psyplot Documentation

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Contents

Welcome! Looking for a fast and flexible visualization software? Here we present **psyplot**, an open source python project that mainly combines the plotting utilities of matplotlib and the data management of the xarray package and integrates them into a software that can be used via command-line and via a GUI!

The main purpose is to have a framework that allows a fast, attractive, flexible, easily applicable, easily reproducible and especially an interactive visualization of your data.

The ultimate goal is to help scientists in their daily work by providing a flexible visualization tool that can be enhanced by their own visualization scripts. `psyplot` can be used via command line and with the graphical user interface (GUI) from the psyplot-gui module.

If you want more motivation: Have a look into the *About psyplot* section.

The package is very new and there are many features that will be included in the future. So we are very pleased for feedback! Please simply raise an issue on GitHub.

CHAPTER 1

Documentation

1.1 About psyplot

1.1.1 Why psyplot?

When visualizing data, one always has to choose:

- Either create the plot with an intuitive graphical user interface (GUI) (e.g. panoply) but less options for customization and difficult to script
- or create the plot from the command line, e.g. via NCL, R or python with more possibilities for customization and scripting but also less intuitive

`psyplot` wants to combine these two worlds: create a well-documented and easy accessible framework to visualize data from a GUI and the command line (and of course through a script).

There exists nothing like that. Of course you can also work with software like Paraview via the built-in python shell. But, if you really want to explore your data it is totally not straightforward to access and explore it from within such a software using numeric functions from numpy, scipy, etc.

Therefore I developed this modular framework that can create and customize plots efficiently with short and comprehensive commands, that can be accessed through a GUI (see *Subprojects*) and where you have always a comprehensive API to access your data.

Different from the usual use with matplotlib, which in the end most of the time results in copy-pasting parts of your code, this software is build on the *don't repeat yourself* principle. Each of the small parts that make up a visualization, whether it is part of the data evaluation or of the appearance of the plot, psyplot puts it into a formatoption can be reused when it is needed.

Nevertheless, it's again a new piece of software. Therefore, if you want to use it, for sure you need a bit of time to get comfortable with the framework. I promise to you, it's worth it. So *get started* and please let me know if you have a different opinion.

1.1.2 About the author

I, (Philipp Sommer), work as a PhD student for climate modeling in the Atmosphere-Regolith-Vegetation (ARVE) group in the Institute of Earth Surface Dynamics (IDYST) at the University of Lausanne. During my time at the Max-Planck-Institute for Meteorology I worked a lot with the Max-Planck-Institute Earth-System-Model (MPI-ESM) and the ICON model in the working group on Terrestrial Hydrology of Stefan Hagemann. This included a lot of evaluation of climate model data. It finally gave the motivation for the visualization framework `psyplot`.

1.1.3 License

psyplot is published under the GNU General Public License v2.0

1.2 Installation

1.2.1 How to install

There basically four different methodologies for the installation. You should choose the one, which is the most appropriate solution concerning your skills and your usage:

The simple installation Use standalone installers which will install all the necessary packages and modules. See *Installation via standalone installers*

The intermediate installation For people coding in python, we recommend to install it through anaconda and the conda-forge channel (see *Installation using conda*) or, if you are not using anaconda, you can use pip (see *Installation using pip*)

The developer installation Install it from source (see *Installation from source*)

Installation via standalone installers

This section contains the necessary informations to install psyplot-conda, a standalone psyplot installation with the most important plugins and the graphical user interface (GUI).

Executables can be downloaded from the links above. Older versions are also available through the the releases page, nightly builds for Linux and OSX are available here.

The installer provided here contain all necessary dependencies for psyplot, psyplot-gui, psy-simple, psy-maps and psy-reg plus the conda package for managing virtual environments. These installers have been created using using the conda constructor package and the packages from the conda-forge channel.

Files for all versions can be found in the psyplot-conda repository and explicitly on the releases page.

Note: Under Linux and MacOSX you can also use `cURL` and to download the latest installer. Just open a terminal and type

```
curl -o psyplot-conda.sh -LO `curl -s https://api.github.com/repos/Chilipp/psyplot-
↪conda/releases/latest | grep browser_download_url | cut -d '"' -f 4 | grep OSNAME`␣
↪| grep .sh
```

where `OSNAME` is one of `Linux` or `MacOSX`.

Then install it simply via

```
bash psyplot-conda.sh
```

Installation on Linux

Download the bash script (file ending on `'.sh'` for linux) from the releases page and open a terminal window.

Type:

```
bash '<path-to-the-downloaded-file.sh>'
```

and simply follow the instructions.

For more information on the command line options type:

```
bash '<Path-to-the-downloaded-file.sh>' --help
```

It will ask you, whether you want to add a `psyplot` alias to your `.bashrc`, such that you can easily start the terminal and type `psyplot` to start the GUI. You can avoid this by setting `NO_PSYPLOT_ALIAS=1`. Hence, to install `psyplot-conda` without any terminal interaction, run:

```
NO_PSYPLOT_ALIAS=1 bash '<Path-to-the-downloaded-file.sh>' -b -p <target-path>
```

Installation on OS X

You can either install it from the terminal using a *bash-script* (`.sh` file), or you can install a standalone app using an *installer* (`.pkg` file).

The bash script will install a conda installation in your desired location. Both will create a `Psyplot.app` (see below).

Installation using the OS X package

This should be straight-forward, however Apple does not provide free Developer IDs for open-source developers. Therefore our installers are not signed and you have to give the permissions to open the files manually. The 4 steps below describe the process.

1. Just download the `.pkg` file
2. To open it, you have to

   Right-click on the file → `Open With` → `Installer`. In the appearing window, click the `Open` button.
3. Follow the instructions. It will create a `Psyplot.app` in the specified location.

4. To open the app the first time, change to the chosen installation directory for the App (by default `$HOME/Applications`), right-click the `Psyplot` app and click on `Open`. In the appearing window, again click on `Open`.

Installation using the bash script

Download the bash script (file ending on `'.sh'` for MacOSX) from the releases page and open a terminal window.

Type:

```
bash '<path-to-the-downloaded-file.sh>'
```

and simply follow the instructions.

For more informations on the command line options type:

```
bash '<Path-to-the-downloaded-file.sh>' --help
```

By default, the installer asks whether you want to install a `Psyplot.app` into your `Applications` directory. You can avoid this be setting `NO_PSYPLOT_APP=1`.

Furthermore it will ask you, whether you want to add a `psyplot` alias to your `.bash_profile`, such that you can easily start the terminal and type `psyplot` to start the GUI. You can avoid this by setting `NO_PSYPLOT_ALIAS=1`. Hence, to install `psyplot-conda` without any terminal interaction, run:

```
NO_PSYPLOT_APP=1 NO_PSYPLOT_ALIAS=1 bash '<Path-to-the-downloaded-file.sh>' -b -p
↪<target-path>
```

Installation on Windows

Just double click the downloaded file and follow the instructions. The installation will create an item in the windows menu (Start -> Programs -> Psyplot) which you can use to open the GUI. You can, however, also download installers that create no shortcut from the releases page.

In any case, if you chose to modify your `PATH` variable during the installation, you can open a command window (`cmd`) and type `psyplot`.

Installation using conda

We highly recommend to use conda for installing psyplot. Here you can install it via manually via the *conda-forge* channel or you can use one of our *preconfigured environment files*.

Manual installation

After downloading the installer from anaconda, you can install psyplot simply via:

```
$ conda install -c conda-forge psyplot
```

However, this only installs the raw framework. For your specific task, you should consider one of the below mentioned plugins (see *Optional dependencies*).

If you want to be able to read and write netCDF files, you can use for example the netCDF4 package via:

```
$ conda install netCDF4
```

If you want to be able to read GeoTiff Raster files, you will need to have gdal installed:

```
$ conda install gdal
```

Please also visit the xarray installation notes for more informations on how to best configure the xarray package for your needs.

Preconfigured environments

There are also some preconfigured environments that you can download which allow an efficient handling of netCDF files and the visualization of data on a globe.

Those environments are

- `psyplot and psy-maps with netCDF4, dask and bottleneck`. This environment contains the recommended modules to view geo-referenced netCDF files without a GUI

  ```
  name: psyplot
  channels:
      - conda-forge
  dependencies:
      - psyplot
      - dask
      - psy-maps
      - psy-reg
      - seaborn
      - bottleneck
      - netCDF4
  ```

- `psyplot with graphical user interface and the above packages`. The same environment as above plus graphical user interface

  ```
  name: psyplot
  channels:
      - conda-forge
  dependencies:
      - psyplot-gui
      - dask
      - netCDF4
      - seaborn
      - bottleneck
      - psy-maps
      - psy-reg
  ```

After you downloaded one of the files, you can create and activate the new virtual environment via:

```
$ conda env create -f <downloaded file>
$ source activate psyplot
```

Installation using pip

If you do not want to use conda for managing your python packages, you can also use the python package manager `pip` and install via:

```
$ pip install psyplot
```

However to be on the safe side, make sure you have the *Dependencies* installed.

Installation from source

To install it from source, make sure you have the *Dependencies* installed, clone the github repository via:

```
git clone https://github.com/Chilipp/psyplot.git
```

and install it via:

```
python setup.py install
```

1.2.2 Dependencies

Required dependencies

Psyplot has been tested for python 2.7, 3.4, 3.5 and 3.6. Furthermore the package is built upon multiple other packages, mainly

- xarray>=0.8: Is used for the data management in the psyplot package
- matplotlib>=1.4.3: **The** python visualiation package
- PyYAML: Needed for the configuration of psyplot

Optional dependencies

We furthermore recommend to use

- psyplot-gui: A graphical user interface to psyplot
- psy-simple: A psyplot plugin to make simple plots
- psy-maps: A psyplot plugin for visualizing data on a map
- psy-reg: A psyplot plugin for visualizing fits to your data
- cdo: The python bindings for cdos (see also the *cdo example*)

1.2.3 Running the tests

We us pytest to run our tests. So you can either run clone out the github repository and run:

```
$ python setup.py test
```

or install pytest by yourself and run

> $ py.test

To also test the plugin functionality, install the `psyplot_test` module in `tests/test_plugin` via:

```
$ cd tests/test_plugin && python setup.py install
```

and run the tests via one of the above mentioned commands.

1.2.4 Building the docs

To build the docs, check out the github repository and install the requirements in `'docs/environment.yml'`. The easiest way to do this is via anaconda by typing:

```
$ conda env create -f docs/environment.yml
$ source activate psyplot_docs
```

Then build the docs via:

```
$ cd docs
$ make html
```

Note: The building of the docs always preprocesses the examples. You might want to disable that by setting `process_examples = False`. Otherwise please note that the examples are written as python3 notebooks. So if you are using python2, you may have to install the python3 kernel. Just create a new environment `'py35'` and install it for IPython via:

```
conda create -n py35 python=3.5
source activate py35
conda install notebook ipykernel
ipython kernel install --user
```

You then have to install the necessary modules for each of the examples in the new `'py35'` environment.

1.2.5 Uninstallation

The uninstallation depends on the system you used to install psyplot. Either you did it via the *standalone installers* (see *Uninstalling standalone app*), via *conda* (see *Uninstallation via conda*), via *pip* or from the *source files* (see *Uninstallation via pip*).

Anyway, if you may want to remove the psyplot configuration files. If you did not specify anything else (see *`psyplot.config.rcsetup.psyplot_fname()`*), the configuration files for psyplot are located in the user home directory. Under linux and OSX, this is `$HOME/.config/psyplot`. On other platforms it is in the `.psyplot` directory in the user home.

Uninstalling standalone app

The complete uninstallation requires three steps:

1. Delete the files (see the OS specific steps below)
2. Unregister the locations from your `PATH` variable (see below)

Uninstallation on Linux

Just delete the folder where you installed `psyplot-conda`. By default, this is `$HOME/psyplot-conda`, so just type:

```
rm -rf $HOME/psyplot-conda
```

If you added a `psyplot` alias to your `.bashrc` (see *installation instructions*) or chose to add the `bin` directory to your `PATH` variable during the installation, open your `$HOME/.bashrc` in an editor of your choice and delete those parts.

Uninstallation on OSX

The uninstallation depends on whether you have used the *package installer* or the *bash script* for the installation.

Uninstall the App installed through the OS X package

Just delete the app from your `Applications` folder. There have been no changes made to your `PATH` variable.

Uninstall the App installed via bash script

As for *linux*, just delete the folder where you installed `psyplot-conda`. By default, this is `$HOME/psyplot-conda`. Open a terminal and just type:

```
rm -rf $HOME/psyplot-conda
```

If you added a `psyplot` alias to your `.bash_profile` (see *installation instructions*) or chose to add the `bin` directory to your `PATH` variable during the installation, open your `$HOME/.bash_profile` in an editor of your choice and delete those parts.

If you chose to add a `Psyplot` app, just delete the symbolic link in `/Applications` or `$HOME/Applications`.

Uninstallation on Windows

Just double-click the `Uninstall-Anaconda.exe` file in the directory where you installed `psyplot-conda` and follow the instructions.

This will also revert the changes in your `PATH` variable.

Uninstallation via conda

If you installed psyplot via *conda*, simply run:

```
conda remove psyplot
```

If you however installed it via a preconfigured environment (see *Preconfigured environments*), you can simply remove the entire virtual environment via:

```
conda env remove -n psyplot
```

Uninstallation via pip

Uninstalling via pip simply goes via:

```
pip uninstall psyplot
```

Note, however, that you should use *conda* if you also installed it via conda.

1.3 Getting started

1.3.1 Initialization and interactive usage

This section shall introduce you how to read data from a netCDF file and visualize it via psyplot. For this, you need to have netCDF4 and the psy-maps psyplot plugin to be installed (see Installation).

Furthermore we use the `demo.nc` netCDF file for our demonstrations.

Note: We recommend to either run this example using our GUI. However, you can also either use IPython from the terminal via

```
conda install ipython  # or pip install ipython
ipython  # starts the ipython console
```

and copy-paste the commands in this example, or you use a jupyter notebook via

```
conda install jupyter  # or pip install jupyter
jupyter notebook  # starts the notebook server
```

Then create a new notebook in the desired location and copy-paste the examples below. If you want, we also recommend to include the following commands in the notebook

```
import psyplot.project as psy
# show the figures inline in the notebook and not in a separate window
%matplotlib inline
# don't close the figures after showing them, because than the update
# would not work
%config InlineBackend.close_figures = False
# show the figures after they are drawn or updated. This is useful
# for the visualization in the jupyter notebook
psy.rcParams['auto_show'] = True
```

After you *installed psyplot*, you can import the package via

```
In [1]: import psyplot
```

Psyplot has several modules and subpackages. The main module for the use of psyplot is the `project` module.

```
In [2]: import psyplot.project as psy
```

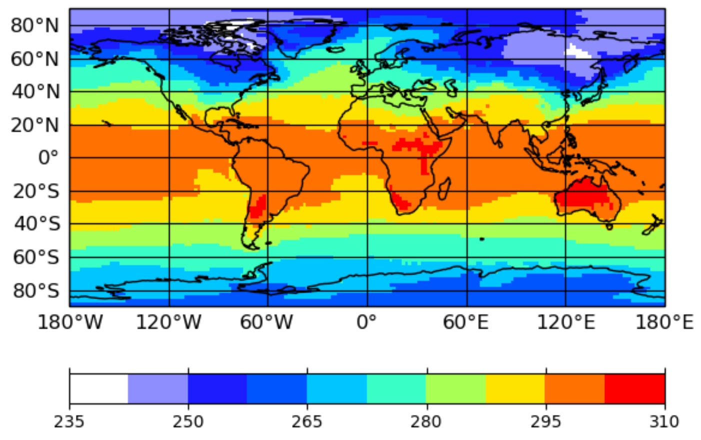
Plots can be created using the attributes of the `plot` instance of the `ProjectPlotter`.

Each new plugin defines several plot methods. In case of the psy-maps package, those are

```
In [3]: psy.plot.show_plot_methods()
barplot
    Make a bar plot of one-dimensional data
combined
    Plot a 2D scalar field with an overlying vector field
density
    Make a density plot of point data
fldmean
    Calculate and plot the mean over x- and y-dimensions
lineplot
    Make a line plot of one-dimensional data
mapcombined
    Plot a 2D scalar field with an overlying vector field on a map
mapplot
    Plot a 2D scalar field on a map
mapvector
    Plot a 2D vector field on a map
plot2d
    Make a simple plot of a 2D scalar field
vector
    Make a simple plot of a 2D vector field
violinplot
    Make a violin plot of your data
```

So to create a simple 2D plot of the temperature field `'t2m'`, you can type

```
In [4]: p = psy.plot.mapplot('demo.nc', name='t2m')
```



Note: If you're not using the GUI, you have to call the *show()* method to display the plot, i.e. just run

```
p.show()
```

Now you created your first project

```
In [5]: p
Out[5]: psyplot.project.Project([    arr0: 2-dim DataArray of t2m, with (lat,␣
↪lon)=(96, 192), lev=100000.0, time=1979-01-31T18:00:00])
```

which contains the `xarray.DataArray` that stores the data and the corresponding plotter that visualizes it

```
In [6]: p[0]
Out[6]:
<xarray.DataArray 't2m' (lat: 96, lon: 192)>
array([[251.41689, 251.454  , 251.48915, ..., 251.29774, 251.33876, 251.37978],
       [254.16493, 254.33095, 254.50087, ..., 253.54774, 253.76845, 253.96376],
       [255.86024, 256.3114 , 256.72742, ..., 254.40712, 254.90517, 255.42665],
       ...,
       [263.70984, 263.6454 , 263.58875, ..., 263.96375, 263.86804, 263.78406],
       [262.4989 , 262.48718, 262.47742, ..., 262.5536 , 262.5321 , 262.51453],
       [260.8485 , 260.8661 , 260.88367, ..., 260.79578, 260.81335, 260.83093]],
      dtype=float32)
Coordinates:
  * lon      (lon) float64 0.0 1.875 3.75 5.625 7.5 9.375 11.25 13.12 15.0 ...
  * lat      (lat) float64 88.57 86.72 84.86 83.0 81.13 79.27 77.41 75.54 ...
    lev      float64 1e+05
    time     datetime64[ns] 1979-01-31T18:00:00
Attributes:
    long_name:  Temperature
    units:      K
    code:       130
    table:      128
    grid_type:  gaussian

In [7]: type(p[0].psy.plotter)
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪psy_maps.plotters.FieldPlotter
```

The visualization and data handling within the psyplot framework is designed to be as easy, flexible and interactive as possible. The appearance of a plot is controlled by the formatoptions of the plotter. In our case, they are the following:

```
In [8]: p.keys()
+-----------------+-----------------+-----------------+-----------------+
| bounds          | cbar            | cbarspacing     | clabel          |
+-----------------+-----------------+-----------------+-----------------+
| clabelprops     | clabelsize      | clabelweight    | clat            |
+-----------------+-----------------+-----------------+-----------------+
| clip            | clon            | cmap            | cticklabels     |
+-----------------+-----------------+-----------------+-----------------+
| ctickprops      | cticks          | cticksize       | ctickweight     |
+-----------------+-----------------+-----------------+-----------------+
| datagrid        | extend          | figtitle        | figtitleprops   |
+-----------------+-----------------+-----------------+-----------------+
| figtitlesize    | figtitleweight  | grid_color      | grid_labels     |
+-----------------+-----------------+-----------------+-----------------+
| grid_labelsize  | grid_settings   | interp_bounds   | levels          |
+-----------------+-----------------+-----------------+-----------------+
| lonlatbox       | lsm             | map_extent      | maskbetween     |
+-----------------+-----------------+-----------------+-----------------+
| maskgeq         | maskgreater     | maskleq         | maskless        |
+-----------------+-----------------+-----------------+-----------------+
| miss_color      | plot            | post            | post_timing     |
```

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```
+----------------+----------------+----------------+----------------+
| projection     | stock_img      | text           | tight          |
+----------------+----------------+----------------+----------------+
| title          | titleprops     | titlesize      | titleweight    |
+----------------+----------------+----------------+----------------+
| transform      | xgrid          | ygrid          |                |
+----------------+----------------+----------------+----------------+
```

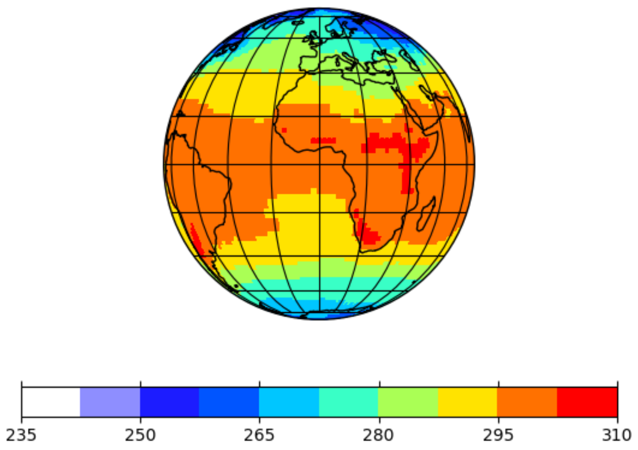
they can be investigated through the `Project.keys()`, `summaries()` and `docs()`, or the corresponding low level methods of the `Plotter` class, `show_keys()`, `show_summaries()` and `show_docs()`.

Updating a formatoption is straight forward. Each formatoption accepts a certain type of data. Let's say, we want to have a different projection. Then we can look at the types this formatoption accepts using the `Project.docs()`

```
In [9]: p.docs('projection')
projection
==========
Specify the projection for the plot

This formatoption defines the projection of the plot

Possible types
--------------
cartopy.crs.CRS
    A cartopy projection instance (e.g. :class:`cartopy.crs.PlateCarree`)
str
    A string specifies the projection instance to use. The centered
    longitude and latitude are determined by the :attr:`clon` and
    :attr:`clat` formatoptions.
    Possible strings are (each standing for the specified projection)

    =========== =======================================
    cyl         :class:`cartopy.crs.PlateCarree`
    robin       :class:`cartopy.crs.Robinson`
    moll        :class:`cartopy.crs.Mollweide`
    geo         :class:`cartopy.crs.Geostationary`
    northpole   :class:`cartopy.crs.NorthPolarStereo`
    southpole   :class:`cartopy.crs.SouthPolarStereo`
    ortho       :class:`cartopy.crs.Orthographic`
    stereo      :class:`cartopy.crs.Stereographic`
    near        :class:`cartopy.crs.NearsidePerspective`
    =========== =======================================

Warnings
--------
An update of the projection clears the axes!
```

Let's use an orthogonal projection. The update goes via the `Project.update()` method which goes all the way down to the `psyplot.plotter.Plotter.update()` and the `psy_maps.plotters.Projection.update()` method of the formatoption.

```
In [10]: p.update(projection='ortho')
```



Note: Actually, in this case an update of the projection requires that the entire axes is cleared and the plot is drawn again. If you want to know more about it, check the *requires_clearing* attribute of the formatoption.

Our framework also let's us update the dimensions of the data we show. For example, if we want to display the field for february, we can type

```
# currently we are displaying january
In [11]: p[0].time.values
Out[11]: numpy.datetime64('1979-01-31T18:00:00.000000000')

In [12]: p.update(time='1979-02', method='nearest')

# now its february
In [13]: p[0].time.values
Out[13]: numpy.datetime64('1979-02-28T18:00:00.000000000')
```

which is in our case equivalent for choosing the second index in our time coordinate via

```
In [14]: p.update(time=1)
```

So far for the first quick introduction. If you are interested you are welcomed to visit our *example galleries* or continue with this guide.

In the end, don't forget to close the project in order to delete the data from the memory and close the figures

```
In [15]: p.close(True, True, True)
```

1.3.2 Choosing the dimension

As you saw already above, the scalar variable `'t2m'` has multiple time steps and we can control what is shown via the `update()` method. By default, the *mapplot()* plot method chooses the first time step and the first vertical level (if those dimensions exist).

However, you can also specify the exact data slice for your visualization based upon the dimensions in you dataset. When doing that, you basically do not have to care about the exact dimension names in the netCDF files, because those are decoded following the CF Conventions. Hence each of the above dimensions are assigned to one of the general dimensions `'t'` (time), `'z'` (vertical dimension), `'y'` (horizontal North-South dimension) and `'x'` (horizontal East-West dimension). In our demo file, the dimensions are therefore decoded as `'time'` → `'t'`, `'lev'` → `'z'`, `'lon'` → `'x'`, `'lat'` → `'y'`.

Hence it is equivalent if you type

```
In [16]: psy.plot.mapplot('demo.nc', name='t2m', t=1)
Out[16]: psyplot.project.Project([    arr0: 2-dim DataArray of t2m, with (lat,␣
↪lon)=(96, 192), lev=100000.0, time=1979-02-28T18:00:00])
```

or

```
In [17]: psy.plot.mapplot('demo.nc', name='t2m', time=1)
Out[17]: psyplot.project.Project([    arr0: 2-dim DataArray of t2m, with (lat,␣
↪lon)=(96, 192), lev=100000.0, time=1979-02-28T18:00:00])
```

Finally you can also be very specific using the *dims* keyword via

```
In [18]: psy.plot.mapplot('demo.nc', name='t2m', dims={'time': 1})
Out[18]: psyplot.project.Project([    arr0: 2-dim DataArray of t2m, with (lat,␣
↪lon)=(96, 192), lev=100000.0, time=1979-02-28T18:00:00])
```

You can also use the *method* keyword from the plotting function to use the advantages of the `xarray.DataArray.sel()` method. E.g. to plot the data corresponding to March 1979 you can use

```
In [19]: psy.plot.mapplot('demo.nc', name='t2m', t='1979-03',
   ....:                  method='nearest', z=100000)
   ....:
Out[19]: psyplot.project.Project([    arr0: 2-dim DataArray of t2m, with (lat,␣
↪lon)=(96, 192), lev=100000.0, time=1979-03-31T18:00:00])
```

Note: If your netCDF file does (for whatever reason) not follow the CF Conventions, we interprete the last dimension as the *x*-dimension, the second last dimension (if existent) as the *y*-dimension, the third last dimension as the *z*-dimension. The time dimension however has to have the name `'time'`. If that still does not fit your netCDF files, you can specify the correct names in the *`rcParams`*, namely

```
In [20]: psy.rcParams.find_all('decoder.(x|y|z|t)')
Out[20]:
RcParams({'decoder.t': {'time'},
          'decoder.x': set(),
          'decoder.y': set(),
          'decoder.z': set()})
```

1.3.3 Configuring the appearance of the plot

psyplot is build upon the great and extensive features of the matplotlib package. Hence, our framework can in principle be seen as a high-level interface to the matplotlib functionalities. However you can always access the basic matplotlib objects like figures and axes if you need.

In the psyplot framework, the communication to matplotlib is done via *formatoptions* that control the appearence of a plot. Each plot method (i.e. each attribute of *`psyplot.project.plot`*) has several a set of them and they set up the corresponding plotter.

Formatoptions are all designed for an interactive usage and can usually be controlled with very simple commands. They range from simple formatoptions like `choosing the title` to `choosing the latitude-longitude box of the data`.

The formatoptions depend on the specific plotting method and can be seen via the methods

`keys`(*args, **kwargs)	Classmethod to return a nice looking table with the given formatoptions
`summaries`(*args, **kwargs)	Method to print the summaries of the formatoptions
`docs`(*args, **kwargs)	Method to print the full documentations of the formatoptions

For example to look at the formatoptions of the *`mapplot`* method in an interactive session, type

```
In [21]: psy.plot.mapplot.keys(grouped=True)  # to see the fmt keys
**************************
Color coding formatoptions
**************************
+-------------+-------------+-------------+-------------+
| bounds      | cbar        | cbarspacing | cmap        |
+-------------+-------------+-------------+-------------+
| ctickprops  | cticksize   | ctickweight | extend      |
+-------------+-------------+-------------+-------------+
| levels      | miss_color  |             |             |
+-------------+-------------+-------------+-------------+

*******************
Label formatoptions
*******************
+----------------+----------------+----------------+----------------+
| clabel         | clabelprops    | clabelsize     | clabelweight   |
+----------------+----------------+----------------+----------------+
| figtitle       | figtitleprops  | figtitlesize   | figtitleweight |
+----------------+----------------+----------------+----------------+
| text           | title          | titleprops     | titlesize      |
+----------------+----------------+----------------+----------------+
| titleweight    |                |                |                |
+----------------+----------------+----------------+----------------+

***************************
Miscallaneous formatoptions
***************************
+----------------+----------------+----------------+----------------+
| clat           | clip           | clon           | datagrid       |
+----------------+----------------+----------------+----------------+
| grid_color     | grid_labels    | grid_labelsize | grid_settings  |
+----------------+----------------+----------------+----------------+
| interp_bounds  | lonlatbox      | lsm            | map_extent     |
+----------------+----------------+----------------+----------------+
| projection     | stock_img      | transform      | xgrid          |
+----------------+----------------+----------------+----------------+
| ygrid          |                |                |                |
+----------------+----------------+----------------+----------------+

***********************
Axis tick formatoptions
***********************
```

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```
+-------------+-------------+
| cticklabels | cticks      |
+-------------+-------------+

*********************
Masking formatoptions
*********************
+-------------+-------------+-------------+-------------+
| maskbetween | maskgeq     | maskgreater | maskleq     |
+-------------+-------------+-------------+-------------+
| maskless    |             |             |             |
+-------------+-------------+-------------+-------------+

******************
Plot formatoptions
******************
+------+
| plot |
+------+

*****************************
Post processing formatoptions
*****************************
+-------------+-------------+
| post        | post_timing |
+-------------+-------------+

******************
Axes formatoptions
******************
+-------+
| tight |
+-------+

In [22]: psy.plot.mapplot.summaries(['title', 'cbar'])  # to see the fmt summaries
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
    Show the title
cbar
    Specify the position of the colorbars

In [23]: psy.plot.mapplot.docs('title')  # to see the full fmt docs
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
=====
Show the title

Set the title of the plot.
You can insert any meta key from the :attr:`xarray.DataArray.attrs` via a
string like ``'%(key)s'``. Furthermore there are some special cases:

- Strings like ``'%Y'``, ``'%b'``, etc. will be replaced using the
  :meth:`datetime.datetime.strftime` method as long as the data has a time
  coordinate and this can be converted to a :class:`~datetime.datetime`
  object.
- ``'%(x)s'``, ``'%(y)s'``, ``'%(z)s'``, ``'%(t)s'`` will be replaced
  by the value of the x-, y-, z- or time coordinate (as long as this
  coordinate is one-dimensional in the data)
- any attribute of one of the above coordinates is inserted via
```

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```
  ``axis + key`` (e.g. the name of the x-coordinate can be inserted via
  ``'%(xname)s'``).
- Labels defined in the :class:`psyplot.rcParams` ``'texts.labels'`` key
  are also replaced when enclosed by '{}'. The standard labels are

  - tinfo: ``%H:%M``
  - dtinfo: ``%B %d, %Y. %H:%M``
  - dinfo: ``%B %d, %Y``
  - desc: ``%(long_name)s [%(units)s]``
  - sdesc: ``%(name)s [%(units)s]``

Possible types
--------------
str
    The title for the :func:`~matplotlib.pyplot.title` function.

Notes
-----
This is the title of this specific subplot! For the title of the whole
figure, see the :attr:`figtitle` formatoption.

See Also
--------
figtitle, titlesize, titleweight, titleprops
```

But of course you can also use the `online documentation` of the method your interested in.

To include a formatoption from the beginning, you can simply pass in the key and the desired value as keyword argument, e.g.

```
In [24]: psy.plot.mapplot('demo.nc', name='t2m', title='my title',
   ....:                  cbar='r')
   ....:
Out[24]: psyplot.project.Project([    arr0: 2-dim DataArray of t2m, with (lat,␣
↪lon)=(96, 192), lev=100000.0, time=1979-01-31T18:00:00])
```

This works generally well as long as there are no dimensions in the desired data with the same name as one of the passed in formatoptions. If you want to be really sure, use the *fmt* keyword via

```
In [25]: p psy.plot.mapplot('demo.nc', name='t2m', fmt={'title': 'my title',
   ....:                                                 'cbar': 'r'})
   ....:
  File "<ipython-input-25-766ec8554a1f>", line 1
    p psy.plot.mapplot('demo.nc', name='t2m', fmt={'title': 'my title',
        ^
SyntaxError: invalid syntax
```

The same methodology works for the interactive usage, i.e. you can use

```
In [26]: p.update(title='my title', cbar='r')

# or
In [27]: p.update(fmt={'title': 'my title', 'cbar': 'r'})
```

1.3.4 Controlling the update

Automatic update

By default, a call of the `update()` method forces an automatic update and redrawing of all the plots. There are however several ways to modify this behavior:

1. Changing the behavior of one single project

   (a) in the initialization of a project using the *auto_update* keyword

   ```
   In [28]: p = psy.plot.mapplot('demo.nc', name='t2m', auto_update=False)
   ```

   (b) setting the `no_auto_update` attribute

   ```
   In [29]: p.no_auto_update = True
   ```

2. Changing the default configuration in the `'lists.auto_update'` key in the `rcParams`

   ```
   In [30]: psy.rcParams['lists.auto_update'] = False
   ```

3. Using the `no_auto_update` attribute as a context manager

   ```
   In [31]: with p.no_auto_update:
      ....:     p.update(title='test')
      ....:
   ```

If you disabled the automatical update via one of the above methods, you have to start the registered updates manually via

```
In [32]: p.update(auto_update=True)

# or
In [33]: p.start_update()
```

Direct control on formatoption update

By default, when updating a formatoption, it is checked for each plot whether the formatoption would change during the update or not. If not, the formatoption is not updated. However, sometimes you may want to do that and for this, you can use the *force* keyword in the `update()` method.

1.3.5 Creating and managing multiple plots

Creating multiple plots

One major advantage of the psyplot framework is the systematic management of multiple plots at the same time. To create multiple plots, simply pass in a list of dimension values and/or names. For example

```
In [34]: psy.plot.mapplot('demo.nc', name='t2m', time=[0, 1])
Out[34]:
psyplot.project.Project([
    arr0: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪01-31T18:00:00,
    arr1: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪02-28T18:00:00])
```

created two plots: one for the first and one for the second time step.

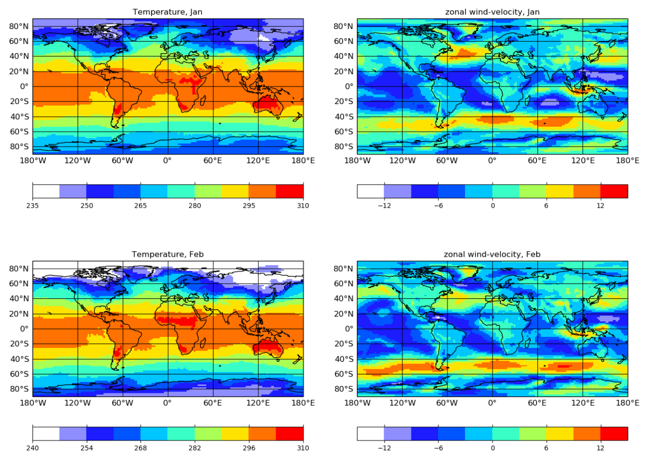
Furthermore

```
In [35]: psy.plot.mapplot('demo.nc', name=['t2m', 'u'], time=[0, 1])
Out[35]:
psyplot.project.Project([
    arr0: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪01-31T18:00:00,
    arr1: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪02-28T18:00:00,
    arr2: 2-dim DataArray of u, with (lat, lon)=(96, 192), lev=100000.0, time=1979-01-
↪31T18:00:00,
    arr3: 2-dim DataArray of u, with (lat, lon)=(96, 192), lev=100000.0, time=1979-02-
↪28T18:00:00])
```

created four plots. By default, each plot is made in an own figure but you can also use the *ax* keyword to setup how the plots will be arranged. The *sort* keyword allows you to sort the plots.

As an example we plot the variables `'t2m'` and `'u'` for the first and second time step into one figure and sort by time. This will produce

```
In [36]: psy.plot.mapplot(
   ....:     'demo.nc', name=['t2m', 'u'], time=[0, 1], ax=(2, 2), sort=['time'],
   ....:     title='%(long_name)s, %b')
   ....:
Out[36]:
psyplot.project.Project([
    arr0: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪01-31T18:00:00,
    arr1: 2-dim DataArray of u, with (lat, lon)=(96, 192), lev=100000.0, time=1979-01-
↪31T18:00:00,
    arr2: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪02-28T18:00:00,
    arr3: 2-dim DataArray of u, with (lat, lon)=(96, 192), lev=100000.0, time=1979-02-
↪28T18:00:00])
```



Warning: As the xarray package, the slicing is based upon positional indexing with lists (see the xarray documentation on ositional indexing). Hence you might think of choosing your data slice via `psy.plot.mapplot(..., x=[1, 2, 3, 4, 5], ...)`. However this would result in 5 different plots! Instead you have to write `psy.plot.mapplot(..., x=[[1, 2, 3, 4, 5]], ...)`. The same is true for plotting methods like the *mapvector* method. Since this method needs two variables (one for the latitudinal and one for the longitudinal direction), typing

```
In [37]:  psy.plot.mapvector('demo.nc', name=['u', 'v'])
ValueError: Can only plot 3-dimensional data!
```

results in a `ValueError`. Instead you have to write

```
In [38]: psy.plot.mapvector('demo.nc', name=[['u', 'v']])
Out[38]: psyplot.project.Project([    arr0: 3-dim DataArray of u, v, with (variable,
↪ lat, lon)=(2, 96, 192), time=1979-01-31T18:00:00, lev=100000.0])
```

Please have a look into the documentations of the *mapvector* and *mapcombined* for getting examples on how to use this methods.

Slicing and filtering the project

Managing a whole lot of plots is basically the same as managing a single plot. However, you can always get the single array and handle it separately.

You can either get it through the usual list slicing (the *Project* class actually is a simple `list` subclass) or you can use meta attributes, dimensions and the specific *arr_name* attribute. For the latter one, just call the project with your filtering attributes

This behavior is especially useful if you want to address only some arrays with your update. For example, let's consider we want to choose a `'winter'` colormap for the zonal wind variable and a colormap ranging from blue to red for the temperature. Then we could do this via

```
In [39]: p(name='t2m').update(cmap='RdBu_r')

In [40]: p(name='u').update(cmap='winter')
```

Note: When doing so, we recommend to temporarily disable the automatic update because then the figure will only be drawn once and the update will be done in parallel.

Hence, it is better to use the context manager *no_auto_update* (see *Automatic update*)

```
In [41]: with p.no_auto_update:
   ....:     p(name='t2m').update(cmap='RdBu_r')
   ....:     p(name='u').update(cmap='winter')
   ....:     p.start_update()
   ....:
```

Finally you can access the plots created by a specific plotting method through the corresponding attribute in the *Project* class. In this case this is of course useless because all plots in `maps` were created by the same plotting method, but it may be helpful when having different plotters in one project (see *The psyplot framework*). Anyway, the plots created by the *mapplot* method could be accessed via

```
In [42]: p.mapplot
Out[42]:
```

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```
psyplot.project.Project([
])
```

1.3.6 Saving and loading your project

Within the psyplot framework, you can also save and restore your plots easily and flexibel.

To save your project, use the *save_project()* method:

```
In [43]: p.save_project('my_project.pkl')
```

This saves the plot-settings into the file `'my_project.pkl'`, a simple pickle file that you could open by yourself using

```
In [44]: import pickle

In [45]: with open('my_project.pkl', 'rb') as f:
   ....:     d = pickle.load(f)
   ....:

In [46]: import os
   ....: os.remove('my_project.pkl')
   ....:
```

In order to not avoid large project files, we do not store the data but only the filenames of the datasets. Hence, if you want to load the project again, make sure that the datasets are accessible through the path as they are listed in the *dsnames* attribute.

Otherwise you have several options to avoid wrong paths:

1. Use the *alternative_paths* parameter and provide for each filename a specific path when you *save* the project

   ```
   In [48]: p.dsnames
   Out[48]: {'demo.nc'}

   In [49]: p.save_project(
      ....:     'test.pkl', alternative_paths={'demo.nc': 'other_path.nc'})
      ....:
   ```

2. pack the whole data to the place where you want to store the project file

   ```
   In [50]: p.save_project('target-folder/test.pkl', pack=True)
   ```

3. specify where the datasets can be found when you *load* the project:

   ```
   In [51]: p = psy.Project.load_project(
      ....:     'test.pkl', alternative_paths={'demo.nc': 'other_path.nc'})
      ....:
   ```

4. Save the data in the pickle file, too

   ```
   In [52]: p.save_project('test.pkl', ds_description={'arr'})
   ```

To restore your project, simply use the *load_project()* method via

```
In [53]: maps = psy.Project.load_project('test.pkl')
```

Note: Saving a project stores the figure informations like axes positions, background colors, etc. However only the axes informations from from the axes within the project are stored. Other axes in the matplotlib figures are not considered and will not be restored. You can, however, use the *alternative_axes* keyword in the `Project.load_project()` method if you want to restore your settings and/or customize your plot with the `post` formatoption (see *Adding your own script: The post formatoption*)

1.3.7 Adding your own script: The `post` formatoption

Very likely, you will face the problem that not all your needs are satisfied by the formatoptions in one plotter. You then have two choices:

1. define your own plotter with new formatoptions (see *How to implement your own plotters and plugins*)

   Pros

   - more structured approach
   - you can enhance the plotter with other formatoptions afterwards and reuse it

   Cons

   - more complicated
   - you always have to ship the module where you define your plotter when you want to *save and load* your project
   - can get messy if you define a lot of different plotters

2. use the `post` formatoption

   Pros

   - fast and easy
   - easy to *save and load*

   Cons

   - may get complicated for large scripts
   - has to be enabled manually by the user

For most of the cases, the `post` formatoptions is probably what you are looking for (the first option is described in our *developers guide*).

This formatoption is designed for applying your own postprocessing script to your plot. It accepts a string that is executed using the built-in `exec()` function and is executed at the very end of the plotting. In this python script, the formatoption itself (and therefore the `plotter` and `axes` can be accessed inside the script through the `self` variable. An example how to handle this formatoption can be found in *our example gallery*.

1.4 Configuration

1.4.1 The `rcParams`

Hint: If you are using the psyplot-gui module, you can also use the preferences widget to modify the configuration. See Configuration of the GUI.

Psyplot, and especially it's plugins have a lot of configuration values. Our rcParams handling is motivated by matplotlib although we extended the possibilities of it's `matplotlib.RcParams` class. Our rcParams are stored in the *`psyplot.rcParams`* object. Without any plugins, this looks like

```
In [1]: from psyplot import rcParams

# is not shown because we have to disable the plugins
In [2]: from psyplot.config.rcsetup import RcParams, defaultParams_orig
   ...: rcParams = RcParams(defaultParams=defaultParams_orig)
   ...: rcParams.update_from_defaultParams()
   ...:

In [5]: print(rcParams.dump(exclude_keys=[]))
# Configuration parameters of the psyplot module
#
# You can copy this file (or parts of it) to another path and save it as
# psyplotrc.yml. The directory should then be stored in the PSYPLOTCONFIGDIR
# environment variable.
#
# Created with python
#
# 3.6.5 | packaged by conda-forge | (default, Apr  6 2018, 13:39:56)
# [GCC 4.8.2 20140120 (Red Hat 4.8.2-15)]
#
#
# Automatically draw the figures if the draw keyword in the update and start_update␣
↪methods is None
auto_draw: true
# Automatically show the figures after the update andstart_update methods
auto_show: false
# path for supplementary data
datapath: null
# interpolation method to calculate 2D-bounds (see the `kind` parameterin the␣
↪:meth:`psyplot.data.CFDecoder.get_plotbounds` method)
decoder.interp_kind: linear
# names that shall be interpreted as the time dimension
decoder.t: !!set
  time: null
# names that shall be interpreted as the longitudinal x dim
decoder.x: !!set {}
# names that shall be interpreted as the latitudinal y dim
decoder.y: !!set {}
# names that shall be interpreted as the vertical z dim
decoder.z: !!set {}
# Boolean flag to control whether CDOs (Climate Data Operators) should be used to␣
↪calculate grid weights. If None, they are tried to be used.
gridweights.use_cdo: null
# default value (boolean) for the auto_update parameter in the initialization of␣
↪Plotter, Project, etc. instances
lists.auto_update: true
# formatoption keys and values that are defined by the user to be used by
# the specified plotters. For example to modify the title of all
# :class:`psyplot.plotter.maps.FieldPlotter` instances, set
```

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```
# ``{'plotter.fieldplotter.title': 'my title'}``
plotter.user: {}
# boolean controlling whether all plotters specified in the project.plotters item␣
↪will be automatically imported when importing the psyplot.project module
project.auto_import: false
# boolean controlling whether the seaborn module shall be imported when importing the␣
↪project module. If None, it is only tried to import the module.
project.import_seaborn: null
# mapping from identifier to plotter definitions for the Project class. See the␣
↪:func:`psyplot.project.register_plotter` function for possible keywords and values.␣
↪See :attr:`psyplot.project.registered_plotters` for examples.
project.plotters: {}
# Plot methods that are defined by the user and overwrite those in the``'project.
↪plotters'`` key. Use this if you want to define your own plotters without writing a␣
↪plugin
project.plotters.user: {}
```

You can use this object like a dictionary and modify the default values. For example, if you do not want, that the seaborn package is imported when the *psyplot.project* module is imported, you can simply do this via:

```
In [6]: rcParams['project.import_seaborn'] = False
```

Additionally, you can make these changes permanent. At every first import of the `psyplot` module, the rcParams are updated from a yaml configuration file. On Linux and OS X, this is stored under `$HOME/.config/psyplot/psyplotrc.yml`, under Windows it is stored at `$HOME/.psyplot/psyplotrc.yml`. But use the *psyplot.config.rcsetup.psyplot_fname()* function, to get the correct location.

To make our changes from above permanent, we could just do:

```
In [7]: import yaml
   ...: from psyplot.config.rcsetup import psyplot_fname
   ...:

In [9]: with open(psyplot_fname(), 'w') as f:
   ...:     yaml.dump(dict{'project.import_seaborn': False}, f)
   ...:
  File "<ipython-input-9-313858e580fd>", line 2
    yaml.dump(dict{'project.import_seaborn': False}, f)
                  ^
SyntaxError: invalid syntax


# or we use the dump method
In [10]: rcParams.dump(psyplot_fname(),
   ....:               overwrite=False,  # update the existing file
   ....:               include_keys=['project.import_seaborn'])
   ....:
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪'# Configuration parameters of the psyplot module\n# \n# You can copy this file (or␣
↪parts of it) to another path and save it as\n# psyplotrc.yml. The directory should␣
↪then be stored in the PSYPLOTCONFIGDIR\n# environment variable.\n# \n# Created with␣
↪python\n# \n# 3.6.5 | packaged by conda-forge | (default, Apr  6 2018, 13:39:56) \n
↪# [GCC 4.8.2 20140120 (Red Hat 4.8.2-15)]\n# \n# \n# boolean controlling whether␣
↪the seaborn module shall be imported when importing the project module. If None, it␣
↪is only tried to import the module.\nproject.import_seaborn: false'
```

1.4.2 Default formatoptions

The psyplot plugins, (`psy_simple.plugin`, `psy_maps.plugin`, etc.) define their own `rcParams` instance. When the plugins are loaded at the first import of `psyplot`, these instances update *`psyplot.rcParams`*.

The update mainly defines the default values for the plotters defined by that plugin. However, it is not always obvious, which key in the *`psyplot.rcParams`* belongs to which formatoption. For this purpose, however, you can use the *`default_key`* attribute. For example, the `title` formatoption has the default_key

```
In [11]: import psyplot.project as psy

In [12]: psy.plot.lineplot.plotter_cls().title.default_key
Out[12]: 'plotter.baseplotter.title'
```

As our plotters are based on inheritance, the default values use it, too. Therefore, the `FieldPlotter`, the underlying plotter for the `mapplot` plot method, uses the same configuration value in the *`psyplot.rcParams`*:

```
In [13]: psy.plot.mapplot.plotter_cls().title.default_key
Out[13]: 'plotter.baseplotter.title'
```

1.5 Subprojects

`psyplot` is only the over-arching framework. It's capabilities are splitted into several subprojects. Each of them is accessible via `https://psyplot.readthedocs.io/projects/<project-name>`

- the psyplot_gui package: The GUI to psyplot
- the psy-simple package: A plugin for simple visualization
- the psy-maps package: A psyplot plugin for visualizing data on a map
- the psy-reg package: A psyplot plugin for visualizing and calculating regression fits
- the psyplot-conda repository. A repository for the creation of standalone installers for psyplot (see *Installation via standalone installers*)

See *Psyplot plugins* for more informations on the plugins.

1.6 xarray Accessors

psyplot defines a `DataArray` and a `Dataset` accessor. You can use these accessors (see xarray Internals) to visualize your data and to update your plots. The following sections will show you how to make and update plots with these accessors. The plotmethods of the accessors are the same as for the *`psyplot.project.plot`* object.

1.6.1 The `DatasetAccessor` dataset accessor

Importing the psyplot package registers a new dataset accessor (see `xarray.register_dataset_accessor()`), the *`DatasetAccessor`*. You can access it via the `psy` attribute of the `Dataset` class, i.e.

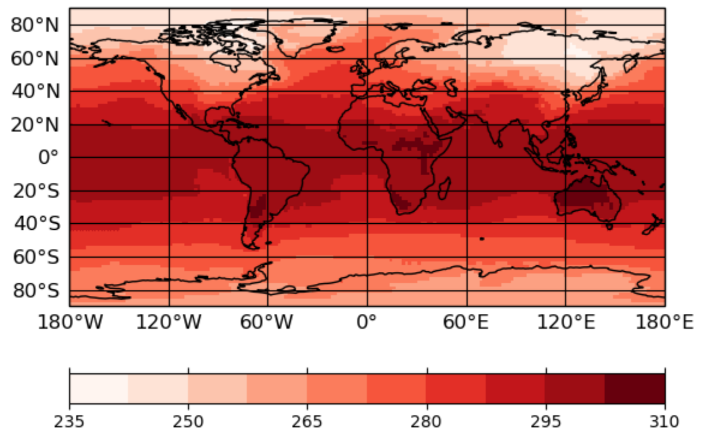
`xarray.Dataset.psy`	alias of *psyplot.data.DatasetAccessor*

It can be used to visualize the variables in the dataset directly from the dataset itself, e.g.

```
In [1]: import psyplot

In [2]: ds = psyplot.open_dataset('demo.nc')

In [3]: sp = ds.psy.plot.mapplot(name='t2m', cmap='Reds')
```



The variable `sp` is a psyplot subproject of the current main project.

```
In [4]: print(sp)
psyplot.project.Project([    arr0: 2-dim DataArray of t2m, with (lat, lon)=(96, 192),␣
↪lev=100000.0, time=1979-01-31T18:00:00])
```

Hence, it would be completely equivalent if you type

```
In [5]: import psyplot.project as psyplot

In [6]: sp = psy.plot.mapplot(ds, name='t2m', cmap='Reds')
```

Note that the *DatasetAccessor.plot* attribute has the same plotmethods as the *psyplot.project.plot* instance.

1.6.2 The `InteractiveArray` dataarray accessor

More advanced then the *dataset accessor* is the registered DataArray accessor, the *InteractiveArray*.

As well as the *DatasetAccessor*, it is registered as the `'psy'` attribute of any `DataArray`, i.e.

`xarray.DataArray.psy`	alias of *psyplot.data.InteractiveArray*

You can use it for two things:

1. create plots of the array
2. update the plots and the array

Creating plots with the dataarray accessor

Just use the `plot` attribute the accessor.

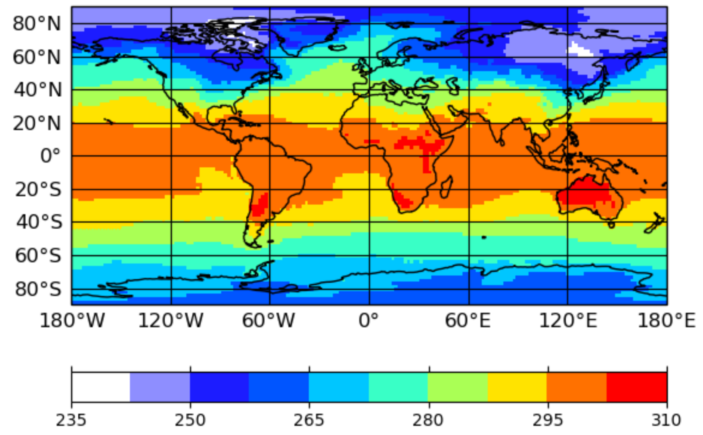
```
In [7]: import psyplot

In [8]: ds = psyplot.open_dataset('demo.nc')

In [9]: da = ds.t2m[0, 0]

# this is a two dimensional array
In [10]: print(da)
<xarray.DataArray 't2m' (lat: 96, lon: 192)>
array([[251.41689, 251.454  , 251.48915, ..., 251.29774, 251.33876, 251.37978],
       [254.16493, 254.33095, 254.50087, ..., 253.54774, 253.76845, 253.96376],
       [255.86024, 256.3114 , 256.72742, ..., 254.40712, 254.90517, 255.42665],
       ...,
       [263.70984, 263.6454 , 263.58875, ..., 263.96375, 263.86804, 263.78406],
       [262.4989 , 262.48718, 262.47742, ..., 262.5536 , 262.5321 , 262.51453],
       [260.8485 , 260.8661 , 260.88367, ..., 260.79578, 260.81335, 260.83093]],
      dtype=float32)
Coordinates:
  * lon      (lon) float64 0.0 1.875 3.75 5.625 7.5 9.375 11.25 13.12 15.0 ...
  * lat      (lat) float64 88.57 86.72 84.86 83.0 81.13 79.27 77.41 75.54 ...
    lev      float64 1e+05
    time     datetime64[ns] 1979-01-31T18:00:00
Attributes:
    long_name:  Temperature
    units:      K
    code:       130
    table:      128
    grid_type:  gaussian

# and we can plot it using the mapplot plot method
In [11]: plotter = da.psy.plot.mapplot()
```



The resulting plotter, an instance of the *psyplot.plotter.Plotter* class, is the object that visualizes the data array. It can also be accessed via the `da.psy.plotter` attribute. Note that the creation of such a plotter overwrites any previous plotter in the `da.psy.plotter` attribute.

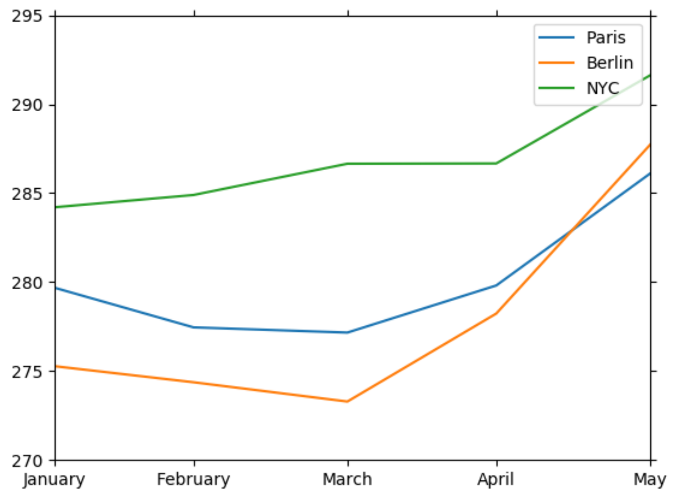
This methodology does not only work for `DataArrays`, but also for multiple DataArrays in a *InteractiveList*. This data structure is, for example, used by the `psyplot.project.plot.lineplot` plot method to visualize multiple lines. Consider the following example:

```
In [12]: ds0 = ds.isel(lev=0)  # select a subset of the dataset

# create a list of arrays at different longitudes
In [13]: l = psyplot.InteractiveList([
   ....:     ds0.t2m.sel(lon=2.35, lat=48.86, method='nearest'),  # Paris
   ....:     ds0.t2m.sel(lon=13.39, lat=52.52, method='nearest'),  # Berlin
   ....:     ds0.t2m.sel(lon=-74.01, lat=40.71, method='nearest'),  # NYC
   ....:     ])
   ....:

In [14]: l.arr_names = ['Paris', 'Berlin', 'NYC']

# plot the list
In [15]: plotter = l.psy.plot.lineplot(xticks='data', xticklabels='%B')
```



Note that for the *InteractiveList*, the *psy* attribute is just the list it self. So it would have been equivalent to call

```
In [16]: l.plot.lineplot()
```

Updating plots and arrays with the dataarray accessor

The *InteractiveArray* accessor is designed for interactive usage of, not only the matplotlib figures, but also of the data. If you selected a subset of a dataset, e.g. via

```
In [17]: da = ds.t2m[0, 0]
   ....: print(da.time)  # January 1979
   ....:
<xarray.DataArray 'time' ()>
array('1979-01-31T18:00:00.000000000', dtype='datetime64[ns]')
Coordinates:
    lev      float64 1e+05
    time     datetime64[ns] 1979-01-31T18:00:00
Attributes:
    standard_name:  time
```

You can change to a different slice using the *InteractiveArray.update()* method.

```
In [19]: da.psy.base = ds   # tell psyplot the source of the dataarray

In [20]: da.psy.update(time=2)
   ....: print(da.time)  # changed to March 1979
   ....:
<xarray.DataArray 'time' ()>
array('1979-03-31T18:00:00.000000000', dtype='datetime64[ns]')
Coordinates:
    lev      float64 1e+05
    time     datetime64[ns] 1979-03-31T18:00:00
Attributes:
    standard_name:  time
```

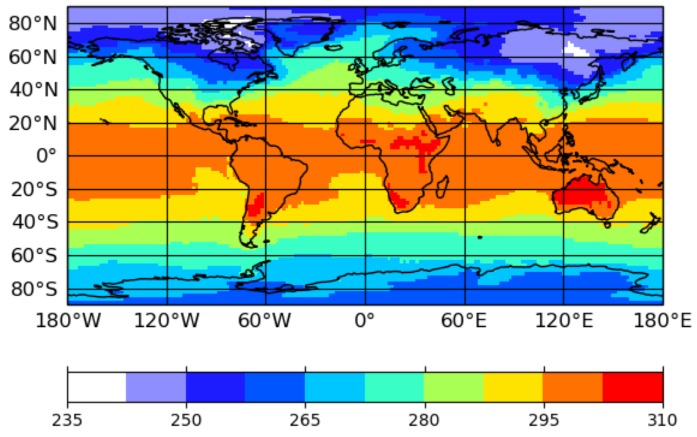
The `da.psy.base = ds` command hereby tells the dataarray, where it is coming from, since this information is not known in the standard xarray framework.

Hint: You can avoid this, using the *DatasetAccessor.create_list()* method of the dataset accessor

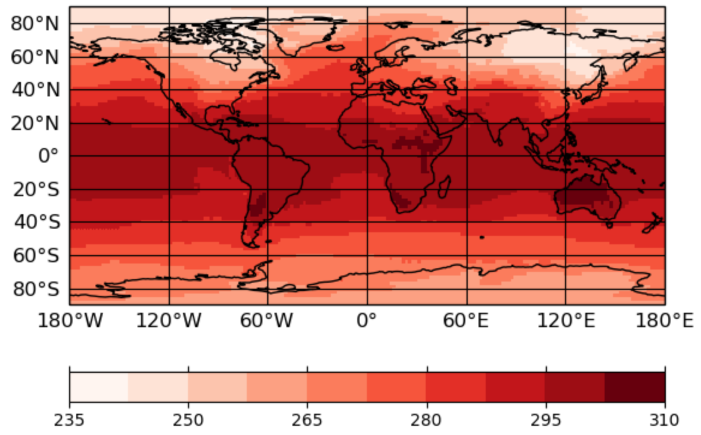
```
In [22]: da = ds.psy.create_list(time=0, lev=0, name='t2m')[0]
   ....: print(da.psy.base is ds)
   ....:
True
```

If you plotted the data, you can also change the formatoptions using the *update()* method, e.g.

```
# create plot
In [24]: da.psy.plot.mapplot();
```

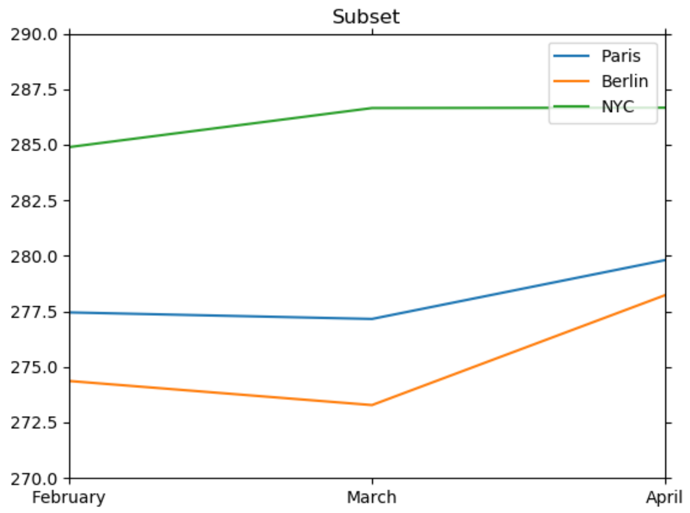


```
In [25]: da.psy.update(cmap='Reds')
```



The same holds for the Interactive list

```
In [26]: l.update(time=slice(1, 4),   # change the data by selecting a subset of the␣
↪timeslice
   ....:           title='Subset',    # change a formatoption, the title of the plot
   ....:           )
   ....:
```



1.7 Psyplot plugins

psyplot only provides the abstract framework on how to make the interactive visualization and data analysis. The real work is implemented in *plugins to this framework*. Each plugin is a separate package that has to be installed independent of psyplot and each plugin registers new plot methods for `psyplot.project.plot`.

1.7.1 Existing plugins

`psy_simple.plugin` A psyplot plugin for simple visualization tasks. This plugin provides a bases for all the other plugins

- Examples Gallery
- plot methods

  `psyplot.project.plot.density` Make a density plot of point data

  `psyplot.project.plot.plot2d` Make a simple plot of a 2D scalar field

  `psyplot.project.plot.combined` Plot a 2D scalar field with an overlying vector field

  `psyplot.project.plot.violinplot` Make a violin plot of your data

  `psyplot.project.plot.lineplot` Make a line plot of one-dimensional data

  `psyplot.project.plot.vector` Make a simple plot of a 2D vector field

  `psyplot.project.plot.barplot` Make a bar plot of one-dimensional data

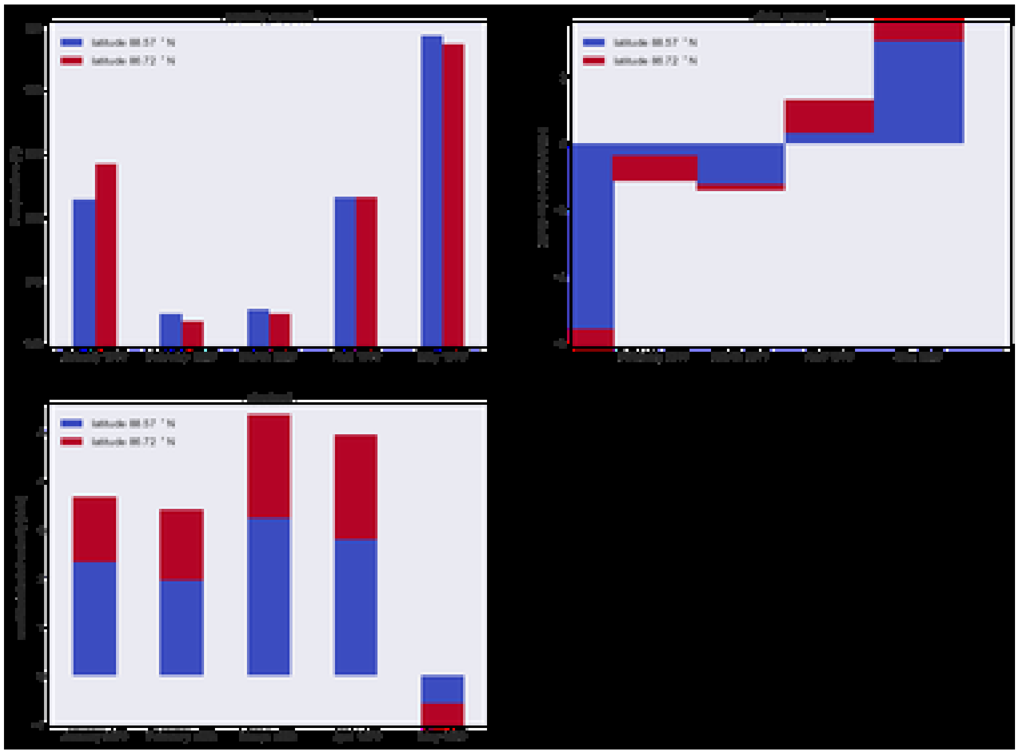


Fig. 1: Bar plot demo

`psy_maps.plugin` A psyplot plugin for visualizing data on a map

- Examples Gallery
- plot methods

  `psyplot.project.plot.mapplot` Plot a 2D scalar field on a map

  `psyplot.project.plot.mapvector` Plot a 2D vector field on a map

  `psyplot.project.plot.mapcombined` Plot a 2D scalar field with an overlying vector field on a map

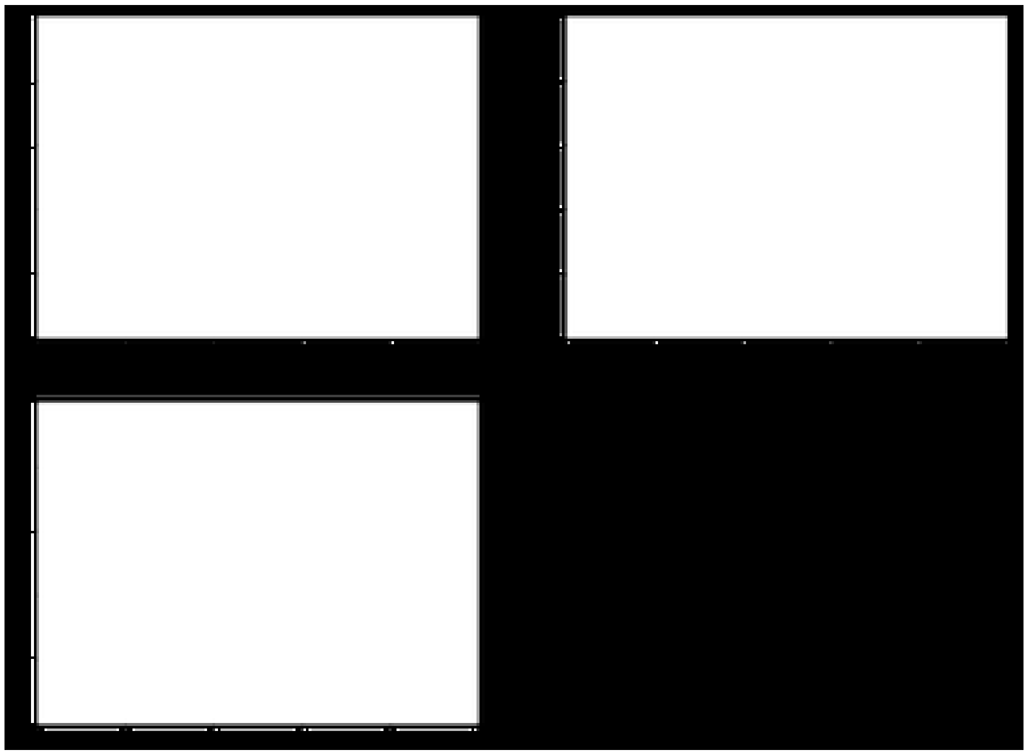


Fig. 2: Line plot demo

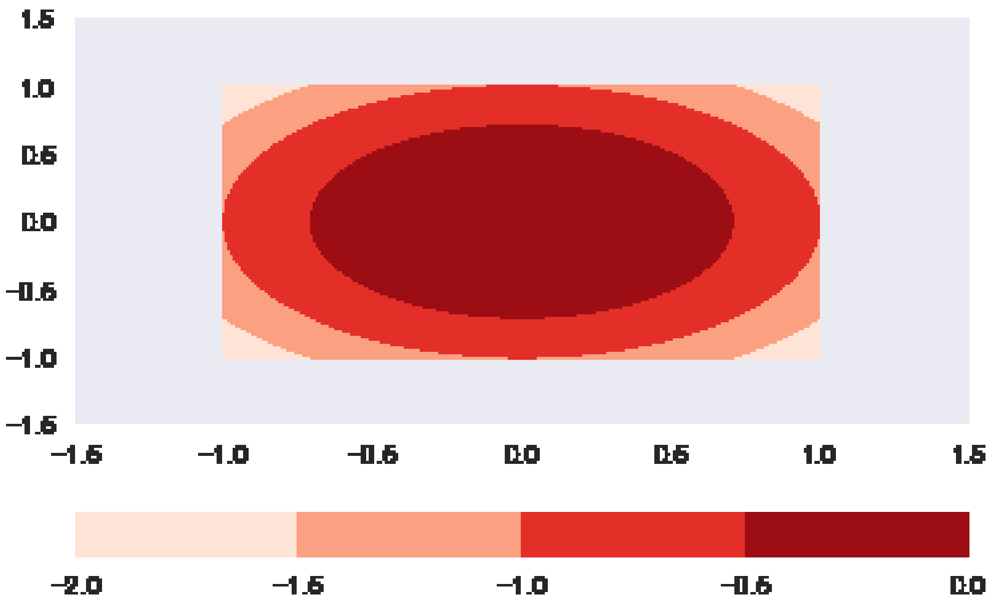


Fig. 3: 2D plots

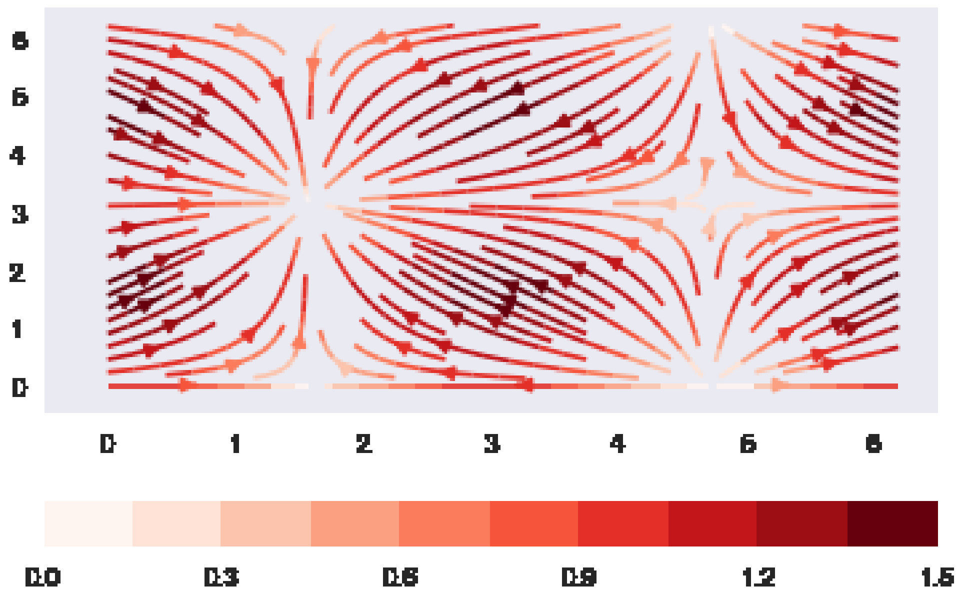


Fig. 4: Vector plot

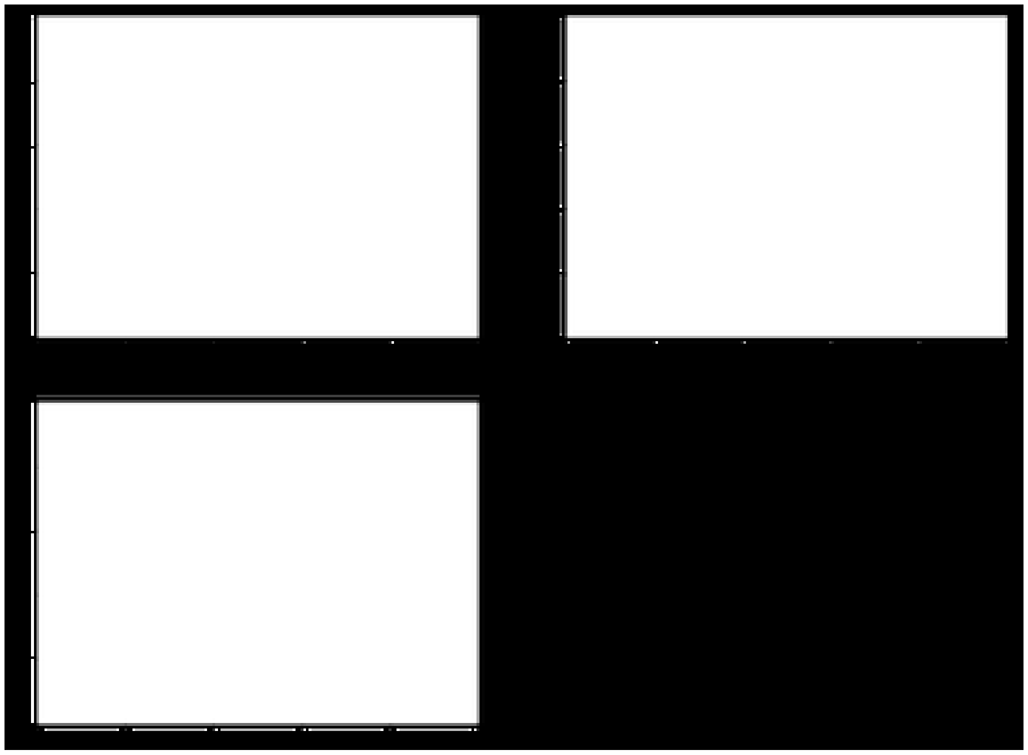


Fig. 5: Violin plot demo

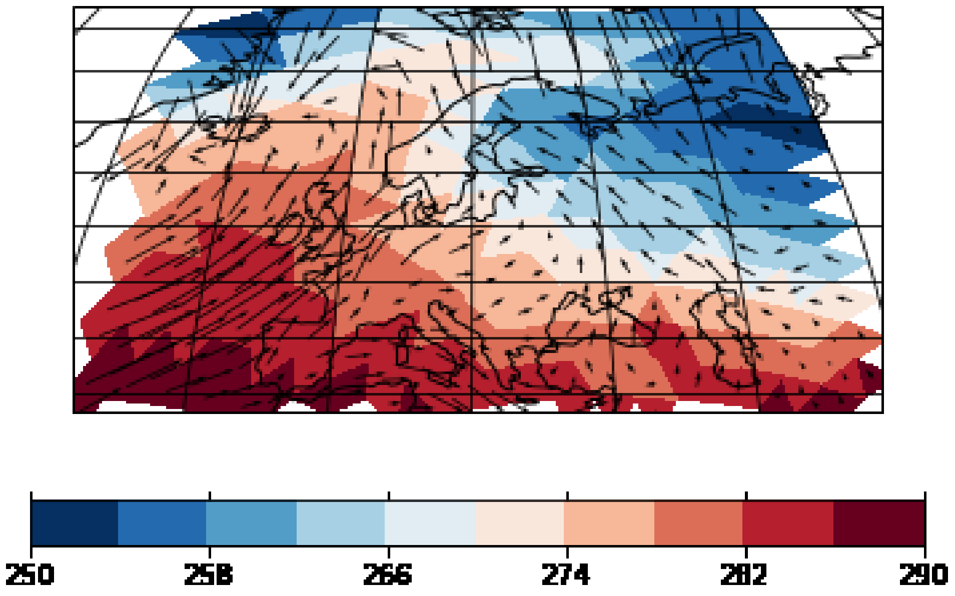


Fig. 6: Visualizing unstructured data

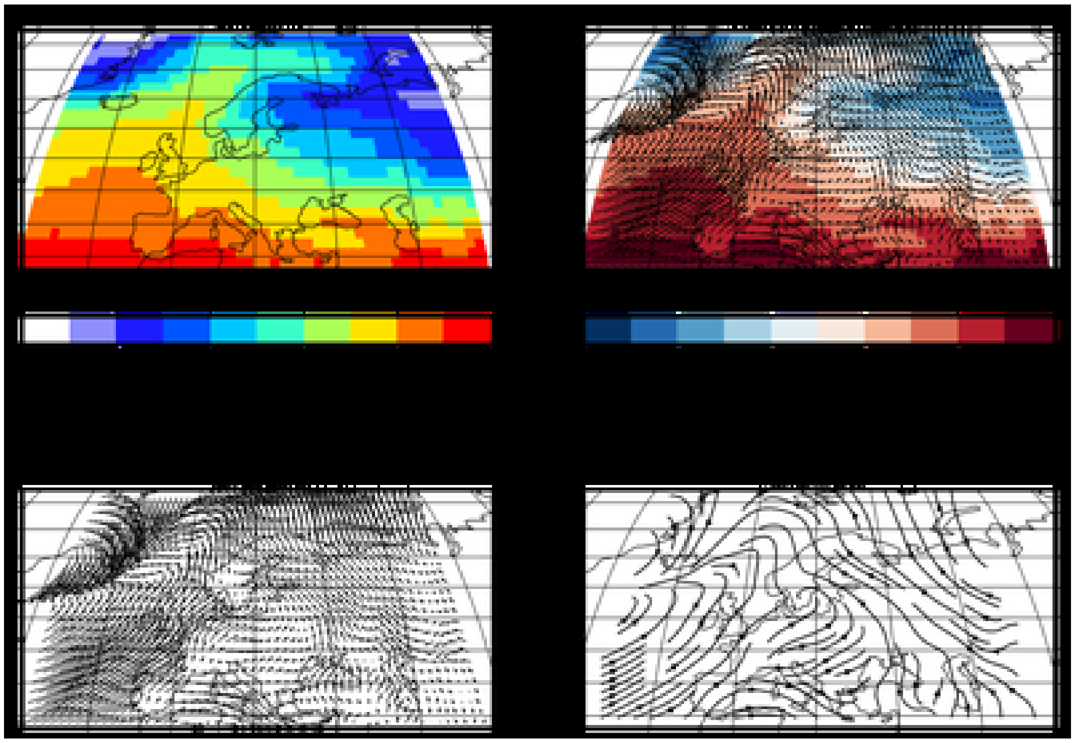


Fig. 7: Basic data visualization on a map

`psy_reg.plugin` A psyplot plugin for visualizing and calculating regression fits

- Examples Gallery
- plot methods

  `psyplot.project.plot.densityreg` Make a density plot and draw a fit from x to y of points

  `psyplot.project.plot.linreg` Draw a fit from x to y

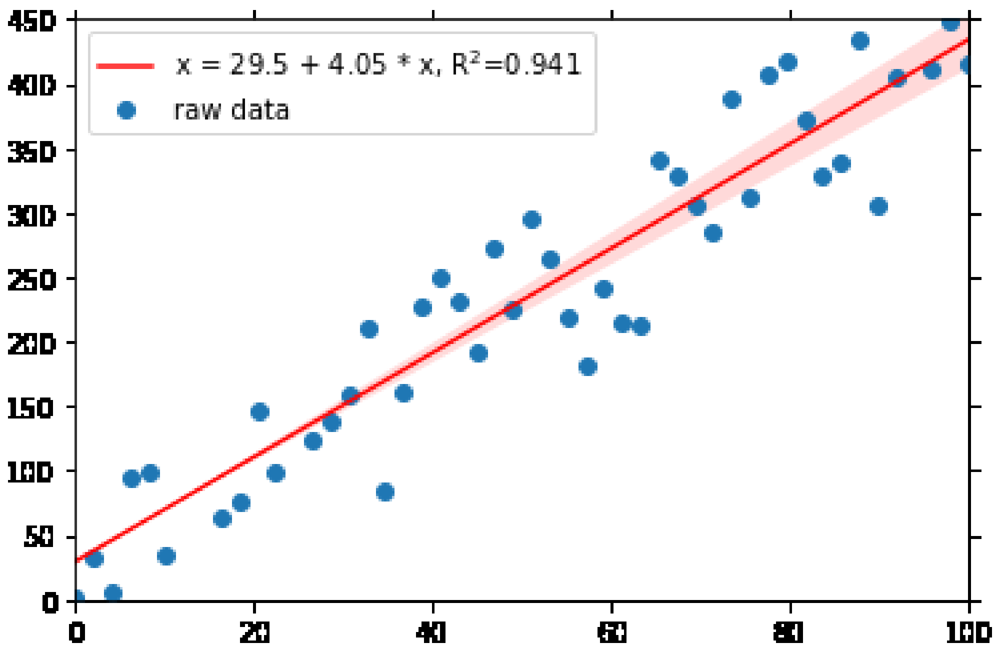


Fig. 8: Creating and accessing a fit

If you have new plugins that you think should be included in this list, please do not hesitate to open an issue on the github project page of psyplot or implement it by yourself in this file and make a pull request.

Note: Because psyplot plugins are imported right at the startup time of psyplot but nevertheless use the *psyplot.config.rcsetup.RcParams* class, you always have to import psyplot first if you want to load a psyplot plugin. In other words, if you want to import one of the above mentiond modules manually, you always have to type

```
import psyplot
import PLUGIN_NAME.plugin
```

instead of

```
import PLUGIN_NAME.plugin
import psyplot
```

where `PLUGIN_NAME` is any of `psy_simple, psy_maps`, etc.

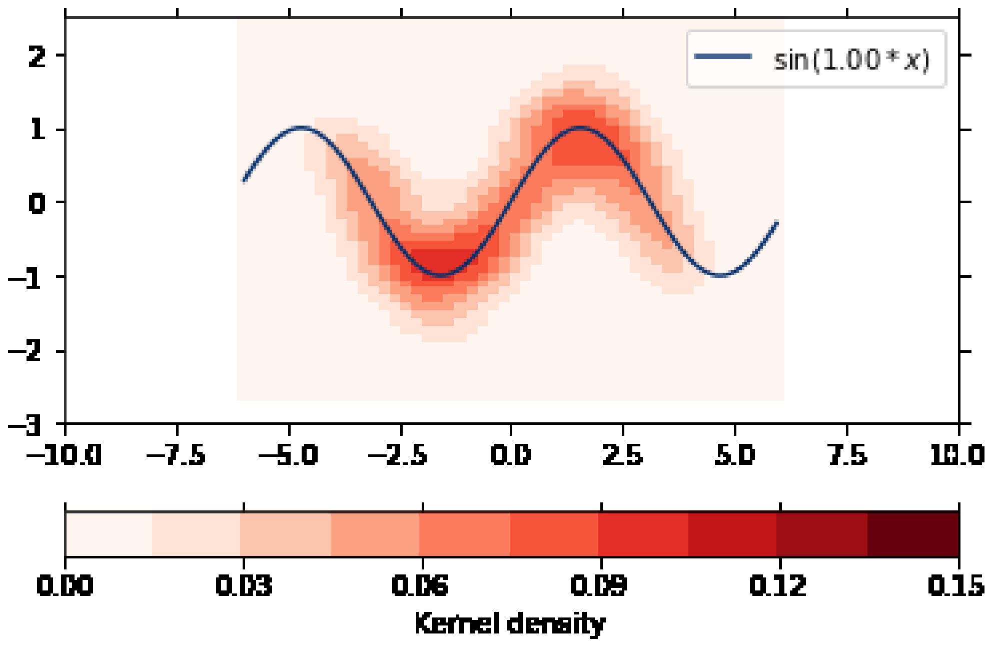


Fig. 9: Plot a fit over a density plot

1.7.2 How to exclude plugins

The psyplot package loads all plugins right when the *psyplot* is imported. In other words, the statement

```
import psyplot
```

already includes that all the psyplot plugin packages are loaded.

You can however exclude plugins from the automatic loading via the `PSYPLOT_PLUGINS` environment variable and exclude specific plot methods of a plugin via the `PSYPLOT_PLOTMETHODS` variable.

The `PSYPLOT_PLUGINS` environment variable

This environment variable is a `::` separated string with plugin names. If a plugin name is preceded by a `no:`, this plugin is excluded. Otherwise, only this plugin is included.

To show this behaviour, we can use `psyplot --list-plugins` which shows the plugins that are used. By default, all plugins are included

```
In [1]: !psyplot --list-plugins
- plugin = psy_simple.plugin
- plugin = psy_maps.plugin
```

Excluding psy-maps works via

```
In [2]: !PSYPLOT_PLUGINS=no:psy_maps.plugin psyplot --list-plugins
- plugin = psy_simple.plugin
```

Including only psy-maps works via

```
In [3]: !PSYPLOT_PLUGINS='yes:psy_maps.plugin' psyplot --list-plugins
- plugin = psy_maps.plugin
```

The PSYPLOT_PLOTMETHODS environment variable

The same principle is used when the plot methods are loaded from the plugins. If you want to manually exclude a plot method from loading, you include it via `no:<plugin-module>:<plotmethod>`. For example, to exclude the :attr:`mapplot <psy_maps:psyplot.project.plot.mapplot>` plot method from the psy-maps plugin, you can use

```
In [4]: !PSYPLOT_PLOTMETHODS=no:psy_maps.plugin:mapplot psyplot --list-plot-methods
barplot: Make a bar plot of one-dimensional data
combined: Plot a 2D scalar field with an overlying vector field
density: Make a density plot of point data
fldmean: Calculate and plot the mean over x- and y-dimensions
lineplot: Make a line plot of one-dimensional data
mapcombined: Plot a 2D scalar field with an overlying vector field on a map
mapvector: Plot a 2D vector field on a map
plot2d: Make a simple plot of a 2D scalar field
vector: Make a simple plot of a 2D vector field
violinplot: Make a violin plot of your data
```

and the same if you only want to include the :attr:`mapplot <psy_maps:psyplot.project.plot.mapplot>` and the :attr:`lineplot <psy_simple:psyplot.project.plot.lineplot>` methods

```
In [5]: !PSYPLOT_PLOTMETHODS='yes:psy_maps.plugin:mapplot::yes:psy_simple.
↪plugin:lineplot' psyplot --list-plot-methods
lineplot: Make a line plot of one-dimensional data
mapplot: Plot a 2D scalar field on a map
```

1.8 Command line usage

The `psyplot.__main__` module defines a simple parser to parse commands from the command line to make a plot of data in a netCDF file. Note that the arguments change slightly if you have the `psyplot-gui` module installed (see psyplot-gui documentation).

It can be run from the command line via:

```
python -m psyplot [options] [arguments]
```

or simply:

```
psyplot [options] [arguments]
```

Load a dataset, make the plot and save the result to a file

```
usage: psyplot [-h] [-V] [-aV] [-lp] [-lpm] [-lds]
               [-n [variable_name [variable_name ...]]]
               [-d dim,val1[,val2[,...]] [dim,val1[,val2[,...]] ...]]
               [-pm {'plot2d', 'barplot', 'violinplot', 'vector', 'combined',
↪'mapvector', 'mapcombined', 'fldmean', 'mapplot', 'density', 'lineplot'}]
               [-o str or list of str] [-p str] [-engine str] [-fmt FILENAME]
```

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```
                [-t] [-rc RC_FILE] [-e str] [--enable-post] [-sns str]
                [-op str] [-cd str]
                [-chname [project-variable,variable-to-use [project-variable,variable-
↪to-use ...]]]
                [str [str ...]]
```

1.8.1 Positional Arguments

str	Either the filenames to show, or, if the *project* parameter is set, the a list of ,-separated filenames to make a mapping from the original filename to a new one Default: []

1.8.2 Named Arguments

-n, --name	The variable names to plot if the *output* parameter is set Default: []
-d, --dims	A mapping from coordinate names to integers if the *project* is not given
-pm, --plot-method	Possible choices: plot2d, barplot, violinplot, vector, combined, mapvector, mapcombined, fldmean, mapplot, density, lineplot The name of the plot_method to use
-p, --project	If set, the project located at the given file name is loaded
-engine	The engine to use for opening the dataset (see `psyplot.data.open_dataset()`)
-fmt, --formatoptions	The path to a yaml (`'.yml'` or `'.yaml'`) or pickle file defining a dictionary of formatoption that is applied to the data visualized by the chosen *plot_method*
-rc, --rc-file	The path to a yaml configuration file that can be used to update the `rcParams`
-e, --encoding	The encoding to use for loading the project. If None, it is automatically determined by pickle. Note: Set this to `'latin1'` if using a project created with python2 on python3.
--enable-post	Enable the `post` processing formatoption. If True/set, post processing scripts are enabled in the given *project*. Only set this if you are sure that you can trust the given project file because it may be a security vulnerability. Default: False
-sns, --seaborn-style	The name of the style of the seaborn package that can be used for the `seaborn.set_style()` function
-cd, --concat-dim	The concatenation dimension if multiple files in *fnames* are provided Default: "__infer_concat_dim__"
-chname	A mapping from variable names in the project to variable names in the datasets that should be used instead. Variable names should be separated by a comma. Default: {}

1.8.3 Info options

Options that print informations and quit afterwards

-V, --version	show program's version number and exit
-aV, --all-versions	Print the versions of all plugins and requirements and exit
-lp, --list-plugins	Print the names of the plugins and exit
-lpm, --list-plot-methods	List the available plot methods and what they do
-lds, --list-datasets	List the used dataset names in the given *project*.

1.8.4 Output options

Options that only have an effect if the *-o* option is set.

-o, --output	If set, the data is loaded and the figures are saved to the specified filename and now graphical user interface is shown
-t, --tight	If True/set, it is tried to figure out the tight bbox of the figure and adjust the paper size of the *output* to it Default: False
-op, --output-project	The name of a project file to save the project to

Examples

Here are some examples on how to use psyplot from the command line.

Plot the variable `'t2m'` in a netCDF file `'myfile.nc'` and save the plot to `'plot.pdf'`:

```
$ psyplot myfile.nc -n t2m -pm mapplot -o test.pdf
```

Create two plots for `'t2m'` with the first and second timestep on the second vertical level:

```
$ psyplot myfile.nc -n t2m  -pm mapplot -o test.pdf -d t,0,1 z,1
```

If you have save a project using the `psyplot.project.Project.save_project()` method into a file named `'project.pkl'`, you can replot this via:

```
$ psyplot -p project.pkl -o test.pdf
```

If you use a different dataset than the one you used in the project (e.g. `'other_ds.nc'`), you can replace it via:

```
$ psyplot other_dataset.nc -p project.pkl -o test.pdf
```

or explicitly via:

```
$ psyplot old_ds.nc,other_ds.nc -p project.pkl -o test.pdf
```

You can also load formatoptions from a configuration file, e.g.:

```
$ echo 'title: my title' > fmt.yaml
$ psyplot myfile.nc -n t2m  -pm mapplot -fmt fmt.yaml -o test.pdf
```

1.9 Example Gallery

The example gallery provides you with some examples on the general usage of the psyplot framework and shows you some applications of the different plotter classes in the psyplot package. You can either download the examples as a Jupyter Notebook or as a converted python script.

After downloading the jupyter-notebook, you can open it by typing:

```
$ jupyter notebook
```

into the terminal and navigate to the file you downloaded.

Note that the examples are python3 notebooks. If you are using python2, you might either open the notebook in an editor and rename `'python3'` in each of the files to `'python3'`, or you create a new conda environment via:

```
conda create -n py35 python=3.5
source activate py35
conda install notebook ipykernel
ipython kernel install --user
```

and install the necessary modules into that environment.

There are lot's of more examples out there for the

- psy-maps plugin
- psy-simple plugin
- psy-reg plugin

1.9.1 Sharing formatoptions

This example shows you the capabilities of sharing formatoptions and what it is all about.

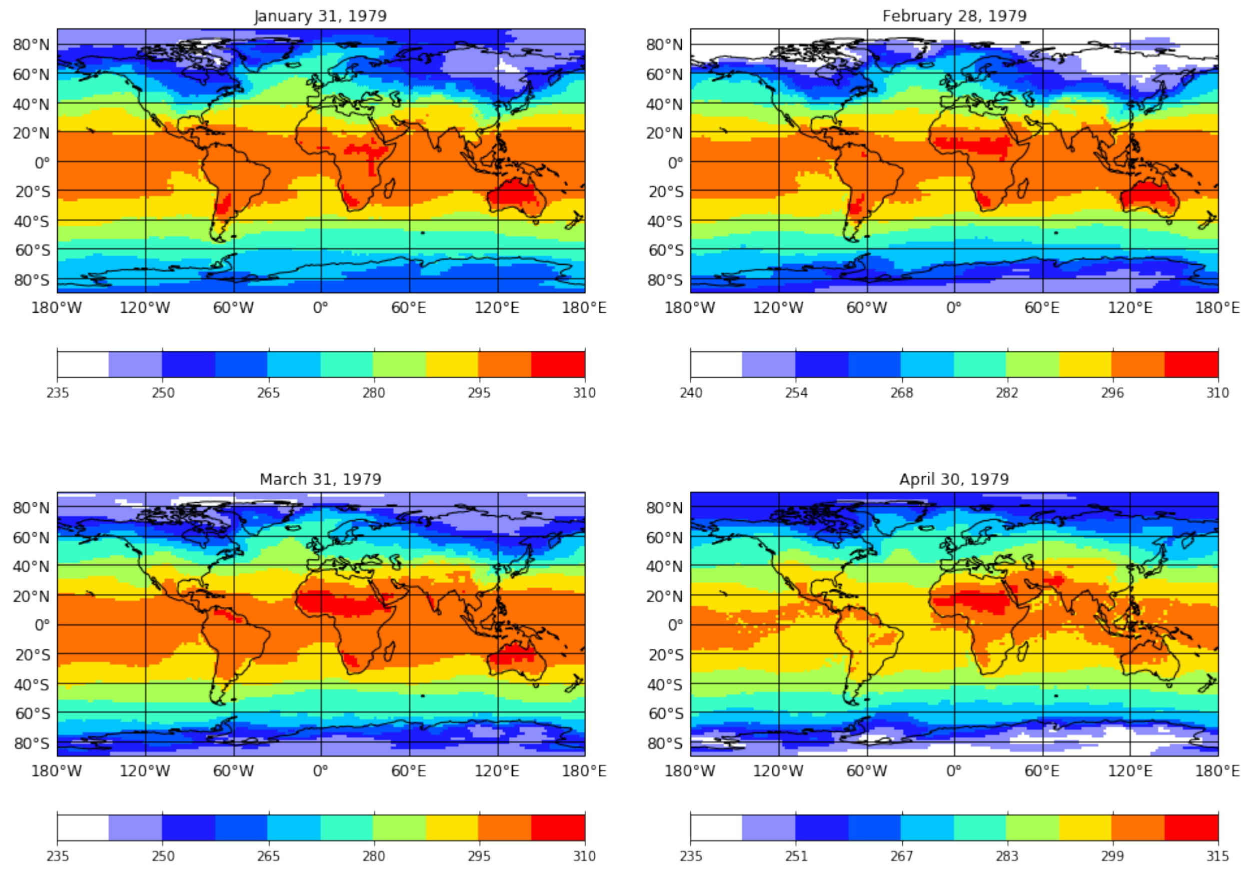
Within the psyplot framework you can easily manage multiple plots and even have interaction between them. This is especially useful if want to compare different variables.

This example requires the file `'sharing_demo.nc'` which contains one variable for the temperature and the psy-maps plugin.

```
import psyplot.project as psy
        fname = 'sharing_demo.nc'
```

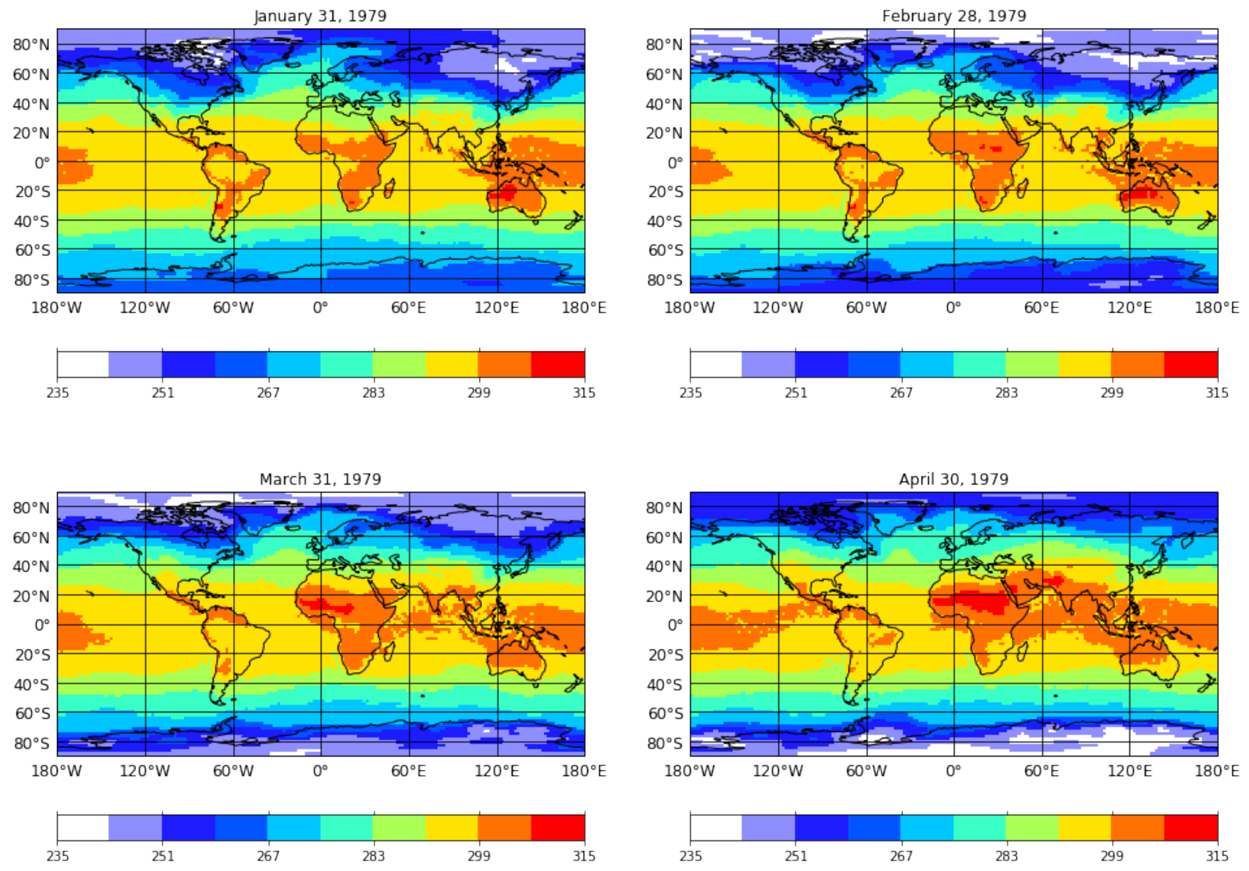
First we create 4 plots into one figure, one for each time step

```
maps = psy.plot.mapplot(fname, name='t2m', title='{dinfo}', ax=(2, 2), time=range(4))
```



As you see, they have slightly different boundaries which can be very annoying if we want to compare them. Therefore we can share the boundaries of the colorbar. The corresponding formatoption is the *bounds* formatoption

```
maps.share(keys='bounds')
maps.show()
```



Now the very first array (January 31st) shares the boundaries with all the other. Furthermore it uses their data as well to calculate the range.

The sharing of formatoptions works for every formatoption key and formatoption groups.

```
maps[0].psy.plotter.groups
```

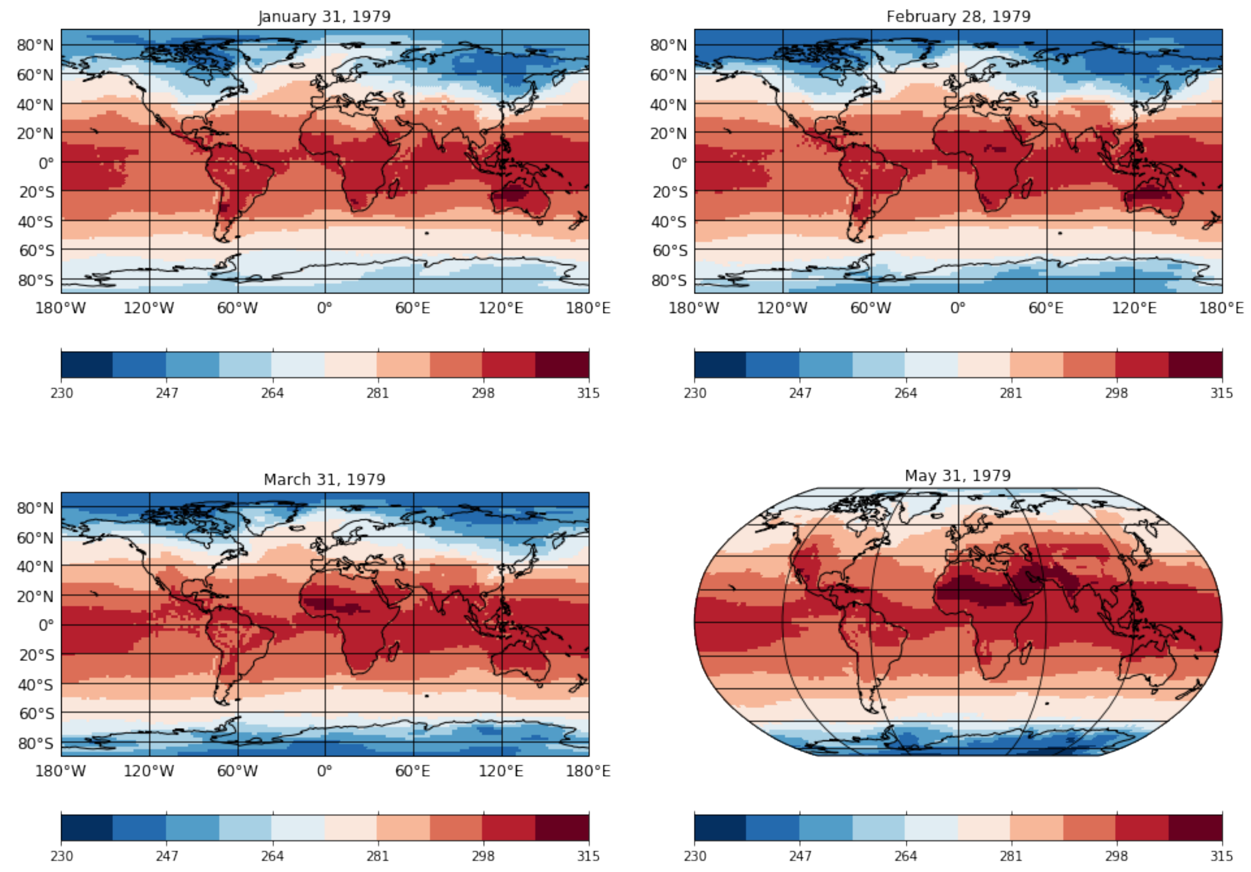
```
{'colors': 'Color coding formatoptions',
 'misc': 'Miscallaneous formatoptions',
 'plotting': 'Plot formatoptions',
 'labels': 'Label formatoptions',
 'ticks': 'Axis tick formatoptions',
 'axes': 'Axes formatoptions',
 'masking': 'Masking formatoptions',
 'post_processing': 'Post processing formatoptions'}
```

Suppose for example, we want to work with only the last array but have the color settings kept equal throughout each plot. For this we can share the `'colors'` group of the formatoption. To do this, we should first unshare the formatoptions currently the first one shares the boundaries with the others.

```
maps.unshare(keys='bounds')
# Now we share the color settings of the last one
arr = maps[-1]
maps[:-1].share(arr, keys='colors')
```

If we now update any of the color formatoptions of the last array, we update them for all the others. However, the other formatoptions (in this example the *projection*) keep untouched

```
arr.psy.update(cmap='RdBu_r', projection='robin', time=4)
maps.show()
```



```
psy.close('all')
```

1.9.2 Applying your own post processing

This demo shows you how to use the `post` formatoption to apply your own post processing scripts.

It requires the `'demo.nc'` netCDF file, `netCDF4` and the psy-maps plugin.

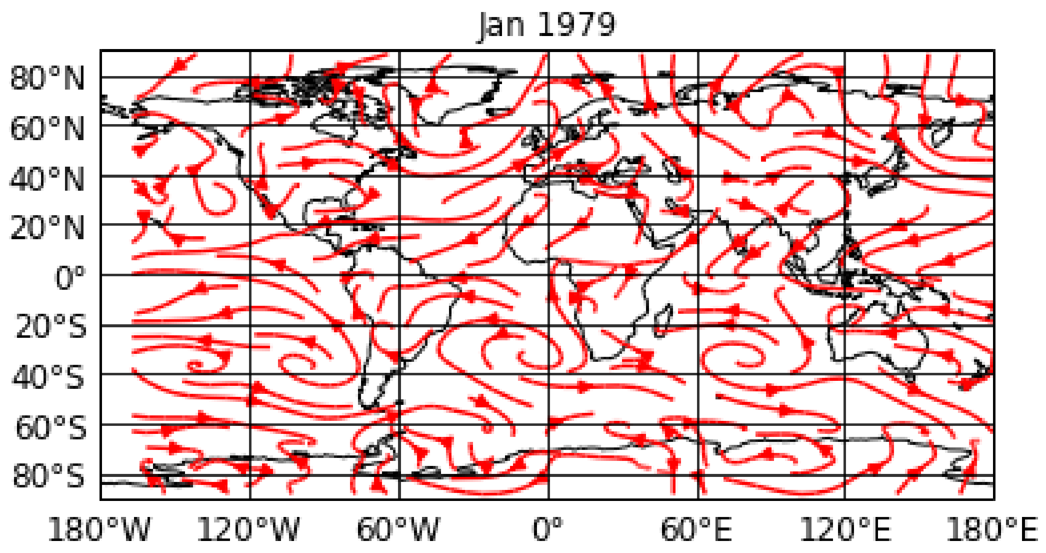
```
import psyplot.project as psy
```

Usage

The `post` formatoption let's you apply your own script to modify your data. Let's start with a simple plot of the wind speed:

```
sp = psy.plot.mapvector('demo.nc', name=[['u', 'v']], plot='stream',
                        color='red', title='%b %Y')
print(sp)
```

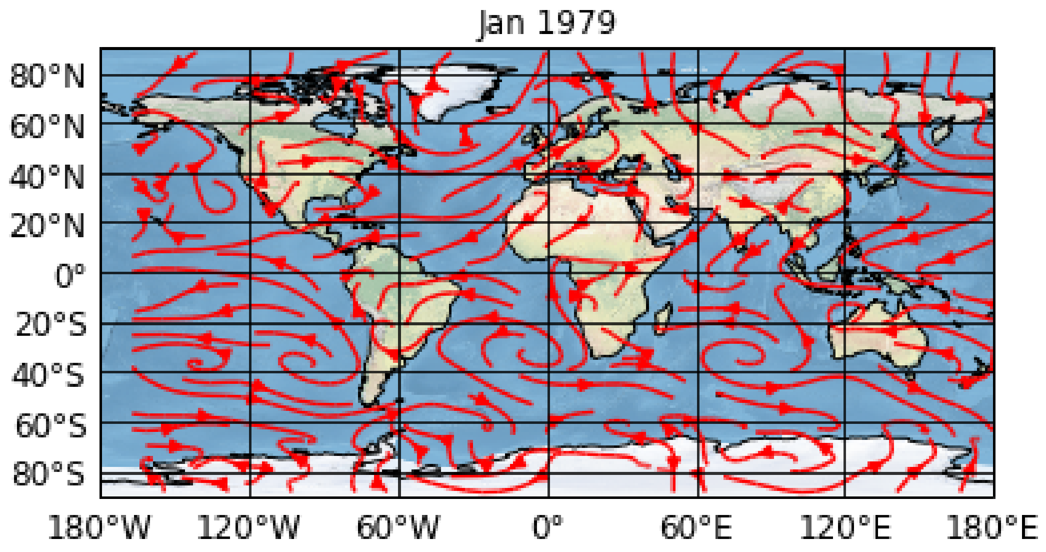
```
psyplot.project.Project([    arr0: 3-dim DataArray of u, v, with (variable, lat,␣
↪lon)=(2, 96, 192), lev=100000.0, time=1979-01-31T18:00:00])
```



It is hard to see the continents below this amount of arrows. So we might want to enhance our plot with cartopy's stock_img.

But since there is now formatoption for it, we can now either define a new plotter and add the formatoption, or we use the `post` formatoption.

```
sp.update(enable_post=True,
          post='self.stock_img = self.ax.stock_img()')
sp.show()
```



The first parameter `enable_post=True` sets the `enable_post` attribute of the plotter to `True`. This attribute is by default set to `False` because it is always a security vulnerability to use the built-in `exec` function which is used by the `post` formatoption. We could, however, already have included this in our first definition of the project via

```
sp = psy.plot.mapvector('demo.nc', name=[['u', 'v']], plot='stream', color='red',
                        enable_post=True)
```

The second parameter `post='self.ax.stock_img()'` updates the `post` formatoption. It accepts an executable python script as a string. Note that we make use of the `self` variable, the only variable that is given to the script. It is the Formatoption instance that performs the update. Hence you can access all the necessary attributes and informations:

- the axes through `self.ax`
- the figure through `self.ax.figure`
- the data that is plotted through `self.data`
- the raw data from the dataset through `self.raw_data`
- the plotter through `self.plotter`
- any other formatoption in the plotter, e.g. the `title` through `self.plotter.title`

For example, let's add another feature that adds the mean of the plotted variables to the plot. For this, let's first have a look into the `plot_data` attribute of the plotter which includes the data that is visualized and that is accessible through the `data` attribute of the `post` formatoption:

```
sp.plotters[0].plot_data
```

```
<xarray.DataArray (variable: 2, lat: 96, lon: 192)>
array([[[-5.548854, -5.470729, ..., -5.680202, -5.618678],
        [-4.17483 , -4.246608, ..., -3.992702, -4.089869],
        ...,
        [-2.664088, -2.547389, ..., -2.911159, -2.785182],
        [-3.48733 , -3.371119, ..., -3.708034, -3.599635]],

       [[ 2.322004,  2.529036, ...,  1.901594,  2.112532],
        [ 1.343489,  1.620344, ...,  0.820051,  1.075911],
        ...,
        [-2.204363, -2.282   , ..., -2.04323 , -2.125261],
        [-1.864519, -1.976824, ..., -1.624773, -1.746843]]], dtype=float32)
Coordinates:
  * lat        (lat) float64 88.57 86.72 84.86 83.0 81.13 79.27 77.41 75.54 ...
    lev        float64 1e+05
    time       datetime64[ns] 1979-01-31T18:00:00
  * lon        (lon) float64 0.0 1.875 3.75 5.625 7.5 9.375 11.25 13.12 15.0 ...
  * variable   (variable) <U1 'u' 'v'
Attributes:
    CDI:           Climate Data Interface version 1.6.8 (http://mpimet.mpg.de/...
    Conventions:   CF-1.4
    history:       Mon Aug 17 22:51:40 2015: cdo -r copy test-t2m-u-v.nc test-...
    title:         Test file
    CDO:           Climate Data Operators version 1.6.8rc2 (http://mpimet.mpg....
    long_name:     zonal wind-velocity
    units:         m/s
    code:          131
    table:         128
    grid_type:     gaussian
```

It is a 3-dimensional array, where the first dimension consists of the zonal wind speed `'u'` and the meridional wind speed `'v'`. So let's add their means as a text to the plot:

```
sp.update(post="""
self.stock_img = self.ax.stock_img()
umean = self.data[0].mean().values
vmean = self.data[1].mean().values
abs_mean = ((self.data[0]**2 + self.data[1]**2)**0.5).mean().values
```

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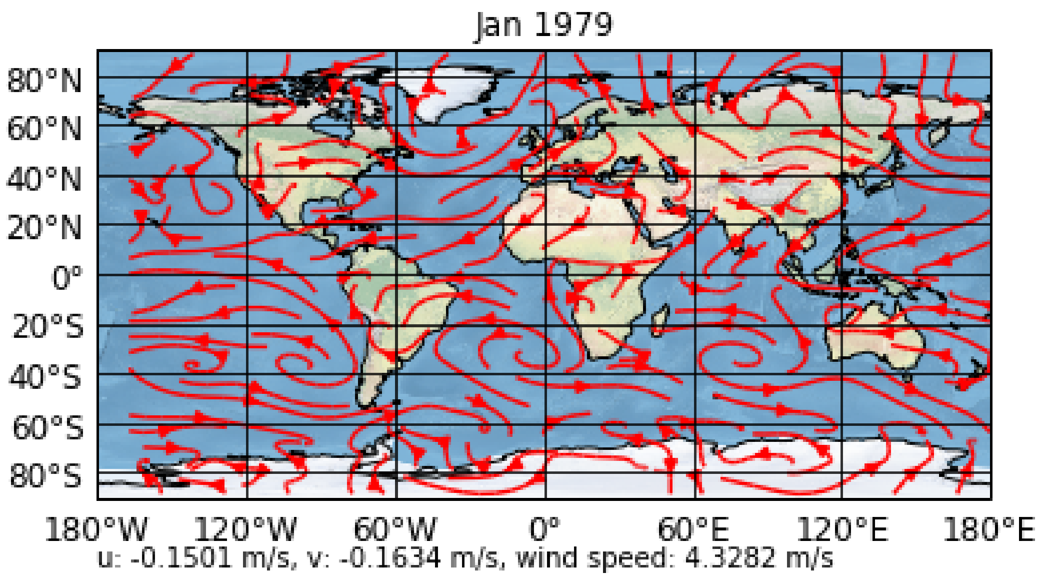
```
self.text = self.ax.text(
    0., -0.15,
    'u: %1.4f m/s, v: %1.4f m/s, wind speed: %1.4f m/s' % (
        umean, vmean, abs_mean),
    transform=self.ax.transAxes)""")
sp.show()
```



Timing

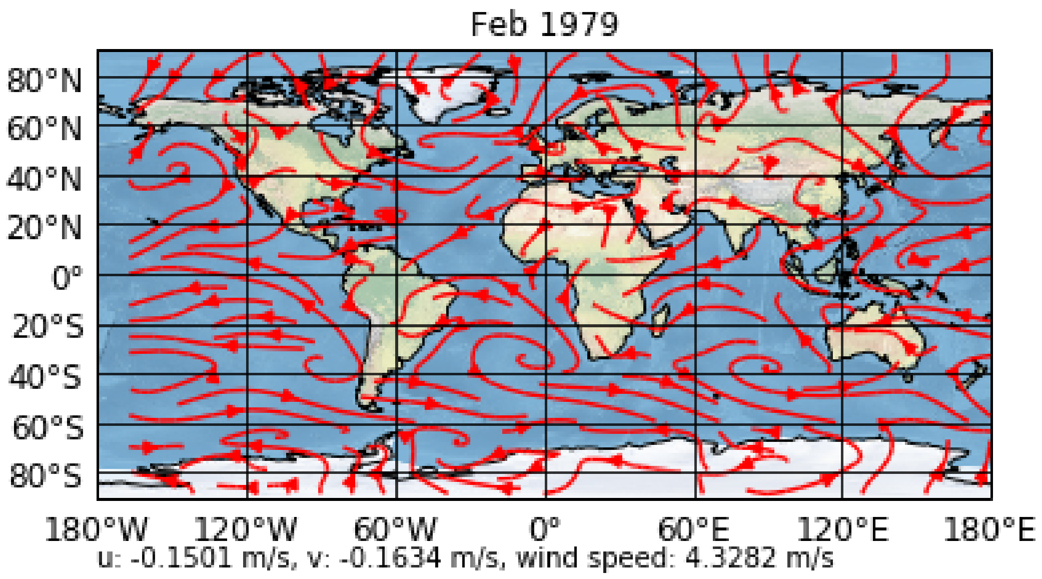
psyplot is intended to work interactively. By default, the `post` formatoption is only updated when you personally update it. However, you can modify this timing using the `post_timing` formatoption. It can be either

- `'never'`: The default which requires a manual update
- `'replot'`: To update it when the data changes
- `'always'`: To always update it.

For example, in the current setting, when we change the data to the second time step via

```
sp.update(time=1)
print(sp)
sp.show()
```

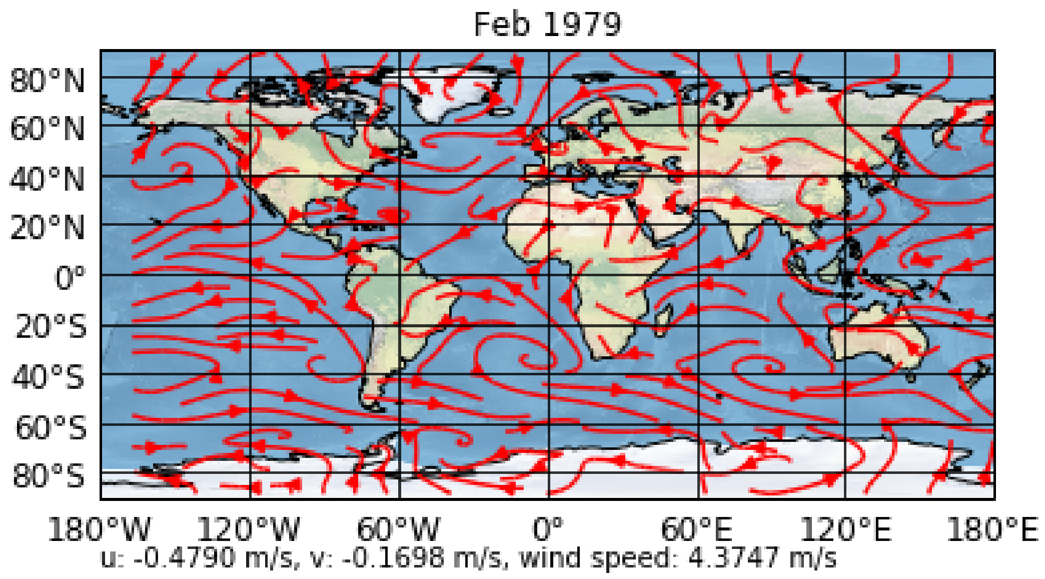
```
psyplot.project.Project([    arr0: 3-dim DataArray of u, v, with (variable, lat,␣
↪lon)=(2, 96, 192), lev=100000.0, time=1979-02-28T18:00:00])
```



Our means are not updated, for this, we have to

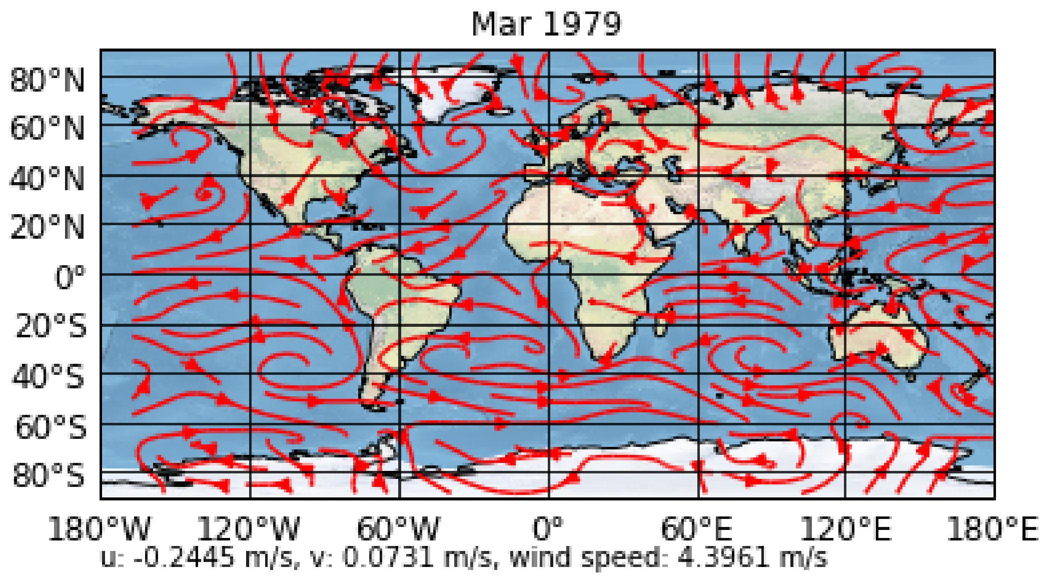
1. set the `post_timing` to `'replot'`
2. slightly modify our `post` script to not plot two texts above each other

```
sp.update(post_timing='replot', post="""
self.stock_img = self.ax.stock_img()
umean = self.data[0].mean().values
vmean = self.data[1].mean().values
abs_mean = ((self.data[0]**2 + self.data[1]**2)**0.5).mean().values
if hasattr(self, 'text'):
    text = self.text
else:
    text = self.ax.text(0., -0.15, '',
                        transform=self.ax.transAxes)
text.set_text(
    'u: %1.4f m/s, v: %1.4f m/s, wind speed: %1.4f m/s' % (
        umean, vmean, abs_mean))""")
sp.show()
```



Now, if we update to the third timestep, our means are also calculated

```
sp.update(time=2)
sp.show()
```



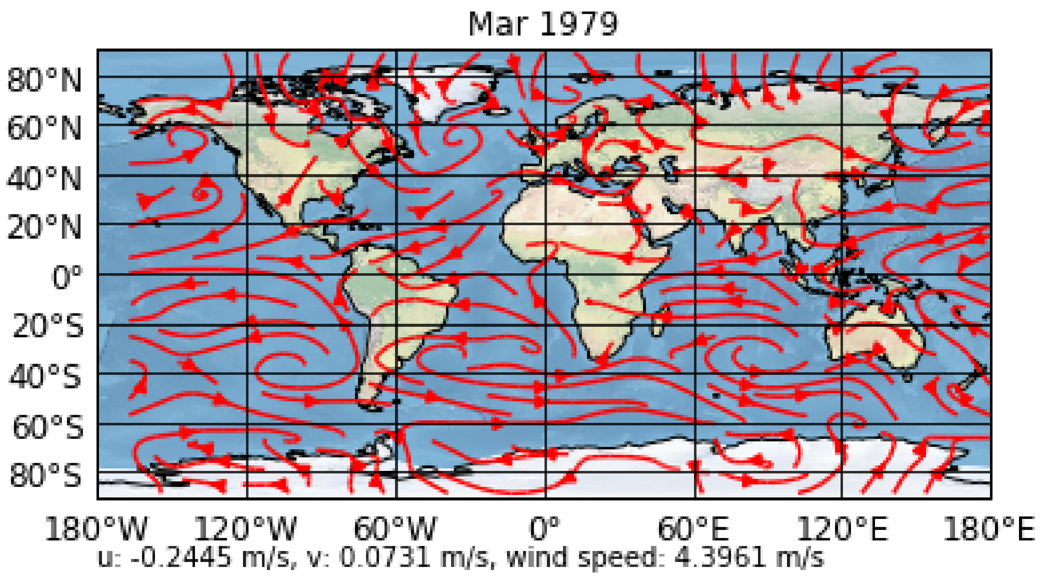
1.9.3 Saving and loading

Saving a project is straight forward via the `save_project` method

```
d = sp.save_project()
```

However, when loading the project, the `enable_post` attribute is (for security reasons) again set to `False`. So if you are sure you can trust the post processing scripts in the `post` formatoption, load your project with `enable_post=True`

```
psy.close('all')
sp = psy.Project.load_project(d, enable_post=True)
```



```
psy.close('all')
```

1.9.4 Usage of Climate Data Operators

This example shows you how CDOs are binded in the psyplot package.

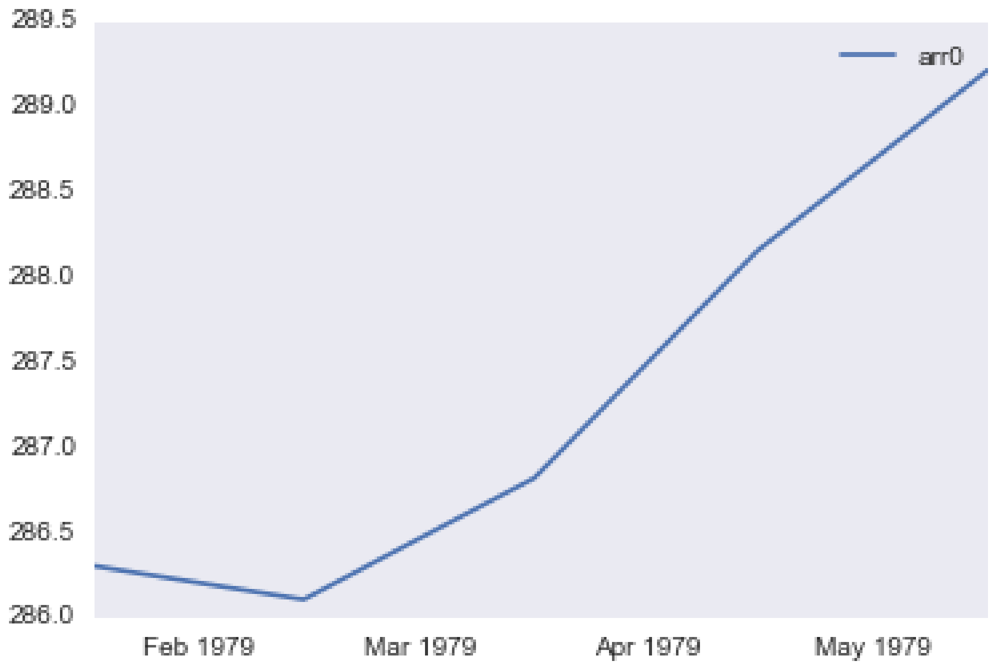
It requires the `'demo.nc'` netCDF file and the psy-maps plugin.

```
import logging
logging.captureWarnings(True)
logging.getLogger('py.warnings').setLevel(logging.ERROR)
```

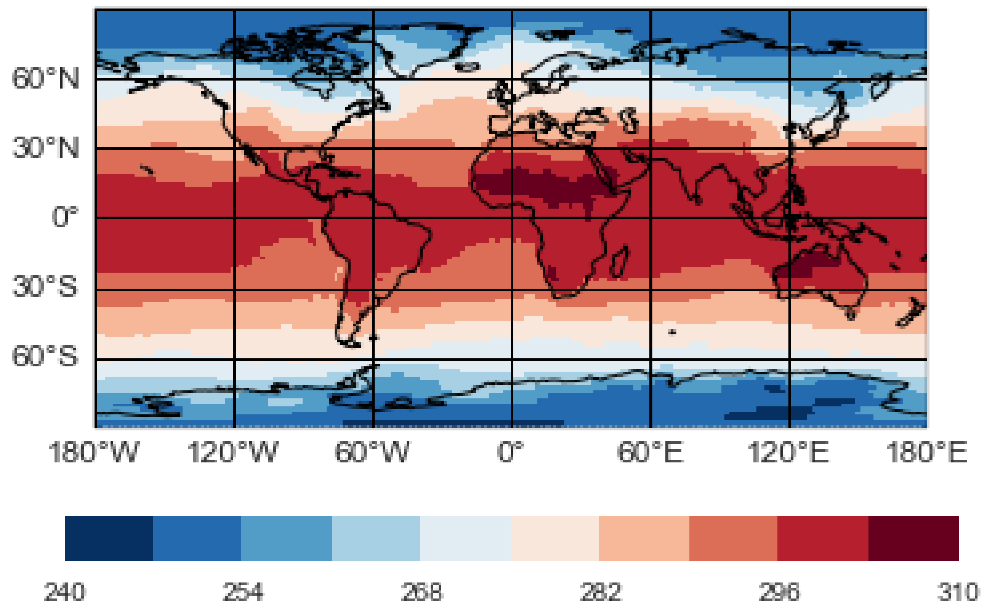
```
import psyplot.project as psy
```

```
cdo = psy.Cdo()
lines = cdo.fldmean(input='-sellevidx,1 demo.nc', plot_method='lineplot', name='t2m',
                    fmt=dict(xticks='month', xticklabels='%b %Y'))
```

```
DatetimeIndex(['1979-01-31 18:00:00', '1979-02-28 18:00:00',
               '1979-03-31 18:00:00', '1979-04-30 18:00:00',
               '1979-05-31 18:00:00'],
              dtype='datetime64[ns]', name='time', freq=None)
```



```
maps = cdo.timmean(input='demo.nc', name='t2m', plot_method='mapplot', fmt=dict(cmap=
↪'RdBu_r'))
```

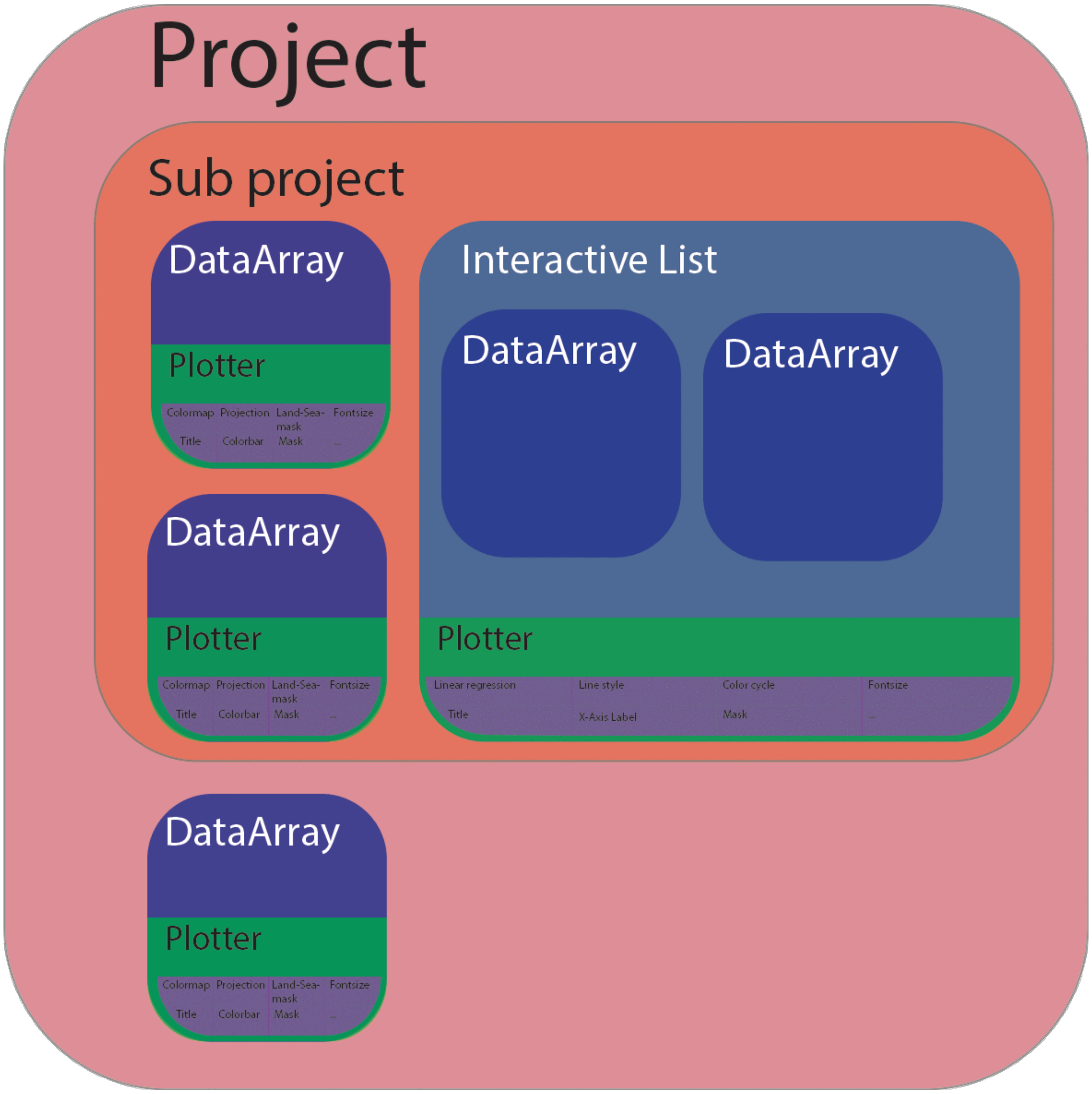


```
psy.close('all')
```

1.10 Developers guide

In this section we provide a deeper overview and introduction in the psyplot frameworks that is necessary for creating new plugins.

1.10.1 The psyplot framework



The main module we used so far, was the `psyplot.project` module. It is the end of a whole framework that is setup by the psyplot package.

This framework is designed in analogy to matplotlibs figure - axes - artist setup, where one figure controls multiple axes, an axes is the manager of multiple artists (e.g. a simple line) and each artist is responsible for visualizing one or more objects on the plot. The psyplot framework instead is defined through the `Project` - (`InteractiveBase` - `Plotter`) - `Formatoption` relationship.

The last to parts in this framework, the `Plotter` and `Formatoption`, are only defined through abstract base classes in this package. They are filled with contents in plugins such as the psy-simple or the psy-maps plugin (see *Psyplot plugins*).

The `project()` function

The *psyplot.project.Project* class (in analogy to matplotlibs `Figure` class) is basically a list that controls multiple plot objects. It comprises the full functionality of the package and packs it into one class, the *Project* class.

In analogy to pyplots `figure()` function, a new project can simply be created via

```
In [1]: import psyplot.project as psy

In [2]: p = psy.project()
```

This automatically sets `p` to be the current project which can be accessed through the *gcp()* method. You can also set the current project by using the *scp()* function.

Note: We highly recommend to use the *project()* function to create new projects instead of creating projects from the *Project*. This ensures the right numbering of the projects of old projects.

The project uses the plotters from the *psyplot.plotter* module to visualize your data. Hence you can add new plots and new data to the project by using the *Project.plot* attribute or the *psyplot.project.plot* attribute which targets the current project. The return types of the plotting methods are again instances of the *Project* class, however we consider them as *subprojects* in contrast *main projects* that are created through the *project()* function. There is basically no difference but the result of the *Project.is_main* attribute which is `False` for subprojects. Hence, each new plot creates a subproject but also stores the data array in the corresponding main project of the *Project* instance from which the plot method has been called. The newly created subproject can be accessed via

```
In [3]: sp = psy.gcp()
```

whereas the current main project can be accessed via

```
In [4]: p = psy.gcp(main=True)
```

Plots created by a specific method of the *Project.plot* attribute may however be accessed via the corresponding attribute of the *Project* class. The following example creates three subprojects, two with the *mapplot* and *mapvector* methods from the psy-maps plugin and one with the simple *lineplot* method from the psy-simple plugin to visualize simple lines.

```
In [5]: import matplotlib.pyplot as plt

In [6]: import cartopy.crs as ccrs

# the subplots for the maps (need cartopy projections)
In [7]: ax = list(psy.multiple_subplots(2, 2, n=3, for_maps=True))

# the subplot for the line plot
In [8]: ax.append(plt.gcf().add_subplot(2, 2, 4))

# scalar field of the zonal wind velocity in the file demo.nc
In [9]: psy.plot.mapplot('demo.nc', name='u', ax=ax[0], clabel='{desc}')
Out[9]: psyplot.project.Project([    arr0: 2-dim DataArray of u, with (lat, lon)=(96,␣
↪192), lev=100000.0, time=1979-01-31T18:00:00])

# a second scalar field of temperature
In [10]: psy.plot.mapplot('demo.nc', name='t2m', ax=ax[1], clabel='{desc}')
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪psyplot.project.Project([    arr1: 2-dim DataArray of t2m, with (lat, lon)=(96,␣
↪192), lev=100000.0, time=1979-01-31T18:00:00])
```

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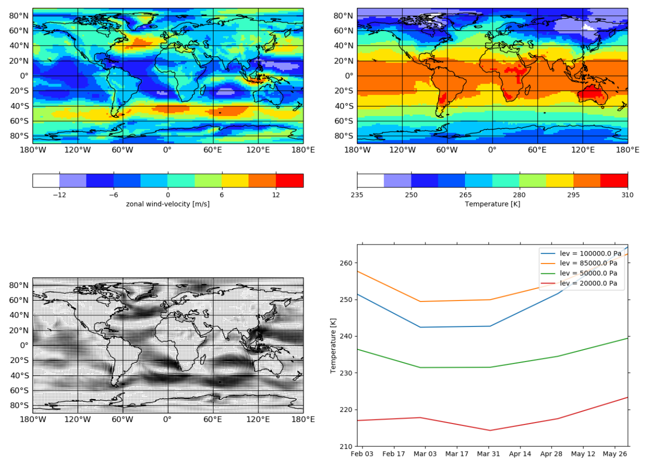
```
# a vector plot projected on the earth
In [11]: psy.plot.mapvector('demo.nc', name=[['u', 'v']], ax=ax[2],
   ....:                    attrs={'long_name': 'Wind speed'})
   ....:
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪psyplot.project.Project([    arr2: 3-dim DataArray of u, v, with (variable, lat,␣
↪lon)=(2, 96, 192), time=1979-01-31T18:00:00, lev=100000.0])

In [12]: psy.plot.lineplot('demo.nc', name='t2m', x=0, y=0, z=range(4),
   ....:                   ax=ax[3], xticklabels='%b %d', ylabel='{desc}',
   ....:                   legendlabels='%(zname)s = %(z)s %(zunits)s')
   ....:
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪
psyplot.project.Project([arr3: psyplot.data.InteractiveList([
    arr0: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=100000.0,
    arr1: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=85000.0,
    arr2: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=50000.0,
    arr3: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=20000.0])])
```



The latter is now the current subproject we could access via *psy.gcp()*. However we can access all of them through the main project

```
In [13]: mp = psy.gcp(True)

In [14]: mp  # all arrays
Out[14]:
2 Main psyplot.project.Project([
    arr0: 2-dim DataArray of u, with (lat, lon)=(96, 192), lev=100000.0, time=1979-01-
↪31T18:00:00,
    arr1: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪01-31T18:00:00,
```

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```
    arr2: 3-dim DataArray of u, v, with (variable, lat, lon)=(2, 96, 192), time=1979-
↪01-31T18:00:00, lev=100000.0,
    arr3: psyplot.data.InteractiveList([
        arr0: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.
↪57216851400727, lev=100000.0,
        arr1: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.
↪57216851400727, lev=85000.0,
        arr2: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.
↪57216851400727, lev=50000.0,
        arr3: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.
↪57216851400727, lev=20000.0])])

In [15]: mp.mapplot  # all scalar fields
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪
psyplot.project.Project([
    arr0: 2-dim DataArray of u, with (lat, lon)=(96, 192), lev=100000.0, time=1979-01-
↪31T18:00:00,
    arr1: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪01-31T18:00:00])

In [16]: mp.mapvector  # all vector plots
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪psyplot.project.Project([    arr2: 3-dim DataArray of u, v, with (variable, lat,␣
↪lon)=(2, 96, 192), time=1979-01-31T18:00:00, lev=100000.0])

In [17]: mp.maps  # all data arrays that are plotted on a map
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪
psyplot.project.Project([
    arr0: 2-dim DataArray of u, with (lat, lon)=(96, 192), lev=100000.0, time=1979-01-
↪31T18:00:00,
    arr1: 2-dim DataArray of t2m, with (lat, lon)=(96, 192), lev=100000.0, time=1979-
↪01-31T18:00:00,
    arr2: 3-dim DataArray of u, v, with (variable, lat, lon)=(2, 96, 192), time=1979-
↪01-31T18:00:00, lev=100000.0])

In [18]: mp.lineplot # the simple plot we created
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪
psyplot.project.Project([arr3: psyplot.data.InteractiveList([
    arr0: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=100000.0,
    arr1: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=85000.0,
    arr2: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=50000.0,
    arr3: 1-dim DataArray of t2m, with (time)=(5,), lon=0.0, lat=88.57216851400727,␣
↪lev=20000.0])])
```

The advantage is, since every plotter has different formatoptions, we can now update them very easily. For example lets update the arrowsize to 1 (which only works for the *mapvector* plots), the projection to an orthogonal (which only works for *maps*), the simple plots to use the `'viridis'` colormap for color coding the lines and for all we choose their title corresponding to the variable names

```
In [19]: p.maps.update(projection='ortho')
```

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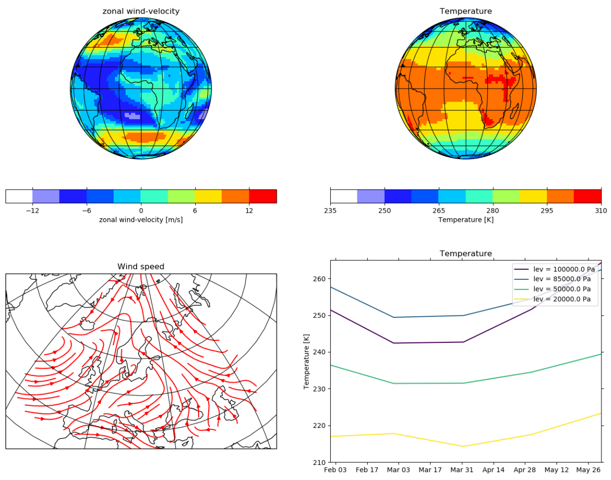
```
In [20]: p.mapvector.update(color='r', plot='stream', lonlatbox='Europe')

In [21]: p.lineplot.update(color='viridis')

In [22]: p.update(title='%(long_name)s')
```



The `InteractiveBase` and the `Plotter` classes

Interactive data objects

The next level are instances of the *InteractiveBase* class. This abstract base class provides an interface between the data and the visualization. Hence a plotter (that's how we call instances of the *Plotter* class) will deal with the subclasses of the *InteractiveBase*:

InteractiveArray(xarray_obj, *args, **kwargs)	Interactive psyplot accessor for the data array
InteractiveList(*args, **kwargs)	List of `InteractiveArray` instances that can be plotted itself

Those classes (in particular the *InteractiveArray*) keep the reference to the base dataset to allow the update of the dataslice you are plotting. The *InteractiveList* class can be used in a plotter for the visualization of multiple *InteractiveArray* instances (see for example the `psyplot.plotter.simple.LinePlotter` and `psyplot.plotter.maps.CombinedPlotter` classes). Furthermore those data instances have a *plotter* attribute that is usually occupied by an instance of a *Plotter* subclass.

Note: The *InteractiveArray* serves as a `DataArray` accessor. After you imported psyplot, you can access it via the `psy` attribute of a `DataArray`, i.e. via

```
In [23]: import xarray as xr

In [24]: xr.DataArray([]).psy
Out[24]: <psyplot.data.InteractiveArray at 0x7fb9cddbd7f0>
```

Visualization objects

Each plotter class is the coordinator of several visualization options. Thereby the `Plotter` class itself contains only the structural functionality for managing the formatoptions that do the real work. The plotters for the real usage are defined in plugins like the psy-simple or the psy-maps package.

Hence each `InteractiveBase` instance is visualized by exactly one `Plotter` class. If you don't want to use the *project framework*, the initialization of such an instance nevertheless straight forward. Just open a dataset, extract the right data array and plot it

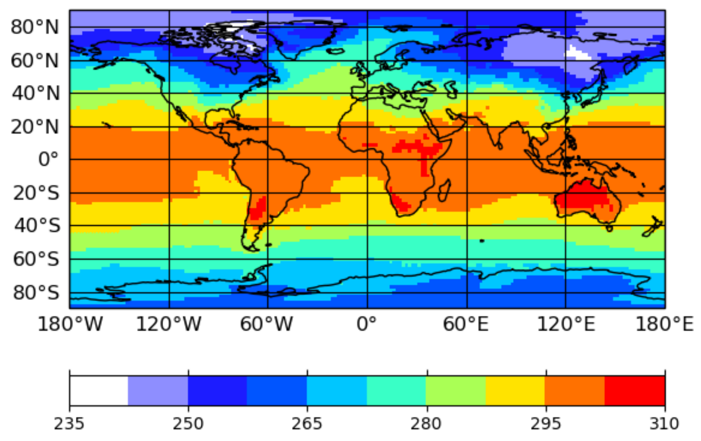
```
In [25]: from psyplot import open_dataset

In [26]: from psy_maps.plotters import FieldPlotter

In [27]: ds = open_dataset('demo.nc')

In [28]: arr = ds.t2m[0, 0]

In [29]: plotter = FieldPlotter(arr)
```



Now we created a plotter with all it's formatoptions:

```
In [30]: type(plotter), plotter
Out[30]:
(psy_maps.plotters.FieldPlotter,
 {'levels': None,
  'interp_bounds': None,
  'plot': 'mesh',
  'miss_color': None,
  'projection': 'cyl',
  'transform': 'cyl',
  'clon': None,
  'clat': None,
  'lonlatbox': None,
```

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```
  'lsm': [True, 1.0],
  'stock_img': False,
  'grid_color': 'k',
  'grid_labels': None,
  'grid_labelsize': 12.0,
  'grid_settings': {},
  'xgrid': True,
  'ygrid': True,
  'map_extent': None,
  'datagrid': None,
  'clip': None,
  'cmap': 'white_blue_red',
  'bounds': ['rounded', None],
  'extend': 'neither',
  'cbar': {'b'},
  'clabel': '',
  'clabelsize': 'medium',
  'clabelweight': None,
  'cbarspacing': 'uniform',
  'clabelprops': {},
  'cticks': None,
  'cticklabels': None,
  'cticksize': 'medium',
  'ctickweight': None,
  'ctickprops': {},
  'tight': False,
  'maskless': None,
  'maskleq': None,
  'maskgreater': None,
  'maskgeq': None,
  'maskbetween': None,
  'title': '',
  'titlesize': 'large',
  'titleweight': None,
  'titleprops': {},
  'figtitle': '',
  'figtitlesize': 12.0,
  'figtitleweight': None,
  'figtitleprops': {},
  'text': [],
  'post_timing': 'never',
  'post': None})
```

You can use the `show_keys()`, `show_summaries()` and `show_docs()` methods to have a look into the documentation into the formatoptions or you simply use the builtin `help()` function for it:

```
>>> help(plotter.clabel)
```

The update methods are the same as for the `Project` class. You can use the `psyplot.data.InteractiveArray.update()` via `arr.psy.update()` which updates the data and forwards the formatoptions to the `Plotter.update()` method.

Note: Plotters are subclasses of dictionaries where each item represents the key-value pair of one formatoption. Anyway, although you could now simply set a formatoption like you set an item for a dictionary via

```
In [31]: plotter['clabel'] = 'my label'
```

or equivalently

```
In [32]: plotter.clabel = 'my label'
```

this would not change the plot! Instead you have to use the *psyplot.plotter.Plotter.update()* method, i.e.

```
In [33]: plotter.update(clabel='my label')
```

Formatoptions

Formatoptions are the core of the visualization in the psyplot framework. They conceptually correspond to the basic `matplotlib.artist.Artist` and inherit from the abstract *Formatoption* class. Each plotter is set up through it's formatoptions where each formatoption has a unique formatoption key inside the plotter. This formatoption key (e.g. 'title' or 'clabel') is what is used for updating the plot etc. You can find more information in *How to implement your own plotters and plugins* .

1.10.2 How to implement your own plotters and plugins

New plotters and plugins to the psyplot framework are highly welcomed. In this guide, we present *how to create new plotters* and explain to you how you can *include them as a plugin in psyplot*.

Creating plotters

Implementing new plotters can be very easy or quite an effort depending on how sophisticated you want to do it. In principle, you only have to implement the *Formatoption.update()* method and a default value. I.e., one simple formatoption would be

```
In [1]: from psyplot.plotter import Formatoption, Plotter

In [2]: class MyFormatoption(Formatoption):
   ...:     default = 'my text'
   ...:     def update(self, value):
   ...:         self.ax.text(0.5, 0.5, value, fontsize='xx-large')
   ...:
```

together with a plotter

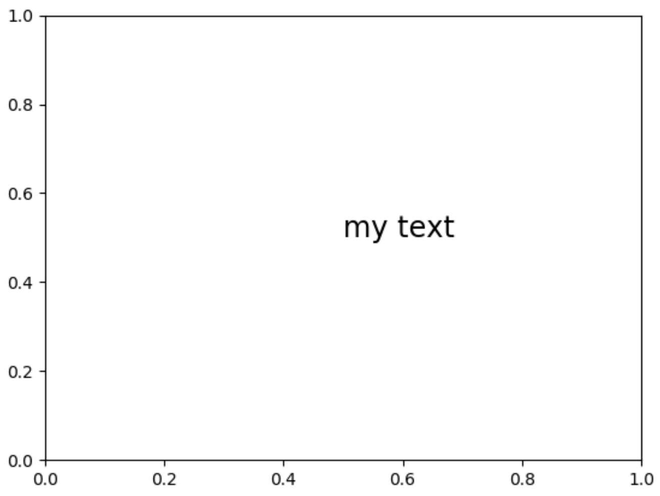
```
In [3]: class MyPlotter(Plotter):
   ...:     my_fmt = MyFormatoption('my_fmt')
   ...:
```

and your done. Now you can make a simple plot

```
In [4]: from psyplot import open_dataset

In [5]: ds = open_dataset('demo.nc')

In [6]: plotter = MyPlotter(ds.t2m)
```



However, if you're using the psyplot framework, you probably will be a bit more advanced so let's talk about attributes and methods of the `Formatoption` class.

If you look into the documentation of the `Formatoption` class, you find quite a lot of attributes and methods which probably is a bit depressing and confusing. But in principle, we can group them into 4 categories, the interface to the data, to the plotter and to other formatoptions. Plus an additional category for some Formatoption internals you definitely have to care about.

Interface for the plotter

The first interface is the one, that interfaces to the plotter. The most important attributes in this group are the `key`, `priority`, `plot_fmt`, `initialize_plot()` and most important the `update()` method.

The `key` is the unique key for the formatoption inside the plotter. In our example above, we assign the `'my_fmt'` key to the `MyFormatoption` class in `MyPlotter`. Hence, this key is defined when the plotter class is defined and will be automatically assigned to the formatoption.

The next important attribute is the `priority` attribute. There are three stages in the update of a plotter:

1. The stage with data manipulation. If formatoptions manipulate the data that shall be visualized (the `data` attribute), those formatoptions are updated first. They have the `psyplot.plotter.START` priority
2. The stage of the plot. Formatoptions that influence how the data is visualized are updated here (e.g. the colormap or formatoptions that do the plotting). They have the `psyplot.plotter.BEFOREPLOTTING` priority.
3. The stage of the plot where additional informations are inserted. Here all the labels are updated, e.g. the title, xlabel, etc.. This is the default priority of the `Formatoption.priority` attribute, the `psyplot.plotter.END` priority.

If there is any formatoption updated within the first two groups, the plot of the plotter is updated. This brings us to the third important attribute, the `plot_fmt`. This boolean tells the plotter, whether the corresponding formatoption is assumed to make a plot at the end of the second stage (the `BEFOREPLOTTING` stage). If this attribute is `True`, then the plotter will call the `Formatoption.make_plot()` method of the formatoption instance.

Finally, the `initialize_plot()` and `update()` methods, this is were your contribution really is required. The `initialize_plot()` method is called when the plot is created for the first time, the `update()` method when it is updated (the default implementation of the `initialize_plot()` simply calls the `update()` method). Implement these methods in your formatoption and thereby make use of the interface to the *data* and other *formatoptions*.

Interface to the data

The next set of attributes help you to interface to the data. There are two important parts in this section the interface to the data and the interpretation of the data.

The first part is mainly represented to the `Formatoption.data` and `Formatoption.raw_data` attributes. The plotter that contains the formatoption often creates a copy of the data because the data for the visualization might be modified (see for example the `psy_reg.plotter.LinRegPlotter`). This modified data can be accessed through the `Formatoption.data` and should be the standard approach to access the data within a formatoption. Nevertheless, the original data can be accessed through the `Formatoption.raw_data` attribute. However, it only makes sense to access this data for formatoption with `START priority`.

The result of these two attributes depend on the `Formatoption.index_in_list` attribute. The data objects in the psyplot framework are either a `xarray.DataArray` or a list of those in a `psyplot.data.InteractiveList`. If the `index_in_list` attribute is not None, and the data object is an `InteractiveList`, then only the array at the specified position is returned. To completely avoid this issue, you might also use the `iter_data` or `iter_raw_data` attributes.

The second part in this section is the interpretation of the data and here, the formatoption can use the `Formatoption.decoder` attribute. This subclass of the `psyplot.data.CFDecoder` helps you to identify the x- and y-variables in the data.

Interfacing to other formatoptions

A formatoption is the lowest level in the psyplot framework. It is represented at multiple levels:

1. at the lowest level through the subclass of the `Formatoption` class
2. at the `Plotter` class level which includes the formatoption class as a descriptor (in our example above it's `MyPlotter.my_fmt`)
3. at the `Plotter` instance level through
   (a) a personalized instance of the corresponding `Formatoption` class (i.e. `plotter = MyPlotter(); plotter.my_fmt is not MyPlotter.my_fmt`)
   (b) an item in the plotter (i.e. `plotter = MyPlotter(); plotter['my_fmt']`)
4. In the update methods of the `Plotter`, `psyplot.data.InteractiveBase` and `psyplot.data.ArrayList` as a keyword (i.e. `plotter = MyPlotter(); plotter.update(my_fmt='new value')`)

Hence, there is one big to the entire framework, that is: the functionality of a new formatoption has to be completely defined through exactly one argument, i.e. it must be possible to assign a value to the formatoption in the plotter.

For complex formatoption, this might indeed be quite a challenge for the developer and there are two solutions to it:

1. The simple solution for the developer: Allow a dictionary as a formatoption, here we also have the `psyplot.plotter.DictFormatoption` to help you.
2. Interface to other formatoptions

First solution: Use a `dict`

That said, to implement a formatoption that inserts a custom text and let the user define the size of the text, you either create a formatoption that accepts a text via

```
class CustomText(DictFormatoption):

    default = {'text': ''}

    text = None

    def validate(self, value):
        if not isinstance(value, dict):
            return {'text': value}
        return value

    def initialize_plot(self, value):
        self.text = self.ax.text(0.2, 0.2, value['text'],
                                 fontsize=value.get('size', 'large'))

    def update(self, value):
        self.text.set_text(value['text'])
        self.text.set_fontsize(value.get('size', 'large'))


class MyPlotter(Plotter):

    my_fmt = CustomText('my_fmt')
```

and then you could create and update a plotter via

```
p = MyPlotter(xarray.DataArray([]))
p.update(my_fmt='my text')  # updates the text
p.update(my_fmt={'size': 14})  # updates the size
p.update(my_fmt={'size': 14, 'text': 'Something'})  # updates text and size
```

This solution has the several advantages:

- The user does not get confused through too many formatoptions
- It is easy to allow more keywords for this formatoption

Indeed, the `psy_simple.plotter.Legend` formatoption uses this framework since the `matplotlib.pyplot.legend()` function accepts that many keywords that it would be not informative to create a formatoption for each of them.

Otherwise you could of course avoid the *`DictFormatoption`* and just force the user to always provide a new dictionary.

Second solution: Interact with other formatoptions

Another possibility is to implement a second formatoption for the size of the text. And here, the psyplot framework helps you with several attributes of the *`Formatoption`* class:

the *`children`* attribute Forces the listed formatoptions in this list to be updated before the current formatoption is updated

the *`dependencies`* attributes Same as *`children`* but also forces an update if one of the named formatoptions are updated

the *`parents`* attribute Skip the update if one of the *`parents`* is updated

the *`connections`* attribute just provides connections to the listed formatoptions

Each of those attributes accept a list of strings that represent the formatoption keys of other formatoptions. Those formatoptions are then accessible within the formatoption via the usual `getattr()`. I.e. if you list a formatoption in the *children* attribute, you can access it inside the formatoption (`self`) via `self.other_formatoption`.

In our example of the `CustomText`, this could be implemented via

```
class CustomTextSize(Formatoption):
    """
    Set the fontsize of the custom text

    Possible types
    --------------
    int
        The fontsize of the text
    """

    default = int

    def validate(self, value):
        return int(value)

    # this text has not to be updated if the custom text is updated
    children = ['text']

    def update(self, value):
        self.text.text.set_fontsize(value)


class CustomText(Formatoption):
    """
    Place a text

    Possible types
    --------------
    str
        The text to display"""

    def initialize_plot(self, value):
        self.text = self.ax.text(0.2, 0.2, value['text'])

    def update(self, value):
        self.text.set_text(value)


class MyPlotter(Plotter):

    my_fmt = CustomText('my_fmt')
    my_fmtsize = CustomTextSize('my_fmtsize', text='my_fmt')
```

the update in that sense would be like

and then you could create and update a plotter via

```
p = MyPlotter(xarray.DataArray([]))
p.update(my_fmt='my text')  # updates the text
p.update(my_fmtsize=14)  # updates the size
p.update(my_fmt='Something', my_fmtsize=14)  # updates text and size
```

The advantages of this methodology are basically:

- The user straight away sees two formatoptions that can be interpreted easiliy
- The formatoption that controls the font size could easily be subclassed and replaced in a subclass of `MyPlotter`. In the first framework using the *`DictFormatoption`*, this would mean that the entire process has to be rewritten.

  As you see in the above definition `my_fmtsize = CustomTextSize('my_fmtsize', text='my_fmt')`, we provide an additional `text` keyword. That is because we explicitly named the `text` key in the `children` attribute of the `CustomTextSize` formatoption. In that way we can tell the `my_fmtsize` formatoption how to find the necessary formatoption. That works for all keys listed in the *`children`*, *`dependencies`*, *`parents`* and *`connections`* attributes.

Creating new plugins

Now that you have created your plotter, you may want to include it in the plot methods of the *`Project`* class such that you can do something like

```
import psyplot.project as psy
psy.plot.my_plotter('netcdf-file.nc', name='varname')
```

There are three possibilities how you can do this:

1. The easy and fast solution for one session: register the plotter using the *`psyplot.project.register_plotter()`* function
2. The easy and steady solution: Save the calls you used in step 1 in the `'project.plotter.user'` key of the *`rcParams`*
3. The steady and shareable solution: Create a new plugin

The third solution has been used for the psy-maps and psy-simple plugins. To create a skeleton for your plugin, you can use the `psyplot-plugin` command that is installed when you install psyplot.

For our demonstration, let's create a plugin named my-plugin. This is simply done via

```
In [7]: !psyplot-plugin my-plugin

In [8]: import glob

In [9]: glob.glob('my-plugin/**', recursive=True)
Out[9]:
['my-plugin/',
 'my-plugin/LICENSE',
 'my-plugin/MANIFEST.in',
 'my-plugin/__pycache__',
 'my-plugin/__pycache__/setup.cpython-36.pyc',
 'my-plugin/my_plugin',
 'my-plugin/my_plugin/plotters.py',
 'my-plugin/my_plugin/__pycache__',
 'my-plugin/my_plugin/__pycache__/__init__.cpython-36.pyc',
 'my-plugin/my_plugin/__pycache__/plugin.cpython-36.pyc',
 'my-plugin/my_plugin/__pycache__/plotters.cpython-36.pyc',
 'my-plugin/my_plugin/plugin.py',
 'my-plugin/my_plugin/__init__.py',
 'my-plugin/README.md',
 'my-plugin/setup.py']
```

The following files are created in a directory named `'my-plugin'`:

`'setup.py'` The installation script

'my_plugin/plugin.py' The file that sets up the configuration of our plugin. This file should define the `rcParams` for the plugin (see also *rcParams handling in plugins*)

'my_plugin/plotters.py' The file in which we define the plotters. This file should define the plotters and formatoptions.

If you want to see more, look into the comments in the created files.

`rcParams` handling in plugins

Every formatoption does have default values. In *our example above*, we simply set it via the *`default`* attribute. This is a hard-coded, but easy, stable and quick solution.

However, your formatoption could also be used in different plotters, each requiring a different default value. Or you want to give the user the possibility to set his own default value. For this, we implemented the

`psyplot.plotter.Plotter._rcparams_string`	List of base strings in the `psyplot.rcParams` dictionary

attribute. Here you can specify a string for this plotter which is used to get the default value of the formatoptions in this plotter from the *`rcParams`*. The expected *`default_key`* for one formatoption would then be `the_chosen_string + fmt_key`.

The following example illustrates this:

```
In [10]: from psyplot.config.rcsetup import rcParams
   ....: from psyplot.plotter import Plotter, Formatoption
   ....:
```

First we define our defaultParams, a mapping from default key to the default value, a validation function, and a description (see the *`psyplot.config.rcsetup.defaultParams`* dictionary).

```
In [12]: defaultParams = {
   ....:     'plotter.example_plotter.fmt1': [
   ....:         1, lambda val: int(val), 'Example formatoption']
   ....:     }
   ....:
```

Then we update the *`defaultParams`* of the *`psyplot.rcParams`* and set the value

```
In [13]: rcParams.defaultParams.update(defaultParams)

In [14]: rcParams.update_from_defaultParams(defaultParams)
   ....: print(rcParams['plotter.example_plotter.fmt1'])
   ....:
1
```

Now we define a formatoption for our new plotter class and implement it in a new plotter object.

```
In [16]: class ExampleFmt(Formatoption):
   ....:     def update(self, value):
   ....:         pass
   ....:

In [17]: class ExamplePlotter(Plotter):
   ....:     # we use our base string, 'plotter.example_plotter.'
   ....:     _rcparams_string = ['plotter.example_plotter.']
```

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```
   ....:     # and register a formatoption for the plotter
   ....:     fmt1 = ExampleFmt('fmt1')
   ....:
```

If we now create a new instance of this `ExamplePlotter`, the `fmt1` formatoption will have a value of `1`, as we defined it in the above `defaultParams`:

```
In [18]: plotter = ExamplePlotter()

In [19]: print(plotter['fmt1'])
1

# and the default_key is our string in the defaultParams, a combination
# of the _rcparams_string and the formatoption key
In [20]: print(plotter.fmt1.default_key)
\\plotter.example_plotter.fmt1

In [21]: print(plotter.fmt1.default)
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\1
```

Changing the value in the *`rcParams`*, also changes the default value for the plotter

```
In [22]: rcParams['plotter.example_plotter.fmt1'] = 2

In [23]: print(plotter.fmt1.default)
2
```

Also, if we subclass this plotter, the default_key will not change

```
In [24]: class SecondPlotter(ExamplePlotter):
   ....:     # we set a new _rcparams_string
   ....:     _rcparams_string = ['plotter.another_plotter.']
   ....:

In [25]: plotter = SecondPlotter()

# still the same key, although we defined a different _rcparams_string
In [26]: print(plotter.fmt1.default_key)
plotter.example_plotter.fmt1
```

If you're developing a new plugin you would then have to define the `rcParams` and `defaultParams` in the `plugin.py` script (see *Creating new plugins*) and they will then be automatically implemented in *`psyplot.rcParams`*.

1.11 How to contribute

psyplot and it's plugins are available open-source on Github. Here we very much welcome your contributions!

In case of any troubles, need for clarification or suggestions, please open an issue on psyplots github page (or on the corresponding plugins github page, see *Subprojects*). If you are not sure, where you should open the issue, just use psyplots repository.

We also very much welcome pull requests for bug fixes, feature improvements or additional examples. If you want to add an example to the documentation, please just fork the correct github repository and add a jupyter notebook in the `examples` directory, together with all the necessary data files. To build our docs, we use the sphinx-nbexamples package to build the examples. Therefore please make sure that your supplementary data files are correctly implemented in the meta data of the notebook (see Providing supplementary files). We are, however, also willing to help you finalizing incomplete pull requests.

1.12 API Reference

psyplot visualization framework

Functions

get_versions([requirements, key])	Get the version information for psyplot, the plugins and its requirements

Data

with_gui	Boolean that is True, if psyplot runs inside the graphical user interface

psyplot.**get_versions**(*requirements=True*, *key=None*)

Get the version information for psyplot, the plugins and its requirements

Parameters

- **requirements** (*bool*) – If True, the requirements of the plugins and psyplot are investigated
- **key** (*func*) – A function that determines whether a plugin shall be considererd or not. The function must take a single argument, that is the name of the plugin as string, and must return True (import the plugin) or False (skip the plugin). If None, all plugins are imported

Returns A mapping from `'psyplot'`/the plugin names to a dictionary with the `'version'` key and the corresponding version is returned. If *requirements* is True, it also contains a mapping from `'requirements'` a dictionary with the versions

Return type dict

Examples

Using the built-in JSON module, we get something like

```
import json
print(json.dumps(psyplot.get_versions(), indent=4))
{
    "psy_simple.plugin": {
        "version": "1.0.0.dev0"
    },
    "psyplot": {
        "version": "1.0.0.dev0",
        "requirements": {
            "matplotlib": "1.5.3",
            "numpy": "1.11.3",
            "pandas": "0.19.2",
            "xarray": "0.9.1"
        }
    },
```

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```
    "psy_maps.plugin": {
        "version": "1.0.0.dev0",
        "requirements": {
            "cartopy": "0.15.0"
        }
    }
}
```

psyplot.**with_gui = False**

Boolean that is True, if psyplot runs inside the graphical user interface by the `psyplot_gui` module

rcParams	*RcParams* instance that stores default formatoptions and configuration settings.
InteractiveArray(xarray_obj, *args, **kwargs)	Interactive psyplot accessor for the data array
InteractiveList(*args, **kwargs)	List of `InteractiveArray` instances that can be plotted itself

1.12.1 Subpackages

psyplot.compat package

Submodules

psyplot.compat.pycompat module

Compatibility module for different python versions

That's a test

Classes

DictMethods

Functions

get_default_value(func, arg)
getcwd(*args, **kwargs)
isstring(s)

class psyplot.compat.pycompat.**DictMethods**

Bases: `object` **Methods**

iteritems()
iterkeys()
itervalues()

static iteritems()

static iterkeys()

static itervalues()

psyplot.compat.pycompat.**get_default_value**(*func*, *arg*)

psyplot.compat.pycompat.**getcwd**(**args*, ***kwargs*)

psyplot.compat.pycompat.**isstring**(*s*)

psyplot.config package

Configuration module of the psyplot package

This module contains the module for managing rc parameters and the logging. Default parameters are defined in the *rcsetup.defaultParams* dictionary, however you can set up your own configuration in a yaml file (see `psyplot.load_rc_from_file()`)

Data

config_path	*class* – *str* or `None`. Path to the yaml configuration file (if found).
logcfg_path	`str`. Path to the yaml logging configuration file

psyplot.config.**config_path = None**
class – *str* or `None`. Path to the yaml configuration file (if found). See *psyplot_fname()* for further information

psyplot.config.**logcfg_path = '/home/docs/checkouts/readthedocs.org/user_builds/psyplot/chec**
`str`. Path to the yaml logging configuration file

Submodules

psyplot.config.logsetup module

Logging configuration module of the psyplot package

This module defines the essential functions for setting up the `logging.Logger` instances that are used by the psyplot package.

Functions

setup_logging([default_path, default_level, . . .])	Setup logging configuration

psyplot.config.logsetup.**setup_logging**(*default_path=None*, *default_level=20*, *env_key='LOG_PSYPLOT'*)
Setup logging configuration

Parameters

- **default_path** (*str*) – Default path of the yaml logging configuration file. If None, it defaults to the 'logging.yaml' file in the config directory
- **default_level** (*int*) – Default: `logging.INFO`. Default level if default_path does not exist
- **env_key** (*str*) – environment variable specifying a different logging file than *default_path* (Default: 'LOG_CFG')

Returns **path** – Path to the logging configuration file

Return type str

Notes

Function taken from http://victorlin.me/posts/2012/08/26/good-logging-practice-in-python

psyplot.config.rcsetup module

Default management of the psyplot package

This module defines the necessary classes, data and functions for the default configuration of the module. The structure is motivated and to larger parts taken from the matplotlib package.

Classes

RcParams(*args, **kwargs)	A dictionary object including validation
SubDict(base, base_str[, pattern, . . .])	Class that keeps week reference to the base dictionary

Functions

get_configdir([name, env_key])	Return the string representing the configuration directory.
psyplot_fname([env_key, fname, if_exists])	Get the location of the config file.
safe_list(l)	Function to create a list
validate_bool(b)	Convert b to a boolean or raise
validate_bool_maybe_none(b)	Convert b to a boolean or raise
validate_dict(d)	Validate a dictionary
validate_path_exists(s)	If s is a path, return s, else False
validate_str(s)	Validate a string
validate_stringlist(s)	Validate a list of strings
validate_stringset(*args, **kwargs)	Validate a set of strings

Data

defaultParams	dict with default values and validation functions
rcParams	*RcParams* instance that stores default

class psyplot.config.rcsetup.**RcParams**(**args*, ***kwargs*)

Bases: dict

A dictionary object including validation

validating functions are defined and associated with rc parameters in *defaultParams*

This class is essentially the same as in maplotlibs RcParams but has the additional *find_and_replace()* method.

Parameters **defaultParams** (*dict*) – The defaultParams to use (see the *defaultParams* attribute). By default, the *psyplot.config.rcsetup.defaultParams* dictionary is used

Other Parameters **‘‘*args, **kwargs‘‘** – Any key-value pair for the initialization of the dictionary

Attributes

HEADER	str(object='') -> str
defaultParams	
descriptions	The description of each keyword in the rcParams dictionary
msg_depr	str(object='') -> str
msg_depr_ignore	str(object='') -> str
validate	Dictionary with validation methods as values

Methods

connect(key, func)	Connect a function to the given formatoption
copy()	Make sure, the right class is retained
disconnect([key, func])	Disconnect the connections to the an rcParams key
dump([fname, overwrite, include_keys, . . .])	Dump this instance to a yaml file
find_all(pattern)	Return the subset of this RcParams dictionary whose keys match, using `re.search()`, the given `pattern`.
find_and_replace(*args, **kwargs)	Like `find_all()` but the given strings are replaced
keys()	Return sorted list of keys.
load_from_file([fname])	Update rcParams from user-defined settings
load_plugins([raise_error])	Load the plotters and defaultParams from the plugins
remove(key, func)	
update([E,]**F)	If E is present and has a .keys() method, then does: for k in E: D[k] = E[k]
update_from_defaultParams([defaultParams, . . .])	Update from the a dictionary like the *defaultParams*
values()	Return values in order of sorted keys.

HEADER = 'Configuration parameters of the psyplot module\n\nYou can copy this file (or

connect (*key*, *func*)
Connect a function to the given formatoption

Parameters

- **key** (*str*) – The rcParams key
- **func** (*function*) – The function that shall be called when the rcParams key changes. It must accept a single value that is the new value of the key.

copy ()
Make sure, the right class is retained

defaultParams

descriptions
The description of each keyword in the rcParams dictionary

disconnect (*key=None*, *func=None*)
Disconnect the connections to the an rcParams key

Parameters

- **key** (*str*) – The rcParams key. If None, all keys are used
- **func** (*function*) – The function that is connected. If None, all functions are connected

dump(*fname=None, overwrite=True, include_keys=None, exclude_keys=['project.plotters'], include_descriptions=True, **kwargs*)

Dump this instance to a yaml file

Parameters

- **fname** (`str or None`) – file name to write to. If None, the string that would be written to a file is returned
- **overwrite** (`bool`) – If True and *fname* already exists, it will be overwritten
- **include_keys** (`None or list of str`) – Keys in the dictionary to be included. If None, all keys are included
- **exclude_keys** (`list of str`) – Keys from the `RcParams` instance to be excluded

Other Parameters **``**kwargs``** – Any other parameter for the `yaml.dump()` function

Returns if fname is `None`, the string is returned. Otherwise, `None` is returned

Return type str or None

Raises `IOError` – If *fname* already exists and *overwrite* is False

See also:

`load_from_file()`

find_all(*pattern*)

Return the subset of this RcParams dictionary whose keys match, using `re.search()`, the given `pattern`.

Parameters **pattern** (`str`) – pattern as suitable for re.compile

Returns RcParams instance with entries that match the given *pattern*

Return type *RcParams*

Notes

Changes to the returned dictionary are (different from `find_and_replace()` are *not* propagated to the parent RcParams dictionary.

See also:

`find_and_replace()`

find_and_replace(**args*, ***kwargs*)

Like `find_all()` but the given strings are replaced

This method returns a dictionary-like object that keeps weak reference to this rcParams instance. The resulting *SubDict* instance takes the keys from this rcParams instance but leaves away what is found in *base_str*.

`*args` and `**kwargs` are determined by the `SubDict` class, where the *base* dictionary is this one.

Parameters

- **base_str** (`str or list of str`) – Strings that are used as to look for keys to get and set keys in the `base` dictionary. If a string does not contain `'%(key)s'`, it will be appended at the end. `'%(key)s'` will be replaced by the specific key for getting and setting an item.

- **pattern** (*str*) – Default: `'.+'`. This is the pattern that is inserted for `%(key)s` in a base string to look for matches (using the `re` module) in the *base* dictionary. The default *pattern* matches everything without white spaces.
- **pattern_base** (*str or list or str*) – If None, the whatever is given in the *base_str* is used. Those strings will be used for generating the final search patterns. You can specify this parameter by yourself to avoid the misinterpretation of patterns. For example for a *base_str* like `'my.str'` it is recommended to additionally provide the *pattern_base* keyword with `'my\.str'`. Like for *base_str*, the `%(key)s` is appended if not already in the string.
- **trace** (*bool*) – Default: False. If True, changes in the SubDict are traced back to the *base* dictionary. You can change this behaviour also afterwards by changing the `trace` attribute
- **replace** (*bool*) – Default: True. If True, everything but the '%(key)s' part in a base string is replaced (see examples below)

Returns SubDict with this rcParams instance as reference.

Return type *SubDict*

Examples

The syntax is the same as for the initialization of the `SubDict` class:

```
>>> from psyplot import rcParams
>>> d = rcParams.find_and_replace(['plotter.baseplotter.',
...                               'plotter.vector.'])
>>> print(d['title'])
None

>>> print(d['arrowsize'])
1.0
```

See also:

find_all(), *SubDict()*

keys()
Return sorted list of keys.

load_from_file(*fname=None*)
Update rcParams from user-defined settings

This function updates the instance with what is found in *fname*

Parameters fname (*str*) – Path to the yaml configuration file. Possible keys of the dictionary are defined by `config.rcsetup.defaultParams`. If None, the `config.rcsetup.psyplot_fname()` function is used.

See also:

`dump_to_file()`, *psyplot_fname()*

load_plugins(*raise_error=False*)
Load the plotters and defaultParams from the plugins

This method loads the *plotters* attribute and *defaultParams* attribute from the plugins that use the entry point specified by *group*. Entry points must be objects (or modules) that have a *defaultParams* and a *plotters* attribute.

Parameters **raise_error** (*bool*) – If True, an error is raised when multiple plugins define the same plotter or rcParams key. Otherwise only a warning is raised

msg_depr = '%s is deprecated and replaced with %s; please use the latter.'

msg_depr_ignore = '%s is deprecated and ignored. Use %s'

remove (*key*, *func*)

update ([*E*], ***F*) → None. Update D from dict/iterable E and F.
If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and lacks a .keys() method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]

update_from_defaultParams (*defaultParams=None*, *plotters=True*)
Update from the a dictionary like the `defaultParams`

Parameters

- **defaultParams** (*dict*) – The `defaultParams` like dictionary. If None, the `defaultParams` attribute will be updated
- **plotters** (*bool*) – If True, `'project.plotters'` will be updated too

validate
Dictionary with validation methods as values

values ()
Return values in order of sorted keys.

class psyplot.config.rcsetup.**SubDict** (*base*, *base_str*, *pattern='.+'*, *pattern_base=None*, *trace=False*, *replace=True*)
Bases: `collections.UserDict`, `dict`

Class that keeps week reference to the base dictionary

This class is used by the `RcParams.find_and_replace()` method to provide an easy handable instance that keeps reference to the base rcParams dictionary.

Parameters

- **base** (*dict*) – base dictionary
- **base_str** (*str or list of str*) – Strings that are used as to look for keys to get and set keys in the `base` dictionary. If a string does not contain `'%(key)s'`, it will be appended at the end. `'%(key)s'` will be replaced by the specific key for getting and setting an item.
- **pattern** (*str*) – Default: `'.+'`. This is the pattern that is inserted for `%(key)s` in a base string to look for matches (using the `re` module) in the *base* dictionary. The default *pattern* matches everything without white spaces.
- **pattern_base** (*str or list or str*) – If None, the whatever is given in the *base_str* is used. Those strings will be used for generating the final search patterns. You can specify this parameter by yourself to avoid the misinterpretation of patterns. For example for a *base_str* like `'my.str'` it is recommended to additionally provide the *pattern_base* keyword with `'my\.str'`. Like for *base_str*, the `%(key)s` is appended if not already in the string.
- **trace** (*bool*) – Default: False. If True, changes in the SubDict are traced back to the *base* dictionary. You can change this behaviour also afterwards by changing the `trace` attribute
- **replace** (*bool*) – Default: True. If True, everything but the '%(key)s' part in a base string is replaced (see examples below)

Methods

add_base_str(base_str[, pattern, …])	Add further base string to this instance
iteritems()	Unsorted iterator over items
iterkeys()	Unsorted iterator over keys
itervalues()	Unsorted iterator over values
update(*args, **kwargs)	Update the dictionary

Attributes

base	dict. Reference dictionary
base_str	list of strings. The strings that are used to set and get a specific key
data	Dictionary representing this *SubDict* instance
patterns	list of compiled patterns from the base_str attribute, that
replace	bool. If True, matching strings in the base_str
trace	bool. If True, changes are traced back to the base dict

Notes

- If a key of matches multiple strings in *base_str*, the first matching one is used.
- the SubDict class is (of course) not that efficient as the *base* dictionary, since we loop multiple times through it's keys

---

Examples

Initialization example:

```
>>> from psyplot import rcParams
>>> d = rcParams.find_and_replace(['plotter.baseplotter.',
...                                'plotter.vector.'])
>>> print d['title']

>>> print d['arrowsize']
1.0
```

To convert it to a usual dictionary, simply use the *data* attribute:

```
>>> d.data
{'title': None, 'arrowsize': 1.0, ...}
```

Note that changing one keyword of your *SubDict* will not change the *base* dictionary, unless you set the *trace* attribute to True:

```
>>> d['title'] = 'my title'
>>> print(d['title'])
my title

>>> print(rcParams['plotter.baseplotter.title'])

>>> d.trace = True
```

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```
>>> d['title'] = 'my second title'
>>> print(d['title'])
my second title
>>> print(rcParams['plotter.baseplotter.title'])
my second title
```

Furthermore, changing the `replace` attribute will change how you can access the keys:

```
>>> d.replace = False

# now setting d['title'] = 'anything' would raise an error (since
# d.trace is set to True and 'title' is not a key in the rcParams
# dictionary. Instead we need
>>> d['plotter.baseplotter.title'] = 'anything'
```

See also:

`RcParams.find_and_replace`

`add_base_str`(*base_str*, *pattern='.+'*, *pattern_base=None*, *append=True*)
Add further base string to this instance

Parameters

- **`base_str`** (*`str or list of str`*) – Strings that are used as to look for keys to get and set keys in the `base` dictionary. If a string does not contain `'%(key)s'`, it will be appended at the end. `'%(key)s'` will be replaced by the specific key for getting and setting an item.
- **`pattern`** (*`str`*) – Default: `'.+'`. This is the pattern that is inserted for `%(key)s` in a base string to look for matches (using the `re` module) in the *base* dictionary. The default *pattern* matches everything without white spaces.
- **`pattern_base`** (*`str or list or str`*) – If None, the whatever is given in the *base_str* is used. Those strings will be used for generating the final search patterns. You can specify this parameter by yourself to avoid the misinterpretation of patterns. For example for a *base_str* like `'my.str'` it is recommended to additionally provide the *pattern_base* keyword with `'my\.str'`. Like for *base_str*, the `%(key)s` is appended if not already in the string.
- **`append`** (*`bool`*) – If True, the given *base_str* are appended (i.e. it is first looked for them in the `base` dictionary), otherwise they are put at the beginning

`base = {}`
`dict`. Reference dictionary

`base_str = []`
list of strings. The strings that are used to set and get a specific key from the `base` dictionary

`data`
Dictionary representing this `SubDict` instance

See also:

`iteritems`

`iteritems`()
Unsorted iterator over items

iterkeys()
Unsorted iterator over keys

itervalues()
Unsorted iterator over values

patterns = []
list of compiled patterns from the `base_str` attribute, that are used to look for the matching keys in `base`

replace
`bool`. If True, matching strings in the `base_str` attribute are replaced with an empty string.

trace = False
`bool`. If True, changes are traced back to the `base` dict

update(**args*, ***kwargs*)
Update the dictionary

psyplot.config.rcsetup.**defaultParams**
`dict` with default values and validation functions

psyplot.config.rcsetup.**get_configdir**(*name='psyplot'*, *env_key='PSYPLOTCONFIGDIR'*)
Return the string representing the configuration directory.

The directory is chosen as follows:

1. If the *env_key* environment variable is supplied, choose that.

2a. On Linux and osx, choose `'$HOME/.config/' + name`.

2b. On other platforms, choose `'$HOME/.' + name`.

3. If the chosen directory exists, use that as the configuration directory.
4. A directory: return None.

Parameters

- **name** (`str`) – The name of the program
- **env_key** (`str`) – The environment variable that can be used for the configuration directory

Notes

This function is motivated by the `matplotlib.matplotlib_fname()` function

psyplot.config.rcsetup.**psyplot_fname**(*env_key='PSYPLOTRC'*, *fname='psyplotrc.yml'*, *if_exists=True*)
Get the location of the config file.

The file location is determined in the following order

- *$PWD/psyplotrc.yml*
- environment variable *PSYPLOTRC* (pointing to the file location or a directory containing the file *psyplotrc.yml*)
- *$PSYPLOTCONFIGDIR/psyplot*
- On Linux and osx,
  - *$HOME/.config/psyplot/psyplotrc.yml*
- On other platforms,

  - *$HOME/.psyplot/psyplotrc.yml* if *$HOME* is defined.
- Lastly, it looks in *$PSYPLOTDATA/psyplotrc.yml* for a system-defined copy.

Parameters

- **env_key** (*str*) – The environment variable that can be used for the configuration directory
- **fname** (*str*) – The name of the configuration file
- **if_exists** (*bool*) – If True, the path is only returned if the file exists

Returns None, if no file could be found and *if_exists* is True, else the path to the psyplot configuration file

Return type None or str

Notes

This function is motivated by the `matplotlib.matplotlib_fname()` function

`psyplot.config.rcsetup.`**`rcParams`**

RcParams instance that stores default formatoptions and configuration settings.

`psyplot.config.rcsetup.`**`safe_list`**`(l)`

Function to create a list

Parameters **l** (*iterable or anything else*) – Parameter that shall be converted to a list.

- If string or any non-iterable, it will be put into a list
- if iterable, it will be converted to a list

Returns *l* put (or converted) into a list

Return type list

`psyplot.config.rcsetup.`**`validate_bool`**`(b)`

Convert b to a boolean or raise

`psyplot.config.rcsetup.`**`validate_bool_maybe_none`**`(b)`

Convert b to a boolean or raise

`psyplot.config.rcsetup.`**`validate_dict`**`(d)`

Validate a dictionary

Parameters **d** (*dict or str*) – If str, it must be a path to a yaml file

Returns

Return type dict

Raises `ValueError`

`psyplot.config.rcsetup.`**`validate_path_exists`**`(s)`

If s is a path, return s, else False

`psyplot.config.rcsetup.`**`validate_str`**`(s)`

Validate a string

Parameters **s** (*str*) –

Returns

Return type str

Raises ValueError

`psyplot.config.rcsetup.`**`validate_stringlist`**`(s)`

Validate a list of strings

Parameters **`val`** (*`iterable of strings`*) –

Returns list of str

Return type list

Raises ValueError

`psyplot.config.rcsetup.`**`validate_stringset`**`(*args, **kwargs)`

Validate a set of strings

Parameters **`val`** (*`iterable of strings`*) –

Returns set of str

Return type set

Raises ValueError

psyplot.sphinxext package

Sphinx extension package of the psyplot module

Submodules

psyplot.sphinxext.extended_napoleon module

Sphinx extension module to provide additional sections for numpy docstrings

This extension extends the `sphinx.ext.napoleon` package with an additional *Possible types* section in order to document possible types for descriptors.

Notes

If you use this module as a sphinx extension, you should not list the `sphinx.ext.napoleon` module in the extensions variable of your conf.py. This module has been tested for sphinx 1.3.1.

Classes

`DocstringExtension`	Class that introduces a “Possible Types” section
`ExtendedGoogleDocstring`(docstring[, config, …])	`sphinx.ext.napoleon.GoogleDocstring` with more sections
`ExtendedNumpyDocstring`(docstring[, config, …])	`sphinx.ext.napoleon.NumpyDocstring` with more sections

Functions

`process_docstring`(app, what, name, obj, …)	Process the docstring for a given python object.
`setup`(app)	Sphinx extension setup function

`class` `psyplot.sphinxext.extended_napoleon.`**`DocstringExtension`**

Bases: `object`

Class that introduces a "Possible Types" section

This class serves as a base class for `sphinx.ext.napoleon.NumpyDocstring` and `sphinx.ext.napoleon.GoogleDocstring` to introduce another section names *Possible types*

Examples

The usage is the same as for the NumpyDocstring class, but it supports the *Possible types* section:

```
>>> from sphinx.ext.napoleon import Config

>>> from psyplot.sphinxext.extended_napoleon import (
...     ExtendedNumpyDocstring)
>>> config = Config(napoleon_use_param=True,
...                 napoleon_use_rtype=True)
>>> docstring = '''
... Possible types
... --------------
... type1
...     Description of `type1`
... type2
...     Description of `type2`'''
>>> print(ExtendedNumpyDocstring(docstring, config))
.. rubric:: Possible types

* *type1* --
  Description of `type1`
* *type2* --
  Description of `type2`
```

class `psyplot.sphinxext.extended_napoleon.`**`ExtendedGoogleDocstring`**(*docstring, config=None, app=None, what='', name='', obj=None, options=None*)

Bases: `sphinx.ext.napoleon.docstring.GoogleDocstring`, *`psyplot.sphinxext.extended_napoleon.DocstringExtension`*

`sphinx.ext.napoleon.GoogleDocstring` with more sections

class `psyplot.sphinxext.extended_napoleon.`**`ExtendedNumpyDocstring`**(*docstring, config=None, app=None, what='', name='', obj=None, options=None*)

Bases: `sphinx.ext.napoleon.docstring.NumpyDocstring`, *`psyplot.sphinxext.extended_napoleon.DocstringExtension`* `sphinx.ext.napoleon.NumpyDocstring` with more sections

`psyplot.sphinxext.extended_napoleon.`**`process_docstring`**(*app*, *what*, *name*, *obj*, *options*, *lines*)

Process the docstring for a given python object.

Called when autodoc has read and processed a docstring. *lines* is a list of docstring lines that *_process_docstring* modifies in place to change what Sphinx outputs.

The following settings in conf.py control what styles of docstrings will be parsed:

- `napoleon_google_docstring` – parse Google style docstrings
- `napoleon_numpy_docstring` – parse NumPy style docstrings

Parameters

- **`app`** (*`sphinx.application.Sphinx`*) – Application object representing the Sphinx process.
- **`what`** (*`str`*) – A string specifying the type of the object to which the docstring belongs. Valid values: "module", "class", "exception", "function", "method", "attribute".
- **`name`** (*`str`*) – The fully qualified name of the object.
- **`obj`** (*`module, class, exception, function, method, or attribute`*) – The object to which the docstring belongs.
- **`options`** (*`sphinx.ext.autodoc.Options`*) – The options given to the directive: an object with attributes inherited_members, undoc_members, show_inheritance and noindex that are True if the flag option of same name was given to the auto directive.
- **`lines`** (*`list of str`*) – The lines of the docstring, see above.

Note: *lines* is modified *in place*

Notes

This function is (to most parts) taken from the `sphinx.ext.napoleon` module, sphinx version 1.3.1, and adapted to the classes defined here

`psyplot.sphinxext.extended_napoleon.`**`setup`**(*app*)

Sphinx extension setup function

When the extension is loaded, Sphinx imports this module and executes the `setup()` function, which in turn notifies Sphinx of everything the extension offers.

Parameters app (*`sphinx.application.Sphinx`*) – Application object representing the Sphinx process

Notes

This function uses the setup function of the `sphinx.ext.napoleon` module

1.12.2 Submodules

psyplot.data module

Classes

`AbsoluteTimeDecoder`(array)	
`AbsoluteTimeEncoder`(array)	
`ArrayList`([iterable, attrs, auto_update, . . .])	Base class for creating a list of interactive arrays from a dataset
`CFDecoder`([ds, x, y, z, t])	Class that interpretes the coordinates and attributes accordings to
`DatasetAccessor`(ds)	A dataset accessor to interface with the psyplot package
`InteractiveArray`(xarray_obj, *args, **kwargs)	Interactive psyplot accessor for the data array
`InteractiveBase`([plotter, arr_name, auto_update])	Class for the communication of a data object with a suitable plotter
`InteractiveList`(*args, **kwargs)	List of `InteractiveArray` instances that can be plotted itself
`Signal`([name, cls_signal])	Signal to connect functions to a specific event
`UGridDecoder`([ds, x, y, z, t])	Decoder for UGrid data sets

Functions

`decode_absolute_time`(times)	
`encode_absolute_time`(times)	
`get_filename_ds`(ds[, dump, paths])	Return the filename of the corresponding to a dataset
`get_index_from_coord`(coord, base_index)	Function to return the coordinate as integer, integer array or slice
`get_tdata`(t_format, files)	Get the time information from file names
`open_dataset`(filename_or_obj[, decode_cf, . . .])	Open an instance of `xarray.Dataset`.
`open_mfdataset`(paths[, decode_cf, . . .])	Open multiple files as a single dataset.
`setup_coords`([arr_names, sort, dims])	Sets up the arr_names dictionary for the plot
`to_netcdf`(ds, *args, **kwargs)	Store the given dataset as a netCDF file
`to_slice`(arr)	Test whether *arr* is an integer array that can be replaced by a slice

Data

`get_fname_funcs`	functions to use to extract the file name from a data store
`t_patterns`	mapping that translates datetime format strings to regex patterns

class psyplot.data.**AbsoluteTimeDecoder**(*array*)

Bases: `xarray.core.utils.NDArrayMixin` **Attributes**

`dtype`

dtype

class psyplot.data.**AbsoluteTimeEncoder**(*array*)

Bases: `xarray.core.utils.NDArrayMixin` **Attributes**

dtype

dtype

class psyplot.data.**ArrayList**(*iterable=[]*, *attrs={}*, *auto_update=None*, *new_name=True*)

Bases: `list`

Base class for creating a list of interactive arrays from a dataset

This list contains and manages *InteractiveArray* instances

Parameters

- **iterable** (*iterable*) – The iterable (e.g. another list) defining this list
- **attrs** (*dict-like or iterable, optional*) – Global attributes of this list
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the *update()* method or not. See also the *no_auto_update* attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Attributes

all_dims	The dimensions for each of the arrays in this list
all_names	The variable names for each of the arrays in this list
arr_names	Names of the arrays (!not of the variables!) in this list
arrays	A list of all the `xarray.DataArray` instances in this list
coords	Names of the coordinates of the arrays in this list
coords_intersect	Coordinates of the arrays in this list that are used in all arrays
dims	Dimensions of the arrays in this list
dims_intersect	Dimensions of the arrays in this list that are used in all arrays
is_unstructured	A boolean for each array whether it is unstructured or not
logger	`logging.Logger` of this instance
names	Set of the variable in this list
no_auto_update	`bool`. Boolean controlling whether the `start_update()`
with_plotter	The arrays in this instance that are visualized with a plotter

Methods

append(value[, new_name])	Append a new array to the list
array_info([dump, paths, attrs, . . .])	Get dimension informations on you arrays
copy([deep])	Returns a copy of the list

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Table 29 – continued from previous page

draw()	Draws all the figures in this instance
extend(iterable[, new_name])	Add further arrays from an iterable to this list
from_dataset(base[, method, default_slice, . . .])	Construct an ArrayList instance from an existing base dataset
from_dict(d[, alternative_paths, datasets, . . .])	Create a list from the dictionary returned by `array_info()`
next_available_name([fmt_str, counter])	Create a new array out of the given format string
remove(arr)	Removes an array from the list
rename(arr[, new_name])	Rename an array to find a name that isn't already in the list
start_update([draw])	Conduct the registered plot updates
update([method, dims, fmt, replot, . . .])	Update the coordinates and the plot

all_dims
The dimensions for each of the arrays in this list

all_names
The variable names for each of the arrays in this list

append(*value*, *new_name=False*)
Append a new array to the list

Parameters

- **value** (`InteractiveBase`) – The data object to append to this list
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Raises

- `ValueError` – If it was impossible to find a name that isn't already in the list
- `ValueError` – If *new_name* is False and the array is already in the list

See also:

`list.append()`, *extend()*, *rename()*

arr_names
Names of the arrays (!not of the variables!) in this list

This attribute can be set with an iterable of unique names to change the array names of the data objects in this list.

array_info(*dump=None*, *paths=None*, *attrs=True*, *standardize_dims=True*, *pwd=None*, *use_rel_paths=True*, *alternative_paths={}*, *ds_description={'fname'*, *'store'}*, *full_ds=True*, *copy=False*, ***kwargs*)
Get dimension informations on you arrays

This method returns a dictionary containing informations on the array in this instance

Parameters

- **dump** (*bool*) – If True and the dataset has not been dumped so far, it is dumped to a temporary file or the one generated by *paths* is used. If it is False or both, *dump* and *paths* are None, no data will be stored. If it is None and *paths* is not None, *dump* is set to True.

- **paths** (*iterable or True*) – An iterator over filenames to use if a dataset has no filename. If paths is `True`, an iterator over temporary files will be created without raising a warning
- **attrs** (*bool, optional*) – If True (default), the `ArrayList.attrs` and `xarray.DataArray.attrs` attributes are included in the returning dictionary
- **standardize_dims** (*bool, optional*) – If True (default), the real dimension names in the dataset are replaced by x, y, z and t to be more general.
- **pwd** (*str*) – Path to the working directory from where the data can be imported. If None, use the current working directory.
- **use_rel_paths** (*bool, optional*) – If True (default), paths relative to the current working directory are used. Otherwise absolute paths to *pwd* are used
- **ds_description** (*'all' or set of {'fname', 'ds', 'num', 'arr', 'store'}*) – Keys to describe the datasets of the arrays. If all, all keys are used. The key descriptions are

  fname the file name is inserted in the `'fname'` key

  store the data store class and module is inserted in the `'store'` key

  ds the dataset is inserted in the `'ds'` key

  num The unique number assigned to the dataset is inserted in the `'num'` key

  arr The array itself is inserted in the `'arr'` key
- **full_ds** (*bool*) – If True and `'ds'` is in *ds_description*, the entire dataset is included. Otherwise, only the DataArray converted to a dataset is included
- **copy** (*bool*) – If True, the arrays and datasets are deep copied

Other Parameters

- **‘‘**kwargs‘‘** – Any other keyword for the `to_netcdf()` function
- **path** (*str, Path or file-like object, optional*) – Path to which to save this dataset. File-like objects are only supported by the scipy engine. If no path is provided, this function returns the resulting netCDF file as bytes; in this case, we need to use scipy, which does not support netCDF version 4 (the default format becomes NETCDF3_64BIT).
- **mode** (*{‘w’, ‘a’}, optional*) – Write (‘w’) or append (‘a’) mode. If mode=’w’, any existing file at this location will be overwritten. If mode=’a’, existing variables will be overwritten.
- **format** (*{‘NETCDF4’, ‘NETCDF4_CLASSIC’, ‘NETCDF3_64BIT’,’NETCDF3_CLASSIC’}, optional*) – File format for the resulting netCDF file:
  - NETCDF4: Data is stored in an HDF5 file, using netCDF4 API features.
  - NETCDF4_CLASSIC: Data is stored in an HDF5 file, using only netCDF 3 compatible API features.
  - NETCDF3_64BIT: 64-bit offset version of the netCDF 3 file format, which fully supports 2+ GB files, but is only compatible with clients linked against netCDF version 3.6.0 or later.
  - NETCDF3_CLASSIC: The classic netCDF 3 file format. It does not handle 2+ GB files very well.

  All formats are supported by the netCDF4-python library. scipy.io.netcdf only supports the last two formats.

The default format is NETCDF4 if you are saving a file to disk and have the netCDF4-python library available. Otherwise, xarray falls back to using scipy to write netCDF files and defaults to the NETCDF3_64BIT format (scipy does not support netCDF4).

- **group** (*str, optional*) – Path to the netCDF4 group in the given file to open (only works for format='NETCDF4'). The group(s) will be created if necessary.
- **engine** (*{'netcdf4', 'scipy', 'h5netcdf'}, optional*) – Engine to use when writing netCDF files. If not provided, the default engine is chosen based on available dependencies, with a preference for 'netcdf4' if writing to a file on disk.
- **encoding** (*dict, optional*) – Nested dictionary with variable names as keys and dictionaries of variable specific encodings as values, e.g., ``{'my_variable': {'dtype': 'int16', 'scale_factor': 0.1,

  'zlib': True}, ...}``
- **unlimited_dims** (*sequence of str, optional*) – Dimension(s) that should be serialized as unlimited dimensions. By default, no dimensions are treated as unlimited dimensions. Note that unlimited_dims may also be set via `dataset.encoding['unlimited_dims']`.

Returns An ordered mapping from array names to dimensions and filename corresponding to the array

Return type OrderedDict

See also:

`from_dict()`

`arrays`
A list of all the `xarray.DataArray` instances in this list

`coords`
Names of the coordinates of the arrays in this list

`coords_intersect`
Coordinates of the arrays in this list that are used in all arrays

`copy`(*deep=False*)
Returns a copy of the list

Parameters deep (`bool`) – If False (default), only the list is copied and not the contained arrays, otherwise the contained arrays are deep copied

`dims`
Dimensions of the arrays in this list

`dims_intersect`
Dimensions of the arrays in this list that are used in all arrays

`draw`()
Draws all the figures in this instance

`extend`(*iterable*, *new_name=False*)
Add further arrays from an iterable to this list

Parameters

- **`iterable`** – Any iterable that contains `InteractiveBase` instances
- **`new_name`** (`bool or str`) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new

array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Raises

- `ValueError` – If it was impossible to find a name that isn't already in the list
- `ValueError` – If *new_name* is False and the array is already in the list

See also:

`list.extend()`, *`append()`*, *`rename()`*

`classmethod from_dataset`(*base*, *method='isel'*, *default_slice=None*, *decoder=None*, *auto_update=None*, *prefer_list=False*, *squeeze=True*, *attrs=None*, *load=False*, ***kwargs*)

Construct an ArrayList instance from an existing base dataset

Parameters

- **`base`** (*`xarray.Dataset`*) – Dataset instance that is used as reference
- **`method`** (*`{'isel', None, 'nearest', ..}`*) – Selection method of the xarray.Dataset to be used for setting the variables from the informations in *dims*. If *method* is 'isel', the `xarray.Dataset.isel()` method is used. Otherwise it sets the *method* parameter for the `xarray.Dataset.sel()` method.
- **`auto_update`** (*`bool`*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the *`update()`* method or not. See also the *`no_auto_update`* attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **`prefer_list`** (*`bool`*) – If True and multiple variable names pher array are found, the *`InteractiveList`* class is used. Otherwise the arrays are put together into one *`InteractiveArray`*.
- **`default_slice`** (*`indexer`*) – Index (e.g. 0 if *method* is 'isel') that shall be used for dimensions not covered by *dims* and *furtherdims*. If None, the whole slice will be used.
- **`decoder`** (`CFDecoder`) – The decoder that shall be used to decoder the *base* dataset
- **`squeeze`** (*`bool, optional`*) – Default True. If True, and the created arrays have a an axes with length 1, it is removed from the dimension list (e.g. an array with shape (3, 4, 1, 5) will be squeezed to shape (3, 4, 5))
- **`attrs`** (*`dict, optional`*) – Meta attributes that shall be assigned to the selected data arrays (additional to those stored in the *base* dataset)
- **`load`** (*`bool or dict`*) – If True, load the data from the dataset using the `xarray.DataArray.load()` method. If `dict`, those will be given to the above mentioned `load` method

Other Parameters

- **arr_names** (*string, list of strings or dictionary*) – Set the unique array names of the resulting arrays and (optionally) dimensions.
  - if string: same as list of strings (see below). Strings may include {0} which will be replaced by a counter.
  - list of strings: those will be used for the array names. The final number of dictionaries in the return depend in this case on the *dims* and `**furtherdims`

  - dictionary: Then nothing happens and an `OrderedDict` version of *arr_names* is returned.

- **sort** (*list of strings*) – This parameter defines how the dictionaries are ordered. It has no effect if *arr_names* is a dictionary (use a `OrderedDict` for that). It can be a list of dimension strings matching to the dimensions in *dims* for the variable.
- **dims** (*dict*) – Keys must be variable names of dimensions (e.g. time, level, lat or lon) or 'name' for the variable name you want to choose. Values must be values of that dimension or iterables of the values (e.g. lists). Note that strings will be put into a list. For example dims = {'name': 't2m', 'time': 0} will result in one plot for the first time step, whereas dims = {'name': 't2m', 'time': [0, 1]} will result in two plots, one for the first (time == 0) and one for the second (time == 1) time step.
- **‘‘**kwargs‘‘** – The same as *dims* (those will update what is specified in *dims*)

Returns The list with the specified `InteractiveArray` instances that hold a reference to the given *base*

Return type *ArrayList*

classmethod from_dict(*d, alternative_paths={}, datasets=None, pwd=None, ignore_keys=['attrs', 'plotter', 'ds'], only=None, chname={}, **kwargs*)

Create a list from the dictionary returned by `array_info()`

This classmethod creates an `ArrayList` instance from a dictionary containing filename, dimension infos and array names

Parameters

- **d** (`dict`) – The dictionary holding the data
- **alternative_paths** (`dict or list or str`) – A mapping from original filenames as used in *d* to filenames that shall be used instead. If *alternative_paths* is not None, datasets must be None. Paths must be accessible from the current working directory. If *alternative_paths* is a list (or any other iterable) is provided, the file names will be replaced as they appear in *d* (note that this is very unsafe if *d* is not and OrderedDict)
- **datasets** (`dict or list or None`) – A mapping from original filenames in *d* to the instances of `xarray.Dataset` to use. If it is an iterable, the same holds as for the *alternative_paths* parameter
- **pwd** (`str`) – Path to the working directory from where the data can be imported. If None, use the current working directory.
- **ignore_keys** (`list of str`) – Keys specified in this list are ignored and not seen as array information (note that `attrs` are used anyway)
- **only** (`string, list or callable`) – Can be one of the following three things:
  - a string that represents a pattern to match the array names that shall be included
  - a list of array names to include
  - a callable with two arguments, a string and a dict such as

```python
def filter_func(arr_name: str, info: dict): -> bool
    '''
    Filter the array names

    This function should return True if the array shall be
    included, else False

```

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```
    Parameters
    ----------
    arr_name: str
        The array name (i.e. the ``arr_name`` attribute)
    info: dict
        The dictionary with the array informations. Common
        keys are ``'name'`` that points to the variable name
        and ``'dims'`` that points to the dimensions and
        ``'fname'`` that points to the file name
    '''
    return True or False
```

The function should return `True` if the array shall be included, else `False`. This function will also be given to subsequents instances of `InteractiveList` objects that are contained in the returned value

- **chname** (`dict`) – A mapping from variable names in the project to variable names that should be used instead

Other Parameters

- **``**kwargs``** – Any other parameter from the *psyplot.data.open_dataset* function
- **filename_or_obj** (*str, Path, file or xarray.backends.*DataStore*) – Strings and Path objects are interpreted as a path to a netCDF file or an OpenDAP URL and opened with python-netCDF4, unless the filename ends with .gz, in which case the file is gunzipped and opened with scipy.io.netcdf (only netCDF3 supported). File-like objects are opened with scipy.io.netcdf (only netCDF3 supported).
- **group** (*str, optional*) – Path to the netCDF4 group in the given file to open (only works for netCDF4 files).
- **decode_cf** (*bool, optional*) – Whether to decode these variables, assuming they were saved according to CF conventions.
- **mask_and_scale** (*bool, optional*) – If True, replace array values equal to *_FillValue* with NA and scale values according to the formula *original_values * scale_factor + add_offset*, where *_FillValue*, *scale_factor* and *add_offset* are taken from variable attributes (if they exist). If the *_FillValue* or *missing_value* attribute contains multiple values a warning will be issued and all array values matching one of the multiple values will be replaced by NA.
- **decode_times** (*bool, optional*) – If True, decode times encoded in the standard NetCDF datetime format into datetime objects. Otherwise, leave them encoded as numbers.
- **autoclose** (*bool, optional*) – If True, automatically close files to avoid OS Error of too many files being open. However, this option doesn't work with streams, e.g., BytesIO.
- **concat_characters** (*bool, optional*) – If True, concatenate along the last dimension of character arrays to form string arrays. Dimensions will only be concatenated over (and removed) if they have no corresponding variable and if they are only used as the last dimension of character arrays.
- **decode_coords** (*bool, optional*) – If True, decode the 'coordinates' attribute to identify coordinates in the resulting dataset.
- **chunks** (*int or dict, optional*) – If chunks is provided, it used to load the new dataset into dask arrays. `chunks={}` loads the dataset with dask using a single chunk for all arrays.
- **lock** (*False, True or threading.Lock, optional*) – If chunks is provided, this argument is passed on to `dask.array.from_array()`. By default, a global lock is used when

reading data from netCDF files with the netcdf4 and h5netcdf engines to avoid issues with concurrent access when using dask's multithreaded backend.

- **cache** (*bool, optional*) – If True, cache data loaded from the underlying datastore in memory as NumPy arrays when accessed to avoid reading from the underlying data- store multiple times. Defaults to True unless you specify the *chunks* argument to use dask, in which case it defaults to False. Does not change the behavior of coordinates corresponding to dimensions, which always load their data from disk into a `pandas.Index`.
- **drop_variables** (*string or iterable, optional*) – A variable or list of variables to exclude from being parsed from the dataset. This may be useful to drop variables with problems or inconsistent values.
- **engine** (*{'netcdf4', 'scipy', 'pydap', 'h5netcdf', 'gdal'}, optional*) – Engine to use when reading netCDF files. If not provided, the default engine is chosen based on available dependencies, with a preference for 'netcdf4'.
- **gridfile** (*str*) – The path to a separate grid file or a xarray.Dataset instance which may store the coordinates used in *ds*

Returns The list with the interactive objects

Return type *psyplot.data.ArrayList*

See also:

`from_dataset()`, `array_info()`

`is_unstructured`
A boolean for each array whether it is unstructured or not

`logger`
`logging.Logger` of this instance

`names`
Set of the variable in this list

`next_available_name` (*fmt_str='arr{0}'*, *counter=None*)
Create a new array out of the given format string

Parameters

- **`format_str`** (`str`) – The base string to use. `'{0}'` will be replaced by a counter
- **`counter`** (`iterable`) – An iterable where the numbers should be drawn from. If None, `range(100)` is used

Returns A possible name that is not in the current project

Return type str

`no_auto_update`
`bool`. Boolean controlling whether the `start_update()` method is automatically called by the `update()` method

Examples

You can disable the automatic update via

```
>>> with data.no_auto_update:
...     data.update(time=1)
...     data.start_update()
```

To permanently disable the automatic update, simply set

```
>>> data.no_auto_update = True
>>> data.update(time=1)
>>> data.no_auto_update = False  # reenable automatical update
```

remove (*arr*)

Removes an array from the list

Parameters **arr** (str or *InteractiveBase*) – The array name or the data object in this list to remove

Raises ValueError – If no array with the specified array name is in the list

rename (*arr*, *new_name=True*)

Rename an array to find a name that isn't already in the list

Parameters

- **arr** (InteractiveBase) – A *InteractiveArray* or *InteractiveList* instance whose name shall be checked
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Returns

- *InteractiveBase* – *arr* with changed `arr_name` attribute
- *bool or None* – True, if the array has been renamed, False if not and None if the array is already in the list

Raises

- ValueError – If it was impossible to find a name that isn't already in the list
- ValueError – If *new_name* is False and the array is already in the list

start_update (*draw=None*)

Conduct the registered plot updates

This method starts the updates from what has been registered by the *update()* method. You can call this method if you did not set the *auto_update* parameter when calling the *update()* method to True and when the *no_auto_update* attribute is True.

Parameters **draw** (*bool or None*) – If True, all the figures of the arrays contained in this list will be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary

See also:

no_auto_update, *update()*

update (*method='isel'*, *dims={}*, *fmt={}*, *replot=False*, *auto_update=False*, *draw=None*, *force=False*, *todefault=False*, *enable_post=None*, ***kwargs*)

Update the coordinates and the plot

This method updates all arrays in this list with the given coordinate values and formatoptions.

Parameters

- **method** (*{'isel', None, 'nearest', ..}*) – Selection method of the xarray.Dataset to be used for setting the variables from the informations in *dims*. If *method* is 'isel', the `xarray.Dataset.isel()` method is used. Otherwise it sets the *method* parameter for the `xarray.Dataset.sel()` method.
- **dims** (*dict*) – Keys must be variable names of dimensions (e.g. time, level, lat or lon) or 'name' for the variable name you want to choose. Values must be values of that dimension or iterables of the values (e.g. lists). Note that strings will be put into a list. For example dims = {'name': 't2m', 'time': 0} will result in one plot for the first time step, whereas dims = {'name': 't2m', 'time': [0, 1]} will result in two plots, one for the first (time == 0) and one for the second (time == 1) time step.
- **replot** (*bool*) – Boolean that determines whether the data specific formatoptions shall be updated in any case or not. Note, if *dims* is not empty or any coordinate keyword is in `**kwargs`, this will be set to True automatically
- **fmt** (*dict*) – Keys may be any valid formatoption of the formatoptions in the `plotter`
- **force** (*str, list of str or bool*) – If formatoption key (i.e. string) or list of formatoption keys, thery are definitely updated whether they changed or not. If True, all the given formatoptions in this call of the are *update()* method are updated
- **todefault** (*bool*) – If True, all changed formatoptions (except the registered ones) are updated to their default value as stored in the *rc* attribute
- **auto_update** (*bool*) – Boolean determining whether or not the *start_update()* method is called after the end.
- **draw** (*bool or None*) – If True, all the figures of the arrays contained in this list will be drawn at the end. If None, it defaults to the *'auto_draw''* parameter in the `psyplot.rcParams` dictionary
- **enable_post** (*bool*) – If not None, enable (`True`) or disable (`False`) the *post* formatoption in the plotters
- ****kwargs** – Any other formatoption or dimension that shall be updated (additionally to those in *fmt* and *dims*)

Notes

If the *no_auto_update* attribute is True and the given *auto_update* parameter are is False, the update of the plots are registered and conducted at the next call of the *start_update()* method or the next call of this method (if the *auto_update* parameter is then True).

See also:

no_auto_update(), *start_update()*

with_plotter
The arrays in this instance that are visualized with a plotter

class `psyplot.data.`**CFDecoder**(*ds=None*, *x=None*, *y=None*, *z=None*, *t=None*)
Bases: `object`

Class that interpretes the coordinates and attributes accordings to cf-conventions **Methods**

can_decode(ds, var)	Class method to determine whether the object can be decoded by this decoder class.

Continued on next page

Table 30 – continued from previous page

correct_dims(var[, dims, remove])	Expands the dimensions to match the dims in the variable
decode_coords([gridfile, inplace])	Sets the coordinates and bounds in a dataset
decode_ds(ds, *args, **kwargs)	Static method to decode coordinates and time informations
get_decoder(ds, var)	Class method to get the right decoder class that can decode the
get_idims(arr[, coords])	Get the coordinates in the `ds` dataset as int or slice
get_plotbounds(coord[, kind, ignore_shape])	Get the bounds of a coordinate
get_t(var[, coords])	Get the time coordinate of a variable
get_tname(var[, coords])	Get the name of the t-dimension
get_triangles(var[, coords, convert_radian, . . .])	Get the triangles for the variable
get_variable_by_axis(var, axis[, coords])	Return the coordinate matching the specified axis
get_x(var[, coords])	Get the x-coordinate of a variable
get_xname(var[, coords])	Get the name of the x-dimension
get_y(var[, coords])	Get the y-coordinate of a variable
get_yname(var[, coords])	Get the name of the y-dimension
get_z(var[, coords])	Get the vertical (z-) coordinate of a variable
get_zname(var[, coords])	Get the name of the z-dimension
is_circumpolar(var)	Test if a variable is on a circumpolar grid
is_triangular(var)	Test if a variable is on a triangular grid
is_unstructured(*args, **kwargs)	Test if a variable is on an unstructered grid
register_decoder([pos])	Register a new decoder
standardize_dims(var[, dims])	Replace the coordinate names through x, y, z and t

Attributes

logger	`logging.Logger` of this instance

classmethod can_decode(*ds*, *var*)

Class method to determine whether the object can be decoded by this decoder class.

Parameters

- **ds** (*xarray.Dataset*) – The dataset that contains the given *var*
- **var** (*xarray.Variable or xarray.DataArray*) – The array to decode

Returns True if the decoder can decode the given array *var*. Otherwise False

Return type bool

Notes

The default implementation returns True for any argument. Subclass this method to be specific on what type of data your decoder can decode

correct_dims(*var*, *dims={}*, *remove=True*)

Expands the dimensions to match the dims in the variable

Parameters

- **var** (*xarray.Variable*) – The variable to get the data for
- **dims** (*dict*) – a mapping from dimension to the slices

- **remove** (*bool*) – If True, dimensions in *dims* that are not in the dimensions of *var* are removed

static decode_coords (*gridfile=None*, *inplace=True*)
Sets the coordinates and bounds in a dataset

This static method sets those coordinates and bounds that are marked marked in the netCDF attributes as coordinates in `ds` (without deleting them from the variable attributes because this information is necessary for visualizing the data correctly)

Parameters

- **ds** (*xarray.Dataset*) – The dataset to decode
- **gridfile** (*str*) – The path to a separate grid file or a xarray.Dataset instance which may store the coordinates used in *ds*
- **inplace** (*bool, optional*) – If True, *ds* is modified in place

Returns *ds* with additional coordinates

Return type xarray.Dataset

classmethod decode_ds (*ds*, **args*, ***kwargs*)
Static method to decode coordinates and time informations

This method interpretes absolute time informations (stored with units `'day as %Y%m%d.%f'`) and coordinates

Parameters

- **ds** (*xarray.Dataset*) – The dataset to decode
- **gridfile** (*str*) – The path to a separate grid file or a xarray.Dataset instance which may store the coordinates used in *ds*
- **inplace** (*bool, optional*) – If True, *ds* is modified in place
- **decode_times** (*bool, optional*) – If True, decode times encoded in the standard NetCDF datetime format into datetime objects. Otherwise, leave them encoded as numbers.
- **decode_coords** (*bool, optional*) – If True, decode the 'coordinates' attribute to identify coordinates in the resulting dataset.

Returns The decoded dataset

Return type xarray.Dataset

classmethod get_decoder (*ds*, *var*)
Class method to get the right decoder class that can decode the given dataset and variable

Parameters

- **ds** (*xarray.Dataset*) – The dataset that contains the given *var*
- **var** (*xarray.Variable or xarray.DataArray*) – The array to decode

Returns The decoder for the given dataset that can decode the variable *var*

Return type *CFDecoder*

get_idims (*arr*, *coords=None*)
Get the coordinates in the `ds` dataset as int or slice

This method returns a mapping from the coordinate names of the given *arr* to an integer, slice or an array of integer that represent the coordinates in the `ds` dataset and can be used to extract the given *arr* via the `xarray.Dataset.isel()` method.

Parameters **arr** (*xarray.DataArray*) – The data array for which to get the dimensions as integers, slices or list of integers from the dataset in the `base` attribute

Returns Mapping from coordinate name to integer, list of integer or slice

Return type dict

See also:

`xarray.Dataset.isel()`, *InteractiveArray.idims()*

get_plotbounds(*coord*, *kind=None*, *ignore_shape=False*)
Get the bounds of a coordinate

This method first checks the `'bounds'` attribute of the given *coord* and if it fails, it calculates them.

Parameters

- **coord** (*xarray.Coordinate*) – The coordinate to get the bounds for
- **kind** (*str*) – The interpolation method (see `scipy.interpolate.interp1d()`) that is used in case of a 2-dimensional coordinate
- **ignore_shape** (*bool*) – If True and the *coord* has a `'bounds'` attribute, this attribute is returned without further check. Otherwise it is tried to bring the `'bounds'` into a format suitable for (e.g.) the `matplotlib.pyplot.pcolormesh()` function.

Returns **bounds** – The bounds with the same number of dimensions as *coord* but one additional array (i.e. if *coord* has shape (4,), *bounds* will have shape (5,) and if *coord* has shape (4, 5), *bounds* will have shape (5, 6)

Return type np.ndarray

get_t(*var*, *coords=None*)
Get the time coordinate of a variable

This method searches for the time coordinate in the `ds`. It first checks whether there is one dimension that holds an `'axis'` attribute with 'T', otherwise it looks whether there is an intersection between the `t` attribute and the variables dimensions, otherwise it returns the coordinate corresponding to the first dimension of *var*

Possible types

- **var** (*xarray.Variable*) – The variable to get the time coordinate for
- **coords** (*dict*) – Coordinates to use. If None, the coordinates of the dataset in the `ds` attribute are used.

Returns The time coordinate or None if no time coordinate could be found

Return type xarray.Coordinate or None

get_tname(*var*, *coords=None*)
Get the name of the t-dimension

This method gives the name of the time dimension

Parameters

- **var** (*xarray.Variables*) – The variable to get the dimension for

- **coords** (*dict*) – The coordinates to use for checking the axis attribute. If None, they are not used

Returns The coordinate name or None if no time coordinate could be found

Return type str or None

See also:

get_t()

get_triangles(*var*, *coords=None*, *convert_radian=True*, *copy=False*, *src_crs=None*, *target_crs=None*, *nans=None*)

Get the triangles for the variable

Parameters

- **var** (*xarray.Variable or xarray.DataArray*) – The variable to use
- **coords** (*dict*) – Alternative coordinates to use. If None, the coordinates of the `ds` dataset are used
- **convert_radian** (*bool*) – If True and the coordinate has units in 'radian', those are converted to degrees
- **copy** (*bool*) – If True, vertice arrays are copied
- **src_crs** (*cartopy.crs.Crs*) – The source projection of the data. If not None, a transformation to the given *target_crs* will be done
- **target_crs** (*cartopy.crs.Crs*) – The target projection for which the triangles shall be transformed. Must only be provided if the *src_crs* is not None.
- **nans** (*{None, 'skip', 'only'}*) – Determines whether values with nan shall be left (None), skipped (`'skip'`) or shall be the only one returned (`'only'`)

Returns The spatial triangles of the variable

Return type matplotlib.tri.Triangulation

Raises `ValueError` – If *src_crs* is not None and *target_crs* is None

get_variable_by_axis(*var*, *axis*, *coords=None*)

Return the coordinate matching the specified axis

This method uses to `'axis'` attribute in coordinates to return the corresponding coordinate of the given variable

Possible types

- **var** (*xarray.Variable*) – The variable to get the dimension for
- **axis** (*{'x', 'y', 'z', 't'}*) – The axis string that identifies the dimension
- **coords** (*dict*) – Coordinates to use. If None, the coordinates of the dataset in the `ds` attribute are used.

Returns The coordinate for *var* that matches the given *axis* or None if no coordinate with the right *axis* could be found.

Return type xarray.Coordinate or None

Notes

This is a rather low-level function that only interpretes the CFConvention. It is used by the `get_x()`, `get_y()`, `get_z()` and `get_t()` methods

> **Warning:** If None of the coordinates have an `'axis'` attribute, we use the `'coordinate'` attribute of *var* (if existent). Since however the CF Conventions do not determine the order on how the coordinates shall be saved, we try to use a pattern matching for latitude (`'lat'`) and longitude (`lon'`). If this patterns do not match, we interpret the coordinates such that x: -1, y: -2, z: -3. This is all not very safe for awkward dimension names, but works for most cases. If you want to be a hundred percent sure, use the `x`, `y`, `z` and `t` attribute.

See also:

`get_x()`, `get_y()`, `get_z()`, `get_t()`

get_x(*var*, *coords=None*)
Get the x-coordinate of a variable

This method searches for the x-coordinate in the `ds`. It first checks whether there is one dimension that holds an `'axis'` attribute with 'X', otherwise it looks whether there is an intersection between the `x` attribute and the variables dimensions, otherwise it returns the coordinate corresponding to the last dimension of *var*

Possible types

- **var** (*xarray.Variable*) – The variable to get the x-coordinate for
- **coords** (*dict*) – Coordinates to use. If None, the coordinates of the dataset in the `ds` attribute are used.

Returns The y-coordinate or None if it could be found

Return type xarray.Coordinate or None

get_xname(*var*, *coords=None*)
Get the name of the x-dimension

This method gives the name of the x-dimension (which is not necessarily the name of the coordinate if the variable has a coordinate attribute)

Parameters

- **var** (`xarray.Variables`) – The variable to get the dimension for
- **coords** (`dict`) – The coordinates to use for checking the axis attribute. If None, they are not used

Returns The coordinate name

Return type str

See also:

`get_x()`

get_y(*var*, *coords=None*)
Get the y-coordinate of a variable

This method searches for the y-coordinate in the `ds`. It first checks whether there is one dimension that holds an `'axis'` attribute with 'Y', otherwise it looks whether there is an intersection between the `y` attribute and the variables dimensions, otherwise it returns the coordinate corresponding to the second last dimension of *var* (or the last if the dimension of var is one-dimensional)

Possible types

- **var** (*xarray.Variable*) – The variable to get the y-coordinate for
- **coords** (*dict*) – Coordinates to use. If None, the coordinates of the dataset in the `ds` attribute are used.

Returns The y-coordinate or None if it could be found

Return type xarray.Coordinate or None

`get_yname`(*var*, *coords=None*)

Get the name of the y-dimension

This method gives the name of the y-dimension (which is not necessarily the name of the coordinate if the variable has a coordinate attribute)

Parameters

- **`var`** (*`xarray.Variables`*) – The variable to get the dimension for
- **`coords`** (*`dict`*) – The coordinates to use for checking the axis attribute. If None, they are not used

Returns The coordinate name

Return type str

See also:

`get_y()`

`get_z`(*var*, *coords=None*)

Get the vertical (z-) coordinate of a variable

This method searches for the z-coordinate in the `ds`. It first checks whether there is one dimension that holds an `'axis'` attribute with 'Z', otherwise it looks whether there is an intersection between the `z` attribute and the variables dimensions, otherwise it returns the coordinate corresponding to the third last dimension of *var* (or the second last or last if var is two or one-dimensional)

Possible types

- **var** (*xarray.Variable*) – The variable to get the z-coordinate for
- **coords** (*dict*) – Coordinates to use. If None, the coordinates of the dataset in the `ds` attribute are used.

Returns The z-coordinate or None if no z coordinate could be found

Return type xarray.Coordinate or None

`get_zname`(*var*, *coords=None*)

Get the name of the z-dimension

This method gives the name of the z-dimension (which is not necessarily the name of the coordinate if the variable has a coordinate attribute)

Parameters

- **var** (*xarray.Variables*) – The variable to get the dimension for
- **coords** (*dict*) – The coordinates to use for checking the axis attribute. If None, they are not used

Returns The coordinate name or None if no vertical coordinate could be found

Return type str or None

See also:

get_z()

is_circumpolar(*var*)
Test if a variable is on a circumpolar grid

Parameters **var** (*xarray.Variable or xarray.DataArray*) – The variable to check

Returns True, if the grid is triangular, else False

Return type bool

is_triangular(*var*)
Test if a variable is on a triangular grid

This method first checks the *grid_type* attribute of the variable (if existent) whether it is equal to `"unstructered"`, then it checks whether the bounds are not two-dimensional.

Parameters **var** (*xarray.Variable or xarray.DataArray*) – The variable to check

Returns True, if the grid is triangular, else False

Return type bool

is_unstructured(**args*, ***kwargs*)
Test if a variable is on an unstructered grid

Parameters **var** (*xarray.Variable or xarray.DataArray*) – The variable to check

Returns True, if the grid is triangular, else False

Return type bool

Notes

Currently this is the same as *is_triangular()* method, but may change in the future to support hexagonal grids

logger
`logging.Logger` of this instance

static register_decoder(*pos=0*)
Register a new decoder

This function registeres a decoder class to use

Parameters

- **decoder_class** (*type*) – The class inherited from the *CFDecoder*
- **pos** (*int*) – The position where to register the decoder (by default: the first position

standardize_dims(*var*, *dims={}*)
Replace the coordinate names through x, y, z and t

Parameters

- **var** (*xarray.Variable*) – The variable to use the dimensions of
- **dims** (*dict*) – The dictionary to use for replacing the original dimensions

Returns The dictionary with replaced dimensions

Return type dict

class psyplot.data.**DatasetAccessor**(*ds*)

Bases: `object`

A dataset accessor to interface with the psyplot package **Methods**

copy([deep])	Copy the array
create_list(*args, **kwargs)	Create a *psyplot.data.ArrayList* with arrays from this dataset
to_array(*args, **kwargs)	Convert this dataset into an xarray.DataArray

Attributes

data_store	The `xarray.backends.common.AbstractStore` used to save the
filename	The name of the file that stores this dataset
num	A unique number for the dataset
plot	An object to generate new plots from this dataset

copy(*deep=False*)

Copy the array

This method returns a copy of the underlying array in the `arr` attribute. It is more stable because it creates a new *psy* accessor

create_list(**args*, ***kwargs*)

Create a *psyplot.data.ArrayList* with arrays from this dataset

Parameters

- **base** (*xarray.Dataset*) – Dataset instance that is used as reference
- **method** (*{'isel', None, 'nearest', ..}*) – Selection method of the xarray.Dataset to be used for setting the variables from the informations in *dims*. If *method* is 'isel', the `xarray.Dataset.isel()` method is used. Otherwise it sets the *method* parameter for the `xarray.Dataset.sel()` method.
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **prefer_list** (*bool*) – If True and multiple variable names pher array are found, the *InteractiveList* class is used. Otherwise the arrays are put together into one *InteractiveArray*.
- **default_slice** (*indexer*) – Index (e.g. 0 if *method* is 'isel') that shall be used for dimensions not covered by *dims* and *furtherdims*. If None, the whole slice will be used.
- **decoder** (*CFDecoder*) – The decoder that shall be used to decoder the *base* dataset

- **squeeze** (*bool, optional*) – Default True. If True, and the created arrays have a an axes with length 1, it is removed from the dimension list (e.g. an array with shape (3, 4, 1, 5) will be squeezed to shape (3, 4, 5))
- **attrs** (*dict, optional*) – Meta attributes that shall be assigned to the selected data arrays (additional to those stored in the *base* dataset)
- **load** (*bool or dict*) – If True, load the data from the dataset using the `xarray.DataArray.load()` method. If `dict`, those will be given to the above mentioned `load` method

Other Parameters

- **arr_names** (*string, list of strings or dictionary*) – Set the unique array names of the resulting arrays and (optionally) dimensions.
  - if string: same as list of strings (see below). Strings may include {0} which will be replaced by a counter.
  - list of strings: those will be used for the array names. The final number of dictionaries in the return depend in this case on the *dims* and `**furtherdims`
  - dictionary: Then nothing happens and an `OrderedDict` version of *arr_names* is returned.
- **sort** (*list of strings*) – This parameter defines how the dictionaries are ordered. It has no effect if *arr_names* is a dictionary (use a `OrderedDict` for that). It can be a list of dimension strings matching to the dimensions in *dims* for the variable.
- **dims** (*dict*) – Keys must be variable names of dimensions (e.g. time, level, lat or lon) or 'name' for the variable name you want to choose. Values must be values of that dimension or iterables of the values (e.g. lists). Note that strings will be put into a list. For example dims = {'name': 't2m', 'time': 0} will result in one plot for the first time step, whereas dims = {'name': 't2m', 'time': [0, 1]} will result in two plots, one for the first (time == 0) and one for the second (time == 1) time step.
- **``**kwargs``** – The same as *dims* (those will update what is specified in *dims*)

Returns The list with the specified *`InteractiveArray`* instances that hold a reference to the given *base*

Return type *ArrayList*

See also:

`psyplot.data.ArrayList.from_dataset()`

`data_store`
The `xarray.backends.common.AbstractStore` used to save the dataset

`filename`
The name of the file that stores this dataset

`num`
A unique number for the dataset

`plot`
An object to generate new plots from this dataset

To make a 2D-plot with the `psy-simple` plugin, you can just type

```
project = ds.psy.plot.plot2d(name='variable-name')
```

It will create a new subproject with the extracted and visualized data.

See also:

`psyplot.project.DatasetPlotter` for the different plot methods

to_array (**args*, ***kwargs*)

Convert this dataset into an xarray.DataArray

The data variables of this dataset will be broadcast against each other and stacked along the first axis of the new array. All coordinates of this dataset will remain coordinates.

Parameters

- **dim** (`str, optional`) – Name of the new dimension.
- **name** (`str, optional`) – Name of the new data array.

Returns array

Return type xarray.DataArray

class psyplot.data.**InteractiveArray** (*xarray_obj*, **args*, ***kwargs*)

Bases: `psyplot.data.InteractiveBase`

Interactive psyplot accessor for the data array

This class keeps reference to the base `xarray.Dataset` where the `array.DataArray` originates from and enables to switch between the coordinates in the array. Furthermore it has a `plotter` attribute to enable interactive plotting via an `psyplot.plotter.Plotter` instance.

The `*args` and `**kwargs` are essentially the same as for the `xarray.DataArray` method, additional `**kwargs` are described below.

Other Parameters

- **base** (*xarray.Dataset*) – Default: None. Dataset that serves as the origin of the data contained in this DataArray instance. This will be used if you want to update the coordinates via the `update()` method. If None, this instance will serve as a base as soon as it is needed.
- **decoder** (*psyplot.CFDecoder*) – The decoder that decodes the *base* dataset and is used to get bounds. If not given, a new `CFDecoder` is created
- **idims** (*dict*) – Default: None. dictionary with integer values and/or slices in the *base* dictionary. If not given, they are determined automatically
- **plotter** (*Plotter*) – Default: None. Interactive plotter that makes the plot via formatoption keywords.
- **arr_name** (*str*) – Default: `'data'`. unique string of the array
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.

Attributes

`base`	Base dataset this instance gets its data from
`base_variables`	A mapping from the variable name to the variablein the `base` dataset.
`decoder`	The decoder of this array

Continued on next page

Table 34 – continued from previous page

`idims`	Coordinates in the `base` dataset as int or slice
`iter_base_variables`	An iterator over the base variables in the `base` dataset
`logger`	`logging.Logger` of this instance
`onbasechange`	`Signal` to be emiited when the base of the object changes

Methods

`copy`([deep])	Copy the array
`fldmean`([keepdims])	Calculate the weighted mean over the x- and y-dimension
`fldpctl`(q[, keepdims])	Calculate the percentiles along the x- and y-dimensions
`fldstd`([keepdims])	Calculate the weighted standard deviation over x- and y-dimension
`get_coord`(what[, base])	The x-coordinate of this data array
`get_dim`(what[, base])	The name of the x-dimension of this data array
`gridweights`([keepdims, keepshape, use_cdo])	Calculate the cell weights for each grid cell
`init_accessor`([base, idims, decoder])	Initialize the accessor instance
`isel`(*args, **kwargs)	Return a new DataArray whose dataset is given by integer indexing along the specified dimension(s).
`sel`(*args, **kwargs)	Return a new DataArray whose dataset is given by selecting index labels along the specified dimension(s).
`start_update`([draw, queues])	Conduct the formerly registered updates
`to_interactive_list`()	Return a `InteractiveList` that contains this object
`update`([method, dims, fmt, replot, . . .])	Update the coordinates and the plot

base
Base dataset this instance gets its data from

base_variables
A mapping from the variable name to the variablein the `base` dataset.

copy(*deep=False*)
Copy the array

This method returns a copy of the underlying array in the `arr` attribute. It is more stable because it creates a new *psy* accessor

decoder
The decoder of this array

fldmean(*keepdims=False*)
Calculate the weighted mean over the x- and y-dimension

This method calculates the weighted mean of the spatial dimensions. Weights are calculated using the `gridweights()` method, missing values are ignored. x- and y-dimensions are identified using the `decoder`s :meth:`~CFDecoder.get_xname` and `get_yname()` methods.

Parameters **keepdims** (`bool`) – If True, the dimensionality of this array is maintained

Returns The computed fldmeans. The dimensions are the same as in this array, only the spatial dimensions are omitted if *keepdims* is False.

Return type xr.DataArray

See also:

fldstd() For calculating the weighted standard deviation

fldpctl() For calculating weighted percentiles

fldpctl(*q*, *keepdims=False*)
Calculate the percentiles along the x- and y-dimensions

This method calculates the specified percentiles along the given dimension. Percentiles are weighted by the *gridweights()* method and missing values are ignored. x- and y-dimensions are estimated through the `decoder`s :meth:`~CFDecoder.get_xname` and *get_yname()* methods

Parameters

- **q** (*float or list of floats between 0 and 100*) – The quantiles to estimate
- **keepdims** (*bool*) – If True, the number of dimensions of the array are maintained

Returns The data array with the dimensions. If *q* is a list or *keepdims* is True, the first dimension will be the percentile `'pctl'`. The other dimensions are the same as in this array, only the spatial dimensions are omitted if *keepdims* is False.

Return type xr.DataArray

See also:

fldstd() For calculating the weighted standard deviation

fldmean() For calculating the weighted mean

Warning: This method does load the entire array into memory! So take care if you handle big data.

fldstd(*keepdims=False*)
Calculate the weighted standard deviation over x- and y-dimension

This method calculates the weighted standard deviation of the spatial dimensions. Weights are calculated using the *gridweights()* method, missing values are ignored. x- and y-dimensions are identified using the `decoder`s :meth:`~CFDecoder.get_xname` and *get_yname()* methods.

Parameters **keepdims** (*bool*) – If True, the dimensionality of this array is maintained

Returns The computed standard deviations. The dimensions are the same as in this array, only the spatial dimensions are omitted if *keepdims* is False.

Return type xr.DataArray

See also:

fldmean() For calculating the weighted mean

fldpctl() For calculating weighted percentiles

get_coord(*what*, *base=False*)
The x-coordinate of this data array

Parameters

- **what** (*{'t', 'x', 'y', 'z'}*) – The letter of the axis
- **base** (*bool*) – If True, use the base variable in the `base` dataset.

get_dim(*what*, *base=False*)

The name of the x-dimension of this data array

Parameters

- **what** (*{'t', 'x', 'y', 'z'}*) – The letter of the axis
- **base** (*bool*) – If True, use the base variable in the *base* dataset.

gridweights(*keepdims=False*, *keepshape=False*, *use_cdo=None*)

Calculate the cell weights for each grid cell

Parameters

- **keepdims** (*bool*) – If True, keep the number of dimensions
- **keepshape** (*bool*) – If True, keep the exact shape as the source array and the missing values in the array are masked
- **use_cdo** (*bool or None*) – If True, use Climate Data Operators (CDOs) to calculate the weights. Note that this is used automatically for unstructured grids. If None, it depends on the `'gridweights.use_cdo'` item in the `psyplot.rcParams`.

Returns The 2D-DataArray with the grid weights

Return type xarray.DataArray

idims

Coordinates in the *base* dataset as int or slice

This attribute holds a mapping from the coordinate names of this array to an integer, slice or an array of integer that represent the coordinates in the *base* dataset

init_accessor(*base=None*, *idims=None*, *decoder=None*, **args*, ***kwargs*)

Initialize the accessor instance

This method initializes the accessor

Parameters

- **base** (*xr.Dataset*) – The base dataset for the data
- **idims** (*dict*) – A mapping from dimension name to indices. If not provided, it is calculated when the *idims* attribute is accessed
- **decoder** (`CFDecoder`) – The decoder of this object
- **%(InteractiveBase.parameters)s** –

isel(**args*, ***kwargs*)

Return a new DataArray whose dataset is given by integer indexing along the specified dimension(s).

See also:

`Dataset.isel()`, `DataArray.sel()`

iter_base_variables

An iterator over the base variables in the *base* dataset

logger

`logging.Logger` of this instance

onbasechange

Signal to be emiited when the base of the object changes

sel(**args*, ***kwargs*)
Return a new DataArray whose dataset is given by selecting index labels along the specified dimension(s).

See also:

`Dataset.sel()`, `DataArray.isel()`

start_update(*draw=None*, *queues=None*)
Conduct the formerly registered updates

This method conducts the updates that have been registered via the `update()` method. You can call this method if the `no_auto_update` attribute of this instance is True and the *auto_update* parameter in the `update()` method has been set to False

Parameters

- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'`* parameter in the `psyplot.rcParams` dictionary
- **queues** (list of `Queue.Queue` instances) – The queues that are passed to the `psyplot.plotter.Plotter.start_update()` method to ensure a thread-safe update. It can be None if only one single plotter is updated at the same time. The number of jobs that are taken from the queue is determined by the `_njobs()` attribute. Note that there this parameter is automatically configured when updating from a `Project`.

Returns A boolean indicating whether a redrawing is necessary or not

Return type bool

See also:

`no_auto_update`, `update()`

to_interactive_list()
Return a `InteractiveList` that contains this object

update(*method='isel'*, *dims={}*, *fmt={}*, *replot=False*, *auto_update=False*, *draw=None*, *force=False*, *todefault=False*, ***kwargs*)
Update the coordinates and the plot

This method updates all arrays in this list with the given coordinate values and formatoptions.

Parameters

- **method** (*{'isel', None, 'nearest', ..}*) – Selection method of the xarray.Dataset to be used for setting the variables from the informations in *dims*. If *method* is 'isel', the `xarray.Dataset.isel()` method is used. Otherwise it sets the *method* parameter for the `xarray.Dataset.sel()` method.
- **dims** (*dict*) – Keys must be variable names of dimensions (e.g. time, level, lat or lon) or 'name' for the variable name you want to choose. Values must be values of that dimension or iterables of the values (e.g. lists). Note that strings will be put into a list. For example dims = {'name': 't2m', 'time': 0} will result in one plot for the first time step, whereas dims = {'name': 't2m', 'time': [0, 1]} will result in two plots, one for the first (time == 0) and one for the second (time == 1) time step.
- **replot** (*bool*) – Boolean that determines whether the data specific formatoptions shall be updated in any case or not. Note, if *dims* is not empty or any coordinate keyword is in `**kwargs`, this will be set to True automatically
- **fmt** (*dict*) – Keys may be any valid formatoption of the formatoptions in the `plotter`

- **force** (*str, list of str or bool*) – If formatoption key (i.e. string) or list of formatoption keys, thery are definitely updated whether they changed or not. If True, all the given formatoptions in this call of the are `update()` method are updated
- **todefault** (*bool*) – If True, all changed formatoptions (except the registered ones) are updated to their default value as stored in the `rc` attribute
- **auto_update** (*bool*) – Boolean determining whether or not the `start_update()` method is called after the end.
- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **queues** (list of `Queue.Queue` instances) – The queues that are passed to the `psyplot.plotter.Plotter.start_update()` method to ensure a thread-safe update. It can be None if only one single plotter is updated at the same time. The number of jobs that are taken from the queue is determined by the `_njobs()` attribute. Note that there this parameter is automatically configured when updating from a `Project`.
- ****kwargs** – Any other formatoption or dimension that shall be updated (additionally to those in *fmt* and *dims*)

Notes

If the `no_auto_update` attribute is True and the given *auto_update* parameter are is False, the update of the plots are registered and conducted at the next call of the `start_update()` method or the next call of this method (if the *auto_update* parameter is then True).

class psyplot.data.**InteractiveBase**(*plotter=None*, *arr_name='arr0'*, *auto_update=None*)
Bases: `object`

Class for the communication of a data object with a suitable plotter

This class serves as an interface for data objects (in particular as a base for `InteractiveArray` and `InteractiveList`) to communicate with the corresponding `Plotter` in the `plotter` attribute

Parameters

- **plotter** (`Plotter`) – Default: None. Interactive plotter that makes the plot via formatoption keywords.
- **arr_name** (*str*) – Default: `'data'`. unique string of the array
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.

Attributes

`arr_name`	`str`. The internal name of the `InteractiveBase`
`ax`	The matplotlib axes the plotter of this data object plots on
`block_signals`	Block the emitting of signals of this instance
`logger`	`logging.Logger` of this instance
`no_auto_update`	`bool`. Boolean controlling whether the `start_update()`

Continued on next page

Table 36 – continued from previous page

onupdate	Signal to be emitted when the object has been updated
plot	An object to visualize this data object
plotter	psyplot.plotter.Plotter instance that makes the interactive

Methods

start_update([draw, queues])	Conduct the formerly registered updates
to_interactive_list()	Return a InteractiveList that contains this object
update([fmt, replot, draw, auto_update, . . .])	Update the coordinates and the plot

arr_name
str. The internal name of the InteractiveBase

ax
The matplotlib axes the plotter of this data object plots on

block_signals
Block the emitting of signals of this instance

logger
logging.Logger of this instance

no_auto_update
bool. Boolean controlling whether the start_update() method is automatically called by the update() method

Examples

You can disable the automatic update via

```
>>> with data.no_auto_update:
...     data.update(time=1)
...     data.start_update()
```

To permanently disable the automatic update, simply set

```
>>> data.no_auto_update = True
>>> data.update(time=1)
>>> data.no_auto_update = False  # reenable automatical update
```

onupdate
Signal to be emitted when the object has been updated

plot
An object to visualize this data object

To make a 2D-plot with the psy-simple plugin, you can just type

```
plotter = da.psy.plot.plot2d()
```

It will create a new psyplot.plotter.Plotter instance with the extracted and visualized data.

See also:

`psyplot.project.DataArrayPlotter` for the different plot methods

plotter
`psyplot.plotter.Plotter` instance that makes the interactive plotting of the data

start_update (*draw=None*, *queues=None*)
Conduct the formerly registered updates

This method conducts the updates that have been registered via the `update()` method. You can call this method if the `no_auto_update` attribute of this instance and the *auto_update* parameter in the `update()` method has been set to False

Parameters

- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **queues** (list of `Queue.Queue` instances) – The queues that are passed to the `psyplot.plotter.Plotter.start_update()` method to ensure a thread-safe update. It can be None if only one single plotter is updated at the same time. The number of jobs that are taken from the queue is determined by the `_njobs()` attribute. Note that there this parameter is automatically configured when updating from a `Project`.

Returns A boolean indicating whether a redrawing is necessary or not

Return type bool

See also:

`no_auto_update`, `update()`

to_interactive_list ()
Return a `InteractiveList` that contains this object

update (*fmt={}*, *replot=False*, *draw=None*, *auto_update=False*, *force=False*, *todefault=False*, ***kwargs*)
Update the coordinates and the plot

This method updates all arrays in this list with the given coordinate values and formatoptions.

Parameters

- **replot** (*bool*) – Boolean that determines whether the data specific formatoptions shall be updated in any case or not. Note, if *dims* is not empty or any coordinate keyword is in `**kwargs`, this will be set to True automatically
- **fmt** (*dict*) – Keys may be any valid formatoption of the formatoptions in the `plotter`
- **force** (*str, list of str or bool*) – If formatoption key (i.e. string) or list of formatoption keys, thery are definitely updated whether they changed or not. If True, all the given formatoptions in this call of the are `update()` method are updated
- **todefault** (*bool*) – If True, all changed formatoptions (except the registered ones) are updated to their default value as stored in the `rc` attribute
- **auto_update** (*bool*) – Boolean determining whether or not the `start_update()` method is called at the end. This parameter has no effect if the `no_auto_update` attribute is set to `True`.
- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary

- **`**kwargs`** – Any other formatoption that shall be updated (additionally to those in *fmt*)

Notes

If the `no_auto_update` attribute is True and the given *auto_update* parameter are is False, the update of the plots are registered and conducted at the next call of the `start_update()` method or the next call of this method (if the *auto_update* parameter is then True).

class psyplot.data.**InteractiveList**(**args*, ***kwargs*)

Bases: `psyplot.data.ArrayList`, `psyplot.data.InteractiveBase`

List of `InteractiveArray` instances that can be plotted itself

This class combines the `ArrayList` and the interactive plotting through `psyplot.plotter.Plotter` classes. It is mainly used by the `psyplot.plotter.simple` module

Parameters

- **iterable** (*iterable*) – The iterable (e.g. another list) defining this list
- **attrs** (*dict-like or iterable, optional*) – Global attributes of this list
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter
- **plotter** (*Plotter*) – Default: None. Interactive plotter that makes the plot via formatoption keywords.
- **arr_name** (*str*) – Default: `'data'`. unique string of the array

Methods

`append`(*args, **kwargs)	Append a new array to the list
`extend`(*args, **kwargs)	Add further arrays from an iterable to this list
`from_dataset`(*args, **kwargs)	Create an InteractiveList instance from the given base dataset
`start_update`([draw, queues])	Conduct the formerly registered updates
`to_dataframe`()	
`to_interactive_list`()	Return a `InteractiveList` that contains this object

Attributes

`logger`	`logging.Logger` of this instance
`no_auto_update`	`bool`. Boolean controlling whether the `start_update()`
`psy`	Return the list itself

append(**args*, ***kwargs*)

Append a new array to the list

Parameters

- **value** (`InteractiveBase`) – The data object to append to this list
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Raises

- `ValueError` – If it was impossible to find a name that isn't already in the list
- `ValueError` – If *new_name* is False and the array is already in the list

See also:

`list.append()`, *`extend()`*, `rename()`

`extend`(**args*, ***kwargs*)
Add further arrays from an iterable to this list

Parameters

- **iterable** – Any iterable that contains *`InteractiveBase`* instances
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Raises

- `ValueError` – If it was impossible to find a name that isn't already in the list
- `ValueError` – If *new_name* is False and the array is already in the list

See also:

`list.extend()`, *`append()`*, `rename()`

`classmethod from_dataset`(**args*, ***kwargs*)
Create an InteractiveList instance from the given base dataset

Parameters

- **base** (*xarray.Dataset*) – Dataset instance that is used as reference
- **method** (*{'isel', None, 'nearest', ..}*) – Selection method of the xarray.Dataset to be used for setting the variables from the informations in *dims*. If *method* is 'isel', the `xarray.Dataset.isel()` method is used. Otherwise it sets the *method* parameter for the `xarray.Dataset.sel()` method.
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the *`no_auto_update`* attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **prefer_list** (*bool*) – If True and multiple variable names pher array are found, the *`InteractiveList`* class is used. Otherwise the arrays are put together into one *`InteractiveArray`*.

- **`default_slice`** (*`indexer`*) – Index (e.g. 0 if *method* is 'isel') that shall be used for dimensions not covered by *dims* and *furtherdims*. If None, the whole slice will be used.
- **`decoder`** (`CFDecoder`) – The decoder that shall be used to decoder the *base* dataset
- **`squeeze`** (*`bool, optional`*) – Default True. If True, and the created arrays have a an axes with length 1, it is removed from the dimension list (e.g. an array with shape (3, 4, 1, 5) will be squeezed to shape (3, 4, 5))
- **`attrs`** (*`dict, optional`*) – Meta attributes that shall be assigned to the selected data arrays (additional to those stored in the *base* dataset)
- **`load`** (*`bool or dict`*) – If True, load the data from the dataset using the `xarray.DataArray.load()` method. If `dict`, those will be given to the above mentioned `load` method
- **`plotter`** (`psyplot.plotter.Plotter`) – The plotter instance that is used to visualize the data in this list
- **`make_plot`** (*`bool`*) – If True, the plot is made

Other Parameters

- **arr_names** (*string, list of strings or dictionary*) – Set the unique array names of the resulting arrays and (optionally) dimensions.
  - if string: same as list of strings (see below). Strings may include {0} which will be replaced by a counter.
  - list of strings: those will be used for the array names. The final number of dictionaries in the return depend in this case on the *dims* and `**furtherdims`
  - dictionary: Then nothing happens and an `OrderedDict` version of *arr_names* is returned.
- **sort** (*list of strings*) – This parameter defines how the dictionaries are ordered. It has no effect if *arr_names* is a dictionary (use a `OrderedDict` for that). It can be a list of dimension strings matching to the dimensions in *dims* for the variable.
- **dims** (*dict*) – Keys must be variable names of dimensions (e.g. time, level, lat or lon) or 'name' for the variable name you want to choose. Values must be values of that dimension or iterables of the values (e.g. lists). Note that strings will be put into a list. For example dims = {'name': 't2m', 'time': 0} will result in one plot for the first time step, whereas dims = {'name': 't2m', 'time': [0, 1]} will result in two plots, one for the first (time == 0) and one for the second (time == 1) time step.
- **``**kwargs``** – Further keyword arguments may point to any of the dimensions of the data (see *dims*)

Returns The list with the specified *`InteractiveArray`* instances that hold a reference to the given *base*

Return type *ArrayList*

`logger`
`logging.Logger` of this instance

`no_auto_update`
`bool`. Boolean controlling whether the *`start_update()`* method is automatically called by the `update()` method

Examples

You can disable the automatic update via

```
>>> with data.no_auto_update:
...     data.update(time=1)
...     data.start_update()
```

To permanently disable the automatic update, simply set

```
>>> data.no_auto_update = True
>>> data.update(time=1)
>>> data.no_auto_update = False  # reenable automatical update
```

---

psy
Return the list itself

start_update (*draw=None*, *queues=None*)
Conduct the formerly registered updates

This method conducts the updates that have been registered via the `update()` method. You can call this method if the `auto_update` attribute of this instance is True and the *auto_update* parameter in the `update()` method has been set to False

Parameters

- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **queues** (list of `Queue.Queue` instances) – The queues that are passed to the `psyplot.plotter.Plotter.start_update()` method to ensure a thread-safe update. It can be None if only one single plotter is updated at the same time. The number of jobs that are taken from the queue is determined by the `_njobs()` attribute. Note that there this parameter is automatically configured when updating from a `Project`.

Returns A boolean indicating whether a redrawing is necessary or not

Return type bool

See also:

`no_auto_update`, `update()`

to_dataframe ()

to_interactive_list ()
Return a `InteractiveList` that contains this object

class psyplot.data.**Signal** (*name=None*, *cls_signal=False*)
Bases: `object`

Signal to connect functions to a specific event

This class behaves almost similar to PyQt's `PyQt4.QtCore.pyqtBoundSignal` **Methods**

`connect`(func)	
`disconnect`([func])	Disconnect a function call to the signal.
`emit`(*args, **kwargs)	

connect (*func*)

disconnect (*func=None*)

Disconnect a function call to the signal. If None, all connections are disconnected

emit (**args*, ***kwargs*)

instance = None

owner = None

class psyplot.data.**UGridDecoder** (*ds=None*, *x=None*, *y=None*, *z=None*, *t=None*)

Bases: `psyplot.data.CFDecoder`

Decoder for UGrid data sets

Warning: Currently only triangles are supported.

Methods

`can_decode`(ds, var)	Check whether the given variable can be decoded.
`decode_coords`([gridfile, inplace])	Reimplemented to set the mesh variables as coordinates
`get_mesh`(var[, coords])	Get the mesh variable for the given *var*
`get_nodes`(coord, coords)	Get the variables containing the definition of the nodes
`get_triangles`(var[, coords, convert_radian, . . .])	Get the of the given coordinate.
`get_x`(var[, coords])	Get the centers of the triangles in the x-dimension
`get_y`(var[, coords])	Get the centers of the triangles in the y-dimension
`is_triangular`(*args, **kwargs)	Reimpletemented to return always True.

classmethod can_decode (*ds*, *var*)

Check whether the given variable can be decoded.

Returns True if a mesh coordinate could be found via the `get_mesh()` method

Parameters **%s** –

Returns

Return type %s

static decode_coords (*gridfile=None*, *inplace=True*)

Reimplemented to set the mesh variables as coordinates

Parameters

- **ds** (`xarray.Dataset`) – The dataset to decode
- **gridfile** (`str`) – The path to a separate grid file or a xarray.Dataset instance which may store the coordinates used in *ds*
- **inplace** (`bool, optional`) – If True, *ds* is modified in place

Returns *ds* with additional coordinates

Return type xarray.Dataset

get_mesh (*var*, *coords=None*)

Get the mesh variable for the given *var*

Parameters

- **var** (`xarray.Variable`) – The data source whith the `'mesh'` attribute
- **coords** (`dict`) – The coordinates to use. If None, the coordinates of the dataset of this decoder is used

Returns The mesh coordinate

Return type xarray.Coordinate

get_nodes(*coord*, *coords*)
Get the variables containing the definition of the nodes

Parameters

- **coord** (*xarray.Coordinate*) – The mesh variable
- **coords** (*dict*) – The coordinates to use to get node coordinates

get_triangles(*var*, *coords=None*, *convert_radian=True*, *copy=False*, *src_crs=None*, *target_crs=None*, *nans=None*)
Get the of the given coordinate.

Parameters

- **var** (*xarray.Variable or xarray.DataArray*) – The variable to use
- **coords** (*dict*) – Alternative coordinates to use. If None, the coordinates of the `ds` dataset are used
- **convert_radian** (*bool*) – If True and the coordinate has units in 'radian', those are converted to degrees
- **copy** (*bool*) – If True, vertice arrays are copied
- **src_crs** (*cartopy.crs.Crs*) – The source projection of the data. If not None, a transformation to the given *target_crs* will be done
- **target_crs** (*cartopy.crs.Crs*) – The target projection for which the triangles shall be transformed. Must only be provided if the *src_crs* is not None.
- **nans** (*{None, 'skip', 'only'}*) – Determines whether values with nan shall be left (None), skipped (`'skip'`) or shall be the only one returned (`'only'`)

Returns The spatial triangles of the variable

Return type matplotlib.tri.Triangulation

Notes

If the `'location'` attribute is set to `'node'`, a delaunay triangulation is performed using the `matplotlib.tri.Triangulation` class.

Todo: Implement the visualization for UGrid data shown on the edge of the triangles

get_x(*var*, *coords=None*)
Get the centers of the triangles in the x-dimension

Returns The y-coordinate or None if it could be found

Return type xarray.Coordinate or None

get_y(*var*, *coords=None*)
Get the centers of the triangles in the y-dimension

Returns The y-coordinate or None if it could be found

Return type xarray.Coordinate or None

is_triangular(**args*, ***kwargs*)
Reimpletemented to return always True. Any `*args` and `**kwargs` are ignored

psyplot.data.**decode_absolute_time**(*times*)

psyplot.data.**encode_absolute_time**(*times*)

psyplot.data.**get_filename_ds**(*ds*, *dump=True*, *paths=None*, ***kwargs*)
Return the filename of the corresponding to a dataset

This method returns the path to the *ds* or saves the dataset if there exists no filename

Parameters

- **ds** (`xarray.Dataset`) – The dataset you want the path information for
- **dump** (`bool`) – If True and the dataset has not been dumped so far, it is dumped to a temporary file or the one generated by *paths* is used
- **paths** (`iterable or True`) – An iterator over filenames to use if a dataset has no filename. If paths is `True`, an iterator over temporary files will be created without raising a warning

Other Parameters

- **``**kwargs``** – Any other keyword for the `to_netcdf()` function
- **path** (*str, Path or file-like object, optional*) – Path to which to save this dataset. File-like objects are only supported by the scipy engine. If no path is provided, this function returns the resulting netCDF file as bytes; in this case, we need to use scipy, which does not support netCDF version 4 (the default format becomes NETCDF3_64BIT).
- **mode** (*{'w', 'a'}, optional*) – Write ('w') or append ('a') mode. If mode='w', any existing file at this location will be overwritten. If mode='a', existing variables will be overwritten.
- **format** (*{'NETCDF4', 'NETCDF4_CLASSIC', 'NETCDF3_64BIT','NETCDF3_CLASSIC'}, optional*) – File format for the resulting netCDF file:
  - NETCDF4: Data is stored in an HDF5 file, using netCDF4 API features.
  - NETCDF4_CLASSIC: Data is stored in an HDF5 file, using only netCDF 3 compatible API features.
  - NETCDF3_64BIT: 64-bit offset version of the netCDF 3 file format, which fully supports 2+ GB files, but is only compatible with clients linked against netCDF version 3.6.0 or later.
  - NETCDF3_CLASSIC: The classic netCDF 3 file format. It does not handle 2+ GB files very well.

  All formats are supported by the netCDF4-python library. scipy.io.netcdf only supports the last two formats.

  The default format is NETCDF4 if you are saving a file to disk and have the netCDF4-python library available. Otherwise, xarray falls back to using scipy to write netCDF files and defaults to the NETCDF3_64BIT format (scipy does not support netCDF4).
- **group** (*str, optional*) – Path to the netCDF4 group in the given file to open (only works for format='NETCDF4'). The group(s) will be created if necessary.
- **engine** (*{'netcdf4', 'scipy', 'h5netcdf'}, optional*) – Engine to use when writing netCDF files. If not provided, the default engine is chosen based on available dependencies, with a preference for 'netcdf4' if writing to a file on disk.

- **encoding** (*dict, optional*) – Nested dictionary with variable names as keys and dictionaries of variable specific encodings as values, e.g., ``{'my_variable': {'dtype': 'int16', 'scale_factor': 0.1,

  'zlib': True}, ...}``
- **unlimited_dims** (*sequence of str, optional*) – Dimension(s) that should be serialized as unlimited dimensions. By default, no dimensions are treated as unlimited dimensions. Note that unlimited_dims may also be set via `dataset.encoding['unlimited_dims']`.

Returns

- *str or None* – None, if the dataset has not yet been dumped to the harddisk and *dump* is False, otherwise the complete the path to the input file
- *str* – The module of the `xarray.backends.common.AbstractDataStore` instance that is used to hold the data
- *str* – The class name of the `xarray.backends.common.AbstractDataStore` instance that is used to open the data

`psyplot.data.`**`get_fname_funcs = [<function _get_fname_netCDF4>, <function _get_fname_scipy>,`**

functions to use to extract the file name from a data store

`psyplot.data.`**`get_index_from_coord`**`(`*coord*, *base_index*`)`

Function to return the coordinate as integer, integer array or slice

If *coord* is zero-dimensional, the corresponding integer in *base_index* will be supplied. Otherwise it is first tried to return a slice, if that does not work an integer array with the corresponding indices is returned.

Parameters

- **`coord`** (*`xarray.Coordinate or xarray.Variable`*) – Coordinate to convert
- **`base_index`** (*`pandas.Index`*) – The base index from which the *coord* was extracted

Returns The indexer that can be used to access the *coord* in the *base_index*

Return type int, array of ints or slice

`psyplot.data.`**`get_tdata`**`(`*t_format*, *files*`)`

Get the time information from file names

Parameters

- **`t_format`** (*`str`*) – The string that can be used to get the time information in the files. Any numeric datetime format string (e.g. %Y, %m, %H) can be used, but not non-numeric strings like %b, etc. See[1] for the datetime format strings
- **`files`** (*`list of str`*) – The that contain the time informations

Returns

- *pandas.Index* – The time coordinate
- *list of str* – The file names as they are sorten in the returned index

References

`psyplot.data.`**`open_dataset`**`(`*filename_or_obj*, *decode_cf=True*, *decode_times=True*, *decode_coords=True*, *engine=None*, *gridfile=None*, ***kwargs*`)`

Open an instance of `xarray.Dataset`.

[1] https://docs.python.org/2/library/datetime.html

This method has the same functionality as the `xarray.open_dataset()` method except that is supports an additional 'gdal' engine to open gdal Rasters (e.g. GeoTiffs) and that is supports absolute time units like `'day as %Y%m%d.%f'` (if *decode_cf* and *decode_times* are True).

Parameters

- **filename_or_obj** (*str, Path, file or xarray.backends.*DataStore*) – Strings and Path objects are interpreted as a path to a netCDF file or an OpenDAP URL and opened with python-netCDF4, unless the filename ends with .gz, in which case the file is gunzipped and opened with scipy.io.netcdf (only netCDF3 supported). File-like objects are opened with scipy.io.netcdf (only netCDF3 supported).
- **group** (*str, optional*) – Path to the netCDF4 group in the given file to open (only works for netCDF4 files).
- **decode_cf** (*bool, optional*) – Whether to decode these variables, assuming they were saved according to CF conventions.
- **mask_and_scale** (*bool, optional*) – If True, replace array values equal to *_FillValue* with NA and scale values according to the formula *original_values * scale_factor + add_offset*, where *_FillValue*, *scale_factor* and *add_offset* are taken from variable attributes (if they exist). If the *_FillValue* or *missing_value* attribute contains multiple values a warning will be issued and all array values matching one of the multiple values will be replaced by NA.
- **decode_times** (*bool, optional*) – If True, decode times encoded in the standard NetCDF datetime format into datetime objects. Otherwise, leave them encoded as numbers.
- **autoclose** (*bool, optional*) – If True, automatically close files to avoid OS Error of too many files being open. However, this option doesn't work with streams, e.g., BytesIO.
- **concat_characters** (*bool, optional*) – If True, concatenate along the last dimension of character arrays to form string arrays. Dimensions will only be concatenated over (and removed) if they have no corresponding variable and if they are only used as the last dimension of character arrays.
- **decode_coords** (*bool, optional*) – If True, decode the 'coordinates' attribute to identify coordinates in the resulting dataset.
- **chunks** (*int or dict, optional*) – If chunks is provided, it used to load the new dataset into dask arrays. `chunks={}` loads the dataset with dask using a single chunk for all arrays.
- **lock** (*False, True or threading.Lock, optional*) – If chunks is provided, this argument is passed on to `dask.array.from_array()`. By default, a global lock is used when reading data from netCDF files with the netcdf4 and h5netcdf engines to avoid issues with concurrent access when using dask's multithreaded backend.
- **cache** (*bool, optional*) – If True, cache data loaded from the underlying datastore in memory as NumPy arrays when accessed to avoid reading from the underlying data- store multiple times. Defaults to True unless you specify the *chunks* argument to use dask, in which case it defaults to False. Does not change the behavior of coordinates corresponding to dimensions, which always load their data from disk into a `pandas.Index`.
- **drop_variables** (*string or iterable, optional*) – A variable or list of variables to exclude from being parsed from the dataset. This may be useful to drop variables with problems or inconsistent values.
- **engine** (*{'netcdf4', 'scipy', 'pydap', 'h5netcdf', 'gdal'}, optional*) – Engine to use when reading netCDF files. If not provided, the default engine is chosen based on available dependencies, with a preference for 'netcdf4'.

- **gridfile** (*str*) – The path to a separate grid file or a xarray.Dataset instance which may store the coordinates used in *ds*

Returns The dataset that contains the variables from *filename_or_obj*

Return type xarray.Dataset

psyplot.data.**open_mfdataset**(*paths*, *decode_cf=True*, *decode_times=True*, *decode_coords=True*, *engine=None*, *gridfile=None*, *t_format=None*, ***kwargs*)

Open multiple files as a single dataset.

This function is essentially the same as the `xarray.open_mfdataset()` function but (as the *open_dataset()*) supports additional decoding and the `'gdal'` engine. You can further specify the *t_format* parameter to get the time information from the files and use the results to concatenate the files

Parameters

- **paths** (*str or sequence*) – Either a string glob in the form `"path/to/my/files/*.nc"` or an explicit list of files to open. Paths can be given as strings or as pathlib Paths.
- **chunks** (*int or dict, optional*) – Dictionary with keys given by dimension names and values given by chunk sizes. In general, these should divide the dimensions of each dataset. If int, chunk each dimension by `chunks`. By default, chunks will be chosen to load entire input files into memory at once. This has a major impact on performance: please see the full documentation for more details [2].
- **concat_dim** (*None, str, DataArray or Index, optional*) – Dimension to concatenate files along. This argument is passed on to `xarray.auto_combine()` along with the dataset objects. You only need to provide this argument if the dimension along which you want to concatenate is not a dimension in the original datasets, e.g., if you want to stack a collection of 2D arrays along a third dimension. By default, xarray attempts to infer this argument by examining component files. Set `concat_dim=None` explicitly to disable concatenation.
- **compat** (*{'identical', 'equals', 'broadcast_equals',)* – 'no_conflicts'}, optional String indicating how to compare variables of the same name for potential conflicts when merging:
  - 'broadcast_equals': all values must be equal when variables are broadcast against each other to ensure common dimensions.
  - 'equals': all values and dimensions must be the same.
  - 'identical': all values, dimensions and attributes must be the same.
  - 'no_conflicts': only values which are not null in both datasets must be equal. The returned dataset then contains the combination of all non-null values.
- **preprocess** (*callable, optional*) – If provided, call this function on each dataset prior to concatenation.
- **autoclose** (*bool, optional*) – If True, automatically close files to avoid OS Error of too many files being open. However, this option doesn't work with streams, e.g., BytesIO.
- **lock** (*False, True or threading.Lock, optional*) – This argument is passed on to `dask.array.from_array()`. By default, a per-variable lock is used when reading data from netCDF files with the netcdf4 and h5netcdf engines to avoid issues with concurrent access when using dask's multithreaded backend.
- **data_vars** (*{'minimal', 'different', 'all' or list of str}, optional*) –

These data variables will be concatenated together:

- ’minimal’: Only data variables in which the dimension already appears are included.
- ’different’: Data variables which are not equal (ignoring attributes) across all datasets are also concatenated (as well as all for which dimension already appears). Beware: this option may load the data payload of data variables into memory if they are not already loaded.
- ’all’: All data variables will be concatenated.
- list of str: The listed data variables will be concatenated, in addition to the ‘minimal’ data variables.

- **coords** (*{'minimal', 'different', 'all' o list of str}, optional*) –

  These coordinate variables will be concatenated together:

  - ’minimal’: Only coordinates in which the dimension already appears are included.
  - ’different’: Coordinates which are not equal (ignoring attributes) across all datasets are also concatenated (as well as all for which dimension already appears). Beware: this option may load the data payload of coordinate variables into memory if they are not already loaded.
  - ’all’: All coordinate variables will be concatenated, except those corresponding to other dimensions.
  - list of str: The listed coordinate variables will be concatenated, in addition the ‘minimal’ coordinates.

- **engine** (*{'netcdf4', 'scipy', 'pydap', 'h5netcdf', 'gdal'}, optional*) – Engine to use when reading netCDF files. If not provided, the default engine is chosen based on available dependencies, with a preference for ‘netcdf4’.
- **t_format** (*str*) – The string that can be used to get the time information in the files. Any numeric datetime format string (e.g. %Y, %m, %H) can be used, but not non-numeric strings like %b, etc. See[1] for the datetime format strings
- **gridfile** (*str*) – The path to a separate grid file or a xarray.Dataset instance which may store the coordinates used in *ds*

Returns The dataset that contains the variables from *filename_or_obj*

Return type xarray.Dataset

`psyplot.data.`**`setup_coords`**(*arr_names=None*, *sort=[]*, *dims={}*, ***kwargs*)

Sets up the arr_names dictionary for the plot

Parameters

- **arr_names** (*string, list of strings or dictionary*) – Set the unique array names of the resulting arrays and (optionally) dimensions.
  - if string: same as list of strings (see below). Strings may include {0} which will be replaced by a counter.
  - list of strings: those will be used for the array names. The final number of dictionaries in the return depend in this case on the *dims* and `**furtherdims`
  - dictionary: Then nothing happens and an `OrderedDict` version of *arr_names* is returned.

- **sort** (*list of strings*) – This parameter defines how the dictionaries are ordered. It has no effect if *arr_names* is a dictionary (use a `OrderedDict` for that). It can be a list of dimension strings matching to the dimensions in *dims* for the variable.
- **dims** (*dict*) – Keys must be variable names of dimensions (e.g. time, level, lat or lon) or 'name' for the variable name you want to choose. Values must be values of that dimension or iterables of the values (e.g. lists). Note that strings will be put into a list. For example dims = {'name': 't2m', 'time': 0} will result in one plot for the first time step, whereas dims = {'name': 't2m', 'time': [0, 1]} will result in two plots, one for the first (time == 0) and one for the second (time == 1) time step.
- ****kwargs** – The same as *dims* (those will update what is specified in *dims*)

Returns A mapping from the keys in *arr_names* and to dictionaries. Each dictionary corresponds defines the coordinates of one data array to load

Return type OrderedDict

`psyplot.data.`**`t_patterns = {'%H': '[0-9]{1,2}', '%M': '[0-9]{1,2}', '%S': '[0-9]{1,2}', '%Y`**

mapping that translates datetime format strings to regex patterns

`psyplot.data.`**`to_netcdf`**(*ds*, **args*, ***kwargs*)

Store the given dataset as a netCDF file

This functions works essentially the same as the usual `xarray.Dataset.to_netcdf()` method but can also encode absolute time units

Parameters

- **ds** (*xarray.Dataset*) – The dataset to store
- **path** (*str, Path or file-like object, optional*) – Path to which to save this dataset. File-like objects are only supported by the scipy engine. If no path is provided, this function returns the resulting netCDF file as bytes; in this case, we need to use scipy, which does not support netCDF version 4 (the default format becomes NETCDF3_64BIT).
- **mode** (*{'w', 'a'}, optional*) – Write ('w') or append ('a') mode. If mode='w', any existing file at this location will be overwritten. If mode='a', existing variables will be overwritten.
- **format** (*{'NETCDF4', 'NETCDF4_CLASSIC', 'NETCDF3_64BIT', 'NETCDF3_CLASSIC'}, optional*) – File format for the resulting netCDF file:
  - NETCDF4: Data is stored in an HDF5 file, using netCDF4 API features.
  - NETCDF4_CLASSIC: Data is stored in an HDF5 file, using only netCDF 3 compatible API features.
  - NETCDF3_64BIT: 64-bit offset version of the netCDF 3 file format, which fully supports 2+ GB files, but is only compatible with clients linked against netCDF version 3.6.0 or later.
  - NETCDF3_CLASSIC: The classic netCDF 3 file format. It does not handle 2+ GB files very well.

  All formats are supported by the netCDF4-python library. scipy.io.netcdf only supports the last two formats.

  The default format is NETCDF4 if you are saving a file to disk and have the netCDF4-python library available. Otherwise, xarray falls back to using scipy to write netCDF files and defaults to the NETCDF3_64BIT format (scipy does not support netCDF4).

- **group** (*str, optional*) – Path to the netCDF4 group in the given file to open (only works for format='NETCDF4'). The group(s) will be created if necessary.
- **engine** (*{'netcdf4', 'scipy', 'h5netcdf'}, optional*) – Engine to use when writing netCDF files. If not provided, the default engine is chosen based on available dependencies, with a preference for 'netcdf4' if writing to a file on disk.
- **encoding** (*dict, optional*) – Nested dictionary with variable names as keys and dictionaries of variable specific encodings as values, e.g., ``{'my_variable': {'dtype': 'int16', 'scale_factor': 0.1,

  'zlib': True}, ...}``
- **unlimited_dims** (*sequence of str, optional*) – Dimension(s) that should be serialized as unlimited dimensions. By default, no dimensions are treated as unlimited dimensions. Note that unlimited_dims may also be set via `dataset.encoding['unlimited_dims']`.

psyplot.data.**to_slice**(*arr*)

Test whether *arr* is an integer array that can be replaced by a slice

Parameters **arr** (*numpy.array*) – Numpy integer array

Returns If *arr* could be converted to an array, this is returned, otherwise *None* is returned

Return type slice or None

See also:

get_index_from_coord()

psyplot.docstring module

Docstring module of the psyplot package

We use the docrep package for managing our docstrings

Classes

PsyplotDocstringProcessor(*args, **kwargs)	A `docrep.DocstringProcessor` subclass with possible types section

Functions

append_original_doc(parent[, num])	Return an iterator that append the docstring of the given *parent*
dedent(func)	Dedent the docstring of a function and substitute with `params`
indent(text[, num])	Indet the given string

Data

docstrings(func)	`docrep.PsyplotDocstringProcessor` instance that simplifies the reuse

class psyplot.docstring.**PsyplotDocstringProcessor**(**args*, ***kwargs*)

Bases: `docrep.DocstringProcessor`

A `docrep.DocstringProcessor` subclass with possible types section

Parameters and `**kwargs` (**args*) – Parameters that shall be used for the substitution. Note that you can only provide either `*args` or `**kwargs`, furthermore most of the methods like *get_sectionsf* require `**kwargs` to be provided.

Methods

get_sections(s, base[, sections])	Extract the specified sections out of the given string

Attributes

param_like_sections	list() -> new empty list

get_sections(*s, base, sections=['Parameters', 'Other Parameters', 'Possible types']*)
Extract the specified sections out of the given string

The same as the `docrep.DocstringProcessor.get_sections()` method but uses the `'Possible types'` section by default, too

Parameters

- **s** (*str*) – Docstring to split
- **base** (*str*) – base to use in the `sections` attribute
- **sections** (*list of str*) – sections to look for. Each section must be followed by a newline character ('n') and a bar of '-' (following the numpy (napoleon) docstring conventions).

Returns The replaced string

Return type str

param_like_sections = ['Parameters', 'Other Parameters', 'Returns', 'Raises', 'Possibl

`psyplot.docstring.`**append_original_doc**(*parent, num=0*)
Return an iterator that append the docstring of the given *parent* function to the applied function

`psyplot.docstring.`**dedent**(*func*)
Dedent the docstring of a function and substitute with `params`

Parameters func (*function*) – function with the documentation to dedent

`psyplot.docstring.`**docstrings**(*func*) **= <psyplot.docstring.PsyplotDocstringProcessor object>**
`docrep.PsyplotDocstringProcessor` instance that simplifies the reuse of docstrings from between different python objects.

`psyplot.docstring.`**indent**(*text, num=4*)
Indet the given string

psyplot.gdal_store module

Gdal Store for reading GeoTIFF files into an `xarray.Dataset`

This module contains the definition of the *GdalStore* class that can be used to read in a GeoTIFF file into an `xarray.Dataset`. It requires that you have the python gdal module installed.

Examples

to open a GeoTIFF file named 'my_tiff.tiff' you can do:

```
>>> from psyplot.gdal_store import GdalStore
>>> from xarray import open_dataset
>>> ds = open_dataset(GdalStore('my_tiff'))
```

Or you use the *engine* of the psyplot.open_dataset() function:

```
>>> ds = open_dataset('my_tiff.tiff', engine='gdal')
```

Classes

GdalStore(filename_or_obj)	Datastore to read raster files suitable for the gdal package

class psyplot.gdal_store.**GdalStore**(*filename_or_obj*)

Bases: xarray.backends.common.AbstractDataStore

Datastore to read raster files suitable for the gdal package

We recommend to use the psyplot.open_dataset() function to open a geotiff file:

```
>>> ds = psyplot.open_dataset('my_geotiff.tiff', engine='gdal')
```

Methods

get_attrs()
get_variables()

Notes

The *GdalStore* object is not as elaborate as, for example, the *gdal_translate* command. Many attributes, e.g. variable names or netCDF dimensions will not be interpreted. We only support two dimensional arrays and each band is saved into one variable named like 'Band1', 'Band2', ... If you want a more elaborate translation of your GDAL Raster, convert the file to a netCDF file using gdal_translate or the gdal.GetDriverByName('netCDF').CreateCopy method. However this class does not create an extra file on your hard disk as it is done by GDAL.

Parameters **filename_or_obj** (*str*) – The path to the GeoTIFF file or a gdal dataset

get_attrs()

get_variables()

psyplot.plotter module

Core package for interactive visualization in the psyplot package

This package defines the *Plotter* and *Formatoption* classes, the core of the visualization in the *psyplot* package. Each *Plotter* combines a set of formatoption keys where each formatoption key is represented by a *Formatoption* subclass.

Classes

DictFormatoption(key[, plotter, . . .])	Base formatoption class defining an alternative set_value that works for dictionaries.
Formatoption(key[, plotter, index_in_list, . . .])	Abstract formatoption
FormatoptionMeta	Meta class for formatoptions
Plotter([data, ax, auto_update, project, . . .])	Interactive plotting object for one or more data arrays
PostProcDependencies	The dependencies of this formatoption
PostProcessing(key[, plotter, . . .])	Apply your own postprocessing script
PostTiming(key[, plotter, index_in_list, . . .])	Determine when to run the `post` formatoption

Data

BEFOREPLOTTING	Priority value of formatoptions that are updated before the plot it made.
END	Priority value of formatoptions that are updated at the end.
START	Priority value of formatoptions that are updated before the data is loaded.
groups	`dict`. Mapping from group to group names

Functions

default_print_func	the default function to use when printing formatoption infos (the default is
format_time(x)	Formats date values
is_data_dependent(fmto, data)	Check whether a formatoption is data dependent

psyplot.plotter.**BEFOREPLOTTING = 20**

Priority value of formatoptions that are updated before the plot it made.

class psyplot.plotter.**DictFormatoption**(*key*, *plotter=None*, *index_in_list=None*, *additional_children=[]*, *additional_dependencies=[]*, ***kwargs*)

Bases: *psyplot.plotter.Formatoption*

Base formatoption class defining an alternative set_value that works for dictionaries.

Parameters

- **key** (*str*) – formatoption key in the *plotter*
- **plotter** (`psyplot.plotter.Plotter`) – Plotter instance that holds this formatoption. If None, it is assumed that this instance serves as a descriptor.
- **index_in_list** (*int or None*) – The index that shall be used if the data is a `psyplot.InteractiveList`
- **additional_children** (*list or str*) – Additional children to use (see the `children` attribute)
- **additional_dependencies** (*list or str*) – Additional dependencies to use (see the `dependencies` attribute)
- ****kwargs** – Further keywords may be used to specify different names for children, dependencies and connection formatoptions that match the setup of the plotter. Hence, keywords may be anything of the `children`, `dependencies` and `connections` attributes, with values being the name of the new formatoption in this plotter.

Methods

`set_value`(value[, validate, todefault])	Set (and validate) the value in the plotter

set_value(*value*, *validate=True*, *todefault=False*)
Set (and validate) the value in the plotter

Parameters

- **value** – Value to set
- **validate** (`bool`) – if True, validate the *value* before it is set
- **todefault** (`bool`) – True if the value is updated to the default value

Notes

- If the current value in the plotter is None, then it will be set with the given *value*, otherwise the current value in the plotter is updated
- If the value is an empty dictionary, the value in the plotter is cleared

psyplot.plotter.**END = 10**
Priority value of formatoptions that are updated at the end.

class psyplot.plotter.**Formatoption**(*key*, *plotter=None*, *index_in_list=None*, *additional_children=[]*, *additional_dependencies=[]*, ***kwargs*)
Bases: `object`

Abstract formatoption

This class serves as an abstract version of an formatoption descriptor that can be used by `Plotter` instances.

Parameters

- **key** (`str`) – formatoption key in the *plotter*
- **plotter** (`psyplot.plotter.Plotter`) – Plotter instance that holds this formatoption. If None, it is assumed that this instance serves as a descriptor.
- **index_in_list** (`int or None`) – The index that shall be used if the data is a `psyplot.InteractiveList`
- **additional_children** (`list or str`) – Additional children to use (see the `children` attribute)
- **additional_dependencies** (`list or str`) – Additional dependencies to use (see the `dependencies` attribute)
- ****kwargs** – Further keywords may be used to specify different names for children, dependencies and connection formatoptions that match the setup of the plotter. Hence, keywords may be anything of the `children`, `dependencies` and `connections` attributes, with values being the name of the new formatoption in this plotter.

Interface to the data

`any_decoder`	Return the first possible decoder
`ax`	The axes this Formatoption plots on

Continued on next page

Table 53 – continued from previous page

`data`	The data that is plotted
`data_dependent`	`bool` or a callable. This attribute indicates whether this
`decoder`	The `CFDecoder` instance that decodes the
`index_in_list`	int or None. Index that is used in case the plotting data is a
`iter_data`	Returns an iterator over the plot data arrays
`iter_raw_data`	Returns an iterator over the original data arrays
`project`	Project of the plotter of this instance
`raw_data`	The original data of the plotter of this formatoption
`set_data`(data[, i])	Replace the data to plot
`set_decoder`(decoder[, i])	Replace the data to plot

Interface for the plotter

`changed`	`bool` indicating whether the value changed compared to the
`check_and_set`(value[, todefault, validate])	Checks the value and sets the value if it changed
`diff`(value)	Checks whether the given value differs from what is currently set
`finish_update`()	Finish the update, initialization and sharing process
`initialize_plot`(value, *args, **kwargs)	Method that is called when the plot is made the first time
`key`	`str`. Formatoption key of this class in the
`lock`	A `threading.Rlock` instance to lock while updating
`plot_fmt`	`bool`. Has to be True if the formatoption has a `make_plot`
`plotter`	`Plotter`. Plotter instance this formatoption
`priority`	`int`. Priority value of the the formatoption determining when
`remove`()	Method to remove the effects of this formatoption
`requires_clearing`	`bool`. True if an update of this formatoption requires a
`requires_replot`	Boolean that is True if an update of the formatoption requires a replot
`set_value`(value[, validate, todefault])	Set (and validate) the value in the plotter.
`share`(fmto[, initializing])	Share the settings of this formatoption with other data objects
`update`(value)	Method that is call to update the formatoption on the axes
`update_after_plot`	`bool`. True if this formatoption needs an update after the plot

Interface to other formatoptions

`children`	*list of str*. List of formatoptions that have to be updated before this
`connections`	*list of str*. Connections to other formatoptions that are (different
`dependencies`	*list of str*. List of formatoptions that force an update of this

Continued on next page

Table 55 – continued from previous page

parents	*list of str.* List of formatoptions that, if included in the update,
shared	`set` of the *Formatoption* instance that are shared
shared_by	None if the formatoption is not controlled by another formatoption

Formatoption intrinsic

default	Default value of this formatoption
validate	Validation method of the formatoption
value	Value of the formatoption in the corresponding `plotter` or
value2pickle	The value that can be used when pickling the information of the project
value2share	The value that is passed to shared formatoptions (by default, the

Information attributes

default_key	The key of this formatoption in the `psyplot.rcParams`
group	`str`. Key of the group name in *groups* of this
groupname	Long name of the group this formatoption belongs too.
name	`str`. A bit more verbose name than the formatoption key to be

Methods

get_fmt_widget(parent, project)	Get a widget to update the formatoption in the GUI

Miscellaneous

init_kwargs	`dict` key word arguments that are passed to the
logger	Logger of the plotter

any_decoder
Return the first possible decoder

ax
The axes this Formatoption plots on

changed
`bool` indicating whether the value changed compared to the default or not.

check_and_set (*value*, *todefault=False*, *validate=True*)
Checks the value and sets the value if it changed

This method checks the value and sets it only if the *diff()* method result of the given *value* is True

Parameters

- **value** – A possible value to set
- **todefault** (*bool*) – True if the value is updated to the default value

Returns A boolean to indicate whether it has been set or not

Return type bool

`children = []`
list of str. List of formatoptions that have to be updated before this one is updated. Those formatoptions are only updated if they exist in the update parameters.

`connections = []`
list of str. Connections to other formatoptions that are (different from *`dependencies`* and *`children`*) not important for the update process

`data`
The data that is plotted

`data_dependent = False`
`bool` or a callable. This attribute indicates whether this *`Formatoption`* depends on the data and should be updated if the data changes. If it is a callable, it must accept one argument: the new data. (Note: This is automatically set to True for plot formatoptions)

`decoder`
The *`CFDecoder`* instance that decodes the *`raw_data`*

`default`
Default value of this formatoption

`default_key`
The key of this formatoption in the `psyplot.rcParams`

`dependencies = []`
list of str. List of formatoptions that force an update of this formatoption if they are updated.

`diff`(*value*)
Checks whether the given value differs from what is currently set

Parameters **`value`** – A possible value to set (make sure that it has been validate via the *`validate`* attribute before)

Returns True if the value differs from what is currently set

Return type bool

`finish_update`()
Finish the update, initialization and sharing process

This function is called at the end of the *`Plotter.start_update()`*, *`Plotter.initialize_plot()`* or the *`Plotter.share()`* methods.

`get_fmt_widget`(*parent, project*)
Get a widget to update the formatoption in the GUI

This method should return a QWidget that is loaded by the psyplot-gui when the formatoption is selected in the `psyplot_gui.main.Mainwindow.fmt_widget`. It should call the **:method:'~psyplot_gui.fmt_widget.FormatoptionWidget.insert_text'** method when the update text for the formatoption should be changed.

Parameters

- **`parent`** (*`psyplot_gui.fmt_widget.FormatoptionWidget`*) – The parent widget that contains the returned QWidget
- **`project`** (`psyplot.project.Project`) – The current subproject (see *`psyplot.project.gcp()`*)

Returns The widget to control the formatoption

Return type PyQt5.QtWidgets.QWidget

`group = 'misc'`
`str`. Key of the group name in *`groups`* of this formatoption keyword

`groupname`
Long name of the group this formatoption belongs too.

`index_in_list = 0`
int or None. Index that is used in case the plotting data is a `psyplot.InteractiveList`

`init_kwargs`
`dict` key word arguments that are passed to the initialization of a new instance when accessed from the descriptor

`initialize_plot`(*value*, **args*, ***kwargs*)
Method that is called when the plot is made the first time

Parameters **`value`** – The value to use for the initialization

`iter_data`
Returns an iterator over the plot data arrays

`iter_raw_data`
Returns an iterator over the original data arrays

`key = None`
`str`. Formatoption key of this class in the *`Plotter`* class

`lock`
A `threading.Rlock` instance to lock while updating

This lock is used when multiple *`plotter`* instances are updated at the same time while sharing formatoptions.

`logger`
Logger of the plotter

`name = None`
`str`. A bit more verbose name than the formatoption key to be included in the gui. If None, the key is used in the gui

`parents = []`
list of str. List of formatoptions that, if included in the update, prevent the update of this formatoption.

`plot_fmt = False`
`bool`. Has to be True if the formatoption has a `make_plot` method to make the plot.

`plotter = None`
`Plotter`. Plotter instance this formatoption belongs to

`priority = 10`
`int`. Priority value of the the formatoption determining when the formatoption is updated.

- 10: at the end (for labels, etc.)
- 20: before the plotting (e.g. for colormaps, etc.)
- 30: before loading the data (e.g. for lonlatbox)

`project`
Project of the plotter of this instance

raw_data
The original data of the plotter of this formatoption

remove()
Method to remove the effects of this formatoption

This method is called when the axes is cleared due to a formatoption with *requires_clearing* set to True. You don't necessarily have to implement this formatoption if your plot results are removed by the usual `matplotlib.axes.Axes.clear()` method.

requires_clearing = False
`bool`. True if an update of this formatoption requires a clearing of the axes and reinitialization of the plot

requires_replot = False
Boolean that is True if an update of the formatoption requires a replot

set_data(*data*, *i=None*)
Replace the data to plot

This method may be used to replace the data that is visualized by the plotter. It changes it's behaviour depending on whether an *psyplot.data.InteractiveList* is visualized or a single `pysplot.data.InteractiveArray`

Parameters

- **data** (`psyplot.data.InteractiveBase`) – The data to insert
- **i** (*int*) – The position in the InteractiveList where to insert the data (if the plotter visualizes a list anyway)

Notes

This method uses the *Formatoption.data* attribute

set_decoder(*decoder*, *i=None*)
Replace the data to plot

This method may be used to replace the data that is visualized by the plotter. It changes it's behaviour depending on whether an *psyplot.data.InteractiveList* is visualized or a single `pysplot.data.InteractiveArray`

Parameters

- **decoder** (`psyplot.data.CFDecoder`) – The decoder to insert
- **i** (*int*) – The position in the InteractiveList where to insert the data (if the plotter visualizes a list anyway)

set_value(*value*, *validate=True*, *todefault=False*)
Set (and validate) the value in the plotter. This method is called by the plotter when it attempts to change the value of the formatoption.

Parameters

- **value** – Value to set
- **validate** (*bool*) – if True, validate the *value* before it is set
- **todefault** (*bool*) – True if the value is updated to the default value

share(*fmto*, *initializing=False*, ***kwargs*)
Share the settings of this formatoption with other data objects

Parameters

- **fmto** (Formatoption) – The *Formatoption* instance to share the attributes with
- ****kwargs** – Any other keyword argument that shall be passed to the update method of *fmto*

shared = set()
set of the *Formatoption* instance that are shared with this instance.

shared_by
None if the formatoption is not controlled by another formatoption of another plotter, otherwise the corresponding *Formatoption* instance

update(*value*)
Method that is call to update the formatoption on the axes

Parameters value – Value to update

update_after_plot = False
bool. True if this formatoption needs an update after the plot has changed

validate
Validation method of the formatoption

value
Value of the formatoption in the corresponding *plotter* or the shared value

value2pickle
The value that can be used when pickling the information of the project

value2share
The value that is passed to shared formatoptions (by default, the *value* attribute)

class psyplot.plotter.**FormatoptionMeta**
Bases: abc.ABCMeta

Meta class for formatoptions

This class serves as a meta class for formatoptions and allows a more efficient docstring generation by using the *psyplot.docstring.docstrings* when creating a new formatoption class

Assign an automatic documentation to the formatoption

class psyplot.plotter.**Plotter**(*data=None*, *ax=None*, *auto_update=None*, *project=None*, *draw=None*, *make_plot=True*, *clear=False*, *enable_post=False*, ***kwargs*)
Bases: dict

Interactive plotting object for one or more data arrays

This class is the base for the interactive plotting with the psyplot module. It capabilities are determined by it's descriptor classes that are derived from the *Formatoption* class

Parameters

- **data** (InteractiveArray *or* ArrayList*, optional*) – Data object that shall be visualized. If given and *plot* is True, the *initialize_plot()* method is called at the end. Otherwise you can call this method later by yourself
- **ax** (*matplotlib.axes.Axes*) – Matplotlib Axes to plot on. If None, a new one will be created as soon as the *initialize_plot()* method is called
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the *update()* method or not. See also

the *no_auto_update* attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.

- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*` parameter in the `psyplot.rcParams` dictionary
- **make_plot** (*bool*) – If True, and *data* is not None, the plot is initialized. Otherwise only the framework between plotter and data is set up
- **clear** (*bool*) – If True, the axes is cleared first
- **enable_post** (*bool*) – If True, the *post* formatoption is enabled and post processing scripts are allowed
- ****kwargs** – Any formatoption key from the `formatoptions` attribute that shall be used

Attributes

ax	Axes instance of the plot
base_variables	A mapping from the base_variable names to the variables
changed	`dict` containing the key value pairs that are not the
data	The `psyplot.InteractiveBase` instance of this plotter
enable_post	`bool` that has to be `True` if the post processing script in
figs2draw	All figures that have been manipulated through sharing and the own figure.
fmt_groups	A mapping from the formatoption group to the formatoptions
groups	A mapping from the group short name to the group description
include_links([value])	Temporarily include links in the key descriptions from `show_keys()`, `show_docs()` and `show_summaries()`.
iter_base_variables	A mapping from the base_variable names to the variables
logger	`logging.Logger` of this plotter
no_auto_update	`bool`. Boolean controlling whether the `start_update()`
no_validation	Temporarily disable the validation
plot_data	The data that is used for plotting
plot_data_decoder	The decoder to use for the formatoptions.
post	Apply your own postprocessing script
post_timing	Determine when to run the `post` formatoption
project	The *psyplot.project.Project* instance this plotter belongs to
rc	Default values for this plotter

Methods

check_data(name, dims, is_unstructured)	A validation method for the data shape
check_key(key[, raise_error])	Checks whether the key is a valid formatoption

Continued on next page

Table 61 – continued from previous page

draw()	Draw the figures and those that are shared and have been changed
get_enhanced_attrs(arr[, axes])	
get_vfunc(key)	Return the validation function for a specified formatoption
has_changed(key[, include_last])	Determine whether a formatoption changed in the last update
initialize_plot([data, ax, make_plot, . . .])	Initialize the plot for a data array
make_plot()	Method for making the plot
reinit([draw, clear])	Reinitializes the plot with the same data and on the same axes.
share(plotters[, keys, draw, auto_update])	Share the formatoptions of this plotter with others
show()	Shows all open figures
show_docs([keys, indent])	Classmethod to print the full documentations of the formatoptions
show_keys([keys, indent, grouped, func, . . .])	Classmethod to return a nice looking table with the given formatoptions
show_summaries([keys, indent])	Classmethod to print the summaries of the formatoptions
start_update([draw, queues, update_shared])	Conduct the registered plot updates
unshare(plotters[, keys, auto_update, draw])	Close the sharing connection of this plotter with others
unshare_me([keys, auto_update, draw, . . .])	Close the sharing connection of this plotter with others
update([fmt, replot, auto_update, draw, . . .])	Update the formatoptions and the plot

ax
Axes instance of the plot

base_variables
A mapping from the base_variable names to the variables

changed
`dict` containing the key value pairs that are not the default

classmethod check_data(*name*, *dims*, *is_unstructured*)
A validation method for the data shape

The default method does nothing and should be subclassed to validate the results. If the plotter accepts a `InteractiveList`, it should accept a list for name and dims

Parameters

- **name** (*str or list of str*) – The variable name(s) of the data
- **dims** (*list of str or list of lists of str*) – The dimension name(s) of the data
- **is_unstructured** (*bool or list of bool*) – True if the corresponding array is unstructured

Returns

- *list of bool or None* – True, if everything is okay, False in case of a serious error, None if it is intermediate. Each object in this list corresponds to one in the given *name*
- *list of str* – The message giving more information on the reason. Each object in this list corresponds to one in the given *name*

check_key(*key*, *raise_error=True*, **args*, ***kwargs*)
Checks whether the key is a valid formatoption

Parameters

- **key** (*str*) – Key to check
- **raise_error** (*bool*) – If not True, a list of similar keys is returned
- **msg** (*str*) – The additional message that shall be used if no close match to key is found
- ***args, **kwargs** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns

- *str* – The *key* if it is a valid string, else an empty string
- *list* – A list of similar formatoption strings (if found)
- *str* – An error message which includes

Raises `KeyError` – If the key is not a valid formatoption and *raise_error* is True

data
The `psyplot.InteractiveBase` instance of this plotter

draw()
Draw the figures and those that are shared and have been changed

enable_post = False
`bool` that has to be `True` if the post processing script in the *post* formatoption should be enabled

figs2draw
All figures that have been manipulated through sharing and the own figure.

Notes

Using this property set will reset the figures too draw

fmt_groups
A mapping from the formatoption group to the formatoptions

get_enhanced_attrs(*arr, axes=['x', 'y', 't', 'z']*)

get_vfunc(*key*)
Return the validation function for a specified formatoption

Parameters **key** (*str*) – Formatoption key in the *rc* dictionary

Returns Validation function for this formatoption

Return type function

groups
A mapping from the group short name to the group description

has_changed(*key*, *include_last=True*)
Determine whether a formatoption changed in the last update

Parameters

- **key** (*str*) – A formatoption key contained in this plotter

- **include_last** (*bool*) – if True and the formatoption has been included in the last update, the return value will not be None. Otherwise the return value will only be not None if it changed during the last update

Returns

- None, if the value has not been changed during the last update or *key* is not a valid formatoption key
- a list of length two with the old value in the first place and the given *value* at the second

Return type None or list

include_links(*value=None*)
Temporarily include links in the key descriptions from *show_keys()*, *show_docs()* and *show_summaries()*. Note that this is a class attribute, so each change to the value of this attribute will affect all instances and subclasses

initialize_plot(*data=None, ax=None, make_plot=True, clear=False, draw=None, remove=False*)
Initialize the plot for a data array

Parameters

- **data** (InteractiveArray *or* ArrayList*, optional*) – Data object that shall be visualized.
  - If not None and *plot* is True, the given data is visualized.
  - If None and the *data* attribute is not None, the data in the *data* attribute is visualized
  - If both are None, nothing is done.
- **ax** (*matplotlib.axes.Axes*) – Matplotlib Axes to plot on. If None, a new one will be created as soon as the *initialize_plot()* method is called
- **make_plot** (*bool*) – If True, and *data* is not None, the plot is initialized. Otherwise only the framework between plotter and data is set up
- **clear** (*bool*) – If True, the axes is cleared first
- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **remove** (*bool*) – If True, old effects by the formatoptions in this plotter are undone first

iter_base_variables
A mapping from the base_variable names to the variables

logger
`logging.Logger` of this plotter

make_plot()
Method for making the plot

This method is called at the end of the *BEFOREPLOTTING* stage if and only if the `plot_fmt` attribute is set to `True`

no_auto_update
`bool`. Boolean controlling whether the *start_update()* method is automatically called by the *update()* method

Examples

You can disable the automatic update via

```
>>> with data.no_auto_update:
...     data.update(time=1)
...     data.start_update()
```

To permanently disable the automatic update, simply set

```
>>> data.no_auto_update = True
>>> data.update(time=1)
>>> data.no_auto_update = False  # reenable automatical update
```

`no_validation`
Temporarily disable the validation

Examples

Although it is not recommended to set a value with disabled validation, you can disable it via:

```
>>> with plotter.no_validation:
...     plotter['ticksize'] = 'x'
```

To permanently disable the validation, simply set

```
>>> plotter.no_validation = True
>>> plotter['ticksize'] = 'x'
>>> plotter.no_validation = False  # reenable validation
```

`plot_data`
The data that is used for plotting

`plot_data_decoder = None`
The decoder to use for the formatoptions. If None, the decoder of the raw data is used

`post`
Apply your own postprocessing script

This formatoption let's you apply your own post processing script. Just enter the script as a string and it will be executed. The formatoption will be made available via the `self` variable

Possible types

- *None* – Don't do anything
- *str* – The post processing script as string

Note: This formatoption uses the built-in `exec()` function to compile the script. Since this poses a security risk when loading psyplot projects, it is by default disabled through the *`Plotter.enable_post`* attribute. If you are sure that you can trust the script in this formatoption, set this attribute of the corresponding *`Plotter`* to `True`

Examples

Assume, you want to manually add the mean of the data to the title of the matplotlib axes. You can simply do this via

```
from psyplot.plotter import Plotter
from xarray import DataArray
plotter = Plotter(DataArray([1, 2, 3]))
# enable the post formatoption
plotter.enable_post = True
plotter.update(post="self.ax.set_title(str(self.data.mean()))")
plotter.ax.get_title()
'2.0'
```

By default, the `post` formatoption is only ran, when it is explicitly updated. However, you can use the *`post_timing`* formatoption, to run it automatically. E.g. for running it after every update of the plotter, you can set

```
plotter.update(post_timing='always')
```

See also:

`post_timing` Determine the timing of this formatoption

`post_timing`

Determine when to run the *`post`* formatoption

This formatoption determines, whether the *`post`* formatoption should be run never, after replot or after every update.

Possible types

- *'never'* – Never run post processing scripts
- *'always'* – Always run post processing scripts
- *'replot'* – Only run post processing scripts when the data changes or a replot is necessary

See also:

`post` The post processing formatoption

`project = None`

The *`psyplot.project.Project`* instance this plotter belongs to

`rc`

Default values for this plotter

This *`SubDict`* stores the default values for this plotter. A modification of the dictionary does not affect other plotter instances unless you set the *`trace`* attribute to True

`reinit`(*draw=None*, *clear=False*)

Reinitializes the plot with the same data and on the same axes.

Parameters

- **`draw`** (*`bool or None`*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary

- **clear** (*bool*) – Whether to clear the axes or not

Warning: The axes may be cleared when calling this method (even if *clear* is set to False)!

share (*plotters*, *keys=None*, *draw=None*, *auto_update=False*)
Share the formatoptions of this plotter with others

This method shares the formatoptions of this `Plotter` instance with others to make sure that, if the formatoption of this changes, those of the others change as well

Parameters

- **plotters** (list of `Plotter` instances or a `Plotter`) – The plotters to share the formatoptions with
- **keys** (*string or iterable of strings*) – The formatoptions to share, or group names of formatoptions to share all formatoptions of that group (see the `fmt_groups` property). If None, all formatoptions of this plotter are unshared.
- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **auto_update** (*bool*) – Boolean determining whether or not the `start_update()` method is called at the end. This parameter has no effect if the `no_auto_update` attribute is set to `True`.

See also:

`unshare()`, `unshare_me()`

show ()
Shows all open figures

classmethod show_docs (*keys=None*, *indent=0*, **args*, ***kwargs*)
Classmethod to print the full documentations of the formatoptions

Parameters

- **keys** (*list of str or None*) – If None, the all formatoptions of the given class are used. Group names from the `psyplot.plotter.groups` mapping are replaced by the formatoptions
- **indent** (*int*) – The indentation of the table
- **grouped** (*bool, optional*) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the `psyplot.plotter.Plotter.include_links` attribute.
- **``\*args,\*\*kwargs``** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

See also:

`show_keys()`, `show_docs()`

classmethod show_keys(*keys=None*, *indent=0*, *grouped=False*, *func=None*, *include_links=False*, **args*, ***kwargs*)

Classmethod to return a nice looking table with the given formatoptions

Parameters

- **keys** (`list of str or None`) – If None, the all formatoptions of the given class are used. Group names from the `psyplot.plotter.groups` mapping are replaced by the formatoptions
- **indent** (`int`) – The indentation of the table
- **grouped** (`bool, optional`) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the `psyplot.plotter.Plotter.include_links` attribute.
- **‘‘*args,**kwargs‘‘** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

See also:

`show_summaries()`, `show_docs()`

classmethod show_summaries(*keys=None*, *indent=0*, **args*, ***kwargs*)

Classmethod to print the summaries of the formatoptions

Parameters

- **keys** (`list of str or None`) – If None, the all formatoptions of the given class are used. Group names from the `psyplot.plotter.groups` mapping are replaced by the formatoptions
- **indent** (`int`) – The indentation of the table
- **grouped** (`bool, optional`) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument

- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the `psyplot.plotter.Plotter.include_links` attribute.
- **``*args,**kwargs``** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

See also:

`show_keys()`, `show_docs()`

start_update (*draw=None*, *queues=None*, *update_shared=True*)

Conduct the registered plot updates

This method starts the updates from what has been registered by the `update()` method. You can call this method if you did not set the *auto_update* parameter to True when calling the `update()` method and when the `no_auto_update` attribute is True.

Parameters

- **draw** (`bool or None`) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*` parameter in the `psyplot.rcParams` dictionary
- **queues** (list of `Queue.Queue` instances) – The queues that are passed to the `psyplot.plotter.Plotter.start_update()` method to ensure a thread-safe update. It can be None if only one single plotter is updated at the same time. The number of jobs that are taken from the queue is determined by the `_njobs()` attribute. Note that there this parameter is automatically configured when updating from a `Project`.

Returns A boolean indicating whether a redrawing is necessary or not

Return type bool

See also:

`no_auto_update`, `update()`

unshare (*plotters*, *keys=None*, *auto_update=False*, *draw=None*)

Close the sharing connection of this plotter with others

This method undoes the sharing connections made by the `share()` method and releases the given *plotters* again, such that the formatoptions in this plotter may be updated again to values different from this one.

Parameters

- **plotters** (list of `Plotter` instances or a `Plotter`) – The plotters to release
- **keys** (`string or iterable of strings`) – The formatoptions to unshare, or group names of formatoptions to unshare all formatoptions of that group (see the `fmt_groups` property). If None, all formatoptions of this plotter are unshared.
- **draw** (`bool or None`) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*` parameter in the `psyplot.rcParams` dictionary
- **auto_update** (`bool`) – Boolean determining whether or not the `start_update()` method is called at the end. This parameter has no effect if the `no_auto_update` attribute is set to `True`.

See also:

`share()`, `unshare_me()`

`unshare_me`(*keys=None*, *auto_update=False*, *draw=None*, *update_other=True*)

Close the sharing connection of this plotter with others

This method undoes the sharing connections made by the `share()` method and release this plotter again.

Parameters

- **keys** (*string or iterable of strings*) – The formatoptions to unshare, or group names of formatoptions to unshare all formatoptions of that group (see the `fmt_groups` property). If None, all formatoptions of this plotter are unshared.
- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **auto_update** (*bool*) – Boolean determining whether or not the `start_update()` method is called at the end. This parameter has no effect if the `no_auto_update` attribute is set to `True`.

See also:

`share()`, `unshare()`

`update`(*fmt={}*, *replot=False*, *auto_update=False*, *draw=None*, *force=False*, *todefault=False*, ***kwargs*)

Update the formatoptions and the plot

If the `data` attribute of this plotter is None, the plotter is updated like a usual dictionary (see `dict.update()`). Otherwise the update is registered and the plot is updated if *auto_update* is True or if the `start_update()` method is called (see below).

Parameters

- **fmt** (*dict*) – Keys can be any valid formatoptions with the corresponding values (see the `formatoptions` attribute)
- **replot** (*bool*) – Boolean that determines whether the data specific formatoptions shall be updated in any case or not.
- **force** (*str, list of str or bool*) – If formatoption key (i.e. string) or list of formatoption keys, thery are definitely updated whether they changed or not. If True, all the given formatoptions in this call of the are `update()` method are updated
- **todefault** (*bool*) – If True, all changed formatoptions (except the registered ones) are updated to their default value as stored in the `rc` attribute
- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **queues** (list of `Queue.Queue` instances) – The queues that are passed to the `psyplot.plotter.Plotter.start_update()` method to ensure a thread-safe update. It can be None if only one single plotter is updated at the same time. The number of jobs that are taken from the queue is determined by the `_njobs()` attribute. Note that there this parameter is automatically configured when updating from a `Project`.
- **auto_update** (*bool*) – Boolean determining whether or not the `start_update()` method is called at the end. This parameter has no effect if the `no_auto_update` attribute is set to `True`.

- `**kwargs` – Any other formatoption that shall be updated (additionally to those in *fmt*)

Notes

If the `no_auto_update` attribute is True and the given *auto_update* parameter are is False, the update of the plots are registered and conducted at the next call of the `start_update()` method or the next call of this method (if the *auto_update* parameter is then True).

class psyplot.plotter.**PostProcDependencies**

Bases: `object`

The dependencies of this formatoption

class psyplot.plotter.**PostProcessing**(*key, plotter=None, index_in_list=None, additional_children=[], additional_dependencies=[], **kwargs*)

Bases: `psyplot.plotter.Formatoption`

Apply your own postprocessing script

This formatoption let's you apply your own post processing script. Just enter the script as a string and it will be executed. The formatoption will be made available via the `self` variable

Possible types

Attributes

`children`	list() -> new empty list
`data_dependent`	True if the corresponding `post_timing`
`dependencies`	list() -> new empty list
`group`	str(object='') -> str
`name`	str(object='') -> str
`post_timing`	post_timing Formatoption instance in the plotter
`priority`	float(x) -> floating point number

Methods

`update`(value)	Method that is call to update the formatoption on the axes
`validate`()	Validation method of the formatoption

- *None* – Don't do anything
- *str* – The post processing script as string

Note: This formatoption uses the built-in `exec()` function to compile the script. Since this poses a security risk when loading psyplot projects, it is by default disabled through the `Plotter.enable_post` attribute. If you are sure that you can trust the script in this formatoption, set this attribute of the corresponding `Plotter` to `True`

Examples

Assume, you want to manually add the mean of the data to the title of the matplotlib axes. You can simply do this via

```python
from psyplot.plotter import Plotter
from xarray import DataArray
plotter = Plotter(DataArray([1, 2, 3]))
# enable the post formatoption
plotter.enable_post = True
plotter.update(post="self.ax.set_title(str(self.data.mean()))")
plotter.ax.get_title()
'2.0'
```

By default, the `post` formatoption is only ran, when it is explicitly updated. However, you can use the *`post_timing`* formatoption, to run it automatically. E.g. for running it after every update of the plotter, you can set

```python
plotter.update(post_timing='always')
```

See also:

`post_timing` Determine the timing of this formatoption

Parameters

- **`key`** (*`str`*) – formatoption key in the *plotter*
- **`plotter`** (`psyplot.plotter.Plotter`) – Plotter instance that holds this formatoption. If None, it is assumed that this instance serves as a descriptor.
- **`index_in_list`** (*`int or None`*) – The index that shall be used if the data is a `psyplot.InteractiveList`
- **`additional_children`** (*`list or str`*) – Additional children to use (see the *`children`* attribute)
- **`additional_dependencies`** (*`list or str`*) – Additional dependencies to use (see the *`dependencies`* attribute)
- **`**kwargs`** – Further keywords may be used to specify different names for children, dependencies and connection formatoptions that match the setup of the plotter. Hence, keywords may be anything of the *`children`*, *`dependencies`* and `connections` attributes, with values being the name of the new formatoption in this plotter.

`children = ['post_timing']`

`data_dependent`

True if the corresponding *`post_timing`* formatoption is set to `'replot'` to run the post processing script after every change of the data

`default = None`

`dependencies = []`

`group = 'post_processing'`

`name = 'Custom post processing script'`

`post_timing`

post_timing Formatoption instance in the plotter

`priority = -inf`

update(*value*)

Method that is call to update the formatoption on the axes

Parameters **value** – Value to update

static validate()

Validation method of the formatoption

class psyplot.plotter.**PostTiming**(*key*, *plotter=None*, *index_in_list=None*, *additional_children=[]*, *additional_dependencies=[]*, ***kwargs*)

Bases: *psyplot.plotter.Formatoption*

Determine when to run the `post` formatoption

This formatoption determines, whether the `post` formatoption should be run never, after replot or after every update.

Possible types

Attributes

default	str(object='') -> str
group	str(object='') -> str
name	str(object='') -> str
priority	float(x) -> floating point number

Methods

get_fmt_widget(parent, project)	Get a widget to update the formatoption in the GUI
update(value)	Method that is call to update the formatoption on the axes
validate()	Validation method of the formatoption

- *'never'* – Never run post processing scripts
- *'always'* – Always run post processing scripts
- *'replot'* – Only run post processing scripts when the data changes or a replot is necessary

See also:

post The post processing formatoption

Parameters

- **key** (*str*) – formatoption key in the *plotter*
- **plotter** (psyplot.plotter.Plotter) – Plotter instance that holds this formatoption. If None, it is assumed that this instance serves as a descriptor.
- **index_in_list** (*int or None*) – The index that shall be used if the data is a `psyplot.InteractiveList`
- **additional_children** (*list or str*) – Additional children to use (see the `children` attribute)
- **additional_dependencies** (*list or str*) – Additional dependencies to use (see the `dependencies` attribute)

- **`**kwargs`** – Further keywords may be used to specify different names for children, dependencies and connection formatoptions that match the setup of the plotter. Hence, keywords may be anything of the `children`, `dependencies` and `connections` attributes, with values being the name of the new formatoption in this plotter.

`default = 'never'`

`get_fmt_widget`(*parent*, *project*)
Get a widget to update the formatoption in the GUI

This method should return a QWidget that is loaded by the psyplot-gui when the formatoption is selected in the `psyplot_gui.main.Mainwindow.fmt_widget`. It should call the **:method:'~psyplot_gui.fmt_widget.FormatoptionWidget.insert_text'** method when the update text for the formatoption should be changed.

Parameters

- **`parent`** (*`psyplot_gui.fmt_widget.FormatoptionWidget`*) – The parent widget that contains the returned QWidget
- **`project`** (`psyplot.project.Project`) – The current subproject (see *`psyplot.project.gcp()`*)

Returns The widget to control the formatoption

Return type PyQt5.QtWidgets.QWidget

`group = 'post_processing'`

`name = 'Timing of the post processing'`

`priority = -inf`

`update`(*value*)
Method that is call to update the formatoption on the axes

Parameters **`value`** – Value to update

`static validate`()
Validation method of the formatoption

`psyplot.plotter.`**`START = 30`**
Priority value of formatoptions that are updated before the data is loaded.

`psyplot.plotter.`**`default_print_func`**()
the default function to use when printing formatoption infos (the default is use print or in the gui, use the help explorer)

`psyplot.plotter.`**`format_time`**(*x*)
Formats date values

This function formats `datetime.datetime` and `datetime.timedelta` objects (and the corresponding numpy objects) using the `xarray.core.formatting.format_timestamp()` and the `xarray.core.formatting.format_timedelta()` functions.

Parameters **`x`** (*`object`*) – The value to format. If not a time object, the value is returned

Returns Either the formatted time object or the initial *x*

Return type str or *x*

`psyplot.plotter.`**`groups = {'axes': 'Axes formatoptions', 'colors': 'Color coding formatopt`**
`dict`. Mapping from group to group names

psyplot.plotter.**is_data_dependent**(*fmto*, *data*)

Check whether a formatoption is data dependent

Parameters

- **fmto** (Formatoption) – The *Formatoption* instance to check
- **data** (*xarray.DataArray*) – The data array to use if the *data_dependent* attribute is a callable

Returns True, if the formatoption depends on the data

Return type bool

psyplot.plugin_template module

Module for creating a new template for a psyplot plugin

Functions

main([args])	
new_plugin(odir[, py_name, version, description])	Create a new plugin for the psyplot package

psyplot.plugin_template.**main**(*args=None*)

psyplot.plugin_template.**new_plugin**(*odir*, *py_name=None*, *version='0.0.1.dev0'*, *description='New plugin'*)

Create a new plugin for the psyplot package

Parameters

- **odir** (*str*) – The name of the directory where the data will be copied to. The directory must not exist! The name of the directory also defines the name of the package.
- **py_name** (*str*) – The name of the python package. If None, the basename of *odir* is used (and `'-'` is replaced by `'_'`)
- **version** (*str*) – The version of the package
- **description** (*str*) – The description of the plugin

psyplot.project module

Project module of the psyplot Package

This module contains the *Project* class that serves as the main part of the psyplot API. One instance of the *Project* class serves as coordinator of multiple plots and can be distributed into subprojects that keep reference to the main project without holding all array instances

Furthermore this module contains an easy pyplot-like API to the current subproject.

Classes

Cdo(*args, **kwargs)	Subclass of the original cdo.Cdo class in the cdo.py module
DataArrayPlotter(da, *args, **kwargs)	Interface between the `xarray.Dataset` and the psyplot project
DataArrayPlotterInterface(methodname, . . . [, . . .])	Interface for the *DataArrayPlotter* to a plotter

Continued on next page

Table 67 – continued from previous page

DatasetPlotter(ds, *args, **kwargs)	Interface between the xarray.Dataset and the psyplot project
DatasetPlotterInterface(methodname, module, …)	Interface for the DatasetPlotter to a plotter
PROJECT_CLS	The project class that is used for creating new projects
PlotterInterface(methodname, module, … [, …])	Base class for visualizing a data array from an predefined plotter
Project(*args, **kwargs)	A manager of multiple interactive data projects
ProjectPlotter([project])	Plotting methods of the psyplot.project.Project class

Functions

close([num, figs, data, ds, remove_only])	Close the project
gcp([main])	Get the current project
get_project_nums()	Returns the project numbers of the open projects
multiple_subplots([rows, cols, maxplots, n, …])	Function to create subplots.
project([num])	Create a new main project
register_plotter(identifier, module, … [, …])	Register a psyplot.plotter.Plotter for the projects
scp(project)	Set the current project
unregister_plotter(identifier[, sorter, …])	Unregister a psyplot.plotter.Plotter for the projects

Data

plot	ProjectPlotter of the current project. See the class documentation

class psyplot.project.**Cdo**(**args*, ***kwargs*)

Bases: `cdo.Cdo`

Subclass of the original cdo.Cdo class in the cdo.py module

Requirements are a working cdo binary and the installed cdo.py python module.

For a documentation of an operator, use the python help function, for a list of operators, use the builtin dir function. Further documentation on the operators can be found here: https://code.zmaw.de/projects/cdo/wiki/Cdo%7Brbpy%7D and on the usage of the cdo.py module here: https://code.zmaw.de/projects/cdo

For a demonstration script on how cdos are implemented, see the examples of the psyplot package

Compared to the original cdo.Cdo class, the following things changed, the default cdf handler is the `psyplot.data.open_dataset()` function and the following keywords are implemented for each cdo operator. If any of those is specified, the return will be a subproject (i.e. an instance of `psyplot.project.Project`)

Other Parameters

- **plot_method** (*str or psyplot.project.PlotterInterface*) – An registered plotting function to plot the data (e.g. *psyplot.project.plot.mapplot* to plot on a map). If `None`, no plot will be created. In any case, the returned value is a subproject. If string, it must correspond to the attribute of the `psyplot.project.ProjectPlotter` class
- **name** (*str or list of str*) – The variable names to plot/extract

- **fmt** (*dict*) – Formatoptions that shall be when initializing the plot (you can however also specify them as extra keyword arguments)
- **make_plot** (*bool*) – If True, the data is plotted at the end. Otherwise you have to call the `psyplot.plotter.Plotter.initialize_plot()` method or the `psyplot.plotter.Plotter.reinit()` method by yourself
- **ax** (*None, tuple (x, y[, z]) or (list of) matplotlib.axes.Axes*) – Specifies the subplots on which to plot the new data objects.
  - If None, a new figure will be created for each created plotter
  - If tuple (x, y[, z]), *x* specifies the number of rows, *y* the number of columns and the optional third parameter *z* the maximal number of subplots per figure.
  - If `matplotlib.axes.Axes` (or list of those, e.g. created by the `matplotlib.pyplot.subplots()` function), the data will be plotted on these subplots
- **method** (*{'isel', None, 'nearest', ...}*) – Selection method of the xarray.Dataset to be used for setting the variables from the informations in *dims*. If *method* is 'isel', the `xarray.Dataset.isel()` method is used. Otherwise it sets the *method* parameter for the `xarray.Dataset.sel()` method.

Methods

`loadCdf`(*args, **kwargs)	Load data handler as specified by self.cdfMod

Examples

Calculate the timmean of a 3-dimensional array and plot it on a map using the psy-maps package

```
cdo = psy.Cdo()
sp = cdo.timmean(input='ifile.nc', name='temperature',
                 plot_method='mapplot')
```

which is essentially the same as

```
sp = cdo.timmean(input='ifile.nc', name='temperature',
                 plot_method=psy.plot.mapplot)
# and
sp = psy.plot.mapplot(
    cdo.timmean(input='ifile.nc', returnCdf=True),
    name='temperature', plot_method=psy.plot.mapplot)
```

loadCdf(**args*, ***kwargs*)
Load data handler as specified by self.cdfMod

class psyplot.project.**DataArrayPlotter**(*da*, **args*, ***kwargs*)
Bases: `psyplot.project.ProjectPlotter`

Interface between the `xarray.Dataset` and the psyplot project

This class can be used to make new plots from a given dataset and add them to the current `psyplot.project()` **Attributes**

`barplot`(*args, **kwargs)	Make a bar plot of one-dimensional data
`combined`(*args, **kwargs)	Plot a 2D scalar field with an overlying vector field

Continued on next page

Table 71 – continued from previous page

density(*args, **kwargs)	Make a density plot of point data
fldmean(*args, **kwargs)	Calculate and plot the mean over x- and y-dimensions
lineplot(*args, **kwargs)	Make a line plot of one-dimensional data
mapcombined(*args, **kwargs)	Plot a 2D scalar field with an overlying vector field on a map
mapplot(*args, **kwargs)	Plot a 2D scalar field on a map
mapvector(*args, **kwargs)	Plot a 2D vector field on a map
plot2d(*args, **kwargs)	Make a simple plot of a 2D scalar field
vector(*args, **kwargs)	Make a simple plot of a 2D vector field
violinplot(*args, **kwargs)	Make a violin plot of your data

barplot (**args*, ***kwargs*)

Make a bar plot of one-dimensional data

This plotting method visualizes the data via a `psy_simple.plotters.BarPlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.barplot()
```

Possible formatoptions are

alpha	axiscolor	color	coord
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	labelprops	labelsize	labelweight
legend	legendlabels	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	sym_lims	text
ticksize	tickweight	tight	title
titleprops	titlesize	titleweight	transpose
widths	xlabel	xlim	xrotation
xticklabels	xtickprops	xticks	ylabel
ylim	yrotation	yticklabels	ytickprops
yticks			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.barplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.barplot.summaries('title')

# show the full documentation
>>> da.psy.plot.barplot.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.barplot.plot
```

combined(**args*, ***kwargs*)
Plot a 2D scalar field with an overlying vector field

This plotting method visualizes the data via a `psy_simple.plotters.CombinedSimplePlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.combined()
```

Possible formatoptions are

arrowsize	arrowstyle	axiscolor	bounds
cbar	cbarspacing	clabel	clabelprops
clabelsize	clabelweight	cmap	color
cticklabels	ctickprops	cticks	cticksize
ctickweight	datagrid	density	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	interp_bounds	labelprops	labelsize
labelweight	levels	linewidth	maskbetween
maskgeq	maskgreater	maskleq	maskless
miss_color	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	vbounds	vcbar
vcbarspacing	vclabel	vclabelprops	vclabelsize
vclabelweight	vcmap	vcticklabels	vctickprops
vcticks	vcticksize	vctickweight	vplot
xlabel	xlim	xrotation	xticklabels
xtickprops	xticks	ylabel	ylim
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.combined.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.combined.summaries('title')

# show the full documentation
>>> da.psy.plot.combined.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.combined.plot
```

density(**args*, ***kwargs*)
Make a density plot of point data

This plotting method visualizes the data via a psy_simple.plotters.DensityPlotter plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.density()
```

Possible formatoptions are

axiscolor	bins	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	cmap	coord	cticklabels
ctickprops	cticks	cticksize	ctickweight
datagrid	density	extend	figtitle
figtitleprops	figtitlesize	figtitleweight	grid
interp_bounds	labelprops	labelsize	labelweight
levels	maskbetween	maskgeq	maskgreater
maskleq	maskless	miss_color	normed
plot	post	post_timing	precision
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrange	xrotation	xticklabels	xtickprops
xticks	ylabel	ylim	yrange
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the keys, summaries and docs methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.density.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.density.summaries('title')

# show the full documentation
>>> da.psy.plot.density.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.density.plot
```

fldmean(**args*, ***kwargs*)

Calculate and plot the mean over x- and y-dimensions

This plotting method visualizes the data via a psy_simple.plotters.FldmeanPlotter plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.fldmean()
```

Possible formatoptions are

axiscolor	color	coord	err_calc
error	erroralpha	figtitle	figtitleprops
figtitlesize	figtitleweight	grid	labelprops
labelsize	labelweight	legend	legendlabels
linewidth	marker	markersize	maskbetween
maskgeq	maskgreater	maskleq	maskless
mean	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrotation	xticklabels	xtickprops	xticks
ylabel	ylim	yrotation	yticklabels
ytickprops	yticks		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.fldmean.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.fldmean.summaries('title')

# show the full documentation
>>> da.psy.plot.fldmean.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.fldmean.plot
```

lineplot(**args*, ***kwargs*)

Make a line plot of one-dimensional data

This plotting method visualizes the data via a `psy_simple.plotters.LinePlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.lineplot()
```

Possible formatoptions are

axiscolor	color	coord	error
erroralpha	figtitle	figtitleprops	figtitlesize
figtitleweight	grid	labelprops	labelsize
labelweight	legend	legendlabels	linewidth
marker	markersize	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	sym_lims	text
ticksize	tickweight	tight	title
titleprops	titlesize	titleweight	transpose
xlabel	xlim	xrotation	xticklabels
xtickprops	xticks	ylabel	ylim
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.lineplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.lineplot.summaries('title')

# show the full documentation
>>> da.psy.plot.lineplot.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.lineplot.plot
```

mapcombined(**args*, ***kwargs*)

Plot a 2D scalar field with an overlying vector field on a map

This plotting method visualizes the data via a `psy_maps.plotters.CombinedPlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.mapcombined()
```

Possible formatoptions are

arrowsize	arrowstyle	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	clat	clip	clon
cmap	color	cticklabels	ctickprops
cticks	cticksize	ctickweight	datagrid
density	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	interp_bounds	levels
linewidth	lonlatbox	lsm	map_extent
maskbetween	maskgeq	maskgreater	maskleq
maskless	miss_color	plot	post
post_timing	projection	stock_img	text
tight	title	titleprops	titlesize
titleweight	transform	vbounds	vcbar
vcbarspacing	vclabel	vclabelprops	vclabelsize
vclabelweight	vcmap	vcticklabels	vctickprops
vcticks	vcticksize	vctickweight	vplot
xgrid	ygrid		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.mapcombined.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.mapcombined.summaries('title')

# show the full documentation
>>> da.psy.plot.mapcombined.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.mapcombined.plot
```

mapplot(**args*, ***kwargs*)

Plot a 2D scalar field on a map

This plotting method visualizes the data via a `psy_maps.plotters.FieldPlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.mapplot()
```

Possible formatoptions are

bounds	cbar	cbarspacing	clabel
clabelprops	clabelsize	clabelweight	clat
clip	clon	cmap	cticklabels
ctickprops	cticks	cticksize	ctickweight
datagrid	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	interp_bounds	levels
lonlatbox	lsm	map_extent	maskbetween
maskgeq	maskgreater	maskleq	maskless
miss_color	plot	post	post_timing
projection	stock_img	text	tight
title	titleprops	titlesize	titleweight
transform	xgrid	ygrid	

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.mapplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.mapplot.summaries('title')

# show the full documentation
>>> da.psy.plot.mapplot.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.mapplot.plot
```

mapvector(**args*, ***kwargs*)

Plot a 2D vector field on a map

This plotting method visualizes the data via a `psy_maps.plotters.VectorPlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.mapvector()
```

Possible formatoptions are

arrowsize	arrowstyle	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	clat	clip	clon
cmap	color	cticklabels	ctickprops
cticks	cticksize	ctickweight	datagrid
density	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	linewidth	lonlatbox
lsm	map_extent	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	projection	stock_img
text	tight	title	titleprops
titlesize	titleweight	transform	xgrid
ygrid			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.mapvector.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.mapvector.summaries('title')

# show the full documentation
>>> da.psy.plot.mapvector.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.mapvector.plot
```

plot2d(**args*, ***kwargs*)

Make a simple plot of a 2D scalar field

This plotting method visualizes the data via a `psy_simple.plotters.Simple2DPlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.plot2d()
```

Possible formatoptions are

axiscolor	bounds	cbar	cbarspacing
clabel	clabelprops	clabelsize	clabelweight
cmap	cticklabels	ctickprops	cticks
cticksize	ctickweight	datagrid	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	interp_bounds	labelprops	labelsize
labelweight	levels	maskbetween	maskgeq
maskgreater	maskleq	maskless	miss_color
plot	post	post_timing	sym_lims
text	ticksize	tickweight	tight
title	titleprops	titlesize	titleweight
transpose	xlabel	xlim	xrotation
xticklabels	xtickprops	xticks	ylabel
ylim	yrotation	yticklabels	ytickprops
yticks			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.plot2d.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.plot2d.summaries('title')

# show the full documentation
>>> da.psy.plot.plot2d.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.plot2d.plot
```

vector(**args*, ***kwargs*)

Make a simple plot of a 2D vector field

This plotting method visualizes the data via a `psy_simple.plotters.SimpleVectorPlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.vector()
```

Possible formatoptions are

arrowsize	arrowstyle	axiscolor	bounds
cbar	cbarspacing	clabel	clabelprops
clabelsize	clabelweight	cmap	color
cticklabels	ctickprops	cticks	cticksize
ctickweight	datagrid	density	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	labelprops	labelsize	labelweight
linewidth	maskbetween	maskgeq	maskgreater
maskleq	maskless	plot	post
post_timing	sym_lims	text	ticksize
tickweight	tight	title	titleprops
titlesize	titleweight	transpose	xlabel
xlim	xrotation	xticklabels	xtickprops
xticks	ylabel	ylim	yrotation
yticklabels	ytickprops	yticks	

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.vector.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.vector.summaries('title')

# show the full documentation
>>> da.psy.plot.vector.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.vector.plot
```

violinplot(**args*, ***kwargs*)

Make a violin plot of your data

This plotting method visualizes the data via a `psy_simple.plotters.ViolinPlotter` plotters

To plot a variable in this dataset, type:

```
>>> da.psy.plot.violinplot()
```

Possible formatoptions are

axiscolor	color	figtitle	figtitleprops
figtitlesize	figtitleweight	grid	labelprops
labelsize	labelweight	legend	legendlabels
maskbetween	maskgeq	maskgreater	maskleq
maskless	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrotation	xticklabels	xtickprops	xticks
ylabel	ylim	yrotation	yticklabels
ytickprops	yticks		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> da.psy.plot.violinplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> da.psy.plot.violinplot.summaries('title')

# show the full documentation
>>> da.psy.plot.violinplot.docs('plot')

# or access the documentation via the attribute
>>> da.psy.plot.violinplot.plot
```

class psyplot.project.**DataArrayPlotterInterface**(*methodname*, *module*, *plotter_name*, *project_plotter=None*)

Bases: `psyplot.project.PlotterInterface`

Interface for the `DataArrayPlotter` to a plotter **Methods**

`check_data`(*args, **kwargs)	Check whether the plotter of this plot method can visualize the data

check_data(**args*, ***kwargs*)
Check whether the plotter of this plot method can visualize the data

class psyplot.project.**DatasetPlotter**(*ds*, **args*, ***kwargs*)
Bases: `psyplot.project.ProjectPlotter`

Interface between the `xarray.Dataset` and the psyplot project

This class can be used to make new plots from a given dataset and add them to the current `psyplot.project()` **Attributes**

`barplot`(*args, **kwargs)	Make a bar plot of one-dimensional data
`combined`(*args, **kwargs)	Plot a 2D scalar field with an overlying vector field

Continued on next page

Table 73 – continued from previous page

`density`(*args, **kwargs)	Make a density plot of point data
`fldmean`(*args, **kwargs)	Calculate and plot the mean over x- and y-dimensions
`lineplot`(*args, **kwargs)	Make a line plot of one-dimensional data
`mapcombined`(*args, **kwargs)	Plot a 2D scalar field with an overlying vector field on a map
`mapplot`(*args, **kwargs)	Plot a 2D scalar field on a map
`mapvector`(*args, **kwargs)	Plot a 2D vector field on a map
`plot2d`(*args, **kwargs)	Make a simple plot of a 2D scalar field
`vector`(*args, **kwargs)	Make a simple plot of a 2D vector field
`violinplot`(*args, **kwargs)	Make a violin plot of your data

barplot (**args*, ***kwargs*)

Make a bar plot of one-dimensional data

This plotting method adds data arrays and plots them via `psy_simple.plotters.BarPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.barplot(name=['my_variable'], ...)
```

Possible formatoptions are

alpha	axiscolor	color	coord
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	labelprops	labelsize	labelweight
legend	legendlabels	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	sym_lims	text
ticksize	tickweight	tight	title
titleprops	titlesize	titleweight	transpose
widths	xlabel	xlim	xrotation
xticklabels	xtickprops	xticks	ylabel
ylim	yrotation	yticklabels	ytickprops
yticks			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.barplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.barplot.summaries('title')

# show the full documentation
>>> ds.psy.plot.barplot.docs('plot')
```

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```
# or access the documentation via the attribute
>>> ds.psy.plot.barplot.plot
```

combined(**args*, ***kwargs*)

Plot a 2D scalar field with an overlying vector field

This plotting method adds data arrays and plots them via `psy_simple.plotters.CombinedSimplePlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.combined(name=[['my_variable', ['u_var', 'v_var']]], ...)
```

Possible formatoptions are

arrowsize	arrowstyle	axiscolor	bounds
cbar	cbarspacing	clabel	clabelprops
clabelsize	clabelweight	cmap	color
cticklabels	ctickprops	cticks	cticksize
ctickweight	datagrid	density	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	interp_bounds	labelprops	labelsize
labelweight	levels	linewidth	maskbetween
maskgeq	maskgreater	maskleq	maskless
miss_color	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	vbounds	vcbar
vcbarspacing	vclabel	vclabelprops	vclabelsize
vclabelweight	vcmap	vcticklabels	vctickprops
vcticks	vcticksize	vctickweight	vplot
xlabel	xlim	xrotation	xticklabels
xtickprops	xticks	ylabel	ylim
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.combined.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.combined.summaries('title')

# show the full documentation
>>> ds.psy.plot.combined.docs('plot')
```

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(continued from previous page)

```
# or access the documentation via the attribute
>>> ds.psy.plot.combined.plot
```

density (**args*, ***kwargs*)

Make a density plot of point data

This plotting method adds data arrays and plots them via `psy_simple.plotters.DensityPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.density(name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	bins	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	cmap	coord	cticklabels
ctickprops	cticks	cticksize	ctickweight
datagrid	density	extend	figtitle
figtitleprops	figtitlesize	figtitleweight	grid
interp_bounds	labelprops	labelsize	labelweight
levels	maskbetween	maskgeq	maskgreater
maskleq	maskless	miss_color	normed
plot	post	post_timing	precision
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrange	xrotation	xticklabels	xtickprops
xticks	ylabel	ylim	yrange
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.density.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.density.summaries('title')

# show the full documentation
>>> ds.psy.plot.density.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.density.plot
```

fldmean(**args*, ***kwargs*)

Calculate and plot the mean over x- and y-dimensions

This plotting method adds data arrays and plots them via `psy_simple.plotters.FldmeanPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.fldmean(name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	color	coord	err_calc
error	erroralpha	figtitle	figtitleprops
figtitlesize	figtitleweight	grid	labelprops
labelsize	labelweight	legend	legendlabels
linewidth	marker	markersize	maskbetween
maskgeq	maskgreater	maskleq	maskless
mean	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrotation	xticklabels	xtickprops	xticks
ylabel	ylim	yrotation	yticklabels
ytickprops	yticks		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.fldmean.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.fldmean.summaries('title')

# show the full documentation
>>> ds.psy.plot.fldmean.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.fldmean.plot
```

lineplot(**args*, ***kwargs*)

Make a line plot of one-dimensional data

This plotting method adds data arrays and plots them via `psy_simple.plotters.LinePlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.lineplot(name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	color	coord	error
erroralpha	figtitle	figtitleprops	figtitlesize
figtitleweight	grid	labelprops	labelsize
labelweight	legend	legendlabels	linewidth
marker	markersize	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	sym_lims	text
ticksize	tickweight	tight	title
titleprops	titlesize	titleweight	transpose
xlabel	xlim	xrotation	xticklabels
xtickprops	xticks	ylabel	ylim
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.lineplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.lineplot.summaries('title')

# show the full documentation
>>> ds.psy.plot.lineplot.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.lineplot.plot
```

mapcombined(**args*, ***kwargs*)

Plot a 2D scalar field with an overlying vector field on a map

This plotting method adds data arrays and plots them via `psy_maps.plotters.CombinedPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.mapcombined(name=[['my_variable', ['u_var', 'v_var']]], ...)
```

Possible formatoptions are

arrowsize	arrowstyle	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	clat	clip	clon
cmap	color	cticklabels	ctickprops
cticks	cticksize	ctickweight	datagrid
density	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	interp_bounds	levels
linewidth	lonlatbox	lsm	map_extent
maskbetween	maskgeq	maskgreater	maskleq
maskless	miss_color	plot	post
post_timing	projection	stock_img	text
tight	title	titleprops	titlesize
titleweight	transform	vbounds	vcbar
vcbarspacing	vclabel	vclabelprops	vclabelsize
vclabelweight	vcmap	vcticklabels	vctickprops
vcticks	vcticksize	vctickweight	vplot
xgrid	ygrid		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.mapcombined.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.mapcombined.summaries('title')

# show the full documentation
>>> ds.psy.plot.mapcombined.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.mapcombined.plot
```

mapplot(**args*, ***kwargs*)

Plot a 2D scalar field on a map

This plotting method adds data arrays and plots them via `psy_maps.plotters.FieldPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.mapplot(name=['my_variable'], ...)
```

Possible formatoptions are

bounds	cbar	cbarspacing	clabel
clabelprops	clabelsize	clabelweight	clat
clip	clon	cmap	cticklabels
ctickprops	cticks	cticksize	ctickweight
datagrid	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	interp_bounds	levels
lonlatbox	lsm	map_extent	maskbetween
maskgeq	maskgreater	maskleq	maskless
miss_color	plot	post	post_timing
projection	stock_img	text	tight
title	titleprops	titlesize	titleweight
transform	xgrid	ygrid	

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.mapplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.mapplot.summaries('title')

# show the full documentation
>>> ds.psy.plot.mapplot.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.mapplot.plot
```

mapvector(**args*, ***kwargs*)

Plot a 2D vector field on a map

This plotting method adds data arrays and plots them via `psy_maps.plotters.VectorPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.mapvector(name=[['u_var', 'v_var']], ...)
```

Possible formatoptions are

arrowsize	arrowstyle	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	clat	clip	clon
cmap	color	cticklabels	ctickprops
cticks	cticksize	ctickweight	datagrid
density	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	linewidth	lonlatbox
lsm	map_extent	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	projection	stock_img
text	tight	title	titleprops
titlesize	titleweight	transform	xgrid
ygrid			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.mapvector.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.mapvector.summaries('title')

# show the full documentation
>>> ds.psy.plot.mapvector.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.mapvector.plot
```

plot2d(**args*, ***kwargs*)

Make a simple plot of a 2D scalar field

This plotting method adds data arrays and plots them via `psy_simple.plotters.Simple2DPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.plot2d(name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	bounds	cbar	cbarspacing
clabel	clabelprops	clabelsize	clabelweight
cmap	cticklabels	ctickprops	cticks
cticksize	ctickweight	datagrid	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	interp_bounds	labelprops	labelsize
labelweight	levels	maskbetween	maskgeq
maskgreater	maskleq	maskless	miss_color
plot	post	post_timing	sym_lims
text	ticksize	tickweight	tight
title	titleprops	titlesize	titleweight
transpose	xlabel	xlim	xrotation
xticklabels	xtickprops	xticks	ylabel
ylim	yrotation	yticklabels	ytickprops
yticks			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.plot2d.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.plot2d.summaries('title')

# show the full documentation
>>> ds.psy.plot.plot2d.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.plot2d.plot
```

vector(**args*, ***kwargs*)

Make a simple plot of a 2D vector field

This plotting method adds data arrays and plots them via `psy_simple.plotters.SimpleVectorPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.vector(name=[['u_var', 'v_var']], ...)
```

Possible formatoptions are

arrowsize	arrowstyle	axiscolor	bounds
cbar	cbarspacing	clabel	clabelprops
clabelsize	clabelweight	cmap	color
cticklabels	ctickprops	cticks	cticksize
ctickweight	datagrid	density	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	labelprops	labelsize	labelweight
linewidth	maskbetween	maskgeq	maskgreater
maskleq	maskless	plot	post
post_timing	sym_lims	text	ticksize
tickweight	tight	title	titleprops
titlesize	titleweight	transpose	xlabel
xlim	xrotation	xticklabels	xtickprops
xticks	ylabel	ylim	yrotation
yticklabels	ytickprops	yticks	

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.vector.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.vector.summaries('title')

# show the full documentation
>>> ds.psy.plot.vector.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.vector.plot
```

violinplot(**args*, ***kwargs*)

Make a violin plot of your data

This plotting method adds data arrays and plots them via `psy_simple.plotters.ViolinPlotter` plotters

To plot a variable in this dataset, type:

```
>>> ds.psy.plot.violinplot(name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	color	figtitle	figtitleprops
figtitlesize	figtitleweight	grid	labelprops
labelsize	labelweight	legend	legendlabels
maskbetween	maskgeq	maskgreater	maskleq
maskless	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrotation	xticklabels	xtickprops	xticks
ylabel	ylim	yrotation	yticklabels
ytickprops	yticks		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
# show the keys corresponding to a group or multiple
# formatopions
>>> ds.psy.plot.violinplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> ds.psy.plot.violinplot.summaries('title')

# show the full documentation
>>> ds.psy.plot.violinplot.docs('plot')

# or access the documentation via the attribute
>>> ds.psy.plot.violinplot.plot
```

class psyplot.project.**DatasetPlotterInterface**(*methodname*, *module*, *plotter_name*, *project_plotter=None*)

Bases: *psyplot.project.PlotterInterface*

Interface for the *DatasetPlotter* to a plotter

`arr_names`	Names of the arrays (!not of the variables!) in this list
`axes`	A mapping from axes to data objects with the plotter in this axes
`barplot`	List of data arrays that are plotted by `psy_simple.plotters.BarPlotter` plotters
`block_signals`([value])	Wrapper around a boolean defining an __enter__ and __exit__ method
`combined`	List of data arrays that are plotted by `psy_simple.plotters.CombinedSimplePlotter` plo
`datasets`	A mapping from dataset numbers to datasets in this list
`density`	List of data arrays that are plotted by `psy_simple.plotters.DensityPlotter` plotters
`dsnames`	The set of dataset names in this instance
`dsnames_map`	A dictionary from the dataset numbers in this list to their
`figs`	A mapping from figures to data objects with the plotter in this
`fldmean`	List of data arrays that are plotted by `psy_simple.plotters.FldmeanPlotter` plotters
`is_main`	`bool`. True if this *Project* is a main project
`lineplot`	List of data arrays that are plotted by `psy_simple.plotters.LinePlotter` plotters
`logger`	`logging.Logger` of this instance

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Table 74 – continued from previous page

main	*Project*. The main project of this subproject
mapcombined	List of data arrays that are plotted by psy_maps.plotters.CombinedPlotter plotters
mapplot	List of data arrays that are plotted by psy_maps.plotters.FieldPlotter plotters
maps	List of data arrays that are plotted by psy_maps.plotters.MapPlotter plotters
mapvector	List of data arrays that are plotted by psy_maps.plotters.VectorPlotter plotters
oncpchange	Signal to connect functions to a specific event
plot	Plotting instance of this *Project*.
plot2d	List of data arrays that are plotted by psy_simple.plotters.Simple2DPlotter plotters
plotters	A list of all the plotters in this instance
simple	List of data arrays that are plotted by psy_simple.plotters.SimplePlotterBase plotters
vector	List of data arrays that are plotted by psy_simple.plotters.SimpleVectorPlotter plotte
violinplot	List of data arrays that are plotted by psy_simple.plotters.ViolinPlotter plotters
with_plotter	The arrays in this instance that are visualized with a plotter

psyplot.project.**PROJECT_CLS**

Methods

append(*args, **kwargs)	Append a new array to the list
close([figs, data, ds, remove_only])	Close this project instance
disable()	Disables the plotters in this list
docs(*args, **kwargs)	Show the available formatoptions in this project and their full docu
enable()	
export(output[, tight, concat, close_pdf, ...])	Exports the figures of the project to one or more image files
extend(*args, **kwargs)	Add further arrays from an iterable to this list
from_dataset(*args, **kwargs)	Construct an ArrayList instance from an existing base dataset
joined_attrs([delimiter, enhanced, ...])	Join the attributes of the arrays in this project
keys(*args, **kwargs)	Show the available formatoptions in this project
load_project(fname[, auto_update, ...])	Load a project from a file or dict
new([num])	Create a new main project
save_project([fname, pwd, pack])	Save this project to a file
scp(project)	Set the current project
share([base, keys, by])	Share the formatoptions of one plotter with all the others
show()	Shows all open figures
summaries(*args, **kwargs)	Show the available formatoptions and their summaries in this project
unshare(**kwargs)	Unshare the formatoptions of all the plotters in this instance

Attributes

The project class that is used for creating new projects

alias of *psyplot.project.Project*

class psyplot.project.**PlotterInterface**(*methodname*, *module*, *plotter_name*, *project_plotter=None*)

Bases: object

Base class for visualizing a data array from an predefined plotter

See the `__call__()` method for details on plotting. **Methods**

`check_data`(ds, name, dims)	A validation method for the data shape
`docs`(*args, **kwargs)	Method to print the full documentations of the formatoptions
`keys`(*args, **kwargs)	Classmethod to return a nice looking table with the given formatoptions
`summaries`(*args, **kwargs)	Method to print the summaries of the formatoptions

Attributes

`plotter_cls`	The plotter class
`print_func`	The function that is used to return a formatoption

check_data (*ds*, *name*, *dims*)

A validation method for the data shape

Parameters

- **name** (*list of lists of strings*) – The variable names (see the `check_data()` method of the `plotter_cls` attribute for details)
- **dims** (*list of dictionaries*) – The dimensions of the arrays. It will be enhanced by the default dimensions of this plot method
- **is_unstructured** (*bool or list of bool*) – True if the corresponding array is unstructured.

Returns

- *list of bool or None* – True, if everything is okay, False in case of a serious error, None if it is intermediate. Each object in this list corresponds to one in the given *name*
- *list of str* – The message giving more information on the reason. Each object in this list corresponds to one in the given *name*

docs (**args*, ***kwargs*)

Method to print the full documentations of the formatoptions

Parameters

- **keys** (*list of str or None*) – If None, the all formatoptions of the given class are used. Group names from the `psyplot.plotter.groups` mapping are replaced by the formatoptions
- **indent** (*int*) – The indentation of the table
- **grouped** (*bool, optional*) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the `psyplot.plotter.Plotter.include_links` attribute.

- **“*args,**kwargs“** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

See also:

keys(), *docs()*

keys(**args*, ***kwargs*)

Classmethod to return a nice looking table with the given formatoptions

Parameters

- **keys** (*list of str or None*) – If None, the all formatoptions of the given class are used. Group names from the *psyplot.plotter.groups* mapping are replaced by the formatoptions
- **indent** (*int*) – The indentation of the table
- **grouped** (*bool, optional*) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the *psyplot.plotter.Plotter.include_links* attribute.
- **“*args,**kwargs“** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

See also:

summaries(), *docs()*

plotter_cls

The plotter class

print_func

The function that is used to return a formatoption

By default the `print()` function is used (i.e. it is printed to the terminal)

summaries(**args*, ***kwargs*)

Method to print the summaries of the formatoptions

Parameters

- **keys** (*list of str or None*) – If None, the all formatoptions of the given class are used. Group names from the *psyplot.plotter.groups* mapping are replaced by the formatoptions
- **indent** (*int*) – The indentation of the table

- **grouped** (*bool, optional*) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the *psyplot.plotter.Plotter.include_links* attribute.
- **``*args,**kwargs``** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

See also:

keys(), *docs()*

class psyplot.project.**Project**(**args*, ***kwargs*)
Bases: *psyplot.data.ArrayList*

A manager of multiple interactive data projects

Parameters

- **iterable** (*iterable*) – The iterable (e.g. another list) defining this list
- **attrs** (*dict-like or iterable, optional*) – Global attributes of this list
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter
- **main** (`Project`) – The main project this subproject belongs to (or None if this project is the main project)
- **num** (*int*) – The number of the project

Methods

append(*args, **kwargs)	Append a new array to the list
close([figs, data, ds, remove_only])	Close this project instance
disable()	Disables the plotters in this list
docs(*args, **kwargs)	Show the available formatoptions in this project and their full docu
enable()	

Continued on next page

Table 78 – continued from previous page

`export`(output[, tight, concat, close_pdf, . . .])	Exports the figures of the project to one or more image files
`extend`(*args, **kwargs)	Add further arrays from an iterable to this list
`from_dataset`(*args, **kwargs)	Construct an ArrayList instance from an existing base dataset
`joined_attrs`([delimiter, enhanced, . . .])	Join the attributes of the arrays in this project
`keys`(*args, **kwargs)	Show the available formatoptions in this project
`load_project`(fname[, auto_update, . . .])	Load a project from a file or dict
`new`([num])	Create a new main project
`save_project`([fname, pwd, pack])	Save this project to a file
`scp`(project)	Set the current project
`share`([base, keys, by])	Share the formatoptions of one plotter with all the others
`show`()	Shows all open figures
`summaries`(*args, **kwargs)	Show the available formatoptions and their summaries in this project
`unshare`(**kwargs)	Unshare the formatoptions of all the plotters in this instance

Attributes

`arr_names`	Names of the arrays (!not of the variables!) in this list
`axes`	A mapping from axes to data objects with the plotter in this axes
`barplot`	List of data arrays that are plotted by `psy_simple.plotters.BarPlotter` plotters
`block_signals`([value])	Wrapper around a boolean defining an __enter__ and __exit__ method
`combined`	List of data arrays that are plotted by `psy_simple.plotters.CombinedSimplePlotter` plotters
`datasets`	A mapping from dataset numbers to datasets in this list
`density`	List of data arrays that are plotted by `psy_simple.plotters.DensityPlotter` plotters
`dsnames`	The set of dataset names in this instance
`dsnames_map`	A dictionary from the dataset numbers in this list to their
`figs`	A mapping from figures to data objects with the plotter in this
`fldmean`	List of data arrays that are plotted by `psy_simple.plotters.FldmeanPlotter` plotters
`is_main`	`bool`. True if this `Project` is a main project
`lineplot`	List of data arrays that are plotted by `psy_simple.plotters.LinePlotter` plotters
`logger`	`logging.Logger` of this instance
`main`	`Project`. The main project of this subproject
`mapcombined`	List of data arrays that are plotted by `psy_maps.plotters.CombinedPlotter` plotters
`mapplot`	List of data arrays that are plotted by `psy_maps.plotters.FieldPlotter` plotters
`maps`	List of data arrays that are plotted by `psy_maps.plotters.MapPlotter` plotters
`mapvector`	List of data arrays that are plotted by `psy_maps.plotters.VectorPlotter` plotters

Continued on next page

Table 79 – continued from previous page

oncpchange	signal to be emiitted when the current main and/or sub-project changes
plot	Plotting instance of this *Project*.
plot2d	List of data arrays that are plotted by `psy_simple.plotters.Simple2DPlotter` plotters
plotters	A list of all the plotters in this instance
simple	List of data arrays that are plotted by `psy_simple.plotters.SimplePlotterBase` plotters
vector	List of data arrays that are plotted by `psy_simple.plotters.SimpleVectorPlotter` plotters
violinplot	List of data arrays that are plotted by `psy_simple.plotters.ViolinPlotter` plotters
with_plotter	The arrays in this instance that are visualized with a plotter

append(**args*, ***kwargs*)

Append a new array to the list

Parameters

- **value** (`InteractiveBase`) – The data object to append to this list
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Raises

- `ValueError` – If it was impossible to find a name that isn't already in the list
- `ValueError` – If *new_name* is False and the array is already in the list

See also:

`list.append()`, *extend()*, `rename()`

arr_names

Names of the arrays (!not of the variables!) in this list

This attribute can be set with an iterable of unique names to change the array names of the data objects in this list.

axes

A mapping from axes to data objects with the plotter in this axes

barplot

List of data arrays that are plotted by `psy_simple.plotters.BarPlotter` plotters

block_signals(*value=None*)

Wrapper around a boolean defining an __enter__ and __exit__ method

Notes

If you want to use this class as an instance property, rather use the `_temp_bool_prop()` because this class as a descriptor is ment to be a class descriptor

close (*figs=True*, *data=False*, *ds=False*, *remove_only=False*)
Close this project instance

Parameters

- **figs** (`bool`) – Close the figures
- **data** (`bool`) – delete the arrays from the (main) project
- **ds** (`bool`) – If True, close the dataset as well
- **remove_only** (`bool`) – If True and *figs* is True, the figures are not closed but the plotters are removed

combined
List of data arrays that are plotted by `psy_simple.plotters.CombinedSimplePlotter` plotters

datasets
A mapping from dataset numbers to datasets in this list

density
List of data arrays that are plotted by `psy_simple.plotters.DensityPlotter` plotters

disable ()
Disables the plotters in this list

docs (**args*, ***kwargs*)
Show the available formatoptions in this project and their full docu

Parameters

- **keys** (`list of str or None`) – If None, the all formatoptions of the given class are used. Group names from the `psyplot.plotter.groups` mapping are replaced by the formatoptions
- **indent** (`int`) – The indentation of the table
- **grouped** (`bool, optional`) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the `psyplot.plotter.Plotter.include_links` attribute.
- **‘‘*args,**kwargs‘‘** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

dsnames
The set of dataset names in this instance

dsnames_map
A dictionary from the dataset numbers in this list to their filenames

enable()

export(*output*, *tight=False*, *concat=True*, *close_pdf=None*, *use_time=False*, ***kwargs*)

Exports the figures of the project to one or more image files

Parameters

- **output** (*str, iterable or* `matplotlib.backends.backend_pdf.PdfPages`) – if string or list of strings, those define the names of the output files. Otherwise you may provide an instance of `matplotlib.backends.backend_pdf.PdfPages` to save the figures in it. If string (or iterable of strings), attribute names in the xarray.DataArray.attrs attribute as well as index dimensions are replaced by the respective value (see examples below). Furthermore a single format string without key (e.g. %i, %s, %d, etc.) is replaced by a counter.
- **tight** (*bool*) – If True, it is tried to figure out the tight bbox of the figure (same as bbox_inches='tight')
- **concat** (*bool*) – if True and the output format is *pdf*, all figures are concatenated into one single pdf
- **close_pdf** (*bool or None*) – If True and the figures are concatenated into one single pdf, the resulting pdf instance is closed. If False it remains open. If None and *output* is a string, it is the same as `close_pdf=True`, if None and *output* is neither a string nor an iterable, it is the same as `close_pdf=False`
- **use_time** (*bool*) – If True, formatting strings for the `datetime.datetime.strftime()` are expected to be found in *output* (e.g. `'%m'`, `'%Y'`, etc.). If so, other formatting strings must be escaped by double `'%'` (e.g. `'%%i'` instead of (`'%i'`))
- ****kwargs** – Any valid keyword for the `matplotlib.pyplot.savefig()` function

Returns a PdfPages instance if output is a string and close_pdf is False, otherwise None

Return type matplotlib.backends.backend_pdf.PdfPages or None

Examples

Simply save all figures into one single pdf:

```
>>> p = psy.gcp()
>>> p.export('my_plots.pdf')
```

Save all figures into separate pngs with increasing numbers (e.g. `'my_plots_1.png'`):

```
>>> p.export('my_plots_%i.png')
```

Save all figures into separate pngs with the name of the variables shown in each figure (e.g. `'my_plots_t2m.png'`):

```
>>> p.export('my_plots_%(name)s.png')
```

Save all figures into separate pngs with the name of the variables shown in each figure and with increasing numbers (e.g. `'my_plots_1_t2m.png'`):

```
>>> p.export('my_plots_%i_%(name)s.png')
```

Specify the names for each figure directly via a list:

```
>>> p.export(['my_plots1.pdf', 'my_plots2.pdf'])
```

extend(**args*, ***kwargs*)
Add further arrays from an iterable to this list

Parameters

- **iterable** – Any iterable that contains `InteractiveBase` instances
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

Raises

- `ValueError` – If it was impossible to find a name that isn't already in the list
- `ValueError` – If *new_name* is False and the array is already in the list

See also:

`list.extend()`, *append()*, `rename()`

figs
A mapping from figures to data objects with the plotter in this figure

fldmean
List of data arrays that are plotted by `psy_simple.plotters.FldmeanPlotter` plotters

classmethod from_dataset(**args*, ***kwargs*)
Construct an ArrayList instance from an existing base dataset

Parameters

- **base** (*xarray.Dataset*) – Dataset instance that is used as reference
- **method** (*{'isel', None, 'nearest', ..}*) – Selection method of the xarray.Dataset to be used for setting the variables from the informations in *dims*. If *method* is 'isel', the `xarray.Dataset.isel()` method is used. Otherwise it sets the *method* parameter for the `xarray.Dataset.sel()` method.
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **prefer_list** (*bool*) – If True and multiple variable names pher array are found, the `InteractiveList` class is used. Otherwise the arrays are put together into one `InteractiveArray`.
- **default_slice** (*indexer*) – Index (e.g. 0 if *method* is 'isel') that shall be used for dimensions not covered by *dims* and *furtherdims*. If None, the whole slice will be used.
- **decoder** (*CFDecoder*) – The decoder that shall be used to decoder the *base* dataset
- **squeeze** (*bool, optional*) – Default True. If True, and the created arrays have a an axes with length 1, it is removed from the dimension list (e.g. an array with shape (3, 4, 1, 5) will be squeezed to shape (3, 4, 5))

- **attrs** (*dict, optional*) – Meta attributes that shall be assigned to the selected data arrays (additional to those stored in the *base* dataset)
- **load** (*bool or dict*) – If True, load the data from the dataset using the `xarray.DataArray.load()` method. If `dict`, those will be given to the above mentioned `load` method
- **main** (`Project`) – The main project that this project corresponds to

Other Parameters

- **arr_names** (*string, list of strings or dictionary*) – Set the unique array names of the resulting arrays and (optionally) dimensions.
  - if string: same as list of strings (see below). Strings may include {0} which will be replaced by a counter.
  - list of strings: those will be used for the array names. The final number of dictionaries in the return depend in this case on the *dims* and `**furtherdims`
  - dictionary: Then nothing happens and an `OrderedDict` version of *arr_names* is returned.
- **sort** (*list of strings*) – This parameter defines how the dictionaries are ordered. It has no effect if *arr_names* is a dictionary (use a `OrderedDict` for that). It can be a list of dimension strings matching to the dimensions in *dims* for the variable.
- **dims** (*dict*) – Keys must be variable names of dimensions (e.g. time, level, lat or lon) or 'name' for the variable name you want to choose. Values must be values of that dimension or iterables of the values (e.g. lists). Note that strings will be put into a list. For example dims = {'name': 't2m', 'time': 0} will result in one plot for the first time step, whereas dims = {'name': 't2m', 'time': [0, 1]} will result in two plots, one for the first (time == 0) and one for the second (time == 1) time step.
- **``**kwargs``** – The same as *dims* (those will update what is specified in *dims*)

Returns The newly created project instance

Return type *Project*

is_main
`bool`. True if this *Project* is a main project

joined_attrs (*delimiter=', '*, *enhanced=True*, *plot_data=False*, *keep_all=True*)
Join the attributes of the arrays in this project

Parameters

- **delimiter** (*str*) – The string that shall be used as the delimiter in case that there are multiple values for one attribute in the arrays. If None, they will be returned as sets
- **enhanced** (*bool*) – If True, the *psyplot.plotter.Plotter.get_enhanced_attrs()* method is used, otherwise the `xarray.DataArray.attrs` attribute is used.
- **plot_data** (*bool*) – It True, use the *psyplot.plotter.Plotter.plot_data* attribute of the plotters rather than the raw data in this project
- **keep_all** (*bool*) – If True, all formatoptions are kept. Otherwise only the intersection

Returns A mapping from the attribute to the joined attributes which are either strings or (if there is only one attribute value), the data type of the corresponding value

Return type dict

keys (**args*, ***kwargs*)
Show the available formatoptions in this project

Parameters

- **keys** (`list of str or None`) – If None, the all formatoptions of the given class are used. Group names from the `psyplot.plotter.groups` mapping are replaced by the formatoptions
- **indent** (`int`) – The indentation of the table
- **grouped** (`bool, optional`) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the `psyplot.plotter.Plotter.include_links` attribute.
- **``*args,**kwargs``** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

lineplot
List of data arrays that are plotted by `psy_simple.plotters.LinePlotter` plotters

classmethod load_project (*fname*, *auto_update=None*, *make_plot=True*, *draw=None*, *alternative_axes=None*, *main=False*, *encoding=None*, *enable_post=False*, *new_fig=True*, *clear=None*, ***kwargs*)
Load a project from a file or dict

This classmethod allows to load a project that has been stored using the `save_project()` method and reads all the data and creates the figures.

Since the data is stored in external files when saving a project, make sure that the data is accessible under the relative paths as stored in the file *fname* or from the current working directory if *fname* is a dictionary. Alternatively use the *alternative_paths* parameter or the *pwd* parameter

Parameters

- **fname** (`str or dict`) – The string might be the path to a file created with the `save_project()` method, or it might be a dictionary from this method
- **auto_update** (`bool`) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **make_plot** (`bool`) – If True, the data is plotted at the end. Otherwise you have to call the `psyplot.plotter.Plotter.initialize_plot()` method or the `psyplot.plotter.Plotter.reinit()` method by yourself
- **draw** (`bool or None`) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*` parameter in the `psyplot.rcParams` dictionary

- **alternative_axes** (*dict, None or list*) – alternative axes instances to use
  - If it is None, the axes and figures from the saving point will be reproduced.
  - a dictionary should map from array names in the created project to matplotlib axes instances
  - a list should contain axes instances that will be used for iteration
- **main** (*bool, optional*) – If True, a new main project is created and returned. Otherwise (by default default) the data is added to the current main project.
- **encoding** (*str*) – The encoding to use for loading the project. If None, it is automatically determined by pickle. Note: Set this to `'latin1'` if using a project created with python2 on python3.
- **enable_post** (*bool*) – If True, the `post` formatoption is enabled and post processing scripts are allowed. Do only set this parameter to `True` if you know you can trust the information in *fname*
- **new_fig** (*bool*) – If True (default) and *alternative_axes* is None, new figures are created if the figure already exists
- **clear** (*bool*) – If True, axes are cleared before making the plot. This is only necessary if the *ax* keyword consists of subplots with projection that differs from the one that is needed
- **pwd** (*str or None, optional*) – Path to the working directory from where the data can be imported. If None and *fname* is the path to a file, *pwd* is set to the directory of this file. Otherwise the current working directory is used.
- **alternative_paths** (*dict or list or str*) – A mapping from original filenames as used in *d* to filenames that shall be used instead. If *alternative_paths* is not None, datasets must be None. Paths must be accessible from the current working directory. If *alternative_paths* is a list (or any other iterable) is provided, the file names will be replaced as they appear in *d* (note that this is very unsafe if *d* is not and OrderedDict)
- **datasets** (*dict or list or None*) – A mapping from original filenames in *d* to the instances of `xarray.Dataset` to use. If it is an iterable, the same holds as for the *alternative_paths* parameter
- **ignore_keys** (*list of str*) – Keys specified in this list are ignored and not seen as array information (note that `attrs` are used anyway)
- **only** (*string, list or callable*) – Can be one of the following three things:
  - a string that represents a pattern to match the array names that shall be included
  - a list of array names to include
  - a callable with two arguments, a string and a dict such as

```python
def filter_func(arr_name: str, info: dict): -> bool
    '''
    Filter the array names

    This function should return True if the array shall be
    included, else False

    Parameters
    ----------
    arr_name: str
```

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```
        The array name (i.e. the ``arr_name`` attribute)
    info: dict
        The dictionary with the array informations. Common
        keys are ``'name'`` that points to the variable name
        and ``'dims'`` that points to the dimensions and
        ``'fname'`` that points to the file name
    '''
    return True or False
```

The function should return `True` if the array shall be included, else `False`. This function will also be given to subsequents instances of `InteractiveList` objects that are contained in the returned value

- **chname** (`dict`) – A mapping from variable names in the project to variable names that should be used instead

Other Parameters

- **d** (*dict*) – The dictionary holding the data
- **alternative_paths** (*dict or list or str*) – A mapping from original filenames as used in *d* to filenames that shall be used instead. If *alternative_paths* is not None, datasets must be None. Paths must be accessible from the current working directory. If *alternative_paths* is a list (or any other iterable) is provided, the file names will be replaced as they appear in *d* (note that this is very unsafe if *d* is not and OrderedDict)
- **datasets** (*dict or list or None*) – A mapping from original filenames in *d* to the instances of `xarray.Dataset` to use. If it is an iterable, the same holds as for the *alternative_paths* parameter
- **pwd** (*str*) – Path to the working directory from where the data can be imported. If None, use the current working directory.
- **ignore_keys** (*list of str*) – Keys specified in this list are ignored and not seen as array information (note that `attrs` are used anyway)
- **only** (*string, list or callable*) – Can be one of the following three things:
  - a string that represents a pattern to match the array names that shall be included
  - a list of array names to include
  - a callable with two arguments, a string and a dict such as

```
def filter_func(arr_name: str, info: dict): -> bool
    '''
    Filter the array names

    This function should return True if the array shall be
    included, else False

    Parameters
    ----------
    arr_name: str
        The array name (i.e. the ``arr_name`` attribute)
    info: dict
        The dictionary with the array informations. Common
        keys are ``'name'`` that points to the variable name
        and ``'dims'`` that points to the dimensions and
        ``'fname'`` that points to the file name
```

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```
    '''
    return True or False
```

The function should return `True` if the array shall be included, else `False`. This function will also be given to subsequents instances of `InteractiveList` objects that are contained in the returned value

- **chname** (*dict*) – A mapping from variable names in the project to variable names that should be used instead

Returns The project in state of the saving point

Return type *Project*

`logger`
`logging.Logger` of this instance

`main`
`Project`. The main project of this subproject

`mapcombined`
List of data arrays that are plotted by `psy_maps.plotters.CombinedPlotter` plotters

`mapplot`
List of data arrays that are plotted by `psy_maps.plotters.FieldPlotter` plotters

`maps`
List of data arrays that are plotted by `psy_maps.plotters.MapPlotter` plotters

`mapvector`
List of data arrays that are plotted by `psy_maps.plotters.VectorPlotter` plotters

`classmethod new`(*num=None*, **args*, ***kwargs*)
Create a new main project

Parameters

- **`num`** (*`int`*) – The number of the project
- **`iterable`** (*`iterable`*) – The iterable (e.g. another list) defining this list
- **`attrs`** (*`dict-like or iterable, optional`*) – Global attributes of this list
- **`auto_update`** (*`bool`*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **`new_name`** (*`bool or str`*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter
- **`main`** (`Project`) – The main project this subproject belongs to (or None if this project is the main project)

Returns The with the given *num* (if it does not already exist, it is created)

Return type *Project*

See also:

`scp()` Sets the current project

`gcp()` Returns the current project

`oncpchange`
signal to be emiitted when the current main and/or subproject changes

`plot`
Plotting instance of this `Project`. See the `ProjectPlotter` class for method documentations

`plot2d`
List of data arrays that are plotted by `psy_simple.plotters.Simple2DPlotter` plotters

`plotters`
A list of all the plotters in this instance

`save_project`(*fname=None*, *pwd=None*, *pack=False*, ***kwargs*)
Save this project to a file

Parameters

- **fname** (*str or None*) – If None, the dictionary will be returned. Otherwise the necessary information to load this project via the `load()` method is saved to *fname* using the `pickle` module
- **pwd** (*str or None, optional*) – Path to the working directory from where the data can be imported. If None and *fname* is the path to a file, *pwd* is set to the directory of this file. Otherwise the current working directory is used.
- **pack** (*bool*) – If True, all datasets are packed into the folder of *fname* and will be used if the data is loaded
- **dump** (*bool*) – If True and the dataset has not been dumped so far, it is dumped to a temporary file or the one generated by *paths* is used. If it is False or both, *dump* and *paths* are None, no data will be stored. If it is None and *paths* is not None, *dump* is set to True.
- **paths** (*iterable or True*) – An iterator over filenames to use if a dataset has no filename. If paths is `True`, an iterator over temporary files will be created without raising a warning
- **attrs** (*bool, optional*) – If True (default), the `ArrayList.attrs` and `xarray.DataArray.attrs` attributes are included in the returning dictionary
- **standardize_dims** (*bool, optional*) – If True (default), the real dimension names in the dataset are replaced by x, y, z and t to be more general.
- **use_rel_paths** (*bool, optional*) – If True (default), paths relative to the current working directory are used. Otherwise absolute paths to *pwd* are used
- **ds_description** (*'all' or set of {'fname', 'ds', 'num', 'arr', 'store'}*) – Keys to describe the datasets of the arrays. If all, all keys are used. The key descriptions are

  fname the file name is inserted in the `'fname'` key

  store the data store class and module is inserted in the `'store'` key

  ds the dataset is inserted in the `'ds'` key

  num The unique number assigned to the dataset is inserted in the `'num'` key

  arr The array itself is inserted in the `'arr'` key

- **full_ds** (*bool*) – If True and `'ds'` is in *ds_description*, the entire dataset is included. Otherwise, only the DataArray converted to a dataset is included

Notes

You can also store the entire data in the pickled file by setting `ds_description={'ds'}`

classmethod scp(*project*)
Set the current project

Parameters project (*Project or None*) – The project to set. If it is None, the current subproject is set to empty. If it is a sub project (see:attr:*Project.is_main*), the current subproject is set to this project. Otherwise it replaces the current main project

See also:

scp() The global version for setting the current project

gcp() Returns the current project

project() Creates a new project

share(*base=None*, *keys=None*, *by=None*, ***kwargs*)
Share the formatoptions of one plotter with all the others

This method shares specified formatoptions from *base* with all the plotters in this instance.

Parameters

- **base** (*None, Plotter, xarray.DataArray, InteractiveList, or list of them*) – The source of the plotter that shares its formatoptions with the others. It can be None (then the first instance in this project is used), a *Plotter* or any data object with a *psy* attribute. If *by* is not None, then it is expected that *base* is a list of data objects for each figure/axes
- **keys** (*string or iterable of strings*) – The formatoptions to share, or group names of formatoptions to share all formatoptions of that group (see the `fmt_groups` property). If None, all formatoptions of this plotter are unshared.
- **by** (*{'fig', 'figure', 'ax', 'axes'}*) – Share the formatoptions only with the others on the same `'figure'` or the same `'axes'`. In this case, base must either be `None` or a list of the types specified for *base*
- **draw** (*bool or None*) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *'auto_draw'*' parameter in the `psyplot.rcParams` dictionary
- **auto_update** (*bool*) – Boolean determining whether or not the `start_update()` method is called at the end. This parameter has no effect if the `no_auto_update` attribute is set to `True`.

See also:

`psyplot.plotter.share()`

static show()
Shows all open figures

simple
List of data arrays that are plotted by `psy_simple.plotters.SimplePlotterBase` plotters

summaries(**args*, ***kwargs*)
Show the available formatoptions and their summaries in this project

Parameters

- **keys** (`list of str or None`) – If None, the all formatoptions of the given class are used. Group names from the `psyplot.plotter.groups` mapping are replaced by the formatoptions
- **indent** (`int`) – The indentation of the table
- **grouped** (`bool, optional`) – If True, the formatoptions are grouped corresponding to the `Formatoption.groupname` attribute

Other Parameters

- **func** (*function or None*) – The function the is used for returning (by default it is printed via the `print()` function or (when using the gui) in the help explorer). The given function must take a string as argument
- **include_links** (*bool or None, optional*) – Default False. If True, links (in restructured formats) are included in the description. If None, the behaviour is determined by the `psyplot.plotter.Plotter.include_links` attribute.
- **‘‘*args,**kwargs‘‘** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns None if *func* is the print function, otherwise anything else

Return type results of *func*

unshare(***kwargs*)
Unshare the formatoptions of all the plotters in this instance

This method uses the `psyplot.plotter.Plotter.unshare_me()` method to release the specified formatoptions in *keys*.

Parameters

- **keys** (`string or iterable of strings`) – The formatoptions to unshare, or group names of formatoptions to unshare all formatoptions of that group (see the `fmt_groups` property). If None, all formatoptions of this plotter are unshared.
- **draw** (`bool or None`) – Boolean to control whether the figure of this array shall be drawn at the end. If None, it defaults to the *‘auto_draw’*‘ parameter in the `psyplot.rcParams` dictionary
- **auto_update** (`bool`) – Boolean determining whether or not the `start_update()` method is called at the end. This parameter has no effect if the `no_auto_update` attribute is set to `True`.

See also:

`psyplot.plotter.Plotter.unshare()`, `psyplot.plotter.Plotter.unshare_me()`

vector
List of data arrays that are plotted by `psy_simple.plotters.SimpleVectorPlotter` plotters

violinplot
List of data arrays that are plotted by `psy_simple.plotters.ViolinPlotter` plotters

with_plotter
The arrays in this instance that are visualized with a plotter

class psyplot.project.**ProjectPlotter**(*project=None*)

Bases: object

Plotting methods of the *psyplot.project.Project* class **Attributes**

barplot(*args, **kwargs)	Make a bar plot of one-dimensional data
combined(*args, **kwargs)	Plot a 2D scalar field with an overlying vector field
density(*args, **kwargs)	Make a density plot of point data
fldmean(*args, **kwargs)	Calculate and plot the mean over x- and y-dimensions
lineplot(*args, **kwargs)	Make a line plot of one-dimensional data
mapcombined(*args, **kwargs)	Plot a 2D scalar field with an overlying vector field on a map
mapplot(*args, **kwargs)	Plot a 2D scalar field on a map
mapvector(*args, **kwargs)	Plot a 2D vector field on a map
plot2d(*args, **kwargs)	Make a simple plot of a 2D scalar field
project	
vector(*args, **kwargs)	Make a simple plot of a 2D vector field
violinplot(*args, **kwargs)	Make a violin plot of your data

Methods

show_plot_methods()	Print the plotmethods of this instance

barplot(**args*, ***kwargs*)

Make a bar plot of one-dimensional data

This plotting method adds data arrays and plots them via psy_simple.plotters.BarPlotter plotters

To plot data from a netCDF file type:

```
>>> psy.plot.barplot(filename, name=['my_variable'], ...)
```

Possible formatoptions are

alpha	axiscolor	color	coord
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	labelprops	labelsize	labelweight
legend	legendlabels	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	sym_lims	text
ticksize	tickweight	tight	title
titleprops	titlesize	titleweight	transpose
widths	xlabel	xlim	xrotation
xticklabels	xtickprops	xticks	ylabel
ylim	yrotation	yticklabels	ytickprops
yticks			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.barplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.barplot.summaries('title')

# show the full documentation
>>> psy.plot.barplot.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.barplot.plot
```

combined(**args*, ***kwargs*)

Plot a 2D scalar field with an overlying vector field

This plotting method adds data arrays and plots them via `psy_simple.plotters.CombinedSimplePlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.combined(filename, name=[['my_variable', ['u_var', 'v_var']]], ..
↪.)
```

Possible formatoptions are

arrowsize	arrowstyle	axiscolor	bounds
cbar	cbarspacing	clabel	clabelprops
clabelsize	clabelweight	cmap	color
cticklabels	ctickprops	cticks	cticksize
ctickweight	datagrid	density	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	interp_bounds	labelprops	labelsize
labelweight	levels	linewidth	maskbetween
maskgeq	maskgreater	maskleq	maskless
miss_color	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	vbounds	vcbar
vcbarspacing	vclabel	vclabelprops	vclabelsize
vclabelweight	vcmap	vcticklabels	vctickprops
vcticks	vcticksize	vctickweight	vplot
xlabel	xlim	xrotation	xticklabels
xtickprops	xticks	ylabel	ylim
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.combined.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.combined.summaries('title')

# show the full documentation
>>> psy.plot.combined.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.combined.plot
```

density (**args*, ***kwargs*)

Make a density plot of point data

This plotting method adds data arrays and plots them via `psy_simple.plotters.DensityPlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.density(filename, name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	bins	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	cmap	coord	cticklabels
ctickprops	cticks	cticksize	ctickweight
datagrid	density	extend	figtitle
figtitleprops	figtitlesize	figtitleweight	grid
interp_bounds	labelprops	labelsize	labelweight
levels	maskbetween	maskgeq	maskgreater
maskleq	maskless	miss_color	normed
plot	post	post_timing	precision
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrange	xrotation	xticklabels	xtickprops
xticks	ylabel	ylim	yrange
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
```

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```
# formatopions
>>> psy.plot.density.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.density.summaries('title')

# show the full documentation
>>> psy.plot.density.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.density.plot
```

fldmean(**args*, ***kwargs*)

Calculate and plot the mean over x- and y-dimensions

This plotting method adds data arrays and plots them via `psy_simple.plotters.FldmeanPlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.fldmean(filename, name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	color	coord	err_calc
error	erroralpha	figtitle	figtitleprops
figtitlesize	figtitleweight	grid	labelprops
labelsize	labelweight	legend	legendlabels
linewidth	marker	markersize	maskbetween
maskgeq	maskgreater	maskleq	maskless
mean	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrotation	xticklabels	xtickprops	xticks
ylabel	ylim	yrotation	yticklabels
ytickprops	yticks		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.fldmean.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.fldmean.summaries('title')
```

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```
# show the full documentation
>>> psy.plot.fldmean.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.fldmean.plot
```

lineplot(**args*, ***kwargs*)

Make a line plot of one-dimensional data

This plotting method adds data arrays and plots them via `psy_simple.plotters.LinePlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.lineplot(filename, name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	color	coord	error
erroralpha	figtitle	figtitleprops	figtitlesize
figtitleweight	grid	labelprops	labelsize
labelweight	legend	legendlabels	linewidth
marker	markersize	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	sym_lims	text
ticksize	tickweight	tight	title
titleprops	titlesize	titleweight	transpose
xlabel	xlim	xrotation	xticklabels
xtickprops	xticks	ylabel	ylim
yrotation	yticklabels	ytickprops	yticks

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.lineplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.lineplot.summaries('title')

# show the full documentation
>>> psy.plot.lineplot.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.lineplot.plot
```

mapcombined(**args*, ***kwargs*)

Plot a 2D scalar field with an overlying vector field on a map

This plotting method adds data arrays and plots them via `psy_maps.plotters.CombinedPlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.mapcombined(filename, name=[['my_variable', ['u_var', 'v_var']]],
↪ ...)
```

Possible formatoptions are

arrowsize	arrowstyle	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	clat	clip	clon
cmap	color	cticklabels	ctickprops
cticks	cticksize	ctickweight	datagrid
density	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	interp_bounds	levels
linewidth	lonlatbox	lsm	map_extent
maskbetween	maskgeq	maskgreater	maskleq
maskless	miss_color	plot	post
post_timing	projection	stock_img	text
tight	title	titleprops	titlesize
titleweight	transform	vbounds	vcbar
vcbarspacing	vclabel	vclabelprops	vclabelsize
vclabelweight	vcmap	vcticklabels	vctickprops
vcticks	vcticksize	vctickweight	vplot
xgrid	ygrid		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.mapcombined.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.mapcombined.summaries('title')

# show the full documentation
>>> psy.plot.mapcombined.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.mapcombined.plot
```

mapplot(**args*, ***kwargs*)

Plot a 2D scalar field on a map

This plotting method adds data arrays and plots them via psy_maps.plotters.FieldPlotter plotters

To plot data from a netCDF file type:

```
>>> psy.plot.mapplot(filename, name=['my_variable'], ...)
```

Possible formatoptions are

bounds	cbar	cbarspacing	clabel
clabelprops	clabelsize	clabelweight	clat
clip	clon	cmap	cticklabels
ctickprops	cticks	cticksize	ctickweight
datagrid	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	interp_bounds	levels
lonlatbox	lsm	map_extent	maskbetween
maskgeq	maskgreater	maskleq	maskless
miss_color	plot	post	post_timing
projection	stock_img	text	tight
title	titleprops	titlesize	titleweight
transform	xgrid	ygrid	

Examples

To explore the formatoptions and their documentations, use the keys, summaries and docs methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.mapplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.mapplot.summaries('title')

# show the full documentation
>>> psy.plot.mapplot.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.mapplot.plot
```

mapvector(**args, **kwargs*)

Plot a 2D vector field on a map

This plotting method adds data arrays and plots them via psy_maps.plotters.VectorPlotter plotters

To plot data from a netCDF file type:

```
>>> psy.plot.mapvector(filename, name=[['u_var', 'v_var']], ...)
```

Possible formatoptions are

arrowsize	arrowstyle	bounds	cbar
cbarspacing	clabel	clabelprops	clabelsize
clabelweight	clat	clip	clon
cmap	color	cticklabels	ctickprops
cticks	cticksize	ctickweight	datagrid
density	extend	figtitle	figtitleprops
figtitlesize	figtitleweight	grid_color	grid_labels
grid_labelsize	grid_settings	linewidth	lonlatbox
lsm	map_extent	maskbetween	maskgeq
maskgreater	maskleq	maskless	plot
post	post_timing	projection	stock_img
text	tight	title	titleprops
titlesize	titleweight	transform	xgrid
ygrid			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.mapvector.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.mapvector.summaries('title')

# show the full documentation
>>> psy.plot.mapvector.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.mapvector.plot
```

plot2d(**args*, ***kwargs*)

Make a simple plot of a 2D scalar field

This plotting method adds data arrays and plots them via `psy_simple.plotters.Simple2DPlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.plot2d(filename, name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	bounds	cbar	cbarspacing
clabel	clabelprops	clabelsize	clabelweight
cmap	cticklabels	ctickprops	cticks
cticksize	ctickweight	datagrid	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	interp_bounds	labelprops	labelsize
labelweight	levels	maskbetween	maskgeq
maskgreater	maskleq	maskless	miss_color
plot	post	post_timing	sym_lims
text	ticksize	tickweight	tight
title	titleprops	titlesize	titleweight
transpose	xlabel	xlim	xrotation
xticklabels	xtickprops	xticks	ylabel
ylim	yrotation	yticklabels	ytickprops
yticks			

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.plot2d.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.plot2d.summaries('title')

# show the full documentation
>>> psy.plot.plot2d.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.plot2d.plot
```

project

show_plot_methods()
Print the plotmethods of this instance

vector(**args*, ***kwargs*)
Make a simple plot of a 2D vector field

This plotting method adds data arrays and plots them via `psy_simple.plotters.SimpleVectorPlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.vector(filename, name=[['u_var', 'v_var']], ...)
```

Possible formatoptions are

arrowsize	arrowstyle	axiscolor	bounds
cbar	cbarspacing	clabel	clabelprops
clabelsize	clabelweight	cmap	color
cticklabels	ctickprops	cticks	cticksize
ctickweight	datagrid	density	extend
figtitle	figtitleprops	figtitlesize	figtitleweight
grid	labelprops	labelsize	labelweight
linewidth	maskbetween	maskgeq	maskgreater
maskleq	maskless	plot	post
post_timing	sym_lims	text	ticksize
tickweight	tight	title	titleprops
titlesize	titleweight	transpose	xlabel
xlim	xrotation	xticklabels	xtickprops
xticks	ylabel	ylim	yrotation
yticklabels	ytickprops	yticks	

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.vector.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.vector.summaries('title')

# show the full documentation
>>> psy.plot.vector.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.vector.plot
```

violinplot(**args*, ***kwargs*)

Make a violin plot of your data

This plotting method adds data arrays and plots them via `psy_simple.plotters.ViolinPlotter` plotters

To plot data from a netCDF file type:

```
>>> psy.plot.violinplot(filename, name=['my_variable'], ...)
```

Possible formatoptions are

axiscolor	color	figtitle	figtitleprops
figtitlesize	figtitleweight	grid	labelprops
labelsize	labelweight	legend	legendlabels
maskbetween	maskgeq	maskgreater	maskleq
maskless	plot	post	post_timing
sym_lims	text	ticksize	tickweight
tight	title	titleprops	titlesize
titleweight	transpose	xlabel	xlim
xrotation	xticklabels	xtickprops	xticks
ylabel	ylim	yrotation	yticklabels
ytickprops	yticks		

Examples

To explore the formatoptions and their documentations, use the `keys`, `summaries` and `docs` methods. For example:

```
>>> import psyplot.project as psy

# show the keys corresponding to a group or multiple
# formatopions
>>> psy.plot.violinplot.keys('labels')

# show the summaries of a group of formatoptions or of a
# formatoption
>>> psy.plot.violinplot.summaries('title')

# show the full documentation
>>> psy.plot.violinplot.docs('plot')

# or access the documentation via the attribute
>>> psy.plot.violinplot.plot
```

`psyplot.project.`**`close`**(*num=None*, *figs=True*, *data=True*, *ds=True*, *remove_only=False*)

Close the project

This method closes the current project (figures, data and datasets) or the project specified by *num*

Parameters

- **num** (*int, None or 'all'*) – if `int`, it specifies the number of the project, if None, the current subproject is closed, if `'all'`, all open projects are closed
- **figs** (*bool*) – Close the figures
- **data** (*bool*) – delete the arrays from the (main) project
- **ds** (*bool*) – If True, close the dataset as well
- **remove_only** (*bool*) – If True and *figs* is True, the figures are not closed but the plotters are removed

See also:

`Project.close()`

`psyplot.project.`**`gcp`**(*main=False*)

Get the current project

Parameters main (*bool*) – If True, the current main project is returned, otherwise the current subproject is returned.

See also:

scp() Sets the current project

project() Creates a new project

psyplot.project.**get_project_nums**()
Returns the project numbers of the open projects

psyplot.project.**multiple_subplots**(*rows=1*, *cols=1*, *maxplots=None*, *n=1*, *delete=True*, *for_maps=False*, **args*, ***kwargs*)
Function to create subplots.

This function creates so many subplots on so many figures until the specified number *n* is reached.

Parameters

- **rows** (*int*) – The number of subplots per rows
- **cols** (*int*) – The number of subplots per column
- **maxplots** (*int*) – The number of subplots per figure (if None, it will be row*cols)
- **n** (*int*) – number of subplots to create
- **delete** (*bool*) – If True, the additional subplots per figure are deleted
- **for_maps** (*bool*) – If True this is a simple shortcut for setting `subplot_kw=dict(projection=cartopy.crs.PlateCarree())` and is useful if you want to use the *mapplot*, *mapvector* or *mapcombined* plotting methods
- **and **kwargs** (**args*) – anything that is passed to the `matplotlib.pyplot.subplots()` function

Returns list of maplotlib.axes.SubplotBase instances

Return type list

psyplot.project.**plot = <psyplot.project.ProjectPlotter object>**
ProjectPlotter of the current project. See the class documentation for available plotting methods

psyplot.project.**project**(*num=None*, **args*, ***kwargs*)
Create a new main project

Parameters

- **num** (*int*) – The number of the project
- **iterable** (*iterable*) – The iterable (e.g. another list) defining this list
- **attrs** (*dict-like or iterable, optional*) – Global attributes of this list
- **auto_update** (*bool*) – Default: None. A boolean indicating whether this list shall automatically update the contained arrays when calling the `update()` method or not. See also the `no_auto_update` attribute. If None, the value from the `'lists.auto_update'` key in the `psyplot.rcParams` dictionary is used.
- **new_name** (*bool or str*) – If False, and the `arr_name` attribute of the new array is already in the list, a ValueError is raised. If True and the `arr_name` attribute of the new array is not already in the list, the name is not changed. Otherwise, if the array name is already in use, *new_name* is set to 'arr{0}'. If not True, this will be used for renaming (if the array name of *arr* is in use or not). `'{0}'` is replaced by a counter

- **main** (Project) – The main project this subproject belongs to (or None if this project is the main project)

Returns The with the given *num* (if it does not already exist, it is created)

Return type *Project*

See also:

scp() Sets the current project

gcp() Returns the current project

psyplot.project.**register_plotter**(*identifier*, *module*, *plotter_name*, *plotter_cls=None*, *sorter=True*, *plot_func=True*, *import_plotter=None*, ***kwargs*)

Register a *psyplot.plotter.Plotter* for the projects

This function registers plotters for the Project class to allow a dynamical handling of different plotter classes.

Parameters

- **identifier** (str) – Name of the attribute that is used to filter for the instances belonging to this plotter
- **module** (str) – The module from where to import the *plotter_name*
- **plotter_name** (str) – The name of the plotter class in *module*
- **sorter** (bool, optional) – If True, the Project class gets a new property with the name of the specified *identifier* which allows you to access the instances that are plotted by the specified *plotter_name*
- **plot_func** (bool, optional) – If True, the ProjectPlotter (the class that holds the plotting method for the Project class and can be accessed via the Project.plot attribute) gets an additional method to plot via the specified *plotter_name* (see *Other Parameters* below.)
- **import_plotter** (bool, optional) – If True, the plotter is automatically imported, otherwise it is only imported when it is needed. If *import_plotter* is None, then it is determined by the `psyplot.rcParams 'project.auto_import'` item.

Other Parameters

- **prefer_list** (*bool*) – Determines the *prefer_list* parameter in the *from_dataset* method. If True, the plotter is expected to work with instances of `psyplot.InteractiveList` instead of `psyplot.InteractiveArray`.
- **default_slice** (*indexer*) – Index (e.g. 0 if *method* is 'isel') that shall be used for dimensions not covered by *dims* and *furtherdims*. If None, the whole slice will be used.
- **default_dims** (*dict*) – Default dimensions that shall be used for plotting (e.g. {'x': slice(None), 'y': slice(None)} for longitude-latitude plots)
- **show_examples** (*bool, optional*) – If True, examples how to access the plotter documentation are included in class documentation
- **example_call** (*str, optional*) – The arguments and keyword arguments that shall be included in the example of the generated plot method. This call will then appear as `>>> psy.plot.%(identifier)s(%(example_call)s)` in the documentation
- **plugin** (*str*) – The name of the plugin

psyplot.project.**scp**(*project*)

Set the current project

Parameters **%(Project.scp.parameters)s** –

See also:

gcp() Returns the current project

project() Creates a new project

psyplot.project.**unregister_plotter**(*identifier*, *sorter=True*, *plot_func=True*)

Unregister a *psyplot.plotter.Plotter* for the projects

Parameters

- **identifier** (*str*) – Name of the attribute that is used to filter for the instances belonging to this plotter or to create plots with this plotter
- **sorter** (*bool*) – If True, the identifier will be unregistered from the *Project* class
- **plot_func** (*bool*) – If True, the identifier will be unregistered from the *ProjectPlotter* class

psyplot.utils module

Miscallaneous utility functions for the psyplot package

Classes

DefaultOrderedDict([default_factory])	An ordered collections.defaultdict

Functions

check_key(key, possible_keys[, raise_error, …])	Checks whether the key is in a list of possible keys
hashable(val)	Test if *val* is hashable and if not, get it's string representation
is_remote_url(path)	
join_dicts(dicts[, delimiter, keep_all])	Join multiple dictionaries into one
sort_kwargs(kwargs, *param_lists)	Function to sort keyword arguments and sort them into dictionaries
unique_everseen(iterable[, key])	List unique elements, preserving order.

class psyplot.utils.**DefaultOrderedDict**(*default_factory=None*, **a*, ***kw*)

Bases: collections.OrderedDict

An ordered collections.defaultdict

Taken from http://stackoverflow.com/a/6190500/562769 **Methods**

copy()	Return a shallow copy of the dictionary

copy()

Return a shallow copy of the dictionary

psyplot.utils.**check_key**(*key*, *possible_keys*, *raise_error=True*, *name='formatoption keyword'*, *msg='See show_fmtkeys function for possible formatopion keywords'*, **args*, ***kwargs*)

Checks whether the key is in a list of possible keys

This function checks whether the given *key* is in *possible_keys* and if not looks for similar sounding keys

Parameters

- **key** (*str*) – Key to check
- **possible_keys** (*list of strings*) – a list of possible keys to use
- **raise_error** (*bool*) – If not True, a list of similar keys is returned
- **name** (*str*) – The name of the key that shall be used in the error message
- **msg** (*str*) – The additional message that shall be used if no close match to key is found
- ***args,**kwargs** – They are passed to the `difflib.get_close_matches()` function (i.e. *n* to increase the number of returned similar keys and *cutoff* to change the sensibility)

Returns

- *str* – The *key* if it is a valid string, else an empty string
- *list* – A list of similar formatoption strings (if found)
- *str* – An error message which includes

Raises `KeyError` – If the key is not a valid formatoption and *raise_error* is True

psyplot.utils.**hashable**(*val*)

Test if *val* is hashable and if not, get it's string representation

Parameters **val** (*object*) – Any (possibly not hashable) python object

Returns The given *val* if it is hashable or it's string representation

Return type val or string

psyplot.utils.**is_remote_url**(*path*)

psyplot.utils.**join_dicts**(*dicts*, *delimiter=None*, *keep_all=False*)

Join multiple dictionaries into one

Parameters

- **dicts** (*list of dict*) – A list of dictionaries
- **delimiter** (*str*) – The string that shall be used as the delimiter in case that there are multiple values for one attribute in the arrays. If None, they will be returned as sets
- **keep_all** (*bool*) – If True, all formatoptions are kept. Otherwise only the intersection

Returns The combined dictionary

Return type dict

psyplot.utils.**sort_kwargs**(*kwargs*, **param_lists*)

Function to sort keyword arguments and sort them into dictionaries

This function returns dictionaries that contain the keyword arguments from *kwargs* corresponding given iterables in `*params`

Parameters

- **kwargs** (*dict*) – Original dictionary

- ***param_lists** – iterables of strings, each standing for a possible key in kwargs

Returns len(params) + 1 dictionaries. Each dictionary contains the items of *kwargs* corresponding to the specified list in `*param_lists`. The last dictionary contains the remaining items

Return type list

psyplot.utils.**unique_everseen**(*iterable*, *key=None*)

List unique elements, preserving order. Remember all elements ever seen.

Function taken from https://docs.python.org/2/library/itertools.html

psyplot.version module

psyplot.warning module

Warning module of the psyplot python module

This module controls the warning behaviour of the module via the python builtin warnings module and introduces three new warning classes:

..autosummay:

```
PsPylotRuntimeWarning
PsyPlotWarning
PsyPlotCritical
```

Exceptions

PsyPlotCritical	Critical UserWarning for psyplot module
PsyPlotRuntimeWarning	Runtime warning that appears only ones
PsyPlotWarning	Normal UserWarning for psyplot module

Functions

critical(message[, category, logger])	wrapper around the warnings.warn function for critical warnings.
customwarn(message, category, filename, . . .)	Use the psyplot.warning logger for categories being out of PsyPlotWarning and PsyPlotCritical and the default warnings.showwarning function for all the others.
disable_warnings([critical])	Function that disables all warnings and all critical warnings (if critical evaluates to True) related to the psyplot Module.
warn(message[, category, logger])	wrapper around the warnings.warn function for non-critical warnings.

exception psyplot.warning.**PsyPlotCritical**

Bases: `UserWarning`

Critical UserWarning for psyplot module

exception psyplot.warning.**PsyPlotRuntimeWarning**

Bases: `RuntimeWarning`

Runtime warning that appears only ones

exception psyplot.warning.**PsyPlotWarning**

Bases: `UserWarning`

Normal UserWarning for psyplot module

`psyplot.warning.`**`critical`**(*message*, *category=<class 'psyplot.warning.PsyPlotCritical'>*, *logger=None*)
wrapper around the warnings.warn function for critical warnings. logger may be a logging.Logger instance

`psyplot.warning.`**`customwarn`**(*message*, *category*, *filename*, *lineno*, **args*, ***kwargs*)
Use the psyplot.warning logger for categories being out of PsyPlotWarning and PsyPlotCritical and the default warnings.showwarning function for all the others.

`psyplot.warning.`**`disable_warnings`**(*critical=False*)
Function that disables all warnings and all critical warnings (if critical evaluates to True) related to the psyplot Module. Please note that you can also configure the warnings via the psyplot.warning logger (logging.getLogger(psyplot.warning)).

`psyplot.warning.`**`warn`**(*message*, *category=<class 'psyplot.warning.PsyPlotWarning'>*, *logger=None*)
wrapper around the warnings.warn function for non-critical warnings. logger may be a logging.Logger instance

1.13 ToDos

Todo: Implement the visualization for UGrid data shown on the edge of the triangles

(The original entry is located in /home/docs/checkouts/readthedocs.org/user_builds/psyplot/checkouts/latest/psyplot/data.py:docstring of psyplot.data.UGridDecoder.get_triangles, line 32.)

1.14 Changelog

1.14.1 v1.1.0

This new release mainly adds new xarray accossors (`psy`) for DataArrays and Datasets. Additionally we provide methods to calculate the spatially weighted mean, such as fldmean, fldstd and fldpctl.

Added

- The yaxis_inverted and xaxis_inverted is now considered when loading and saving a matplotlib axes
- Added the `seaborn-style` command line argument
- Added the `concat_dim` command line argument
- Added the plot attribute to the DataArray and Dataset accessors. It is now possible to plot directly from the dataset and the data array
- Added `requires_replot` attribute for the `Formatoption` class. If this attribute is True and the formatoption is contained in an update, it is the same as calling `Plotter.update(replot=True))`.
- We added support for multifile datasets when saving a project. Multifile datasets are datasets that have been opened with, e.g. `psyplot.data.open_mfdataset` or `psyplot.project.plot.<plotmethod>(..., mfmode=True)`. This however does not always work with datasets opened with `xarray.open_mfdataset`. In these cases, you have to set the `Dataset.psy._concat_dim` attribute manually

- Added the `chname` parameter when loading a project. This parameter can be used to display another variable from the dataset than the one stored in the psyplot project file
- Added the `gridweights`, `fldmean`, `fldstd` and `fldpctl` methods to the `psy` DataArray accessor to calculate weighted means, standard deviations and percentiles over the spatial dimensions (x- and y).
- Added the `additional_children` and `additional_dependencies` parameters to the Formatoption intialization. These parameters can be used to provide additional children for a formatoption for one plotter class
- We added the `psyplot.plotter.Formatoption.get_fmt_widget` method which can be implemented to insert widgets in the formatoptions widget of the graphical user interface

1.14.2 v1.0.0

Added

- Changelog

Changed

- When creating new plots using the `psyplot.project.Project.plot` attribute, `scp` for the newly created subproject is only called when the corresponding `Project` is the current main project (`gcp(True)`)
- The `alternate_paths` keyword in the `psyplot.project.Project.save_project` and `psyplot.data.ArrayList.array_info` methods has been changed to `alternative_paths`
- The `psyplot.project.Cdo` class does not accept any of the keywords `returnDA, returnMaps` or `returnLine` anymore. Instead it takes the `plot_method` keyword and several others.
- The `psyplot.project.close` method by default now removes the data from the current project and closes attached datasets
- The modules in the psyplot.plotter modules have been moved to separate packages to make the debugging and testing easier
  - The psyplot.plotter.simple, baseplotter and colors modules have been moved to the psy-simple package
  - The psyplot.plotter.maps and boxes modules have been moved to the psy-maps package
  - The psyplot.plotter.linreg module has been moved to the psy-reg package
- The endings of the yaml configuration files are now all *.yml*. Hence,
  - the configuration file name is now *psyplotrc.yml* instead of *psyplotrc.yaml*
  - the default logging configuration file name is now *logging.yml* instead of *logging.yaml*
- Under osx, the configuration directory is now also expected to be in `$HOME/.config/psyplot` (as it is for linux)

CHAPTER 2

Examples

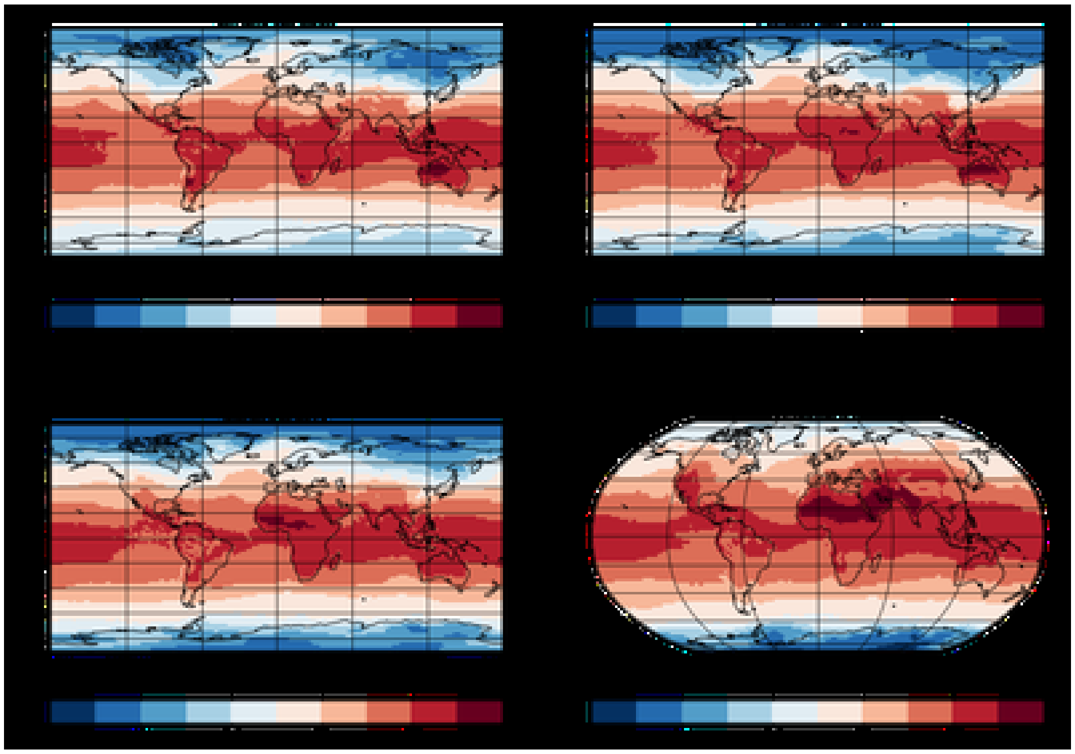

Fig. 1: *Sharing formatoptions*

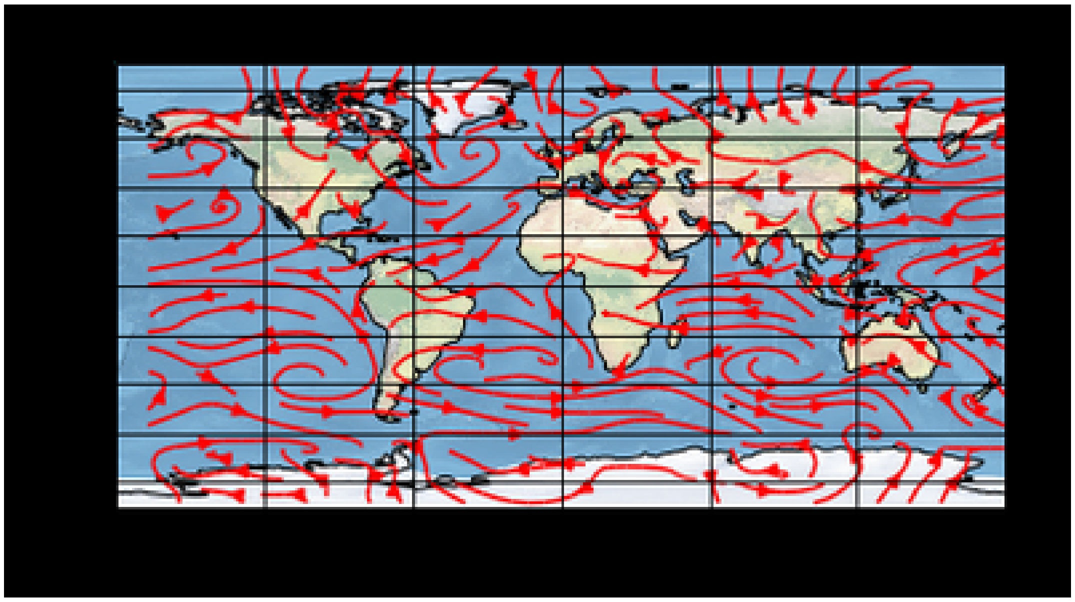

Fig. 2: *Applying your own post processing*

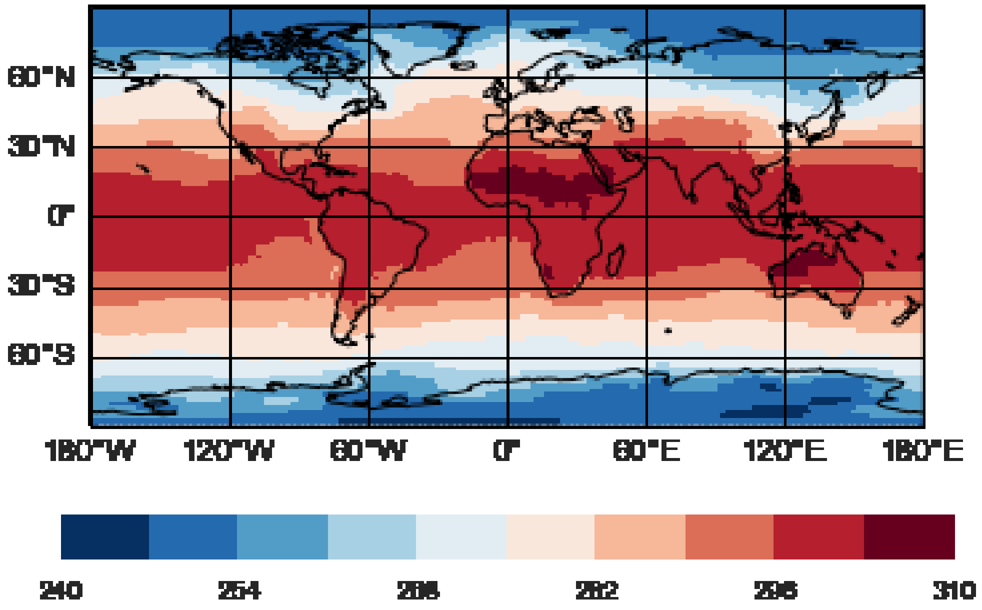

Fig. 3: *Usage of Climate Data Operators*

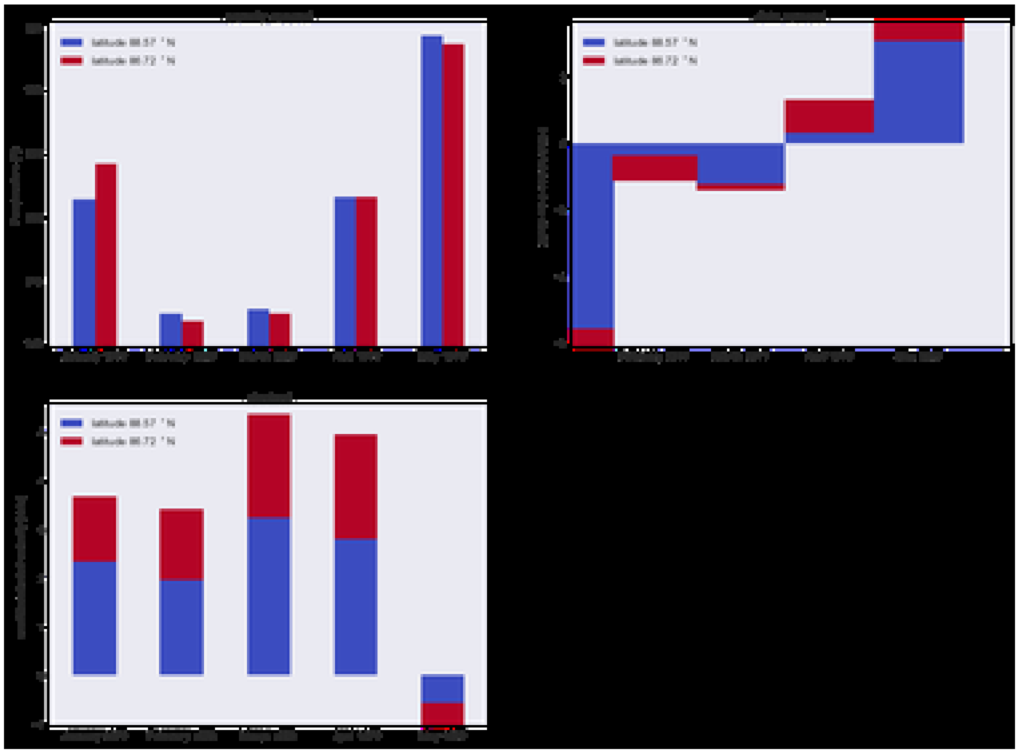
Fig. 4: Bar plot demo

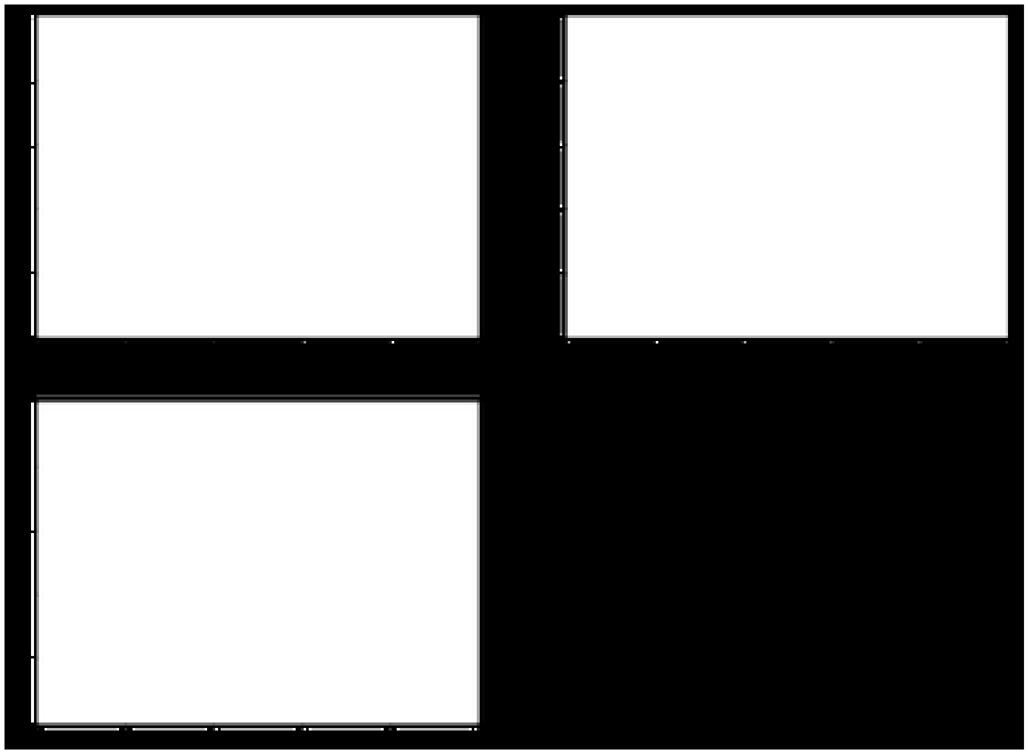
Fig. 5: Line plot demo

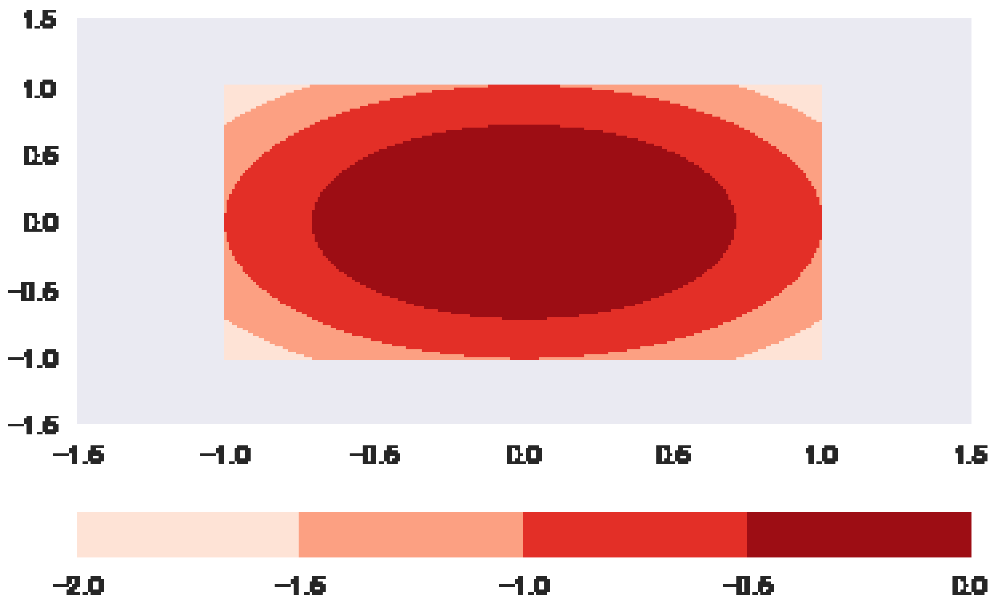

Fig. 6: 2D plots

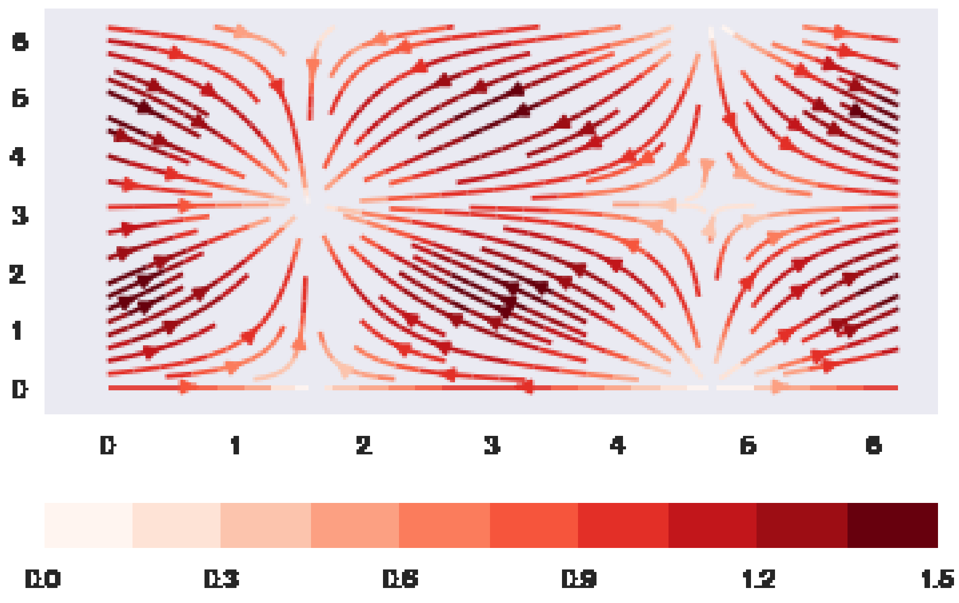

Fig. 7: Vector plot

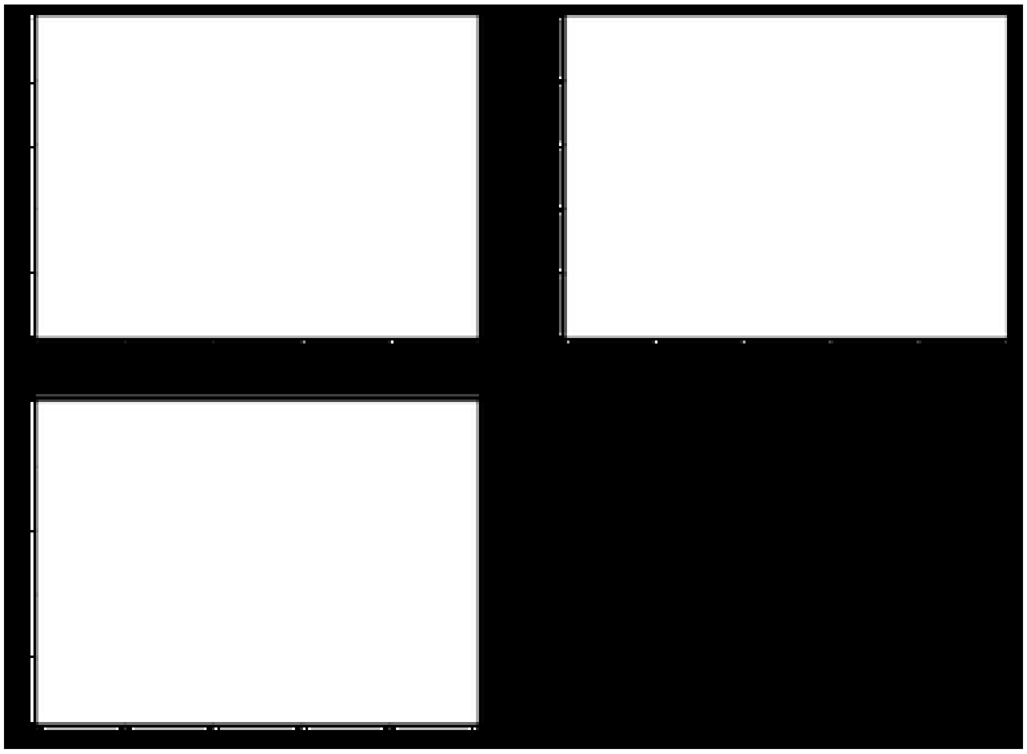

Fig. 8: Violin plot demo

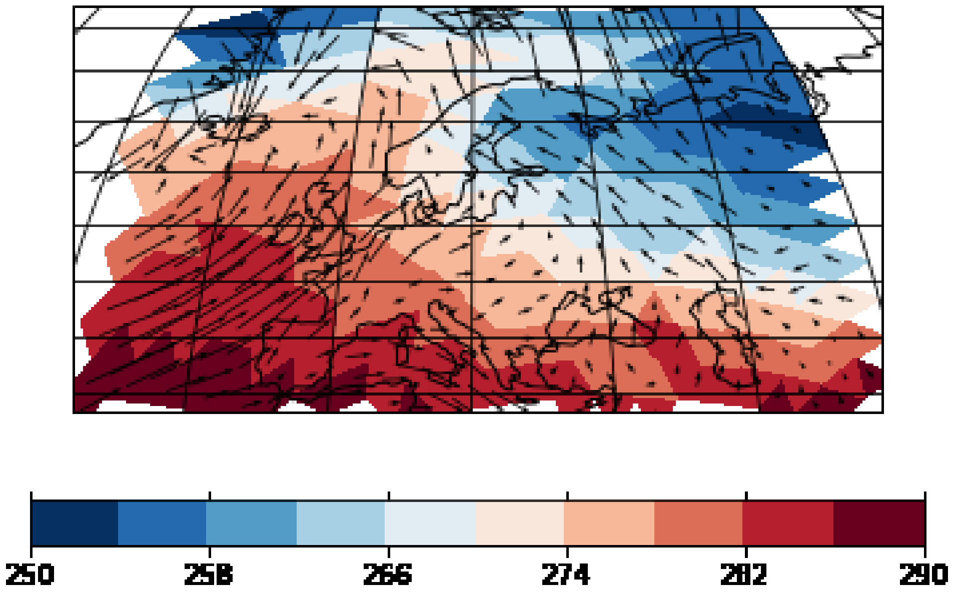

Fig. 9: Visualizing unstructured data

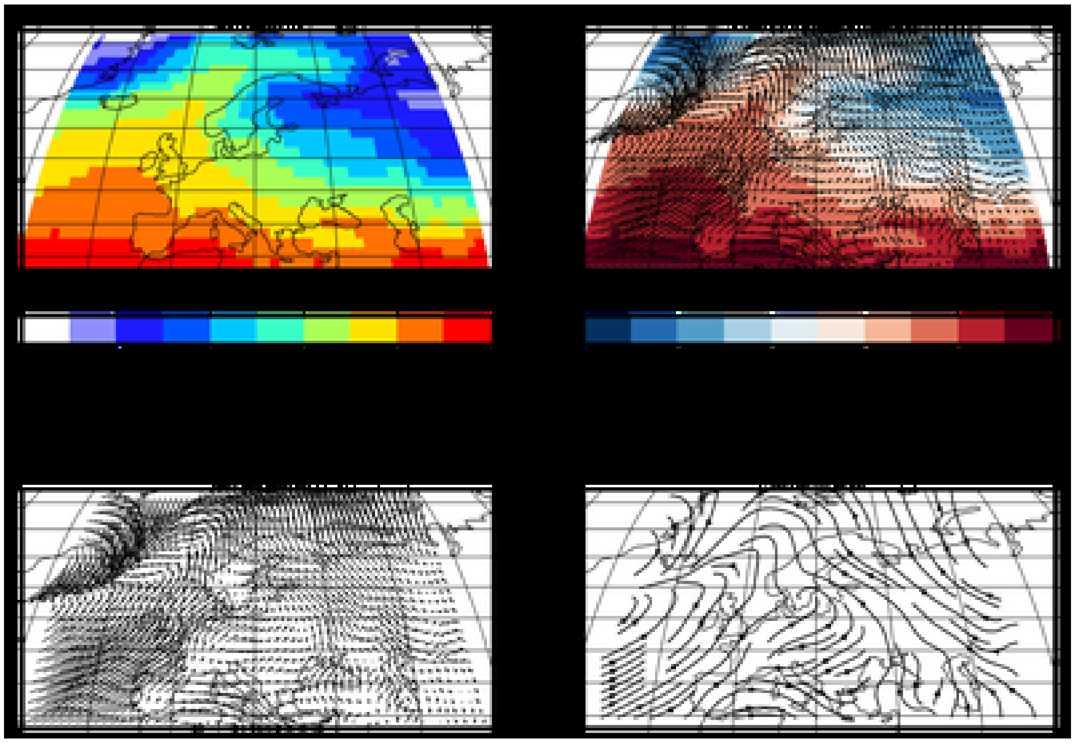

Fig. 10: Basic data visualization on a map

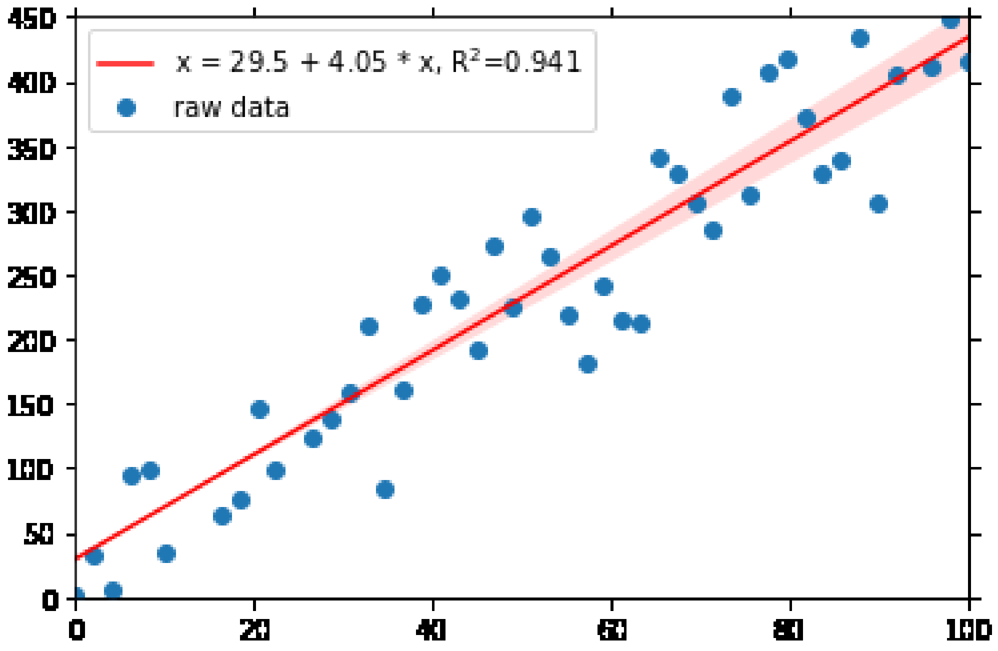

Fig. 11: Creating and accessing a fit

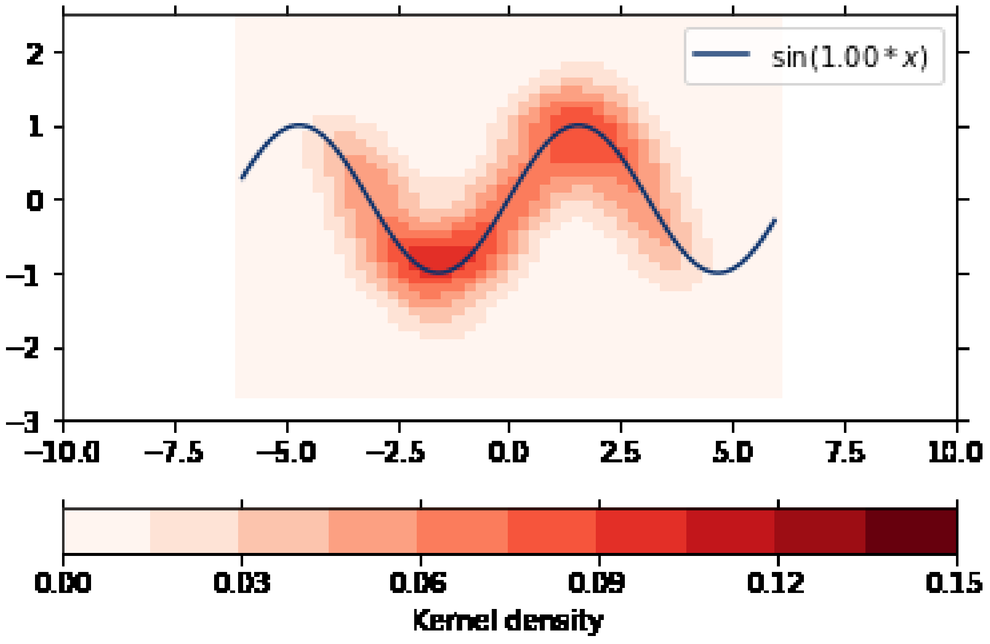

Fig. 12: Plot a fit over a density plot

CHAPTER 3

How to cite psyplot

When using psyplot, you should at least cite the publication in the Journal of Open Source Software:

Sommer, P. S.: The psyplot interactive visualization framework, *The Journal of Open Source Software*, 2, doi:10.21105/joss.00363, https://doi.org/10.21105/joss.00363, 2017.

`BibTex` - `EndNote`

Furthermore, each release of psyplot and it's *subprojects* is associated with a DOI using zenodo.org. If you want to cite a specific version or plugin, please refer to the *releases page of psyplot* or the releases page of the corresponding subproject.

CHAPTER 4

Acknowledgment

This package has been developed by Philipp Sommer.

I want to thank the matplotlib, xarray and cartopy developers for their great packages and of course the python developers for their fascinating work on this beautiful language.

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CHAPTER 5

Indices and tables

- genindex
- modindex
- search

Python Module Index

Index