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- photograph, video or broadcast
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this presentation

Provided that

you attribute the work to its author and respect the rights and licenses associated with its components













Best practices for research reproducibility

part I: Introduction to the FAIR principles for software and data management

https://tinyurl.com/reproducible1

why reproducible research?

because it's good for science

SPECIAL | 18 OCTOBER 2018

Challenges in irreproducible research

Science moves forward by corroboration – when researchers verify others' results. Science advances faster when people waste less time pursuing false leads. No research paper can ever be considered to be the final word, but there are too many that do not stand up to further study.



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because it's good for you



Comment | Open Access | Published: 08 December 2015

Five selfish reasons to work reproducibly

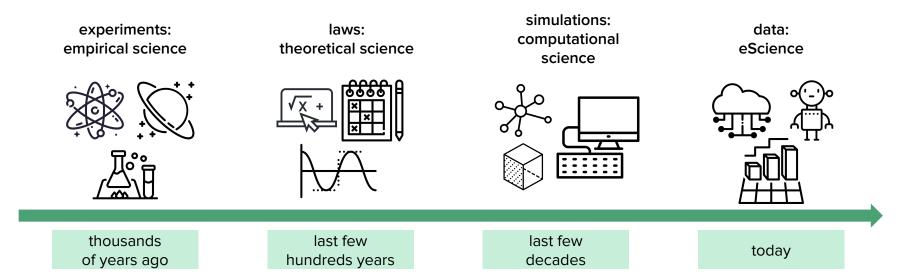
Florian Markowetz

Genome Biology 16, Article number: 274 (2015) | Cite this article

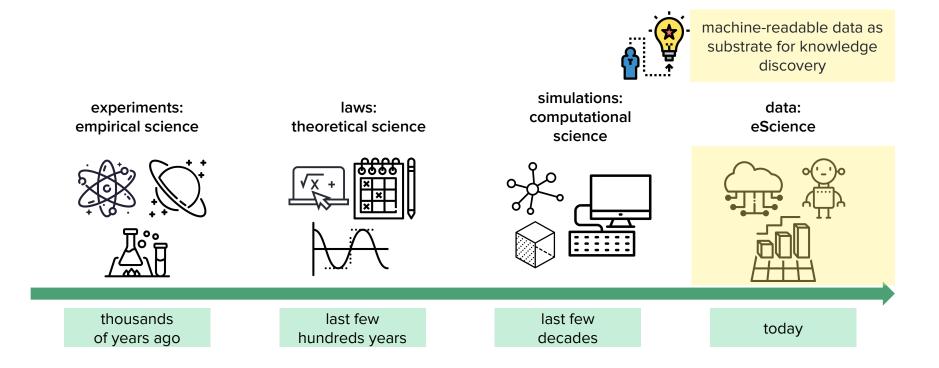
13k Accesses 21 Citations 403 Altmetric Metrics



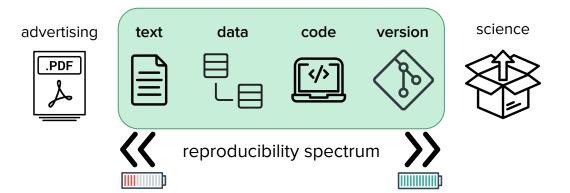
the 4th paradigm: data-driven science



the 4th paradigm: data-driven science



discovering and using research objects on the web



		Data		
		Same	Different	
nalysis	Same	Reproducible	Replicable	
Ana	Different	Robust	Generalisable	

reproducibility is the minimum standard for research validity



the FAIR principles: guidance for data stewardship



assist discovery and reuse through the web

Findable: sufficiently rich metadata + unique and persistent identifiers

Accessible: metadata and data are understandable to humans and machines and deposited in a trusted repository

Interoperable: metadata use a formal language for knowledge representation

Reusable: data have clear usage licenses and provide accurate information on provenance

FAIR != OPEN

FAIR comes in degrees

FAIR = agnostic of technical implementations



F for findable: persistent identifiers

- a PID is a globally unique and long-lasting reference to something, e.g., documents, files, books, people
- a PID is separated from location: if a web document is moved, the PID points to the same object in the new location (URLs)

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Digital Object Identifier: DOI

 the DOI is a common identifier used for academic, professional, and governmental information such as articles, datasets, reports, and other supplemental information



https://doi.org/10.5281/zenodo.3679141

resolver service directory indicator suffix +prefix



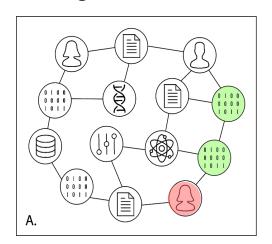
author identifier: ORCID



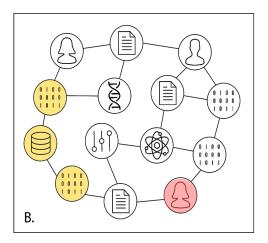
PIDs need to be connected

Connecting Research and Researchers

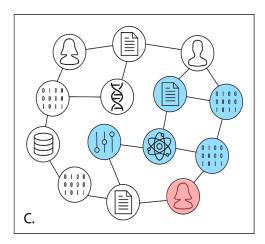
get an ORCID and tell your ORCID about your other identifiers



Different versions of software code



Datasets hosted by a particular repository



All digital objects connected to a research object



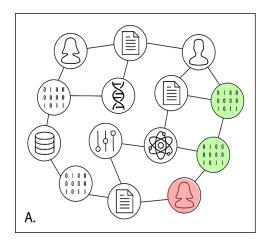
author identifier: ORCID



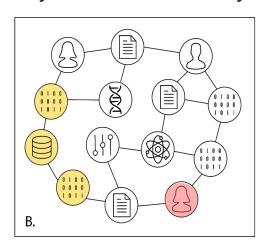
PIDs need to be connected

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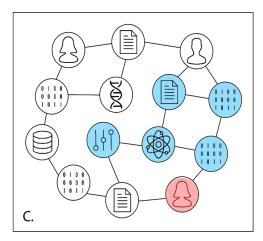
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All digital objects connected to a research object



data repositories and data journals

- choose the right repository
- orun a query on https://www.re3data.org/search?query= and filter by the PID service)
- list of databases at the https://fairsharing.org/databases/
 - the Open Source Brain the OpenNEURO...



PID systems ⊟

ARK (24) DOI (749) PURL (28)

URN (41) hdl (195)

none (1362)

other (94)

data repositories and data journals

* \$\frac{1}{2} \frac{1}{2} \fra

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- list of databases at the https://fairsharing.org/databases/
 - the Open Source Brain the OpenNEURO...
- data citation is necessary to give credit, incentive FAIR behaviors, track impact of datasets, measure return of investment and easily locate and access data
- when using data of others → cite both the related peer-reviewed
 literature and the actual datasets

PID systems ⊟

ARK (24) DOI (749)

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[dataset] 34. Frazier, JA, Hodge, SM, Breeze, JL, Giuliano, AJ, Terry, JE, Moore, CM, Makris, N. CANDI Share Schizophrenia Bulletin 2008 data; 2008. Child and Adolescent NeuroDevelopment Initiative. https://dx.doi.org/10.18116/C6159Z

A for accessible: protocols

- accessible does not imply open
- data and metadata need to be retrievable by their identifier using a standardized communications protocol
- research repositories often use the OAI-PMH or REST API protocols to interface with data in the repository

A for accessible: protocols

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- research repositories often use the OAI-PMH or REST API protocols to interface with data in the repository
- example: Zenodo has a REST API which you can also use to programmatically upload and publish your research outputs

have you deposited any research output on Zenodo?

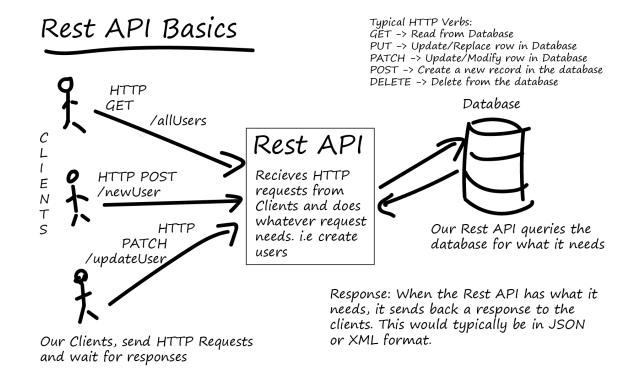




https://zenodo.org/



REST API



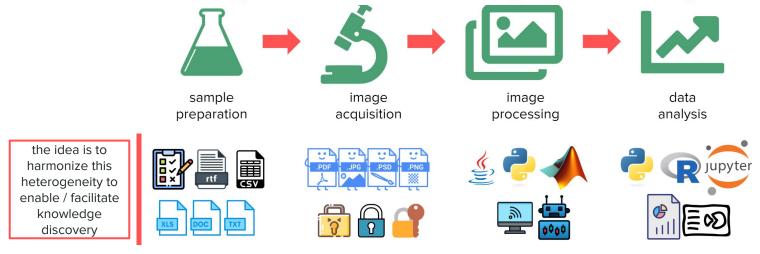
I for interoperable: standards

 data and metadata use a formal, accessible, shared, and broadly applicable language for knowledge representation

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Community standards for open cell migration data



standards for the Life Sciences

 the <u>ISA framework</u>: 'Investigation' (the project context), 'Study' (a unit of research) and 'Assay' (analytical measurement)



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- the <u>ISA framework</u>: 'Investigation' (the project context), 'Study' (a unit of research) and 'Assay' (analytical measurement)
- the <u>FAIRSharing catalogue</u> for standards: a comprehensive list of terminology artifacts (ontologies, controlled vocabularies), data formats, models and reporting guidelines
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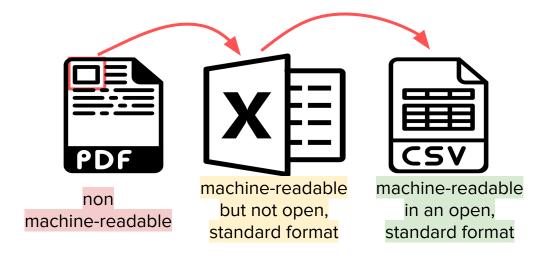
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- the <u>BioSchemas</u>: extends Schema.org (semantic markup for the web) to allow specifically for the description of life science resources
 - e.g. specification for the type BioSample:
 https://bioschemas.org/types/BioSample/0.1-RELEASE-2019_06_19/



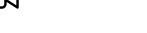
R for reusable: human- and machine-readable

- data and metadata come with clear license usage
- human-readable (PDF OK) is not the same as machine-readable (PDF not OK, CSV, JSON, XML OK)
- both need to be ensured



best practices: file formats

- text
 - **README files** should be in plain text format (ASCII, UTF-8)
 - (see here for a ref on how to best write a README file)
 - o Comma-separated values (CSV) for tabular data
 - Semi-structured plain text formats for non-tabular data (e.g., protein sequences)
 - Structured plain text (XML, JSON)
- images: PDF, JPEG, PNG, TIFF, SVG
- audio: FLAC, AIFF, WAV, MP3, OG
- video: AVI, MPEG, MP4
- compressed file archive: TAR.GZ, 7Z, ZIP







best practices: file naming

- the Stanford Libraries <u>quidance on file naming</u> is a great place to start
- general rule: know what a file is before you double-click on it
- avoid spaces and special characters



- use <u>common letter case patterns</u> such as *kebab-case*, *camelCase*, or *snake_case*
- include author name, project name, type of data, type of analysis, date, and file extension
 - o some examples from **Dryad**:
 - 1900-2000_sasquatch_migration_coordinates.csv
 - Smith-fMRI-neural-response-to-cupcakes-vs-vegetables.nii.gz
 - 2015-SimulationOfTropicalFrogEvolution.R

best practices: data directories



- A) Organized by File type
- B) Organized by Analysis

Dataset.A |- Code | |- Step.1 | |- Step.2 |- Data | |- Processed | |- Raw |- Results/ | |- Figure.1

|- Figure.2

- Models

readme.txt

```
Dataset.B
 - Figure.1
   - Code
    - Data
   - Results
  - Figure.2
   - Code
   - Data
   |- Results
  - Table.1
    - Code
   - Data
   - Results
   readme.txt
```

- governamental data belong to the public domain
- the new H2020 credo for research data is 'as open as possible, as closed as necessary'



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- for data accompanying scientific publications, the Creative Commons licences are recommended



orun a query on https://www.re3data.org/search?query= filtering by data licenses: what do you find?

Data licenses □

```
Apache License 2.0 (39)
BSD (33)
CC (875)
CC0 (171)
Copyrights (975)
ODC (97)
OGL (55)
OGLC (55)
Public Domain (367)
RL (4)
none (1)
other (1151)
```

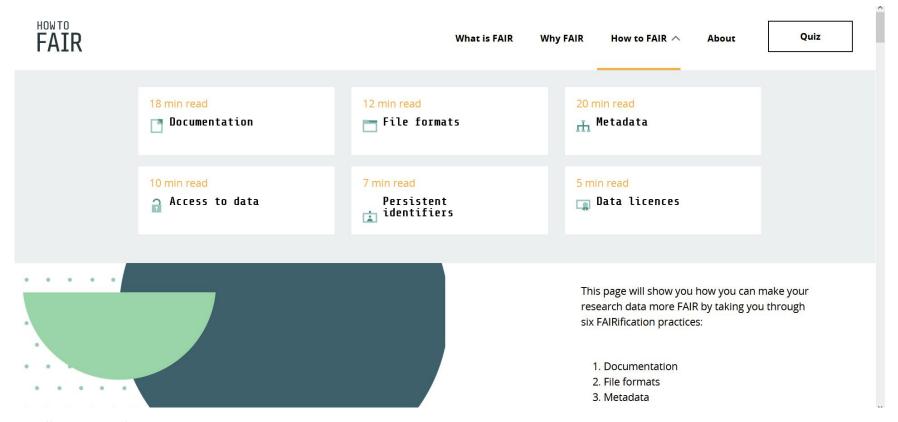




- governamental data belong to the public domain
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- for data accompanying scientific publications, the Creative Commons licences are recommended
- o run a query on https://www.re3data.org/search?query= filtering by data licenses: what do you find?
- open data and content can be freely used, modified, and shared by anyone for any purpose (from the <u>Open Definition</u>)
- look for conformant licenses <u>here</u> (and next slide)

License	Domain	Ву	SA	Comments
Creative Commons CCZero (CC0)	Content, Data	N	N	Dedicate to the Public Domain (all rights waived)
Open Data Commons Public Domain Dedication and Licence (PDDL)	Data	N	N	Dedicate to the Public Domain (all rights waived)
Creative Commons Attribution 4.0 (CC-BY-4.0)	Content, Data	Υ	N	
Open Data Commons Attribution License (ODC-BY)	Data	Υ	N	Attribution for data(bases)
Creative Commons Attribution Share-Alike 4.0 (CC-BY-SA-4.0)	Content, Data	Y	Y	
Open Data Commons Open Database License (ODbL)	Data	Y	Y	Attribution-ShareAlike for data(bases)

how to FAIR



Best practices for research reproducibility

part II: Working with data in a robust, reliable and replicable manner

https://tinyurl.com/reproducible2

version control

use Git to enhance your research reproducibility

"FINAL".doc







FINAL doc!

FINAL_rev. 2. doc







FINAL_rev.6.COMMENTS.doc

FINAL_rev.8.comments5 CORRECTIONS. doc









FINAL_rev.18.comments7. corrections9.MORE.30.doc

FINAL_rev.22.comments49. corrections.10.#@\$%WHYDID ICOMETOGRADSCHOOL?????.doc

WWW. PHDCOMICS. COM

version control

 version control helps you record changes you make to the files in a directory on your computer; version control software & tools are increasingly being used to collaborate in research and academic environments

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Benefits of using version control

- collaboration → define formalized ways to work together and share writing and code
- versioning → robust and rigorous log of changes to a file, without renaming files (v1, v2, final_copy)
- rolling back → quickly undo a set of changes; this can be useful when new writing or new additions to code introduce problems
- understanding → understand how the code or writing came to be, who wrote or contributed particular parts, and who you might ask to help understand it better
- backup → while not meant to be a backup solution, using version control systems mean that your code and writing can be stored on multiple other computers



version control: what we are going to do

setting things up





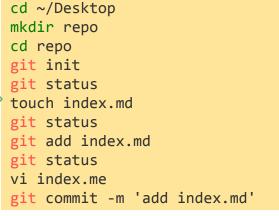
install git on your machine



create a

remote

repository



git remote add origin https://github.com/youruser/repo.git
git remote -v
git push -u origin master

git and GitHub



- <u>git</u> is the most used version control system
- <u>GitHub</u> is a popular website for hosting and sharing Git repositories remotely

setting up git + GitHub

if you do not have it on your machine yet, download git from https://qit-scm.com/downloads



if you do not have one yet, create a GitHub account at https://github.com/



git: create a local repository + adding/committing

```
cd ~/Desktop → move to Desktop
mkdir repo → create a directory called "repo" (use a name of your choice!)
cd repo → move to the directory
git init → initialize an empty repository
ls -a → show content of the directory, including hidden files
git status → show the status of the repository
```



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git init → initialize an empty repository
1s -a → show content of the directory, including hidden files
git status → show the status of the repository
touch index.md → create an empty markdown file called index
git status
git add index.md → add the index file to the tracked files
git status
vi index.me → write some text to the index file (press i, type # Hello, world!, press esc, type :wq)
git commit -m 'add index.md' → commit our changes to git
```



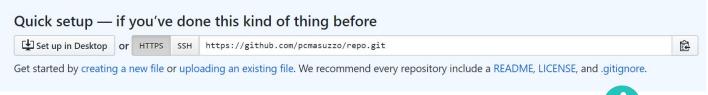


git: create a remote repository on GitHub

create a new repository on GitHub

- 3
- o use this resource to choose an open source license: https://choosealicense.com/
- connect your local repository with the remote repository





push an existing repository from the command line



```
git remote add origin <a href="https://github.com/pcmasuzzo/repo.git">https://github.com/pcmasuzzo/repo.git</a>
git remote -v
git push -u origin master → pushes our local changes to the remote repository
git status
modify the index file and then run:
git diff
```



git: pull changes from the remote repository

- when working with others, or when we are making our own changes from different machines, we need a way of pulling those remote changes back into our local copy
- let's go to our repository in GitHub and add there a README file
- we then have to pull the remote changes we made to keep our local repository in sync



git pull → pulls changes from the remote repository to the local one

additional resources

<u>Git Cheatsheets for Quick Reference by The Carpentries</u> <u>GitHub Help Documentation</u>



best practices for a (code) repository





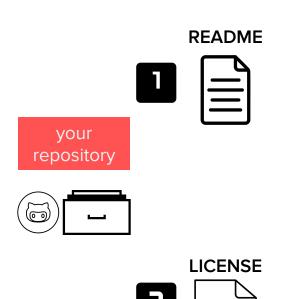


your repository



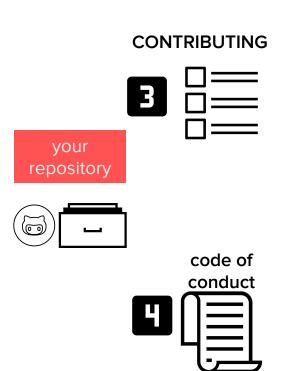
- a clear README is super important if you want people to understand the scope of your project, how to use it, the current status of it, how to get involved (more later...)
- when the README file is included in the root directory, GitHub will automatically display this on the homepage of your repository: this means it is the first thing people will often see!
 resource → A curated list of awesome READMEs

best practices for a (code) repository



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- MIT License: permissive license that lets people do whatever they want with your code as long as they provide appropriate attribution to you, and do not hold you liable
- Apache License 2.0: similar permissions to the MIT License, but also provides an express grant of patent rights from contributors to users
- GNU General Public License (GPL) v3: a copyleft license that requires anyone who redistributes your code, or a derivative work, to make the source available under the same terms as the original license resource → Choose a License

best practices for a (code) repository



- a CONTRIBUTING file serves as a guide to potential contributors on how to engage with your project (and community)
- a CONTRIBUTING file can include: which protocol to use to suggest features/raise issues (e.g. via pull requests), which type of contributions are welcome/prioritized, link to additional external documentations, how to contact you...
 - resource → How to write CONTRIBUTING files
- a code of conduct is important for setting the ground rules for expected behaviour and participation for project contributors
- it is a critical element for creating and maintaining a healthy community that engages in a constructive and productive manner within a positive social atmosphere
- it is important not only to have a CoC, but, should violation of it occur, to also enforce this (never an easy task...)
 resource → The Contributor Covenant

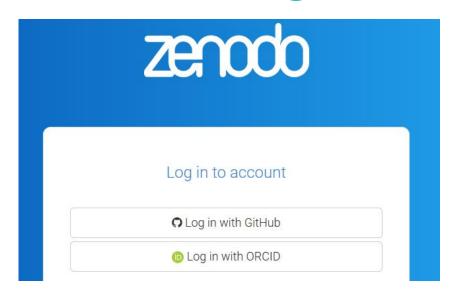


- we have seen how DOIs are the backbone of the academic reference and metrics system
- if you write software for your research, you might want to make it citable
- we are going to do this by archiving one of your GitHub repositories and assigning a DOI with the data archiving tool Zenodo

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choose a repository
important → at this stage, you should tell people how they can reuse your work
by including a license in your repository!

login into Zenodo 🕏



link GitHub and Zenodo (authorize Zenodo to connect with GitHub) 😘







4. on the Zenodo website navigate to the <u>GitHub repository listing page</u> and simply click the 'ON' button next to the repository you want to archive



- 5. make a new release of your code
 - a. if this is your first formal release, call it v1.0.0 or v1.0



 get a DOI: go to the Upload tab in Zenodo, select your uploaded repository, fill in some additional info and get a DOI

April 19, 2019 (v1.0) Software Open Access

pcmasuzzo/hot_topics_scholarly_publishing: Hot Topics Scholarly Publishing v1.0

Created Apr 19, 2019 10:36:43 AM, modified Apr 19, 2019 1:33:11 PM



best practices to make your code citable

FI README.md

Ten hot topics around scholarly publishing

A repo to host data and code to reproduce Figures 3 and 4 from: https://doi.org/10.7287/peerj.preprints.27580v1

Figure 3

Data are from: Lariviere et al. 2016.

Citations data have been extracted from the MS Excel file in Supplementary Information and saved as csv.

Figure 4

Data are DOAJ metadata extra date version of the file to your

DOI 10.5281/zenodo.2647404

add a human-readable citation

Paola Masuzzo. (2019, April 19). pcmasuzzo/hot_topics_scholarly_publish ing: Hot Topics Scholarly Publishing v1.0 (Version v1.0). Zenodo.

http://doi.org/10.5281/zenodo.2647404

get a nice DOI badge

copy the URL for the DOI into the README file of your GitHub repo: the DOI badge will be automatically added and users will know how to cite your code (you only need to do this for your first release, the GitHub/Zenodo integration will assign a DOI to each version/release of your project repository)

e this link to download an

OpenRefine

working with (messy) data in a reproducible way





OpenRefine: working with messy data



powerful tool for working

with messy data

<u>https://openrefine.org/</u> → download & install OpenRefine



(this might take a couple of minutes)

note → a Java Runtime Environment is needed, if you do not have one installed, get it here: https://www.java.com/en/

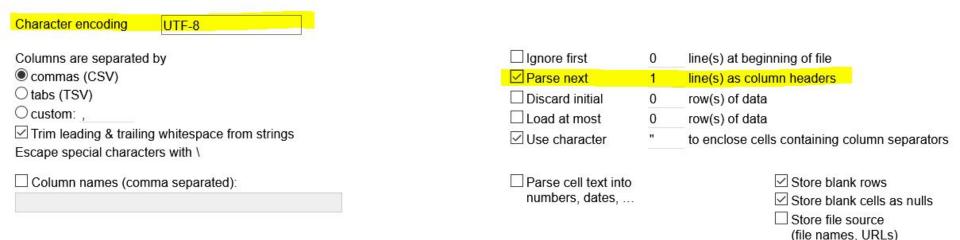
- OpenRefine is 'a tool for working with messy data'
- it uses your web browser as a graphical interface
- it works best with data in a simple tabular format and is ideal to fix inconsistencies in a data set (e.g., standardizing date formatting)
- it can help you accomplish several tasks, such as split data up into more granular parts, match local data up to other data sets, enhance a data set with data from other sources



OpenRefine: create a project



- OpenRefine interface runs at: http://127.0.0.1:3333/
- create a project by importing a file (for our exercises, download the DOAJ journals metadata csv file → https://doaj.org/csv)

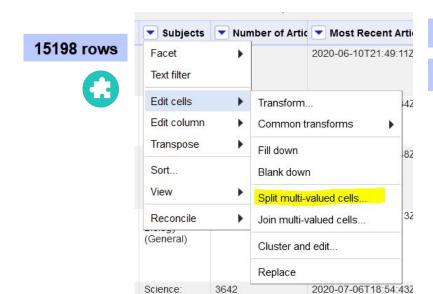




in each row

OpenRefine: split & merge

- rows & records views
 - o in rows mode, each row represents a single record in the dataset
 - o in records mode, OpenRefine links together multiple rows as belonging to the same record
- try out split cells & merge cells (→ edit cells / split multi-valued cells)



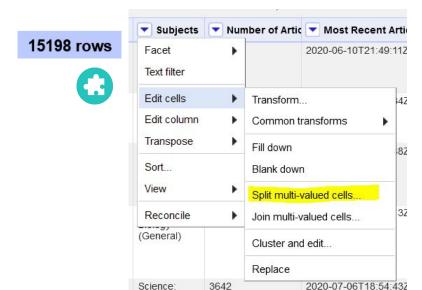
15921 rows

15198 records



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15921 rows

15198 records

best practice → when creating a spreadsheet with multi-valued cells, it is important to choose a separator that will never appear in the cell values themselves; this is why the pipe character (|) is often a good choice, while commas, colons and semi-colons should be avoided as separators

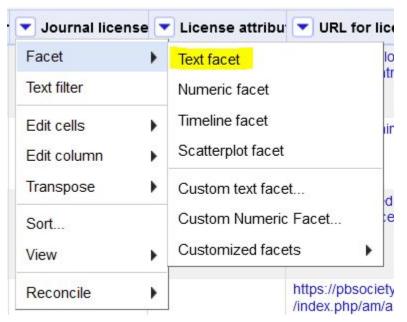


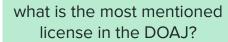
OpenRefine: facets

- facets are one of the most useful features of OpenRefine and can help in both getting an overview of the data and to improve the consistency of the data
- a facet groups all the values that appear in a column, and then allows you to filter the data by these values and edit values across many records at the same time
- the simplest type of facet is a text facet: it groups all the text values in a column and lists each value with the number of records it appears in
- the facet information always appears in the left hand panel in the OpenRefine interface

OpenRefine: facets











OpenRefine: filters & transformations

- filter journals which charge an APC (text filter = Yes)
- use a text facet on APC currency and include only EUR
- use a customized facet facet by blank to see how many of these journals have/have not reported the APC amount (this is very useful to look for missing data)

Facet by blank (null or empty string)





OpenRefine: filters & transformations

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- use a text facet on APC currency and include only EUR
- use a customized facet facet by blank to see how many of these journals have/have not reported the APC amount (this is very useful to look for missing data)
- common transformations

transform column to date → value.toDate("dd/MM/yyyy")

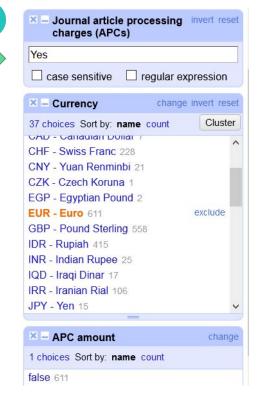


- edit column → add column based on this column →
- value.toString("dd MMMM yyyy")



Added on Date	date string
2004-04- 23T21:31:00Z	23 April 2004
2004-04- 23T21:31:00Z	23 April 2004

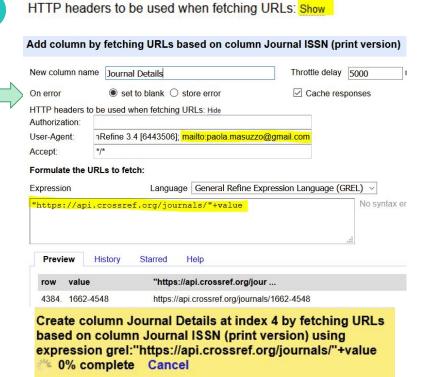
Facet by blank (null or empty string)





OpenRefine: advanced functions

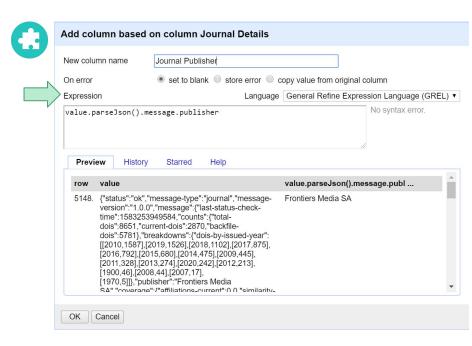
- text filter Journal Title on Frontiers in Neuroscience (might need to reset other filters)
 - on the ISSN column → edit column → add
 column by fetching URLs
 - we're going to use the CrossRef REST API https://github.com/CrossRef/rest-api-doc
- expression →"https://api.crossref.org/journals/"+value
- this will generate a new column named Journal
 Details → this column will be a JSON object
- we will then use this object to get the Publisher Name (amongst other details)





OpenRefine: advanced functions

column Journal Details → edit column
 → add column based on this column → value.parseJson().message.publisher



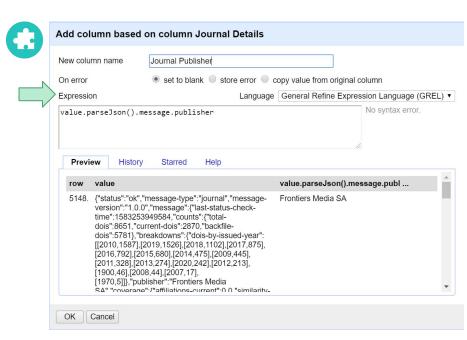


OpenRefine: advanced functions

column Journal Details → edit column
 → add column based on this column → value.parseJson().message.publisher

* VIB plugins → https://www.bits.vib.be/index.php/software-overview/o penrefine (history tools, pivot tool, cross function gui, and scatterplot tool using D3)

* more resources/tutorial → https://libjohn.github.io/openrefine/preamble.html





^{*} plugins available for OpenRefine → http://openrefine.org/download.html (e.g. FAIR metadata)

literate programming

and reproducible research

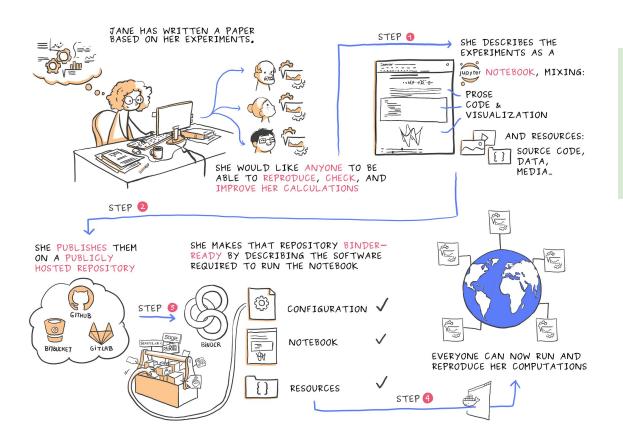
Donald Knuth. "Literate Programming (1984)" in Literate Programming. CSLI, 1992, pg. 99.

believe that the time is ripe for significantly better documentation of programs, and that we can best achieve this by considering programs to be works of literature. Hence, my title: "Literate Programming."

Let us change our traditional attitude to the construction of programs: Instead of imagining that our main task is to instruct a computer what to do, let us concentrate rather on explaining to human beings what we want a computer to do.

The practitioner of literate programming can be regarded as an essayist, whose main concern is with exposition and excellence of style. Such an author, with thesaurus in hand, chooses the names of variables carefully and explains what each variable means. He or she strives for a program that is comprehensible because its concepts have been introduced in an order that is best for human understanding, using a mixture of formal and informal methods that reinforce each other.





literate
programming =
human-readable
(text) +
machine-readable
(code)

literate programming and Binder

- literate programming is a paradigm in which a computer program is given an
 explanation of its logic in a natural language (e.g. English), together with snippets of
 source code. The approach is used in scientific computing and in data science
 routinely for reproducible research and open access purposes
- Binder is an open-source, free service that hosts fully functional Jupyter
 Notebooks, which you can open in an executable environment, making the code immediately reproducible by anyone, anywhere





Reproducible, sharable, interactive computing environments

why do we need all of this?

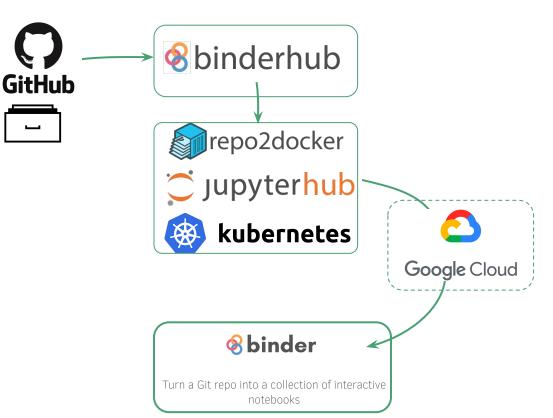
to be able to run code, we need

- hardware to run the code on
- software, including:
 - o the code itself
 - the programming language (e.g. Python, R, Julia, and so on)
 - relevant packages (e.g. pandas, matplotlib, tidyverse, ggplot)

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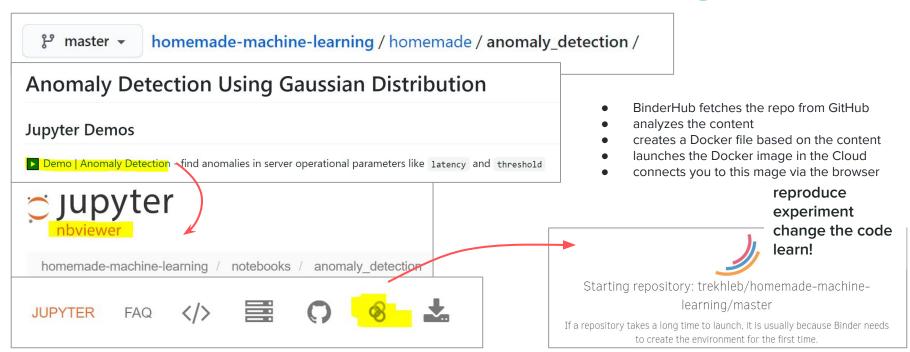




an example

GitHub repo: https://github.com/trekhleb/homemade-machine-learning





let's binderize a repository



- go to https://mybinder.org and type the URL of your repo into the "GitHub repo or URL" box it should look like this:
 - https://github.com/your-username/my-first-binder (I'll use this repo of mine: https://github.com/pcmasuzzo/modelli_epidemiologici)
- as you type, the webpage generates a link in the "Copy the URL below..." box;
 it should look like this: https://mybinder.org/v2/gh/pcmasuzzo/modelli_epidemiologici.git/master)
- copy it, open a new browser tab and visit that URL;
 you will see a "spinner" as Binder launches the repo;
 if everything ran smoothly, you'll see a Jupyter Notebook interface
 note: pushing changes back to the GitHub repo through the container is not possible with Binder
 - show a binder badge via the README file



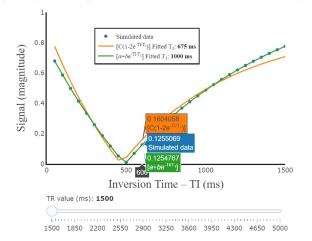


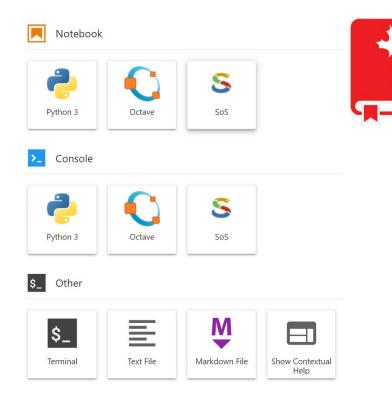
Neurolibre: interactive & reproducible neuroscience



Quantitative T₁ Mapping

This Jupyter Book is a series of interactive tutorials about quantitative T_1 mapping, powered by qMRLab. Most figures are generated with Plot.ly – you can play with them by hovering your mouse over the data, zooming in (click and drag) and out (double click), moving the sliders, and changing the drop-down options. To view the code that was used to generate the figures in this blog post, hover your cursor in the top left corner of the frame that contains the tutorial and click the checkbox "All







towards reproducible publishing



Welcome to a new ERA of reproducible publishing

New open-source technology lets eLife authors publish Executable Research Articles that treat live code and data as first-class citizens.



Replication Study: Transcriptional amplification in tumor cells with elevated c-Myc

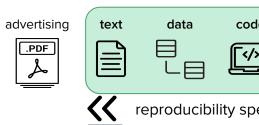


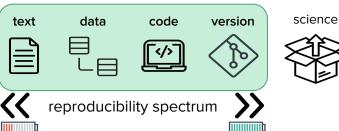
re-execute, validate, reproduce... learn!

Figure 7E

```
#' @width 13
    #' @height 7
                                                                                 PC1
    all.pca.x <- bind_cols(as_tibble(all.pca$x), drop_na(data.pca, fi
    out.pca.x g1 5 <- all.pca.x %>%
      gather("component", "value", 1:5)
 8
      pc1to5 plot <-
        ggplot(data = out.pca.x_g1_5, aes(
10
         x = dvlocmm, y = value, colour = housing
11
12
        )) +
                                                                                                     DV location (mm)
13
        geom point(alpha = 0.5) +
14
        facet wrap(\sim component, ncol = 5) +
        scale_x_continuous("DV location (mm)", c(0, 1, 2)) +
15
16
        theme_classic() +
        PCA_theme +
17
        theme(legend.position = "bottom")
18
19 )
                                                             > R
```

reproducible? not without people





WORLD VIEW . 25 FEBRUARY 2020

Invest 5% of research funds in ensuring data are reusable



It is irresponsible to support research but not data stewardship, says Barend Mons.



data stewards and managers



software developers



(open) champions



people who believe in people



Thank you



@pcmasuzzo



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