github.com/IBT-FMI/SAMRI

# SAMRI — Comprehensive Small Animal Magnetic Resonance Imaging Workflows

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## Abstract

Magnetic Resonance Imaging (MRI) is a measurement method with high depth penetration, which enjoys extensive use in imaging organs with an intricate holistic mode of function, such as the brain. MRI has significant translational potential, constituting a mainstay of human brain imaging, and finding increased use in preclinica model animal research. A core challenge in the analysis of preclinical MRI data is the adaptation of existing toolkits, designed primarily for human use, to the constraints and capabilities accessible in small animals.

SAMRI distributes high-level workflows, containing extensive procedural knowledge associated with MRI data handling, as well as domain knowledge regarding small animal neuroimaging. These workflows:

- cover conversion from the proprietary Bruker format to BIDS[1], preprocessing, and scan-level and population-level neuroimaging statistics.
- are integrated with reference data sources, which can automatically be queried:
  - standardized animal brain atlases,
  - connectivity and gene expression data from the Allen Institute.
- make use exclusively of free and open source software, and can thus be fully managed by an effective package manager with access to neuroscience packages (e.g. Portage [2]).

## Example Workflows

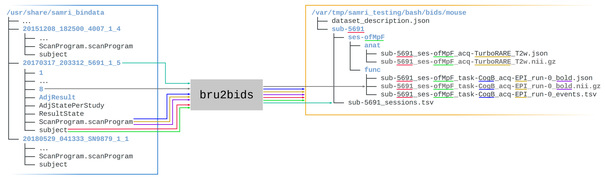



Figure 1: File-detail input/output view of Bruker-to-BIDS repositing workflow [3], with the Bruker data structure summarized on the left and the BIDS data structure exemplified in the right panel. Processing step corresponds to the colored multi-arrow step highlighted in fig. 3.

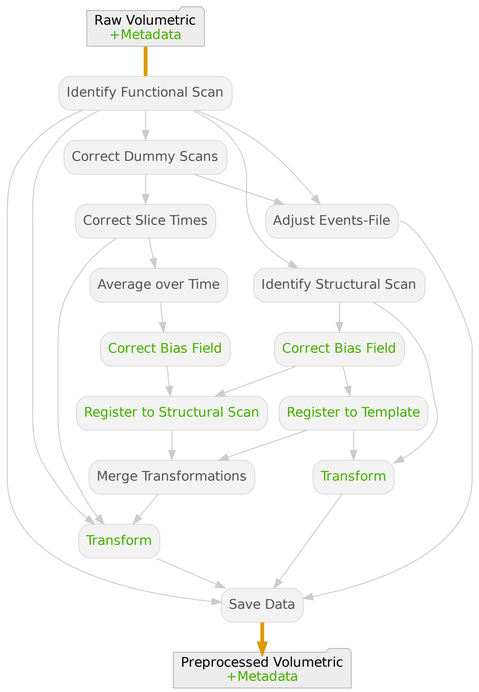



Figure 2: Atomized process overview of the "SAMRI Generic" preprocessing workflow [4], with green nodes representing specific nodes which were optimized for small animal mouse brain parameters. Processing step corresponds to the bold orange arrow highlight from fig. 3.

## Methods

SAMRI's front end interfaces, which provide access to the workflows, are available in Bash and Python (usage examples in fig. 6). The workflow control is implemented in Python, using construction and execution support from the nipype package. Plotting functions (using matplotlib and Blender) are distributed alongside the workflows, enabling operator quality control and the generation of publication-ready plots without the need of graphical editing. Established toolkits from human brain imaging are leveraged for atomized data processing applications (e.g. the nodes of fig. 2), including:

- ANTs
- AFNI
- scikit-learn
- PyBIDS
- FSL
- SciPy
- pandas
- nilearn

## Data-to-Figure Overview

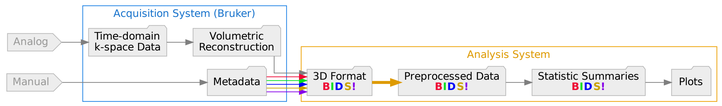



Figure 3: Graph representation of data provenance across an integrated MRI raw-data to plot pipeline, from [3]. All intermediary data processing stages are structured according to the BIDS specification. The processing step highlighted with multiple colored arrows is detailed in fig. 1, and the edge highlighted with a bold orange arrow is detailed in fig. 2.

## Package Structure

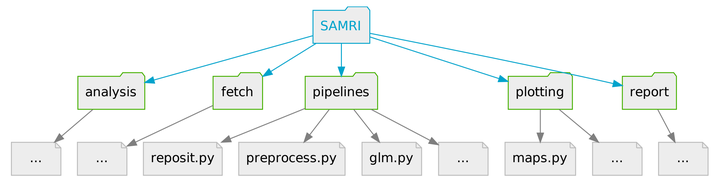



Figure 4: Graph representation of the package structure.

Module contents:

- **analysis**: High-level analysis functions.
- **fetch**: Feature extraction from standardized projection/expression packages.
- **pipelines**: Repositing, preprocessing, and first/second level modelling workflows.
- **plotting**: Small-animal-brain optimized 2D/3D plotting functions.
- **analysis**: High-level timecourse debugging and reporting functions.

## Outlook

- We are looking for **collaborators**, to expand the animal range currently covered (mice, rats) to further model animals.
- We are extending the test suite of the package to improve sustainability.
- We are working on a full stack integration testing infrastructure.
- We are working on a machine-learning based brain extraction solution for the preprocessing workflow.
- We are drafting a full length article detailing the package.

## References

[1] K. J. Gorgolewski, T. Auer, V. D. Calhoun, R. C. Craddock, S. Das, E. P. Duff, G. Flandin, S. S. Ghosh, T. Glatard, Y. O. Halchenko, *et al.*, "The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments," *Scientific Data*, vol. 3, p. 160044, June 2016.

[2] H.-I. Ioanas, B. Saab, and M. Rudin, "Gentoo linux for neuroscience - a replicable, flexible, scalable, rolling-release environment that provides direct access to development software," *Research Ideas and Outcomes*, vol. 3, p. e12095, Feb. 2017.

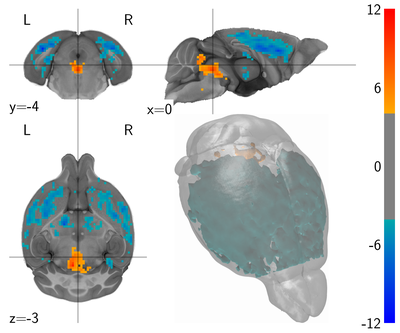
[3] H.-I. Ioanas, M. Marks, C. M. Garin, M. Dhenain, M. F. Yanik, and M. Rudin, "An automated open-source workflow for standards-compliant integration of small animal magnetic resonance imaging data," *Frontiers in neuroinformatics*, vol. 14, p. 5, Feb. 2020.

[4] H.-I. Ioanas, M. Marks, M. F. Yanik, and M. Rudin, "An optimized registration workflow and standard geometric space for small animal brain imaging," *bioRxiv*, 2019.

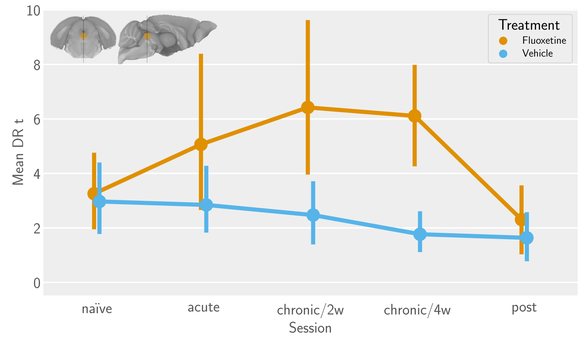
[5] H.-I. Ioanas, B. J. Saab, and M. Rudin, "Whole-brain longitudinal profiling of serotonergic reuptake inhibition," *bioRxiv*, Aug. 2020.

[6] H.-I. Ioanas, B. J. Saab, and M. Rudin, "A whole-brain map and assay parameter analysis of mouse vta dopaminergic activation," *bioRxiv*, Apr. 2020.

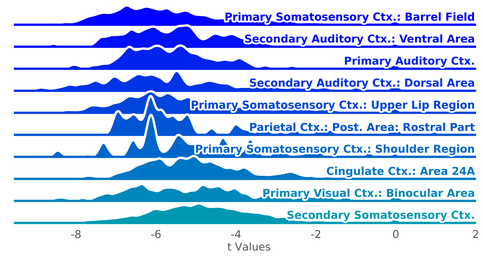
## Figure Examples



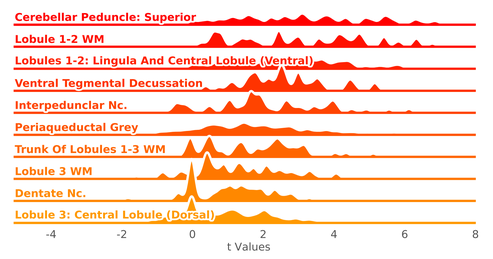

(a) Thresholded volumetric map and dynamically generated mesh for a second-level analysis pattern.



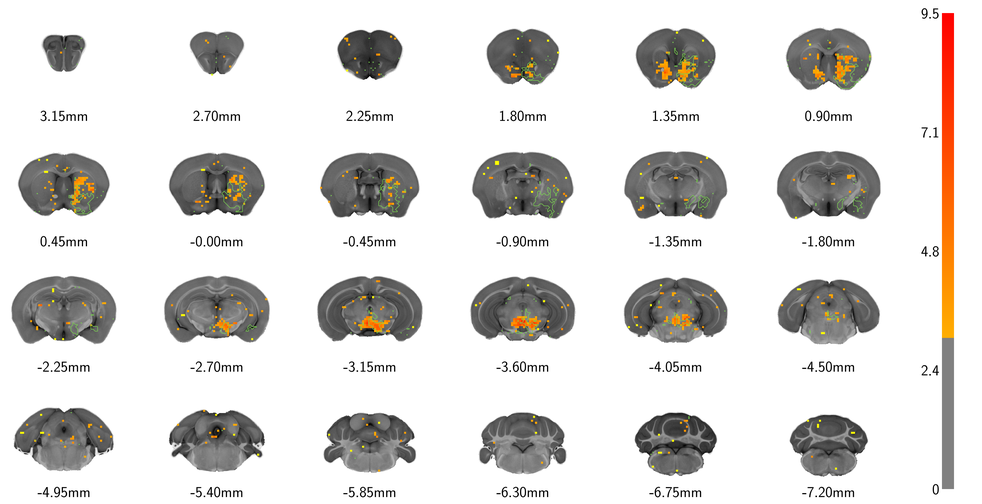

(b) Region of interest measurement session timecourse, split across treatment groups, and with within-population 95 % confidence interval error bars.




(c) Distribution of t-statistic values in the 10 most strongly inhibited atlas parcellation areas, for the statistc map shown in **(a)**.




(d) Distribution of t-statistic values in the 10 most strongly activated atlas parcellation areas, for the statistc map shown in **(a)**.




(e) Qualitative slice-wise comparison of thresholded t-statistic maps, with a functional projections highlighted in a warm heatmap, and structural projections outlined along the same threshold.

Figure 5: Figures, as can be automatically produced by SAMRI via a single function execution. From neuroimaging articles detailing monoaminergic drug profiling [5] **(a, b, c, d)** and monoaminergic assay development [6] **(e)**.

## Interface Examples

```
user@host ~ $ SAMRI bru2bids\
  -o /var/tmp/samri_testing/bash\
  -f '{"acquisition":["EPI"]}'\
  -s '{"acquisition":["TurboRARE"]}'\
  /usr/share/samri_bindata
```

(a) Bash interface

```
from samri.pipelines.reposit import bru2bids
bru2bids('/usr/share/samri_bindata/',
  functional_match={'acquisition':['EPI']}\closecurl,
  structural_match={'acquisition':['TurboRARE']}\closecurl,
  out_base='/var/tmp/samri_testing/pytest/',)
```

(b) Python interface

Figure 6: Bash and Python interfaces, made synchronously available via the Argh package (article fig. 3)

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