Tools and standards to make neuroimaging derived data reusable
Camille Maumet

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Tools and standards to make neuroimaging derived data reusable

Camille Maumet

Univ Rennes, Inria, CNRS, Inserm, IRISA UMR 6074, VisAGeS ERL U-1228
Sample sizes in neuroimaging

2015: 30 subjects / study

Poldrack et. al (2017)
1. Towards large-scale brain imaging studies
More and more shared data available

Single study
30 subjects

Consortium
1000 subjects

Cohort
1 000 - 100 000 subjects

+ Images
+ Homogeneous
- Fewer datasets
New challenges when working with open data

1. Raw data
2. Feature extraction
3. Derived data
4. Statistical analysis
5. Results
New challenges when working with open data
New challenges when working with open data

- Raw data
- Feature extraction
- Derived data
- Statistical analysis
- Results

- Raw data
- Feature extraction
- Derived data
New challenges when working with open data

Feature extraction

Derived data

Raw data

Feature extraction

Derived data

Statistical analysis

Results

Feature extraction

Derived data

Raw data
New challenges when working with open data

Meta-analyses

Feature extraction

Derived data

Statistical analysis

Results

Raw data

Feature extraction

Derived data

Statistical analysis

Results

Raw data

Feature extraction

Derived data

Meta-analyses
2. Analytic variability?
Analytic variability

“Different acceptable analysis methods”
Carp et al. (2012)
Analytic variability
Analytic variability

Spatial registration
Segmentation
Cross-modality registration

etc.
Analytic variability
Analytic variability

≠ algorithm

≠ algorithm
Analytic variability

≠ software

≠ algorithm

≠ software
Analytic variability
Analytic variability

≠ parameters

≠ algorithm

≠ software

≠ software version

≠ parameters
Analytic variability

≠ environment

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Analytic variability

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Question?

How does analytic variability impact neuroimaging results?
Background

- **Choice of Analysis Pipeline (functional MRI)**
  *Carp (2012)*

- **Choice of Analysis Software Version**
  *Groenenschild et al (2012)*

- **Choice of operating system**
  *Glatard et al (2015)*

- **Choice of analysis software package**
  *Pauli et al (2016)*
  *Bowring et al (2018) (preprint)*
Background

- Choice of Analysis Pipeline (functional MRI)
  Carp (2012)

- Choice of Analysis Software Version
  Groenenschild et al (2012)

- Choice of operating system

- Choice of analysis software package
  Pauli et al (2016)

Joint work with Alexander Bowring and Thomas Nichols
Three published studies with available data.

Pipelines aimed to replicate the original analyses.

Impact of Analysis Software on Task fMRI Results

Reproducing the main figure

Impact of Analysis Software on Task fMRI Results

Reproducing the main figure

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Dice coefficients

Impact of Analysis Software on Task fMRI Results

Reproducing the main figure

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Dice coefficients

Unthresholded statistics

3. Transparency
Disclosing analytical details

Details about the analysis pipeline are in the code.

In manuscripts, it is best practice to:

- Cite custom code
- Cite libraries and tools
How to cite software? The software citation principles

Software is a critical part of modern research...

...yet there is little support for its acknowledgement and citation.

https://blog.datacite.org/software-citation-principles/ by Laura Rueda, adapted.

Smith et al (2016)
3. Results

[...] All analysis scripts, results reports, and notebooks for each of study are available through Zenodo (Nielsen and Smith, 2014) at https://zenodo.org/record/1203654 (Alexander Bowring et al., 2018).
Let others cite your code

![GitHub page for NIS0x-BDI/Software_Comparison: Version 0.2](https://zenodo.org/record/1248809)

**Attribution:**
- AlexBowring, Camille Maumet, Thomas Nichols
- No description provided.

**Unique identifier:**
- [DOI](https://doi.org/10.5281/zenodo.1248809)

**Specificity:**
- Files included:
  - `AFNI`
  - `LEVEL2`
  - `euler_chars.csv`
  - `permutation_test`
  - `euler_chars.csv`

**Versions:**
- Version 0.2: 10.5281/zenodo.1248809
- Version v0.1: 10.5281/zenodo.1235695
2.2 Data Analyses

All data analyses were conducted using AFNI 17.0.18 (RRID:SCR_005927, (Cox, 1996)), FSL 5.0.10 (RRID:SCR_002823, (Jenkinson et al., 2012)), and SPM12 v6906 (RRID:SCR_007037, (Penny et al., 2011)).
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Citing libraries and tools

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https://fsl.fmrib.ox.ac.uk/fsl/fslwiki
Citing libraries and tools

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Also applies to other (non-neuroimaging) tools, repositories and libraries...

2.5 Scripting of analyses and figures

A Python Jupyter Notebook (Kluyver et al., 2016) was created for each of the three studies. Each notebook harvests our results data from Neurovault (RRID:SCR_003806) and applies the variety of methods discussed in the previous section using NiBabel 2.2.0 (Brett et al., 2017), NumPy 1.13.3 (Walt et al., 2011) and Pandas 0.20.3 (McKinney and Others, 2010) packages. Figures were created using Matplotlib 2.1.0 (Hunter, 2007) and Nilearn 0.4.0 (Abraham et al., 2014).
"Provenance is information about entities, activities, and people involved in producing a piece of data or thing" — W3C PROV
Machine-readable provenance
Machine-readable provenance

NIDM Experiment

- OpenfMRI
- XNAT
- INS
- Human Connectome Project

Raw data

NIDM Workflow

- FSL
- SPM
- NITRC
- CE

Pipelines

NIDM Results

Results

NIDM: neuroimaging data model
International collaboration with INCF SIG on Reproducibility and Best Practices in Human Brain Imaging
Machine-readable provenance

NIDM: neuroimaging data model
International collaboration with INCF SIG on Reproducibility and Best Practices in Human Brain Imaging.

NIDM-Results → fMRI, VBM results
Harmonised model and provenance.

Joint work with INCF NIDASH working group - https://github.com/incf-nidash/
NIDM-Results in brief

Maumet et al., (2016)
NIDM-Results in brief

Maumet et. al, (2016)
Derived data reuse with NIDM-Results: meta-analysis

Coordinate-based meta-analysis

Image-based meta-analysis


Maumet et. al, (2016)
Derived data inspection with NIDM-Results: SPM- and FSL-like views

https://github.com/incf-nidash/nidmresults-spmhtml
https://github.com/incf-nidash/nidmresults-fslhtm
Derived data inspection with NIDM-Results: SPM- and FSL-like views
How to use NIDM-Results for my study?

1. Export

   $ nidmfs $ fsl_ds107_group 49 -g Control

https://github.com/incf-nidash/nidmresults-spm
https://github.com/incf-nidash/nidmresults-fsl

2. Publication on NeuroVault

   A Correspondence between Individual Differences in the Brain’s Intrinsic Functional Architecture and the Content and Form of Self-Generated Thoughts

   Contributed by ChrisFosGorgolewski, Dan Lurie, Sebastian Urchs, Judy A. Kipping, R. Cameron Craddock, Michael P. Mithum, Daniel S. Margules, Jonathan Smallwood

   Link to the paper

   ![NeuroVault Interface](image)
One step further: linking it all together!

“Gather, view and monitor all research outcomes”

https://beta.connect.openaire.eu/

Principe (2018)
One step further: linking it all together!

“Gather, view and monitor all research outcomes”

https://beta.connect.openaire.eu/

Principe (2018)
Many ways to contribute

You can...

- Make your research outputs available and citable
- Cite existing software
- Use derived data standards and tools
- Contribute to the development of new specifications and their ecosystems
- Make datasets in neuroimaging data repository discoverable

Join the NIDASH community! [https://github.com/incf-nidash/nidm-specs](https://github.com/incf-nidash/nidm-specs)

References


Photo and template credits

Brains on slide 4: Neil Conway - [link](#)
Transparency on slide 29: Public domain (CC0) - [link](#)
Presentation template by [SlidesCarnival](#), adapted.
Acknowledgements

**NIDM working group**


**Neuroimaging software teams**

Gang Chen, Richard Reynolds, Robert Cox (AFNI), Mark Jenkinson, Matthew Webster, Paul McCarthy, Eugene Duff, Steve Smith (FSL), Guillaume Flandin (SPM).

**Meta-analysis datasets** Tracey group at FMRIB.

Thank you! To all INCF NIDASH task force members.
Thank you!

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Join the NIDASH community:
https://github.com/incf-nidash/nidm-specs