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Tools and standards to make neuroimaging derived data reusable

Camille Maumet

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Submitted on 2 Oct 2018

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Tools and standards to make neuroimaging derived data reusable

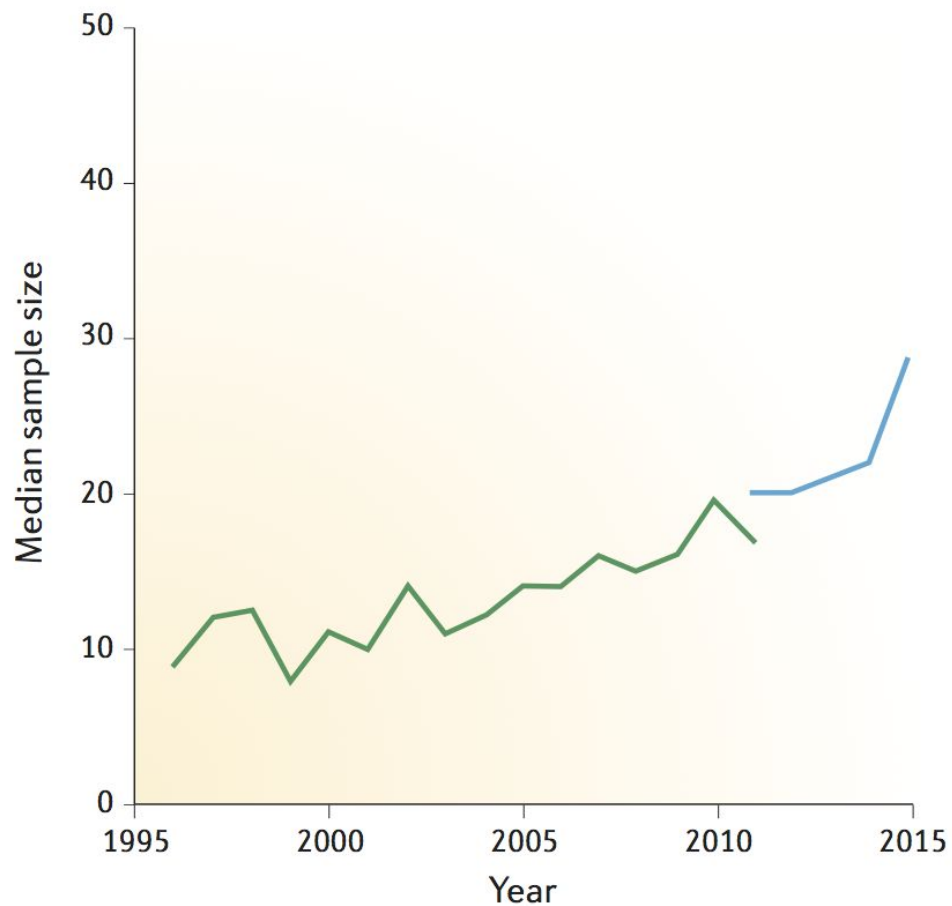
Camille Maumet



Univ Rennes, Inria, CNRS, Inserm, IRISA UMR 6074, VisAGeS ERL U-1228

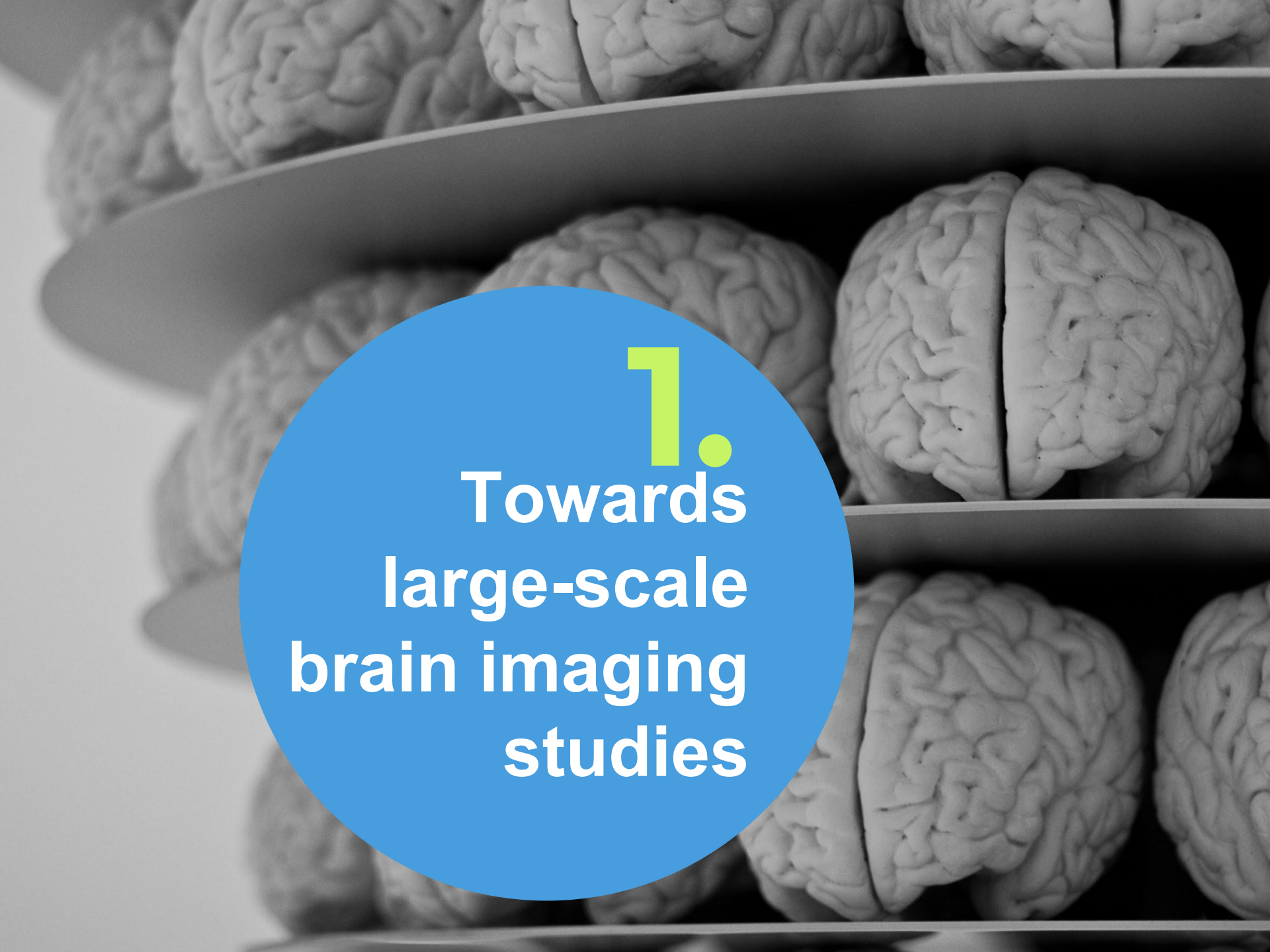


Sample sizes in neuroimaging



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



OpenNEURO

studyforrest.org



NEUROVAULT

L I E L N L F T Q K T Q R V
S M Y C O N N E C T O M E Q
G S P K K W A R R G K E H R

NITRC

OSF

Consortium

1000 subjects



ABIDE

Autism Brain Imaging
Data Exchange

1000 Functional
Connectomes Project



CORR

CONSORTIUM FOR
RELIABILITY AND
REPRODUCIBILITY



HUMAN
Connectome
PROJECT

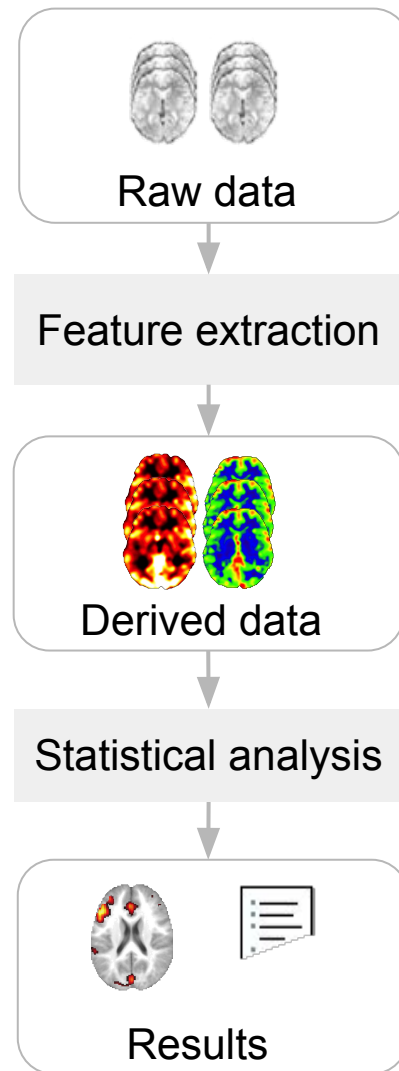
biobank^{uk}
Improving the health of future generations

Cohort

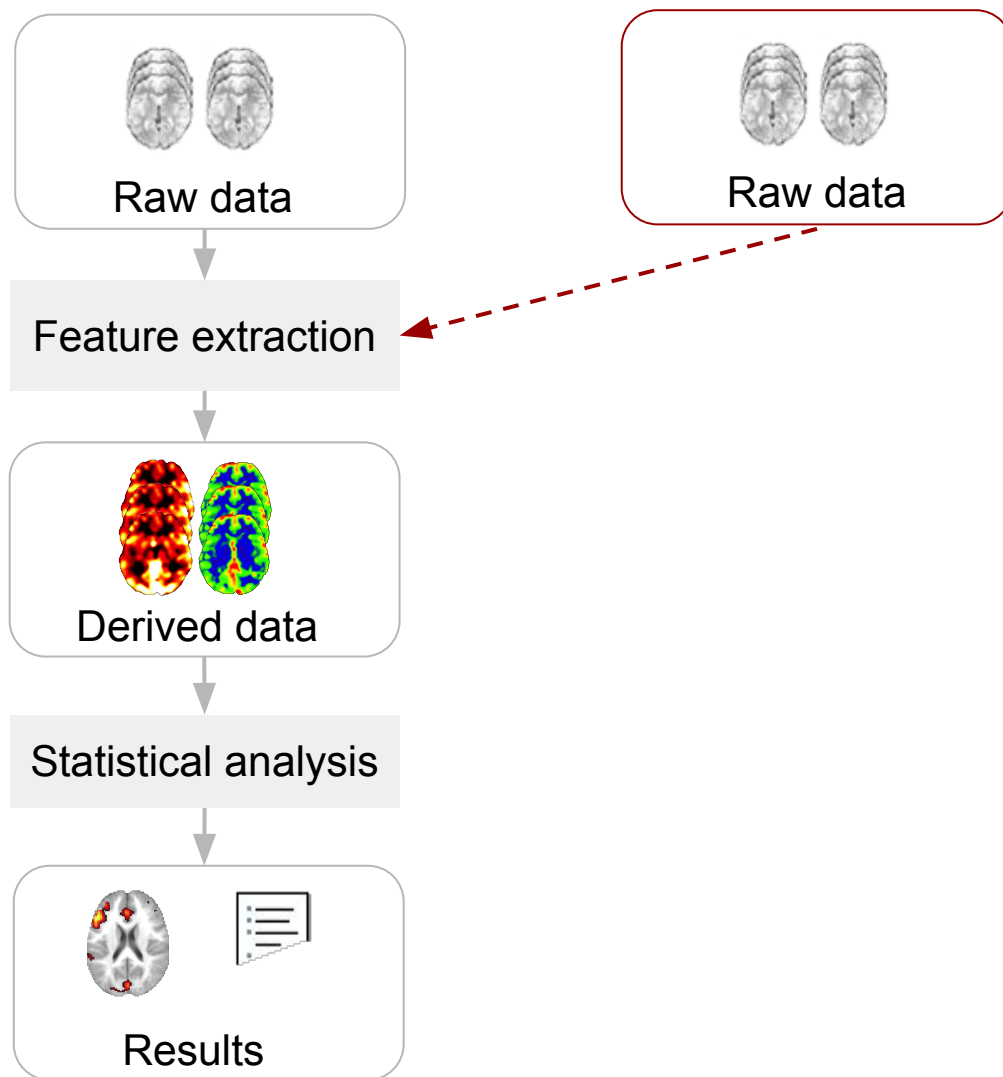
1 000 - 100 000 subjects

- + Images
- + Homogeneous
- Fewer datasets

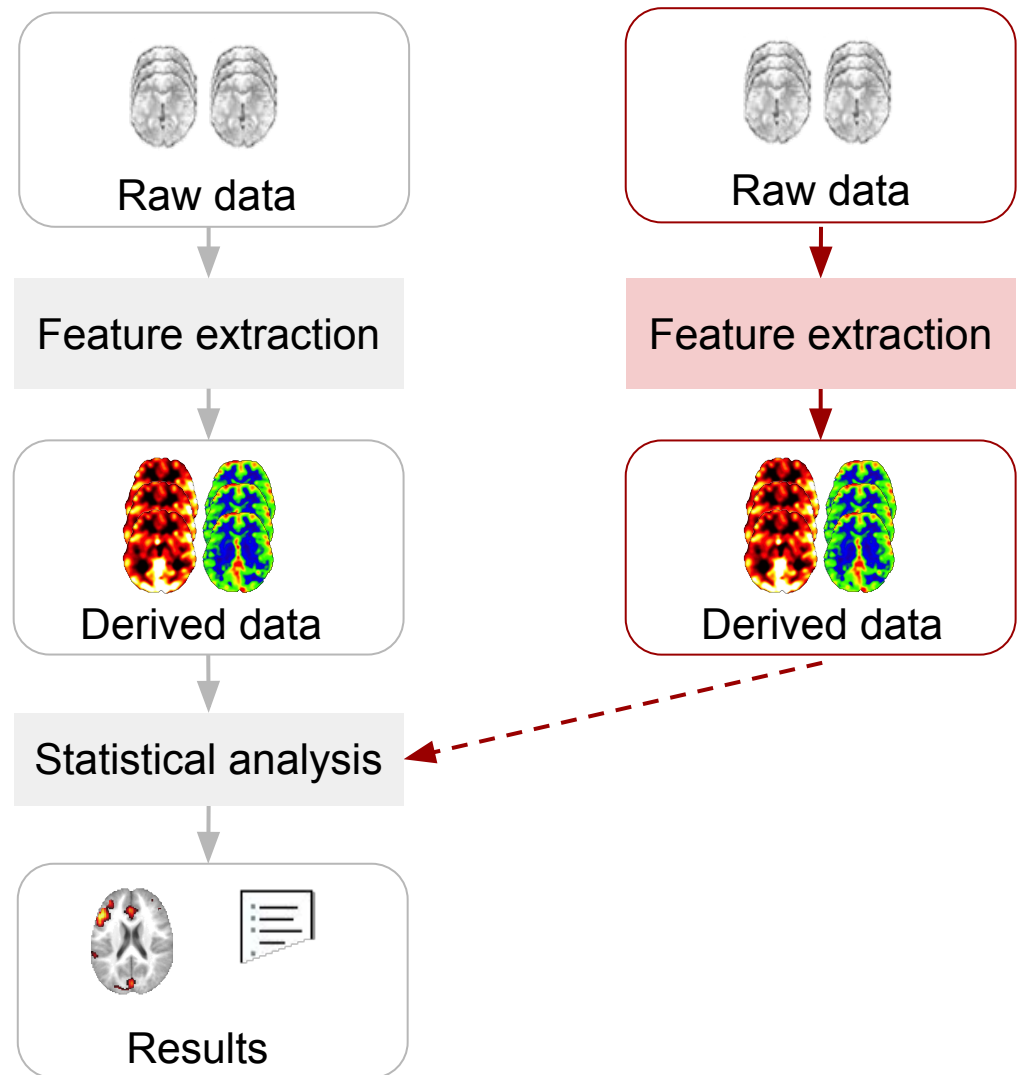
New challenges when working with open data



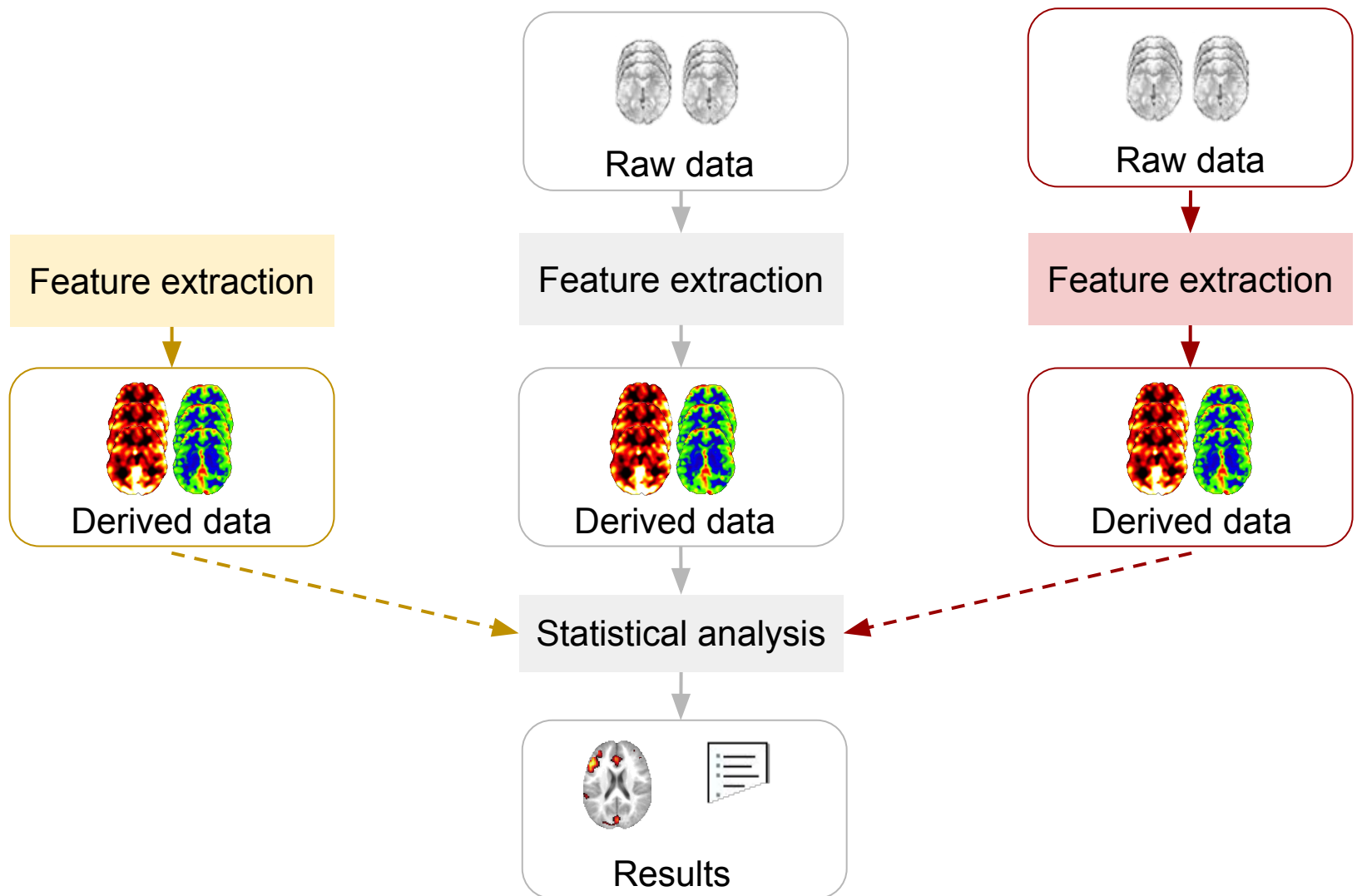
New challenges when working with open data



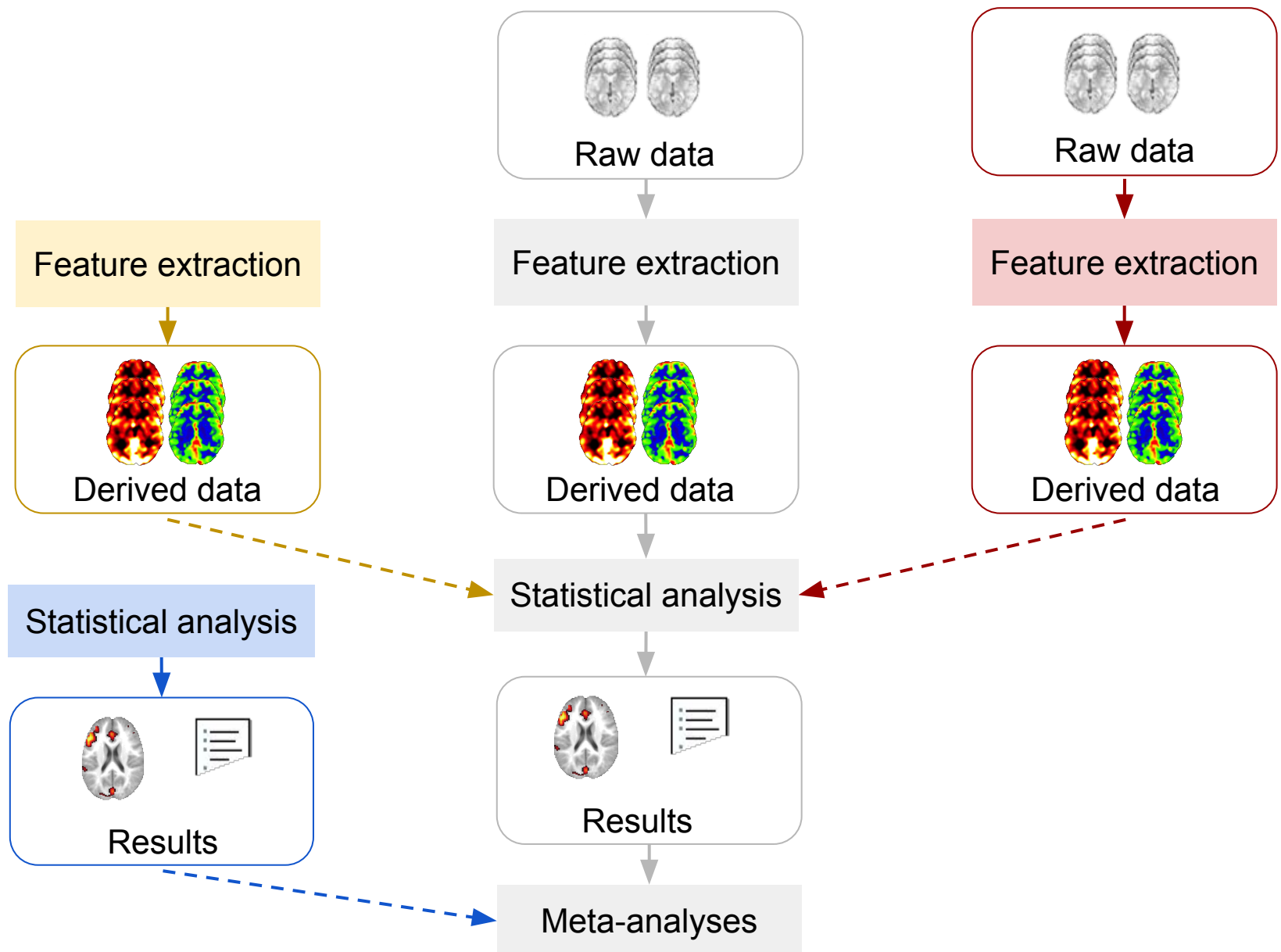
New challenges when working with open data



New challenges when working with open data



New challenges when working with open data

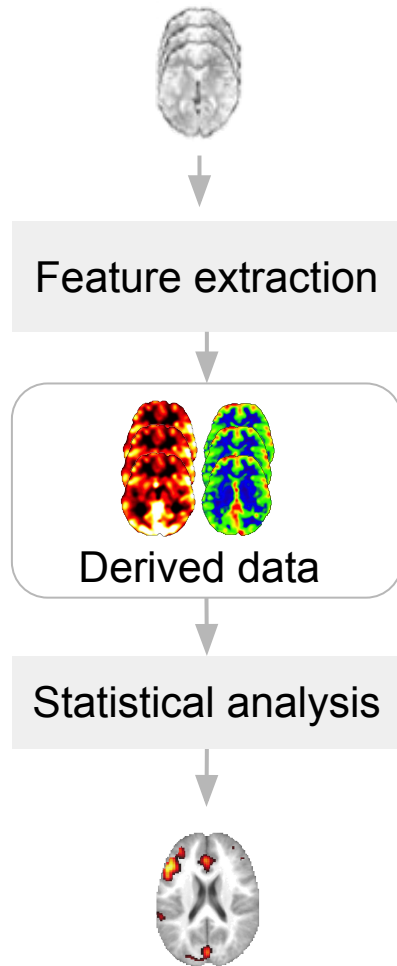


The background features six vertical columns of circles. The first column has 10 circles in shades of gray. The second column has a diamond shape at the top, followed by 4 circles. The third column has 4 circles with a cross-hatch pattern. The fourth column has 10 circles in shades of gray. The fifth column has 10 circles in shades of gray. The sixth column has 10 circles in shades of gray. A large blue circle is centered in the foreground.

2.

**Analytic
variability?**

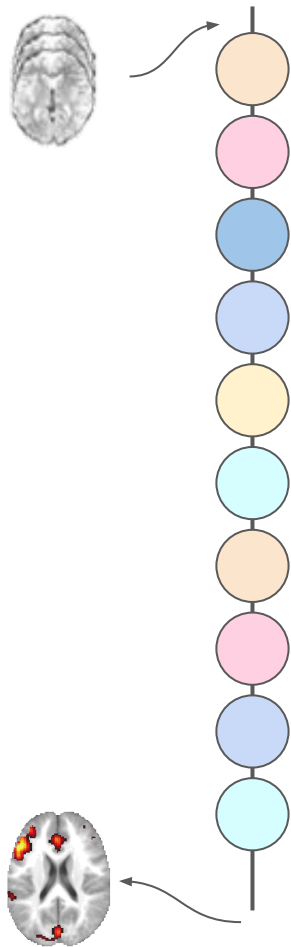
Analytic variability



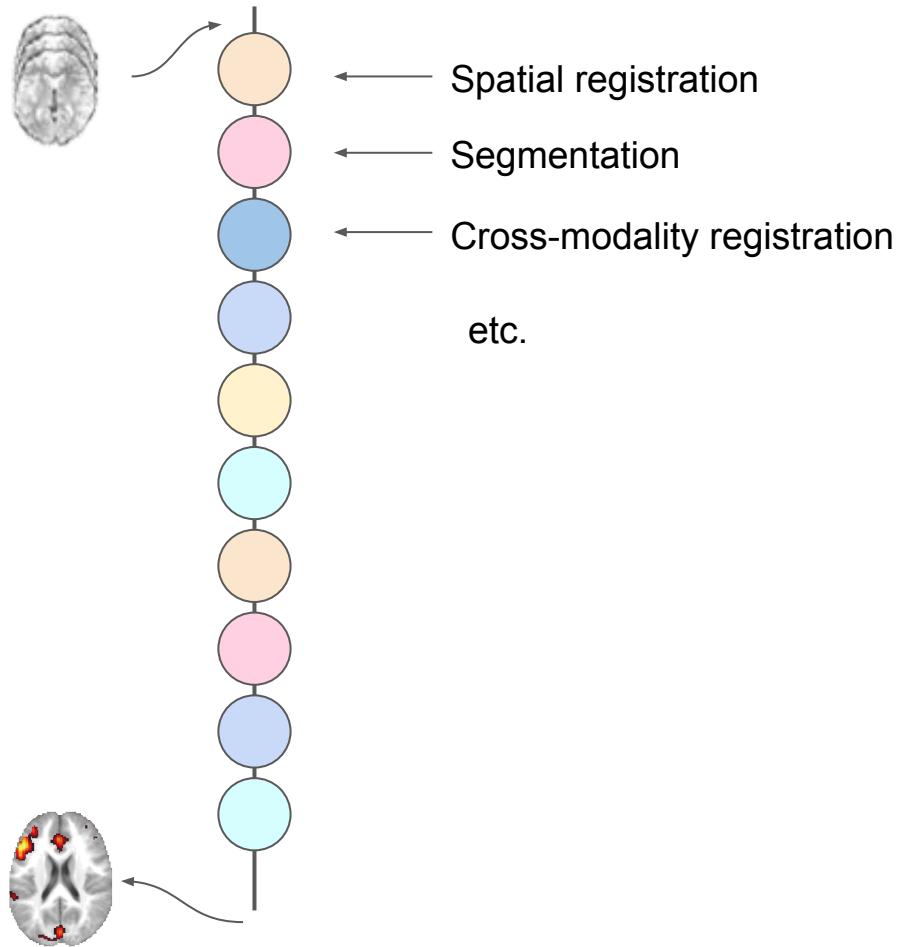
“Different **acceptable** analysis methods”

Carp et al. (2012)

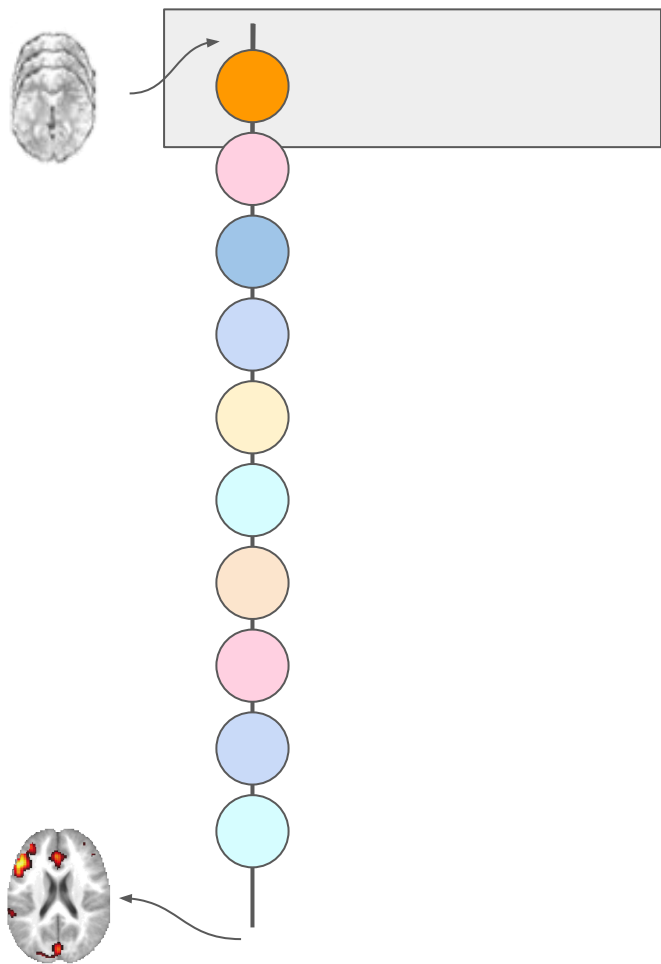
Analytic variability



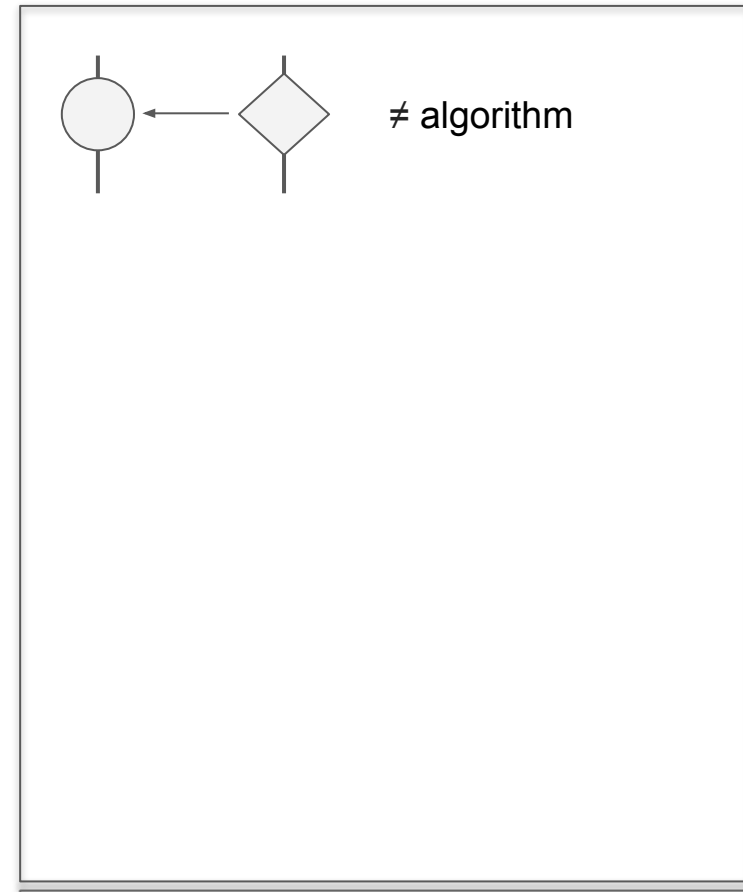
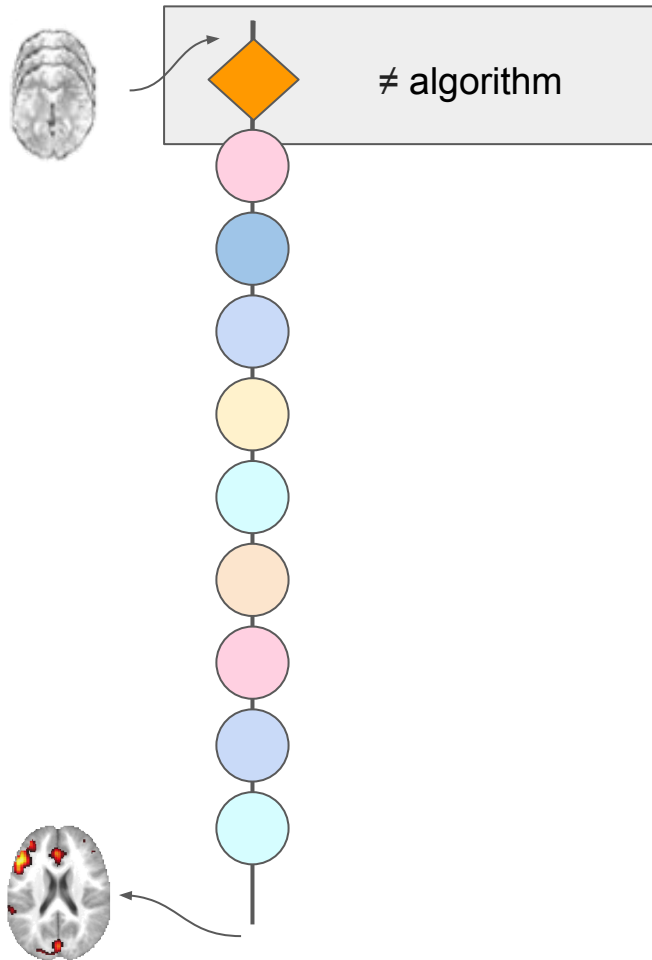
Analytic variability



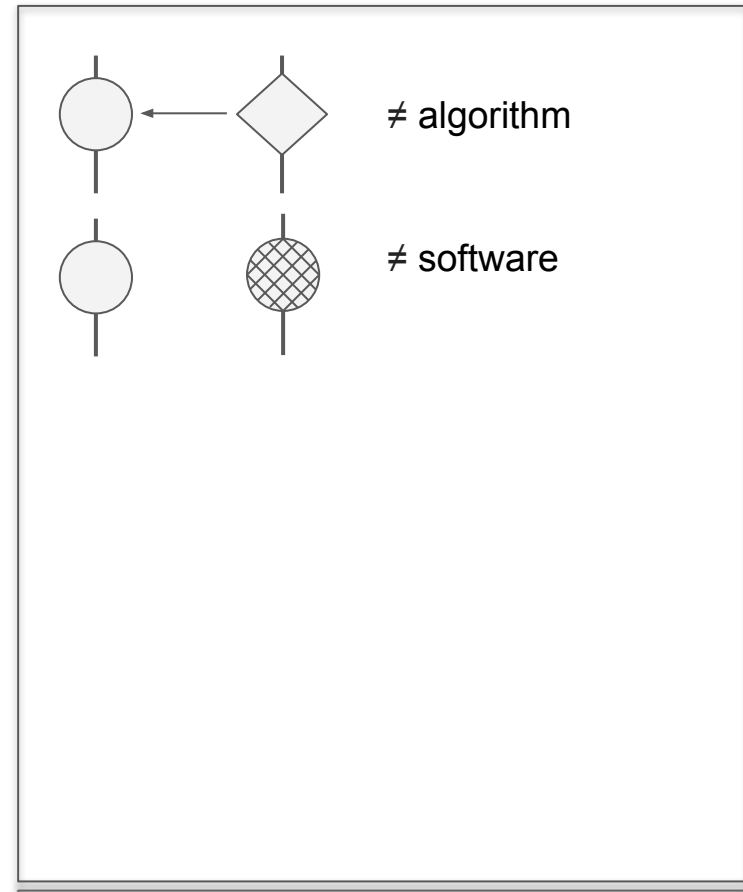
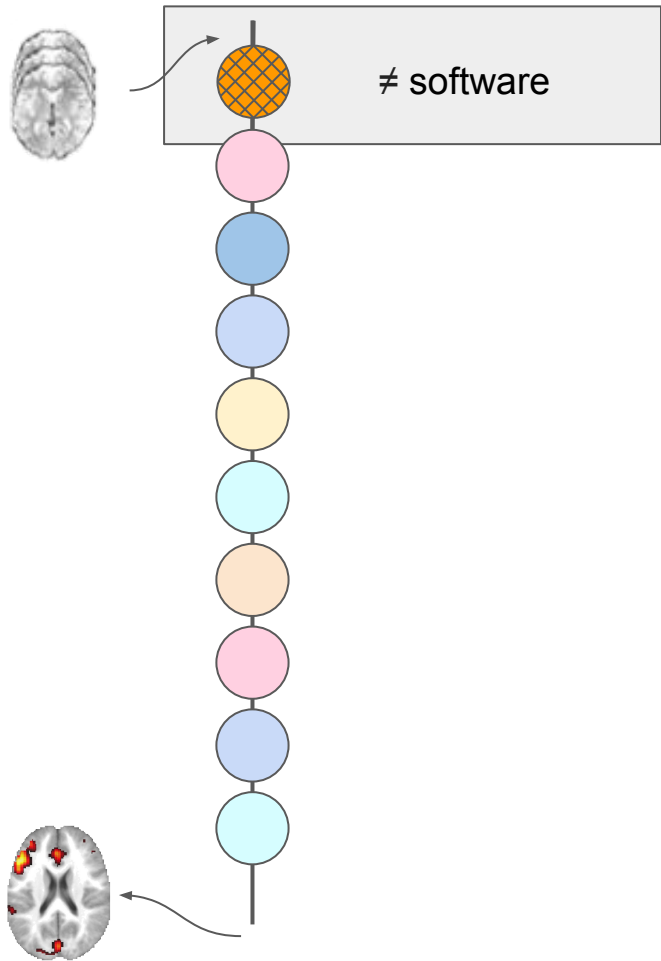
Analytic variability



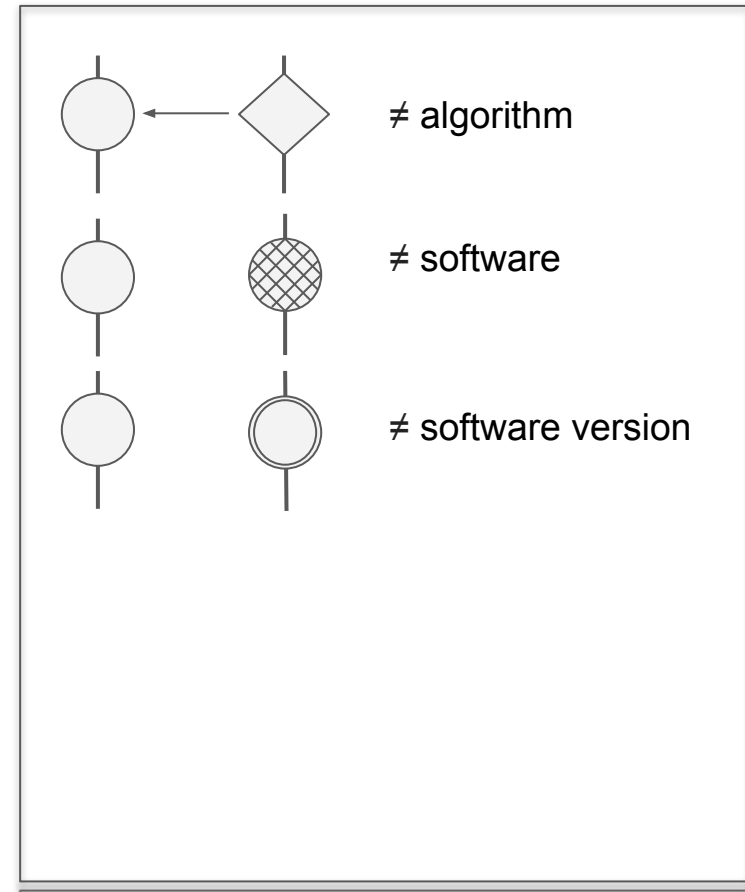
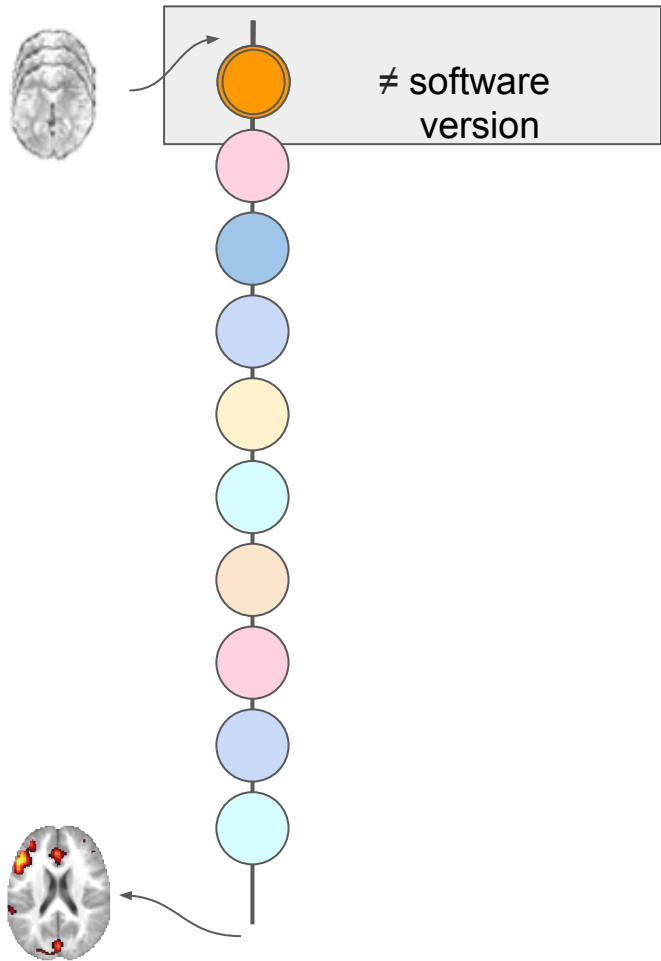
Analytic variability



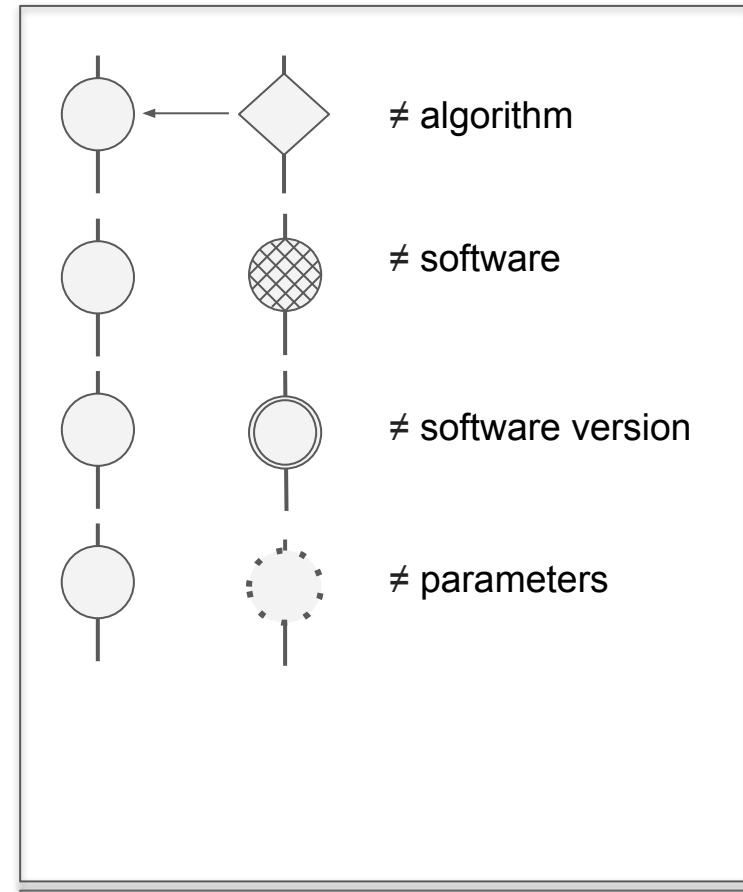
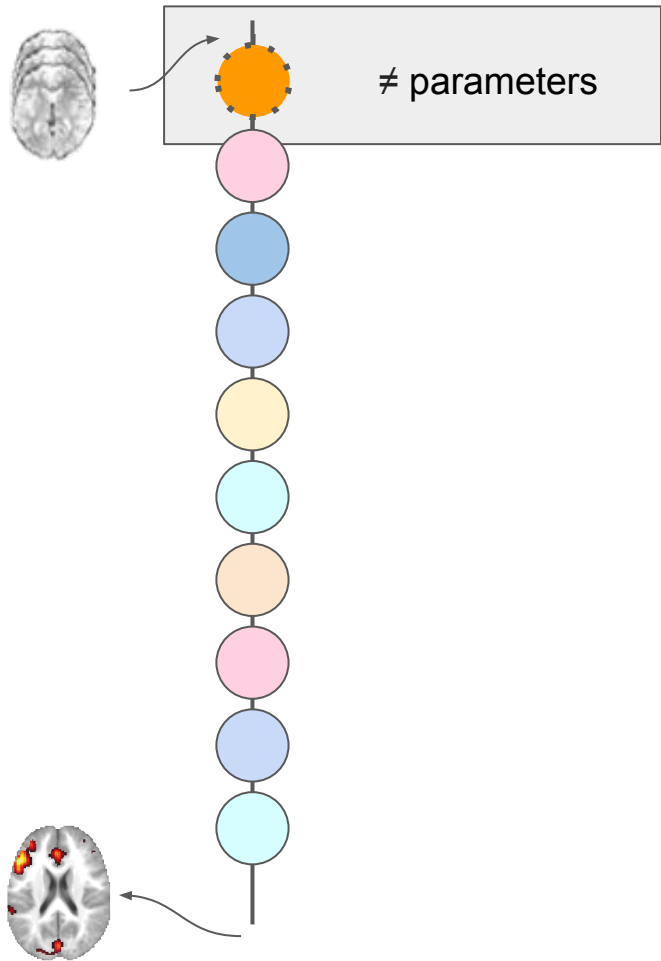
Analytic variability



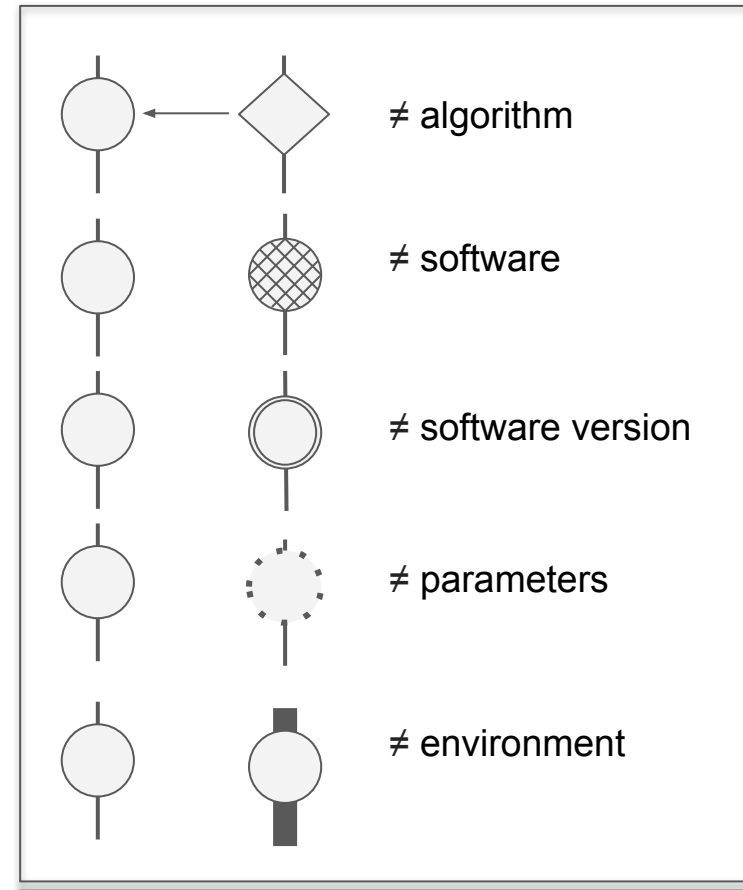
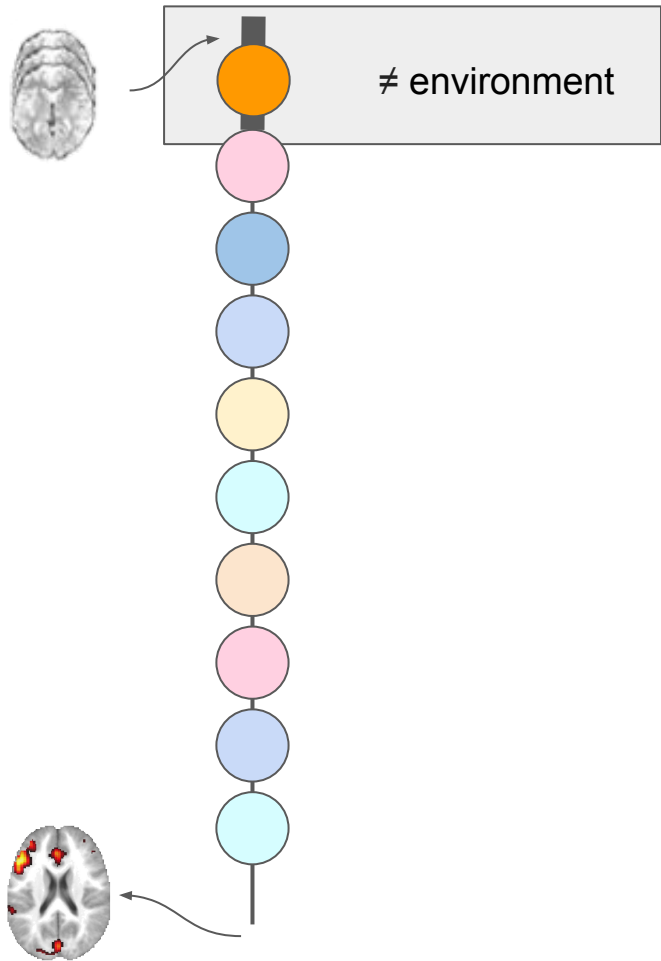
Analytic variability



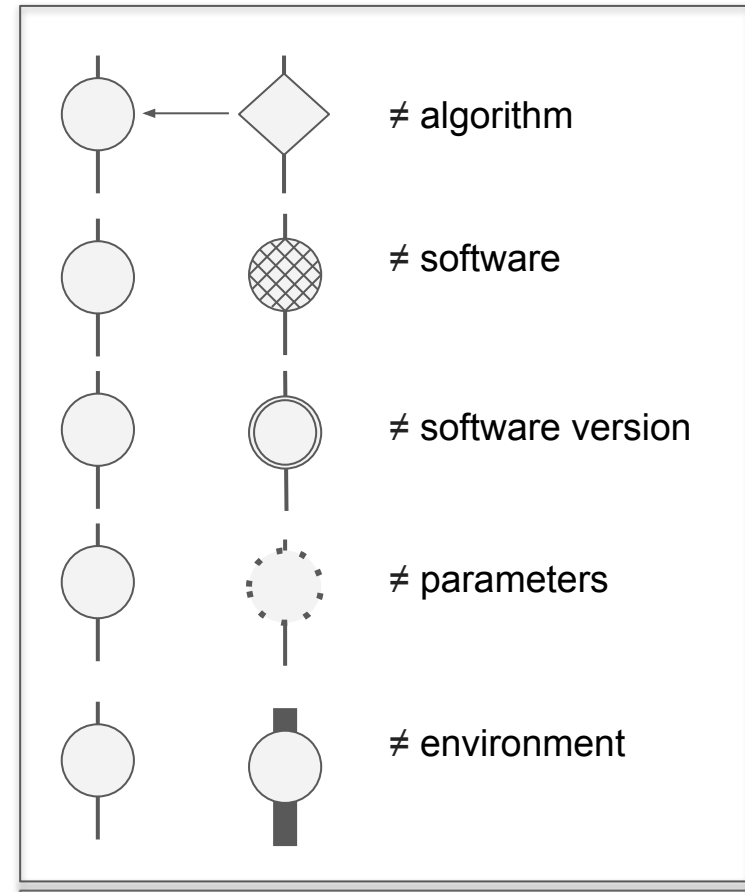
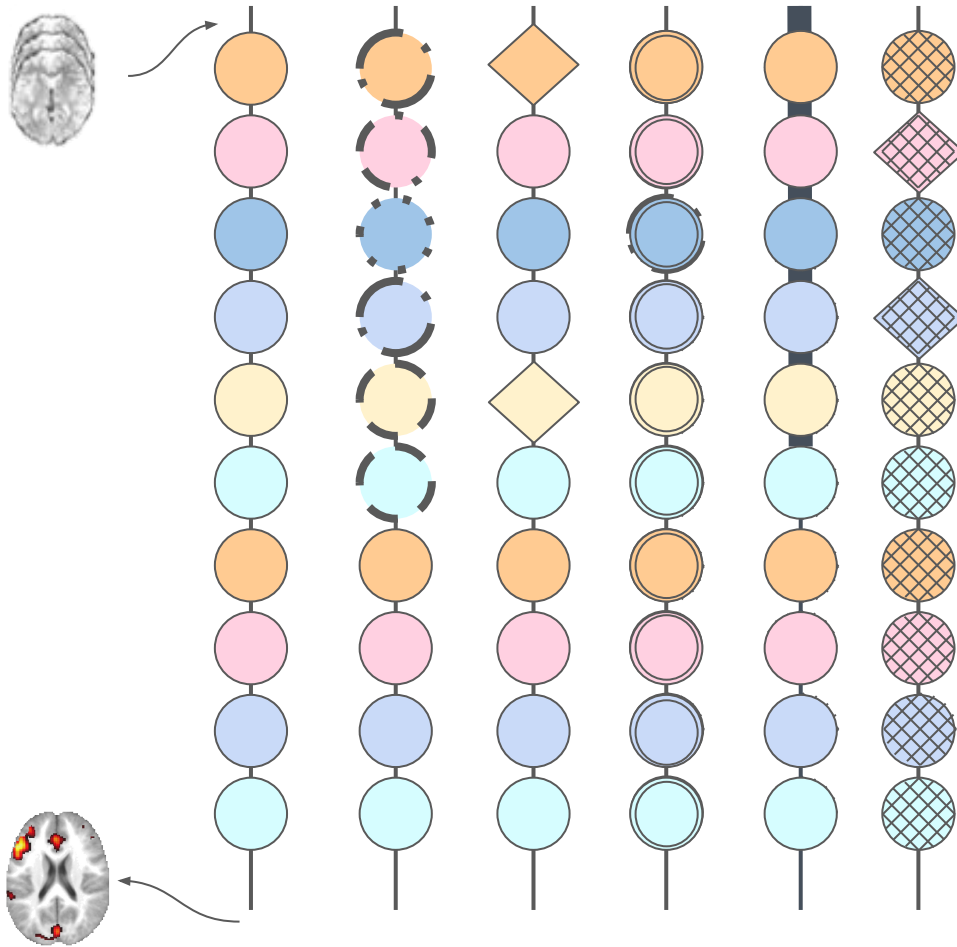
Analytic variability



Analytic variability



Analytic variability





Question?

**How does analytic variability impact
neuroimaging results?**

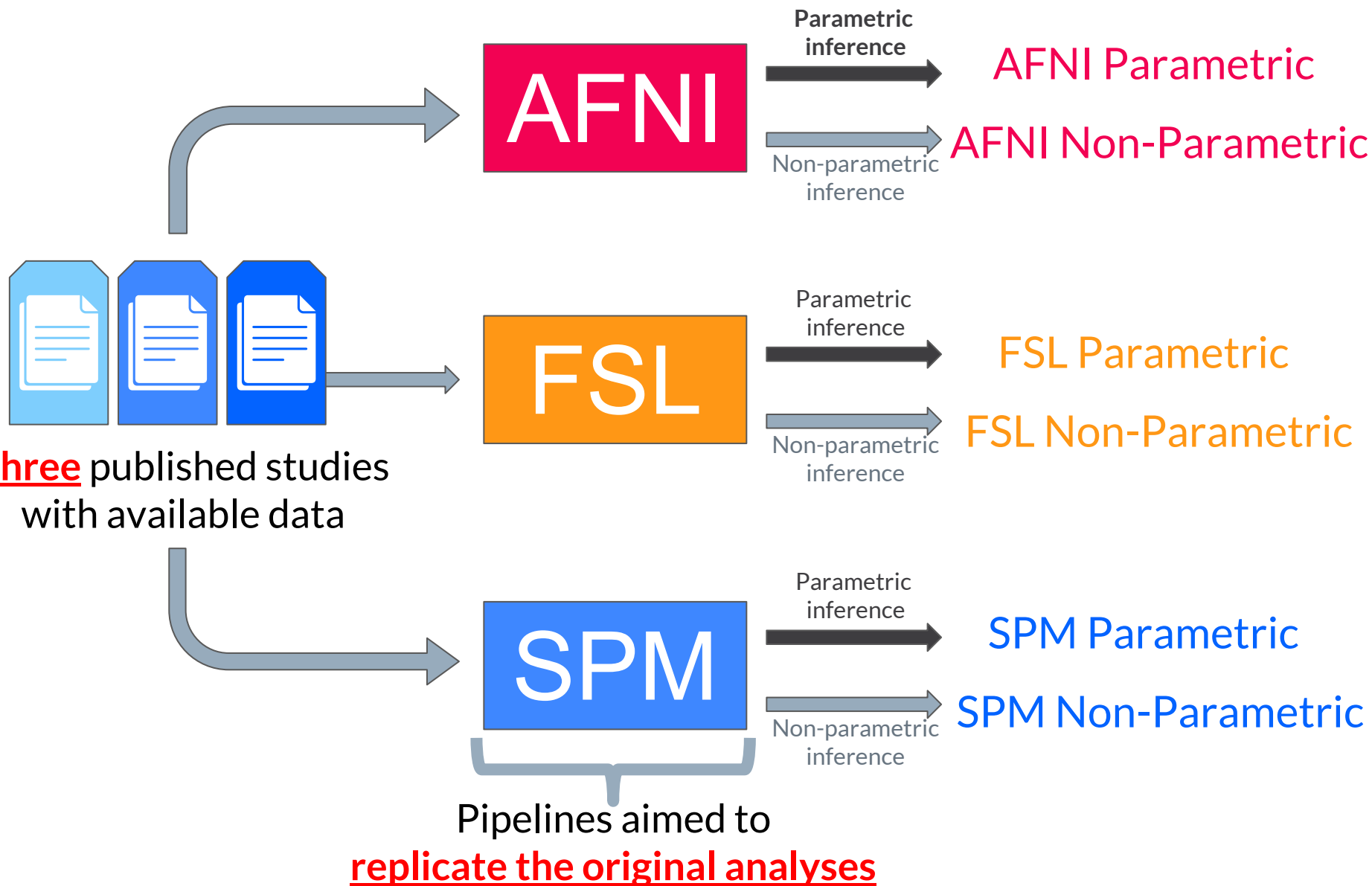
Background

- ▷ **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

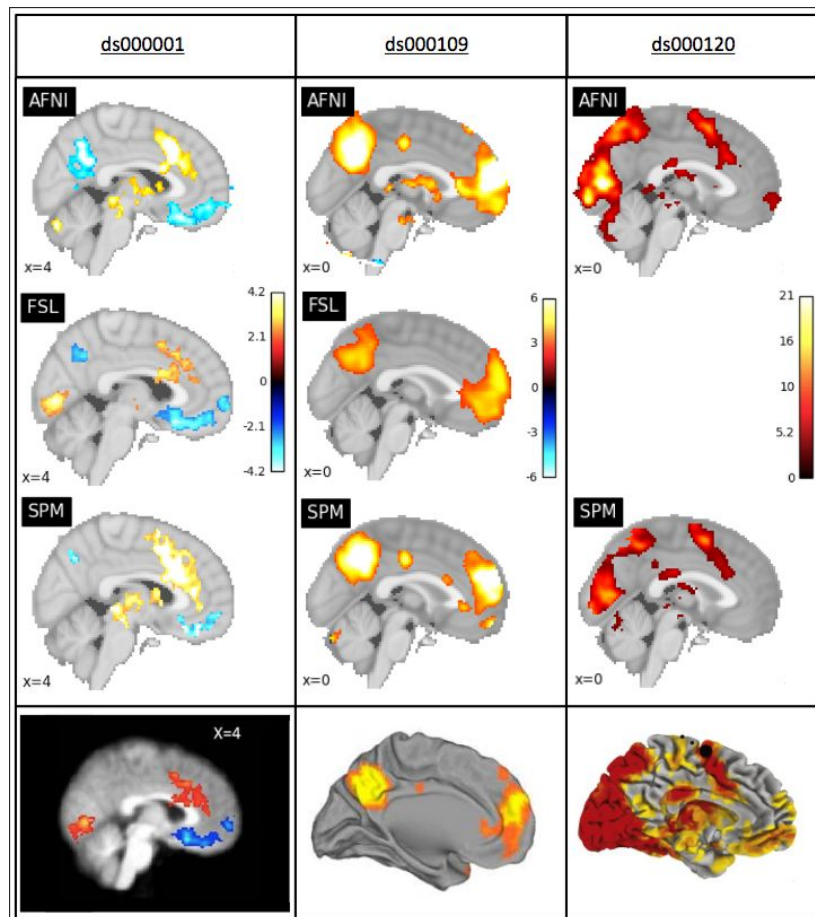
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Pauli et al (2016)
Bowring et al (2018) (preprint)

Joint work with Alexander Bowring and Thomas Nichols



Impact of Analysis Software on Task fMRI Results

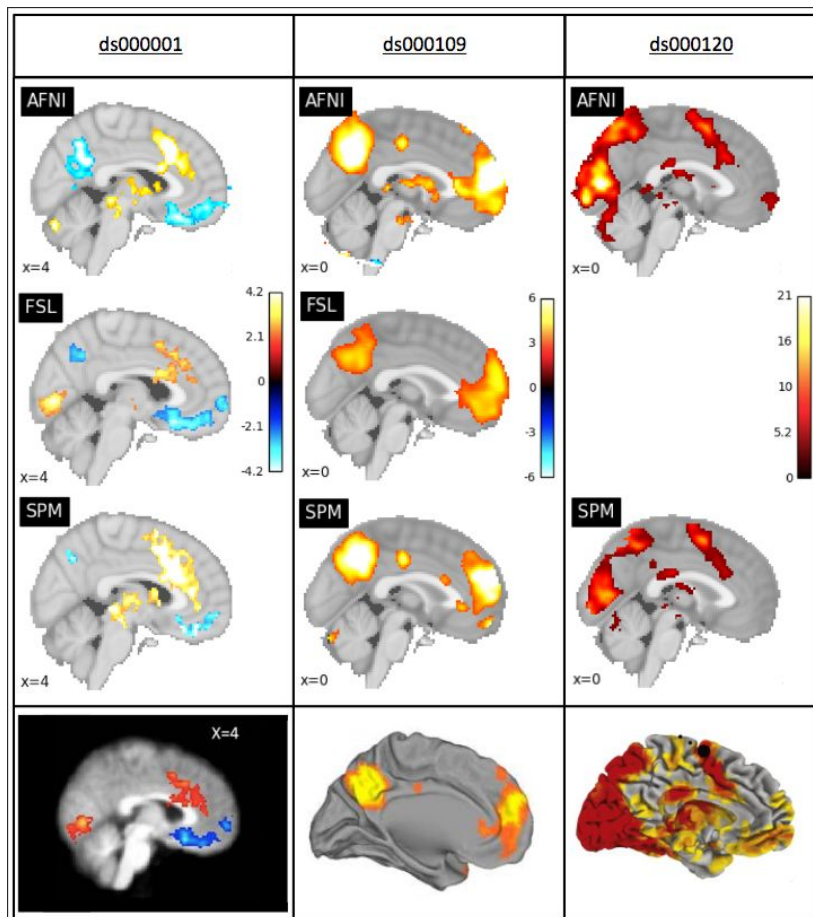
Reproducing the main figure



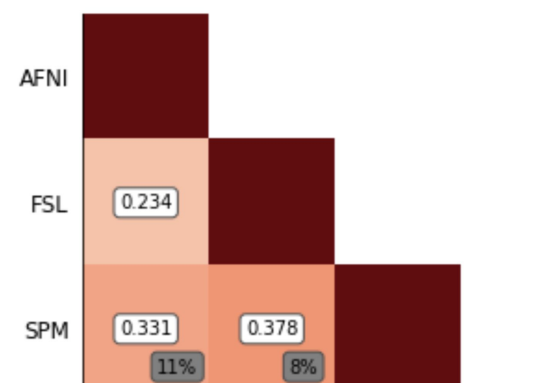
Bowring et al (2018) (preprint)

Impact of Analysis Software on Task fMRI Results

Reproducing the main figure

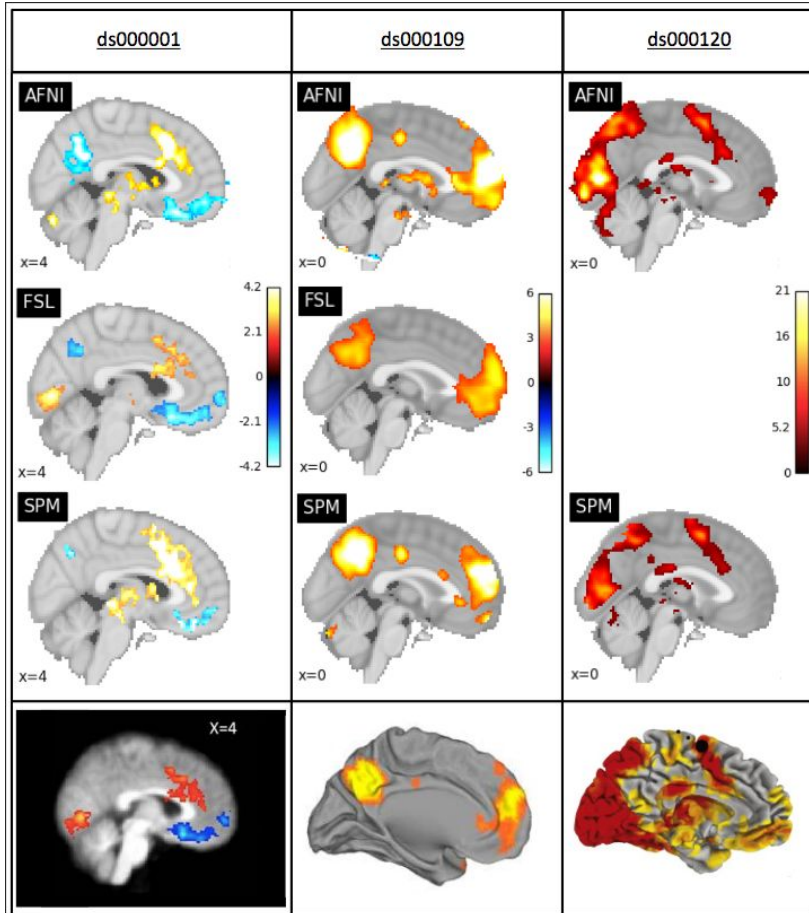


Dice coefficients

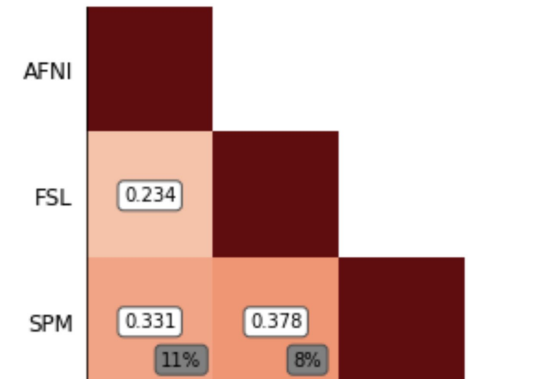


Impact of Analysis Software on Task fMRI Results

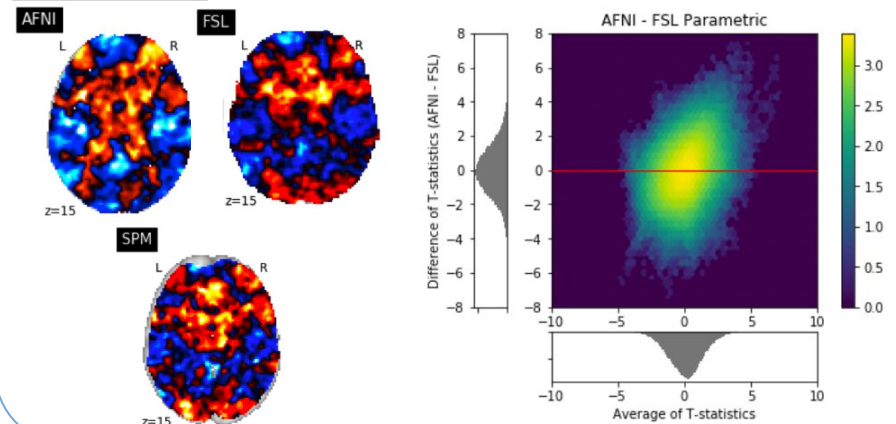
Reproducing the main figure



Dice coefficients



Unthresholded statistics

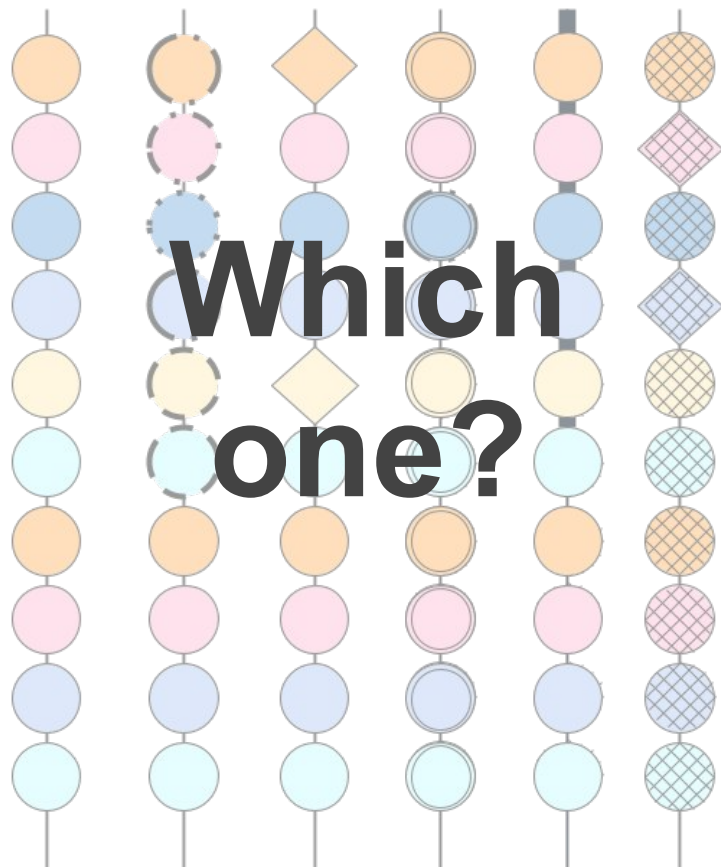




3.

Transparency

Disclosing analytical details



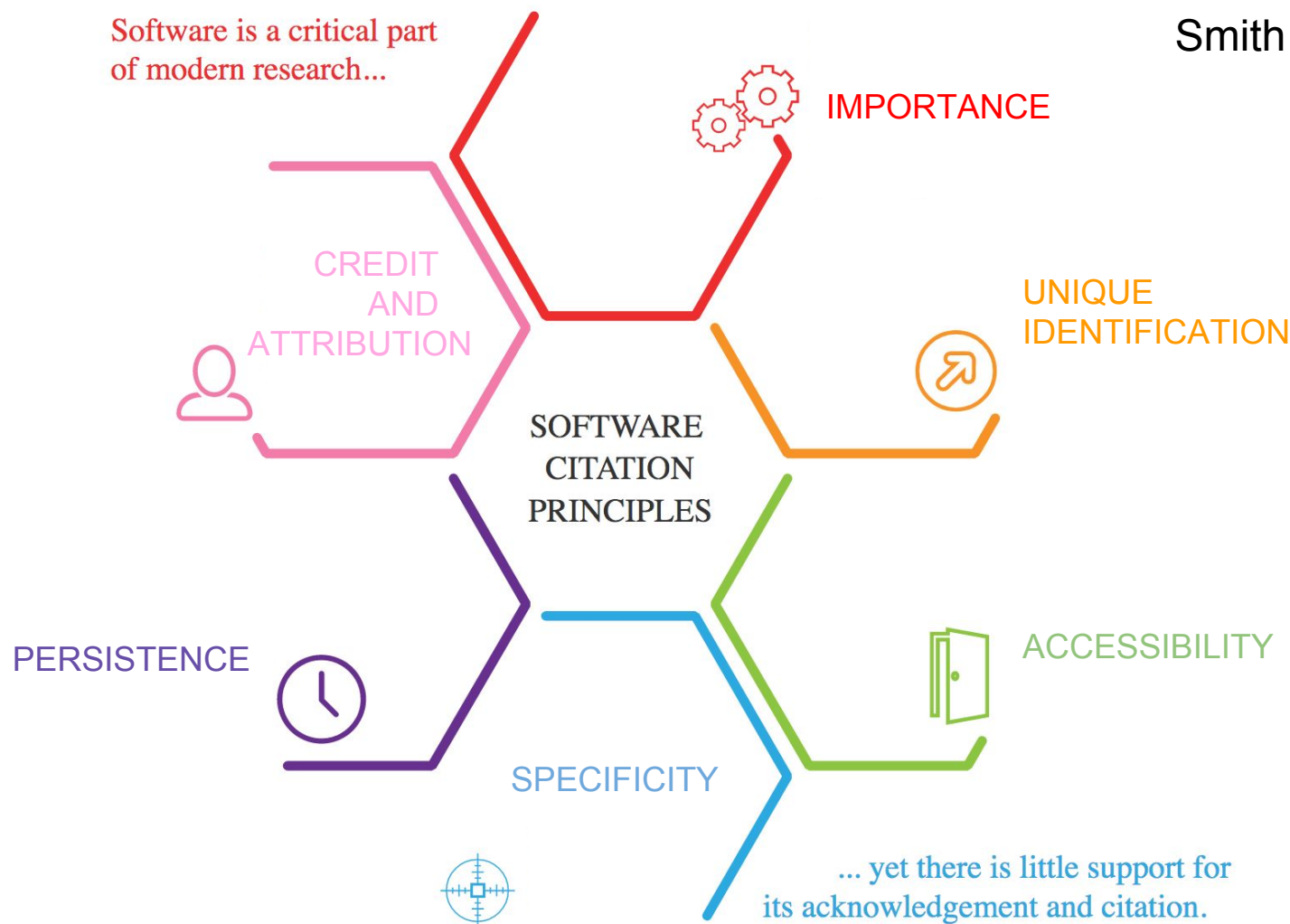
Details about the analysis pipeline are in the code.

In manuscripts, it is best practice to:

- Cite custom code
- Cite libraries and tools

How to cite software? The software citation principles

Smith et al (2016)



Citing custom code

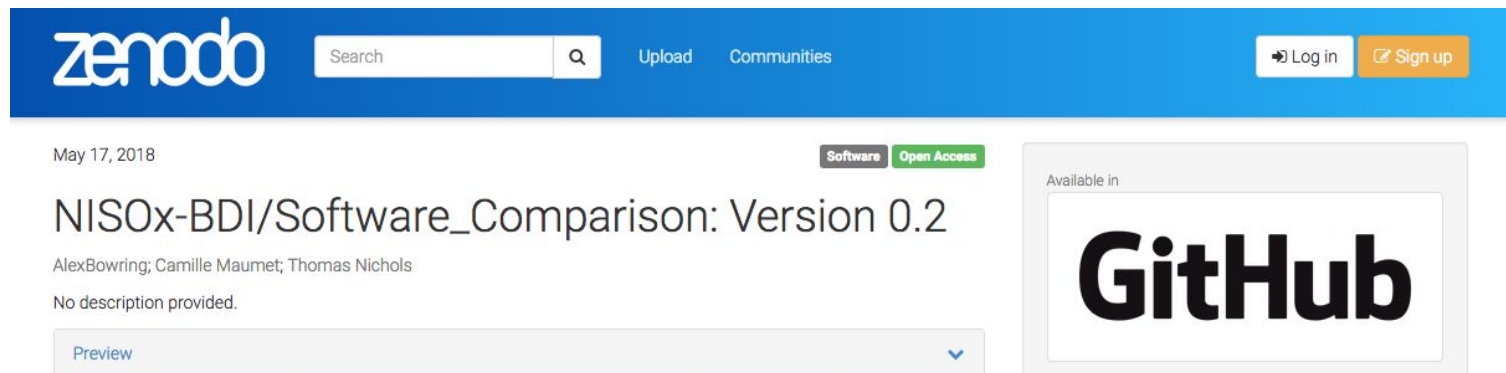
3. Results

Bowring et al (2018)

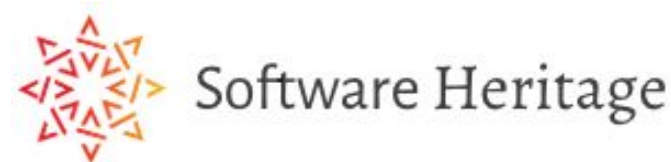
[...] All analysis scripts, results reports, and notebooks for each of study are available through Zenodo (Nielsen and Smith, 2014) at <https://zenodo.org/record/1203654> (Alexander Bowring et al., 2018).

Persistence

Accessibility



The screenshot shows the Zenodo website interface. At the top is a blue navigation bar with the Zenodo logo, a search bar, and links for 'Upload' and 'Communities'. On the right side of the bar are 'Log in' and 'Sign up' buttons. Below the navigation bar, the record details are displayed: the date 'May 17, 2018', the title 'NISOx-BDI/Software_Comparison: Version 0.2', and the authors 'AlexBowring; Camille Maumet; Thomas Nichols'. There are 'Software' and 'Open Access' tags. A note states 'No description provided.' Below this is a 'Preview' button with a dropdown arrow. To the right, a box indicates the record is 'Available in' GitHub, with the GitHub logo prominently displayed.



Let others cite your code

The screenshot shows the Zenodo interface for a software repository. The main title is "NISOx-BDI/Software_Comparison: Version 0.2" with authors "AlexBowring; Camille Maumet; Thomas Nichols". A callout box labeled "Attribution" points to the author information. The file list shows a directory structure with files like ".gitignore", "README.md", "ds001", "AFNI", "LEVEL2", and "SCRIPTS". A callout box labeled "Unique identifier" points to the DOI "10.5281/zenodo.1248809". A callout box labeled "Specificity" points to the "Versions" section, which lists "Version 0.2" and "Version v0.1".

zenodo Search Upload Communities Log in Sign up

May 17, 2018 Software Open Access

NISOx-BDI/Software_Comparison: Version 0.2

AlexBowring; Camille Maumet; Thomas Nichols

No description provided.

Preview Attribution

Software_Comparison-0.2.0.zip

- Software_Comparison-0.2.0
 - .gitignore 482 Bytes
 - README.md 7.4 kB
 - ds001
 - AFNI
 - LEVEL2
 - euler_chars.csv 941 Bytes
 - permutation_test
 - euler_chars.csv 933 Bytes
 - SCRIPTS
 - level2.sh 7.7 kB
 - permutation_test.sh 4.8 kB
 - sub-01_level1.sh 4.3 kB
 - sub-02_level1.sh 4.3 kB
 - sub-03_level1.sh 4.3 kB
 - sub-04_level1.sh 4.3 kB
 - sub-05_level1.sh 4.3 kB
 - sub-06_level1.sh 4.3 kB

Files (11.3 MB)

Name	Size	Preview	Download
Software_Comparison-0.2.0.zip	11.3 MB		

md5:418825948cf76d92c4943714fcc96af0

Available in

GitHub

Publication date: May 17, 2018

DOI: 10.5281/zenodo.1248809 Unique identifier

Related identifiers: Supplement to: https://github.com/NISOx-BDI/Software_Comparison/tree/v0.1

License (for files): [Other \(Open\)](#)

Specificity

Versions

- Version 0.2 10.5281/zenodo.1248809 May 17, 2018
- Version v0.1 10.5281/zenodo.1203655 Mar 19, 2018

Cite all versions? You can cite all versions by using the DOI 10.5281/zenodo.1203654. This DOI represents all versions, and will always resolve to the latest one. [Read more.](#)

Share

Citing libraries and tools

2.2 Data Analyses

Bowring et al (2018)

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)).

Citing libraries and tools

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Specificity



Citing libraries and tools

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Specificity

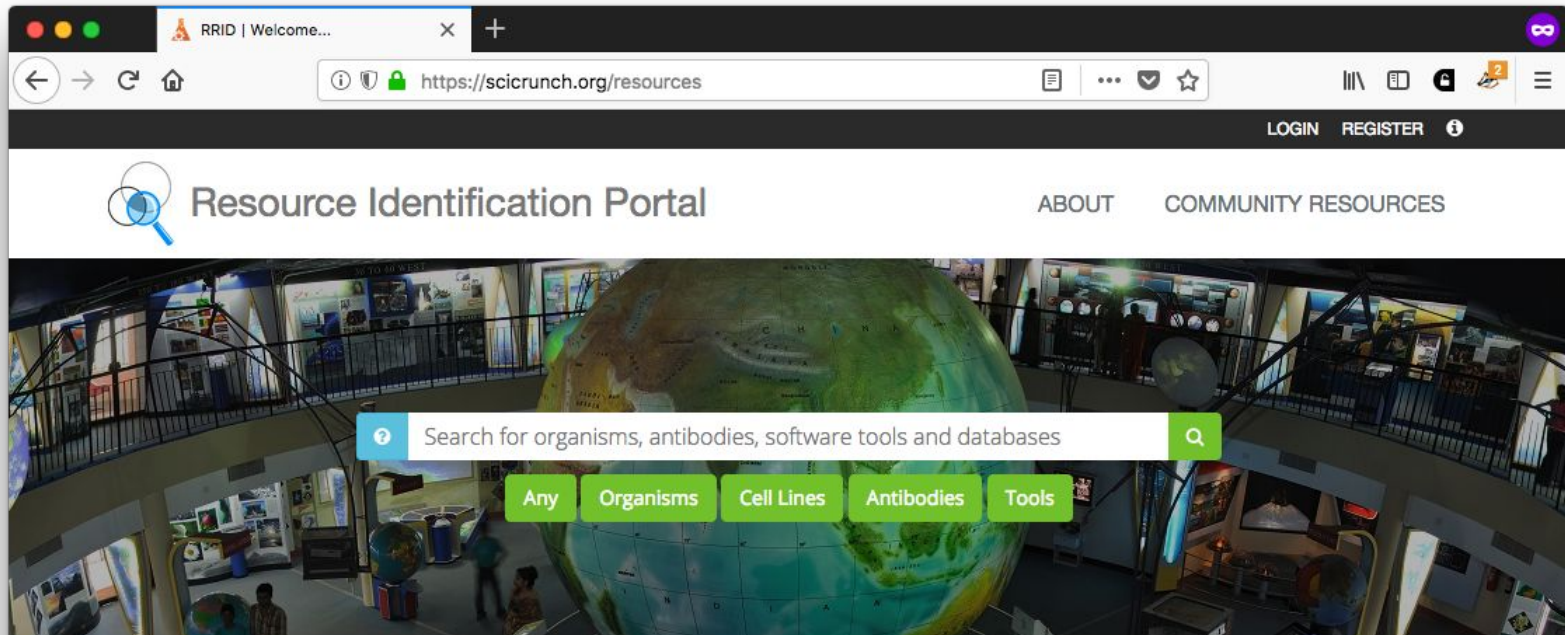
Unique identifier

Citing libraries and tools

2.2 Data Analyses

Bowring et al (2018)

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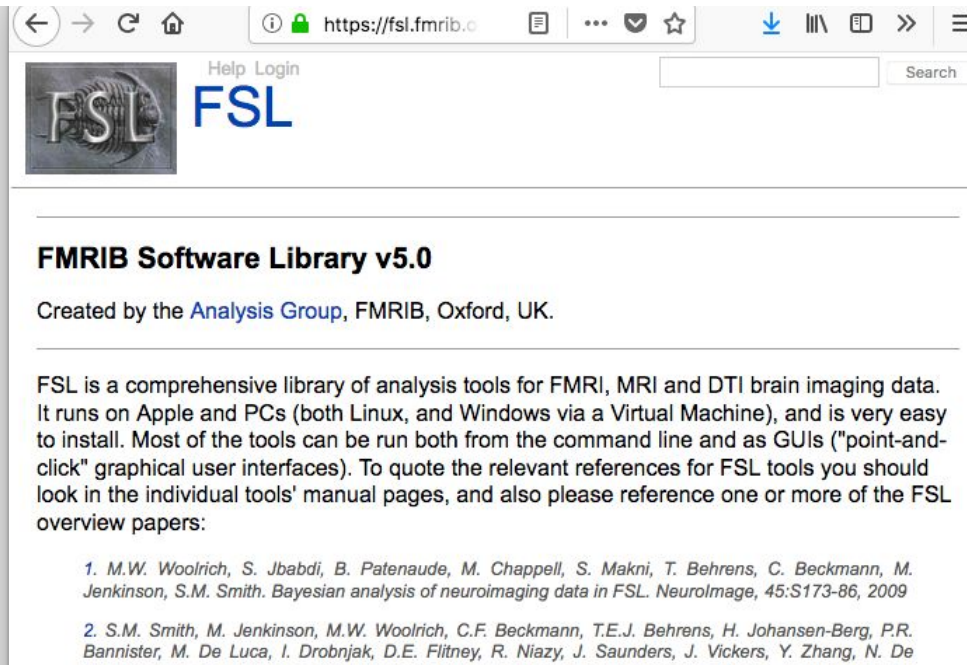


Citing libraries and tools

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Bowring et al (2018)

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The screenshot shows the FSL website homepage. The browser address bar displays "https://fsl.fmrib.ox.ac.uk". The page features the FSL logo, a search bar, and the title "FMRIB Software Library v5.0". Below the title, it states "Created by the Analysis Group, FMRIB, Oxford, UK." The main content describes FSL as a comprehensive library of analysis tools for FMRI, MRI, and DTI brain imaging data, mentioning its availability on Apple and PCs (Linux and Windows via VM) and its ease of installation. It also provides references for FSL tools and manual pages.

FMRIB Software Library v5.0

Created by the [Analysis Group](#), FMRIB, Oxford, UK.

FSL is a comprehensive library of analysis tools for FMRI, MRI and DTI brain imaging data. It runs on Apple and PCs (both Linux, and Windows via a Virtual Machine), and is very easy to install. Most of the tools can be run both from the command line and as GUIs ("point-and-click" graphical user interfaces). To quote the relevant references for FSL tools you should look in the individual tools' manual pages, and also please reference one or more of the FSL overview papers:

1. M.W. Woolrich, S. Jbabdi, B. Patenaude, M. Chappell, S. Makni, T. Behrens, C. Beckmann, M. Jenkinson, S.M. Smith. Bayesian analysis of neuroimaging data in FSL. *NeuroImage*, 45:S173-86, 2009
2. S.M. Smith, M. Jenkinson, M.W. Woolrich, C.F. Beckmann, T.E.J. Behrens, H. Johansen-Berg, P.R. Bannister, M. De Luca, I. Drobnjak, D.E. Flitney, R. Niazy, J. Saunders, J. Vickers, Y. Zhang, N. De

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki>

Citing libraries and tools

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Bowring et al (2018)

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

2.5 Scripting of analyses and figures

Bowring et al (2018)

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).

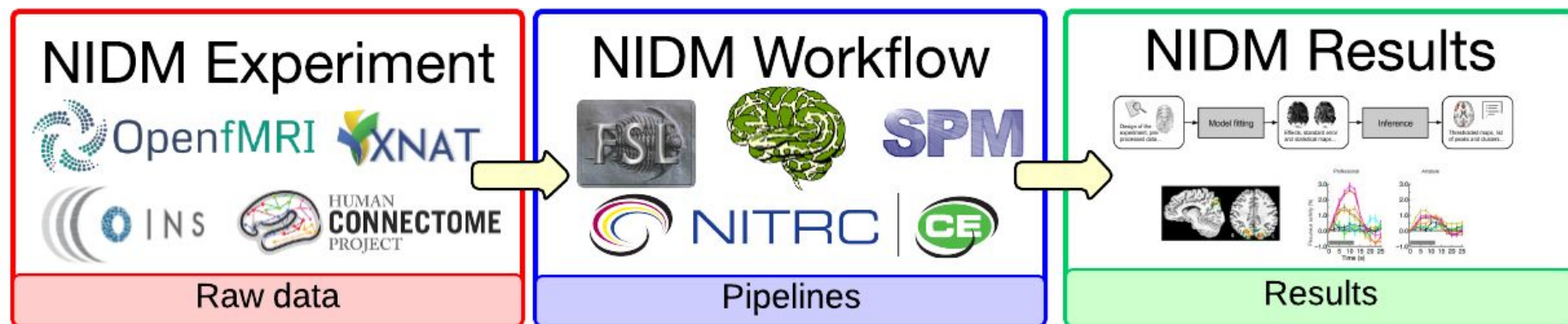


Provenance

“Provenance is information about entities, activities, and people involved in producing a piece of data or thing” — W3C PROV

Machine-readable provenance

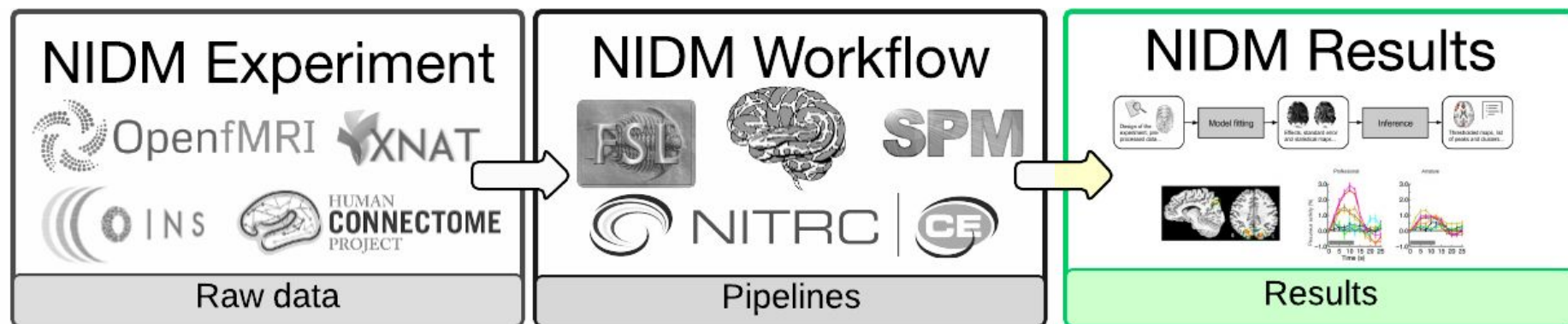
Machine-readable provenance



NIDM: neuroimaging data model

International collaboration with INCF SIG on Reproducibility and Best Practices in Human Brain Imaging

Machine-readable provenance



NIDM: neuroimaging data model

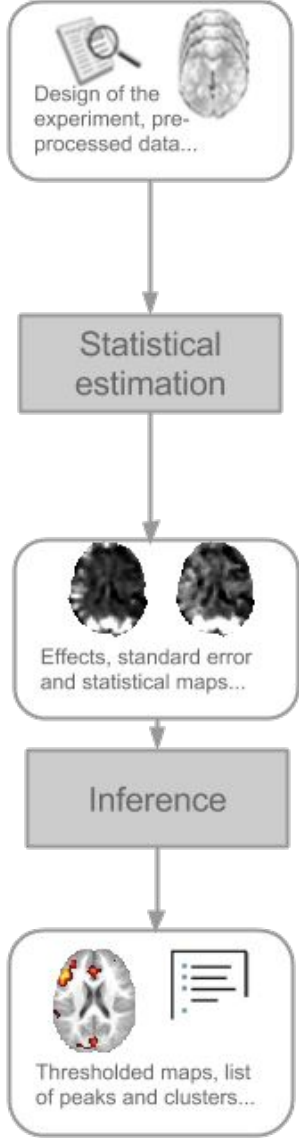
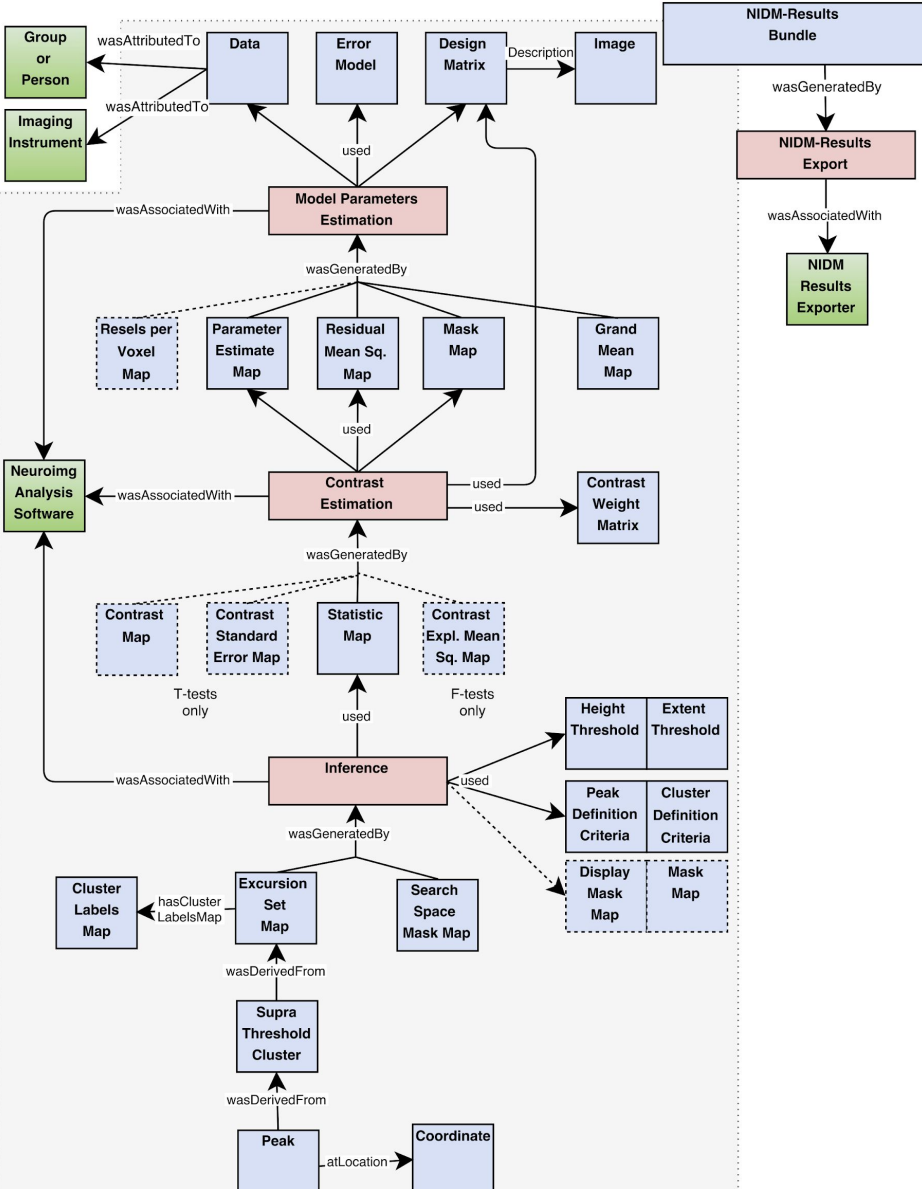
International collaboration with INCF SIG on Reproducibility and Best Practices in Human Brain Imaging.

NIDM-Results → fMRI, VBM results

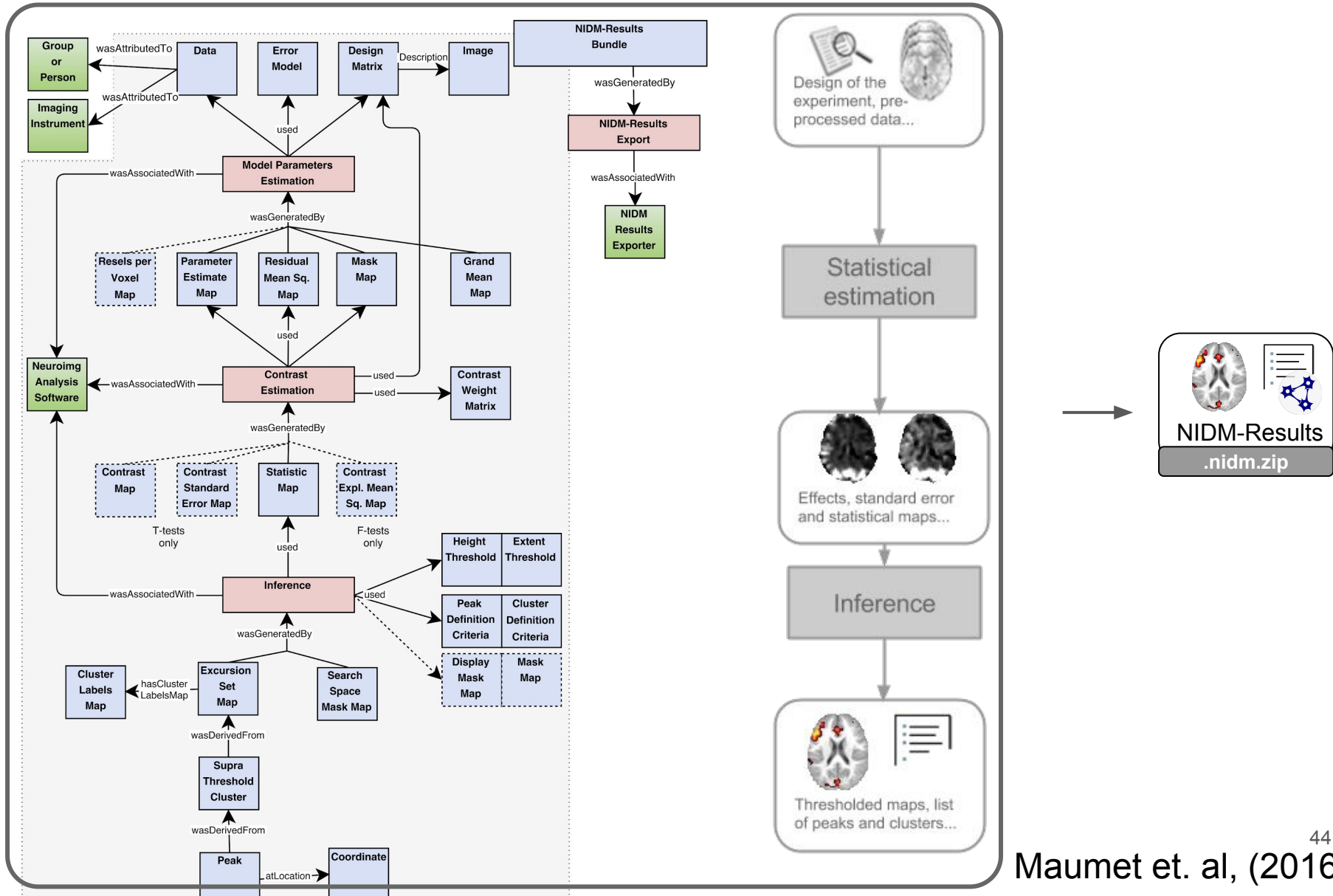
Harmonised model and provenance.

Joint work with INCF NIDASH working group - <https://github.com/incf-nidash/>

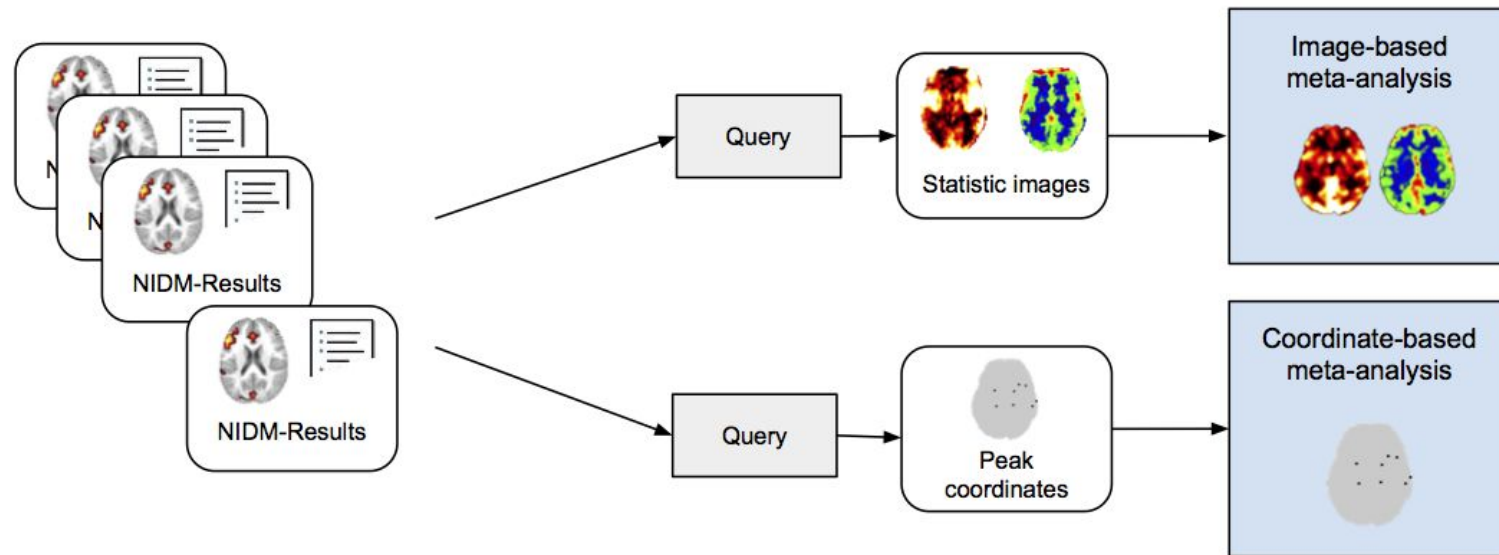
NIDM-Results in brief



NIDM-Results in brief



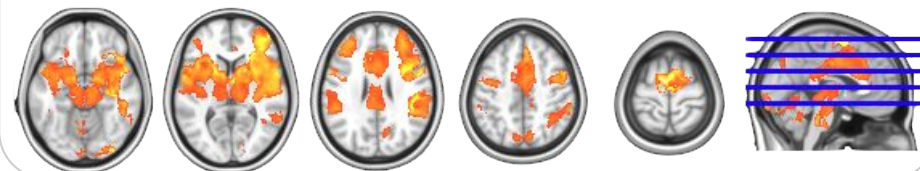
Derived data reuse with NIDM-Results: meta-analysis



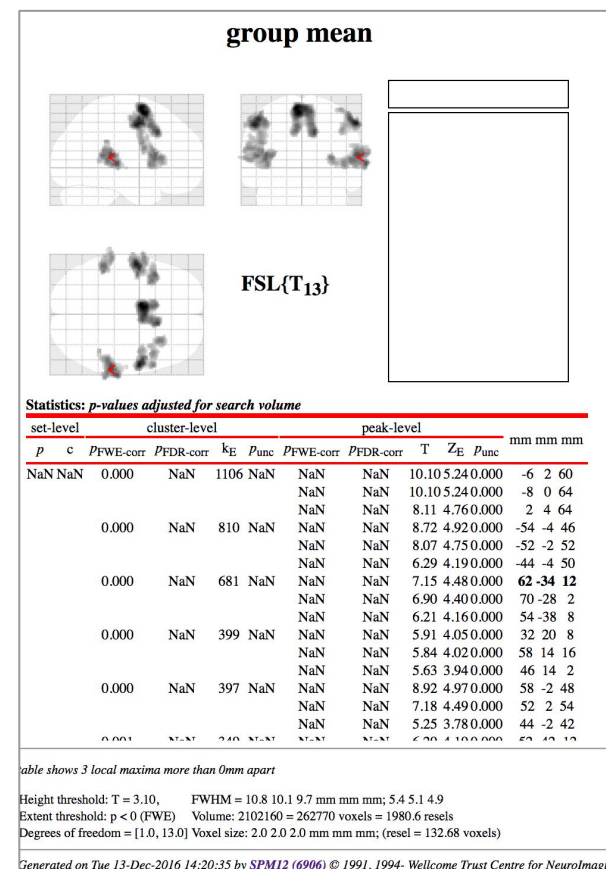
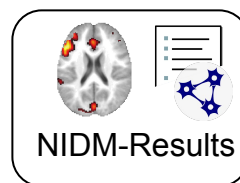
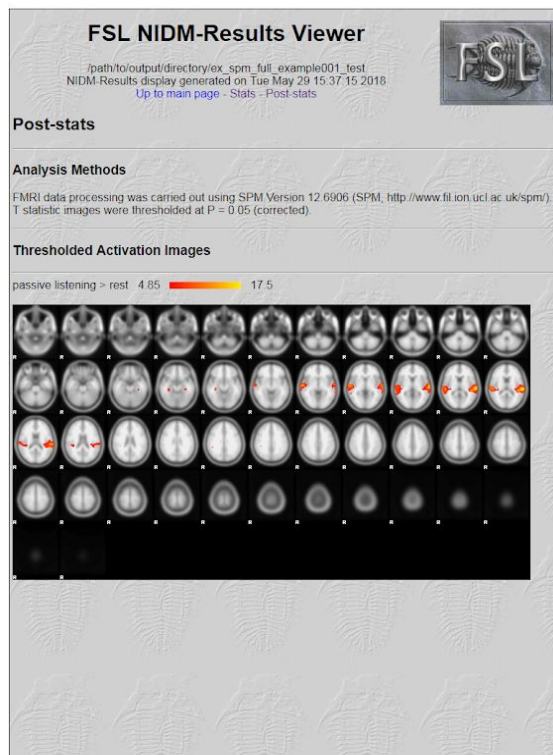
Coordinate-based meta-analysis



Image-based meta-analysis



Derived data inspection with NIDM-Results: SPM- and FSL-like views

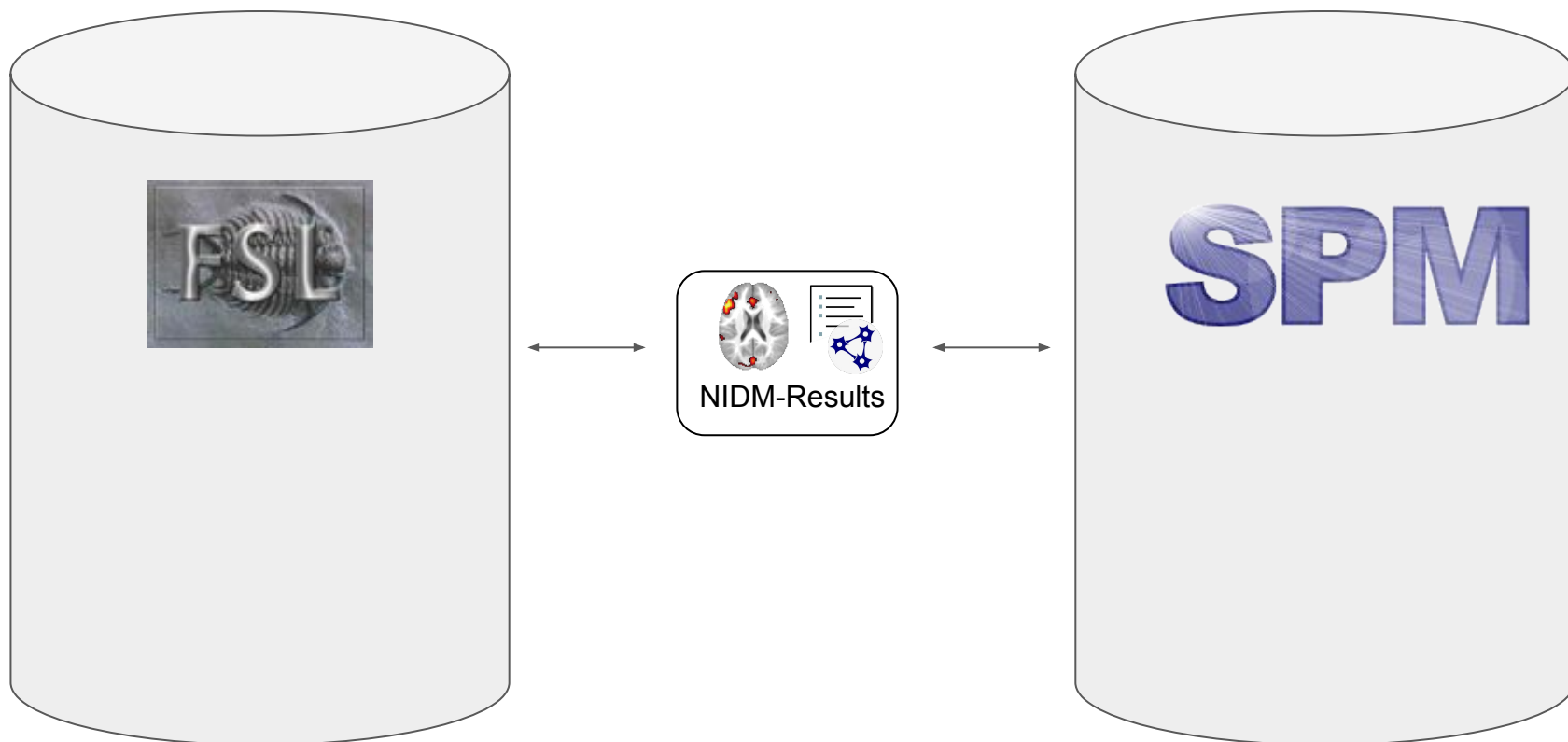


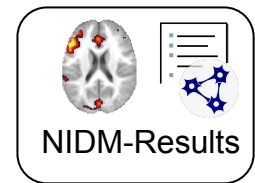
<https://github.com/incf-nidash/nidmresults-spmhtml>

<https://github.com/incf-nidash/nidmresults-fslhtml>

Maullin-Sapey et al (2017)

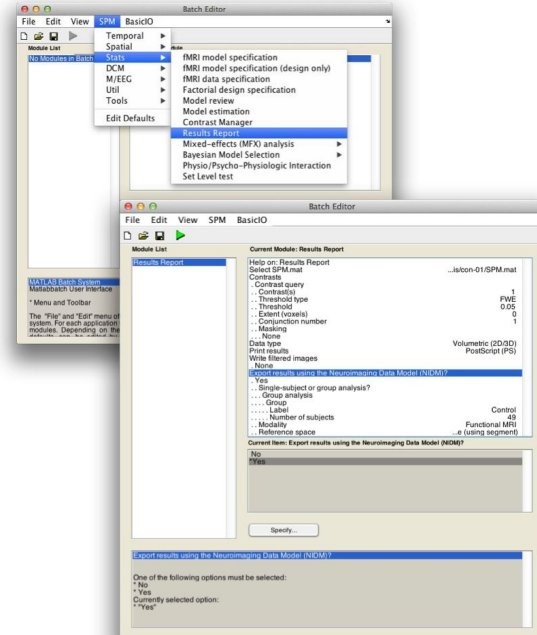
Derived data inspection with NIDM-Results: SPM- and FSL-like views





How to use NIDM-Results for my study?

SPM



1. Export



```
$ nidmfsfsl fsl_ds107_group 49 -g Control
```

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

2. Publication on NeuroVault



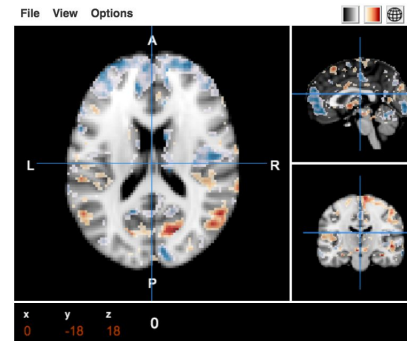
A Correspondence between Individual Differences in the Brain's Intrinsic Functional Architecture and the Content and Form of Self-Generated Thoughts

Contributed by ChrisFiloGorgolewski

Krzysztof J. Gorgolewski, Dan Lurie, Sebastian Urchs, Judy A. Kipping, R. Cameron Craddock, Michael P. Milham, Daniel S. Margulies, Jonathan Smallwood

[Link to the paper](#)

3D View



Images Details

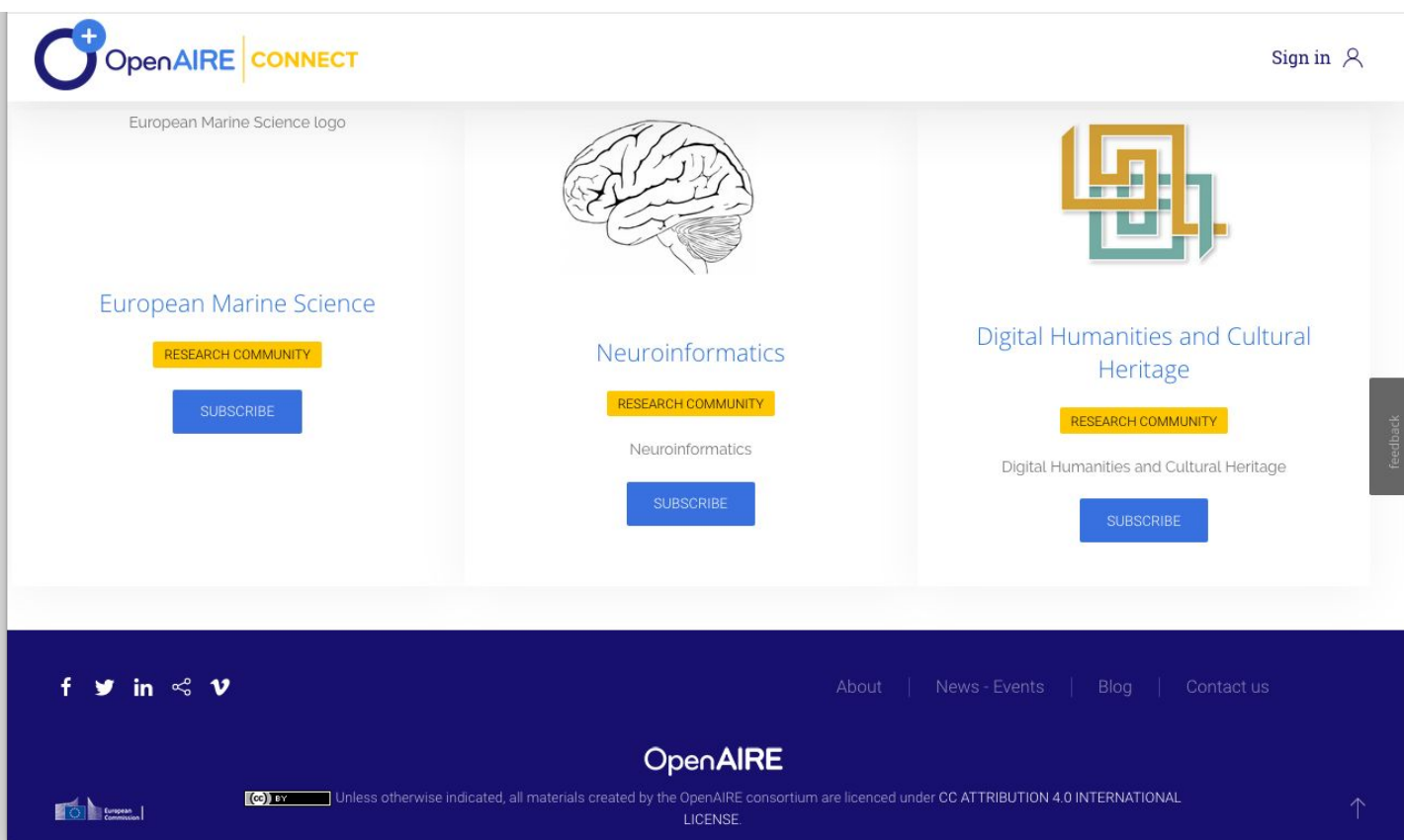
Show 7 entries Search:

View	ID	Name	Type
<input type="checkbox"/>	25	fALFF: Past	Z map
<input type="checkbox"/>	26	fALFF: Future	Z map
<input type="checkbox"/>	27	fALFF: Past > Future	Z map
<input type="checkbox"/>	28	fALFF: Positive	Z map
<input type="checkbox"/>	29	fALFF: Negative	T map
<input type="checkbox"/>	30	fALFF: Positive > Negative	Z map
<input type="checkbox"/>	31	fALFF: Social Cognition	Z map

Showing 1 to 7 of 30 entries First Previous Next Last

One step further: linking it all together!

“Gather, view and monitor all research outcomes”



One step further: linking it all together!

“Gather, view and monitor all research outcomes”



A screenshot of the OpenAIRE CONNECT website's 'Neuroinformatics' page. The page has a header with a brain icon, the title 'Neuroinformatics', and navigation links for 'Search', 'Monitor', 'Share', and 'Link'. There is a 'Sign in' link and a 'SUBSCRIBE' button. Below the header, there are two 'Neuroinformatics' labels, a row of topic tags (BRAIN MAPPING, BRAIN IMAGING, ELECTROENCEPHALOGRAPHY, ARTERIAL SPIN LABELLING, BRAIN FINGERPRINTING, BRAIN, NEUROIMAGING, MULTIMODAL BRAIN IMAGE ANALYSIS, FMRI, NEUROINFORMATICS), and a 'show more' link. A section 'Curated by: sorina.pop, camille.maumet, christian.barillot' is followed by 'Created: 18-04-2018' and 'Members: 4'. A statistics row shows: 87 publications, 1 research data, 0 software, 10 projects, and 5 content providers. Below this are three sections: 'Recent publications' with a link to 'TOWARDS INTEGRATING SPATIAL LOCALIZATION IN CONVOLUTIONAL NEURAL NETWORKS FOR BRAIN IMAGE SEGMENTATION' (UNKNOWN, 2018), 'Recent research data' with a link to 'BROCCOLI: SOFTWARE FOR FAST FMRI ANALYSIS ON MANY-CORE CPUS AND GPUS' (OPEN, Anders Eklund (2014)), and 'Recent software' which shows 'No results found'. A 'feedback' button is on the right side of the page.

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>

OpenAIRE-connect portal: <https://beta.ni.connect.openaire.eu/> and
guidelines for data repository managers:

<https://www.openaire.eu/openaire-guide-for-repository-managers>

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NIDM working group

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Thank you!



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Join the NIDASH community:

<https://github.com/incf-nidash/nidm-specs>