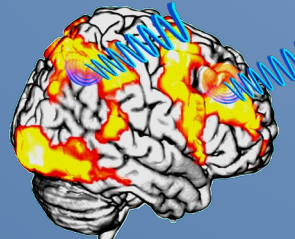


Automatic Analysis for more efficient and reproducible M/EEG pipelines

Tibor Auer

University of Surrey, School of Psychology
NeuroModulation Lab



Challenge

- **Increasingly large cohort sizes**
 - <10 (in 2005) → hundreds (in 2020)
 - **Multimodality: structure, function, diffusion**
 - Offers a more integrated view of the brain
 - Supported by several open research tools such as SPM, FSL, Freesurfer, EEGLAB, FieldTrip, and MNE
- ↓
- **Issues**
 - Requires integration of different tools → Efficiency
 - Difficult documentation → Reproducibility
 - Increased risk of human error
 - Harder to detect errors
- } Transparency



Challenge

- **Tools**

- EEGLAB: more established (since 2004, ~2000 citations/year), great for pre-processing, plugins
- FieldTrip: newer (since 2011, ~900 citations/year), great for analysis and visualisation, stats tools
- MNE(-Python): newest (since 2013, ~300 citations/year), great for visualisation, Python ecosystem
- ...

- **Guidelines**

- [Makoto's preprocessing pipeline](#), [Makoto's code](#): more like considerations and code snippets
- [FieldTrip tutorial](#): well-structured, stand-alone, with example data and code
- [MNE tutorial](#): well-prepared, illustrated, with example data and code

Challenge

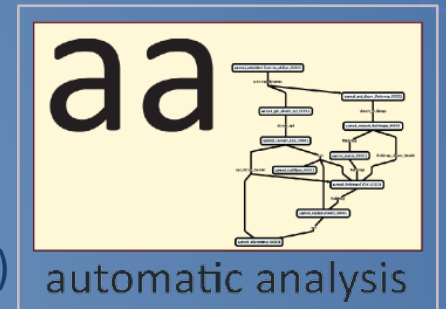
- Pipelines

- NiPy: uniform interface for pre-compiled and Python-based tools
 - Configurability, reproducibility, scalability
 - Loose integration of tools, large technical debt
- MATLAB: Script from analysis
 - EEGLAB: EEGLAB history (*eegh*): command-line back-end for GUI
 - FieldTrip: *reproducescript*: generates code and (intermediate) derived data
 - *Post-hoc* → Rather for documentation
 - Generalisation requires extra work
 - No interoperability
 - Parallelisation depends on user

Solution

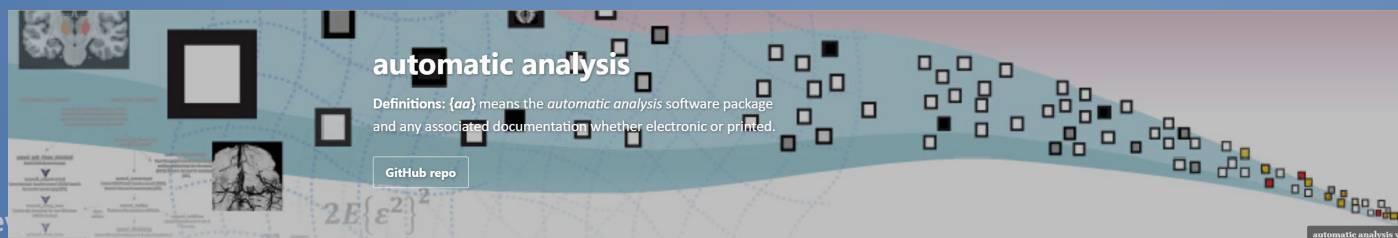
- **Description**

- A pipeline system for neuroimaging written in MATLAB
- Multimodal support: structure, function (EEG, fMRI), diffusion (DTI/DKI), ...
- Integrates major MATLAB-based tools (e.g. SPM, EEGLAB, FieldTrip, CoSMoMVPA, TDT) and some functions from FSL, Freesurfer and other toolboxes
- Disseminates code from contributors and external scientists



- **Availability**

- <https://automaticanalysis.github.io>
- <https://github.com/automaticanalysis/automaticanalysis>



Solution

- **Configurable, automatic workflow**

- Tracks processes → Restartable
- Notifies via e-mail

Efficiency

- **Provides high-level workflow description**

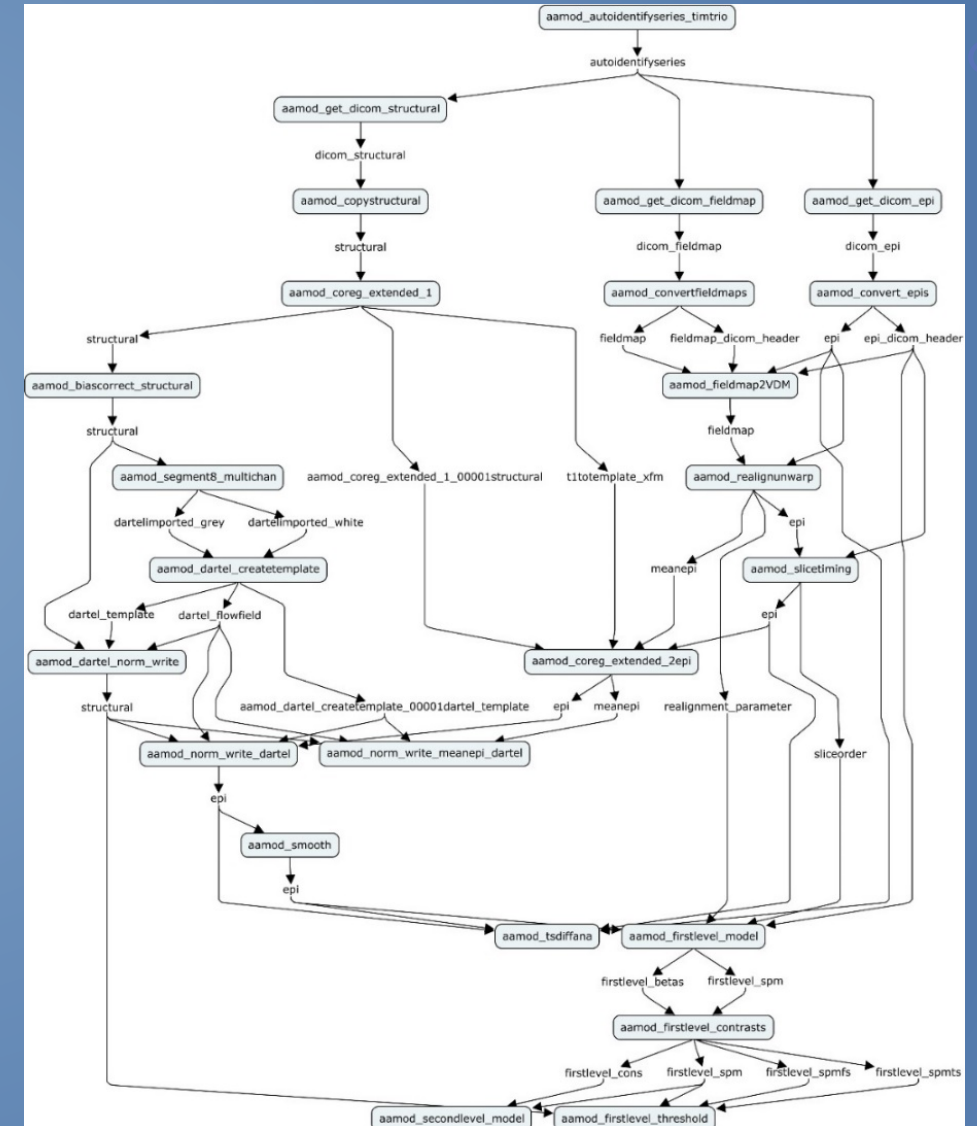
- Replicable
- Code recycling/sharing/publishing

Reproducibility

- **Record keeping**

- Diagnostics
- Captures provenance

Transparency



Solution

USPs

- **Deep level of integration of tools**
 - Site-/user-/study-specific definition and configuration
 - Dynamic loading → reduced ambiguity and 'shadowing'
- **Lower technical debt**
 - Automatic linkage between steps
 - Information on execution → debugging
 - Workflow visualisation
 - Interlinked diagnostics for quality awareness
- **Pipeline connection: takes data from a previous workflow**
 - Multimodal study: separate workflow for each modality
 - Complex study: common preprocessing workflow + multiple analyses

Development

- **Decisions**

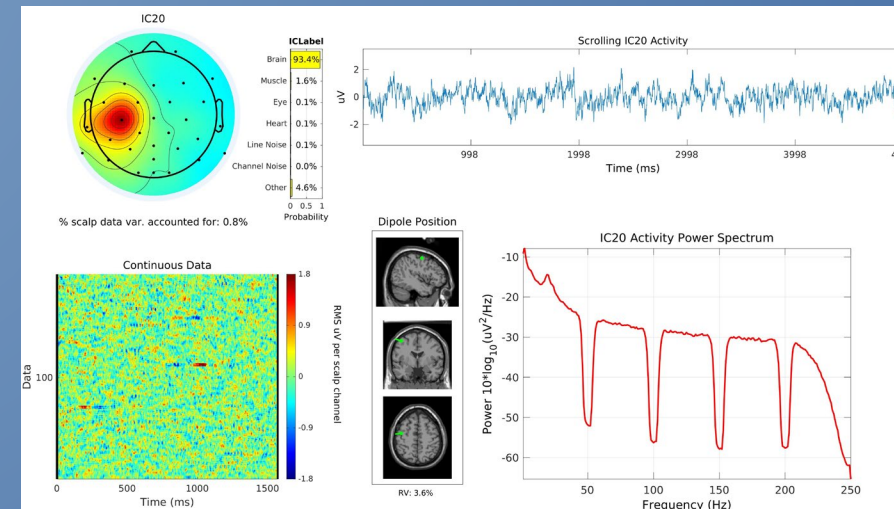
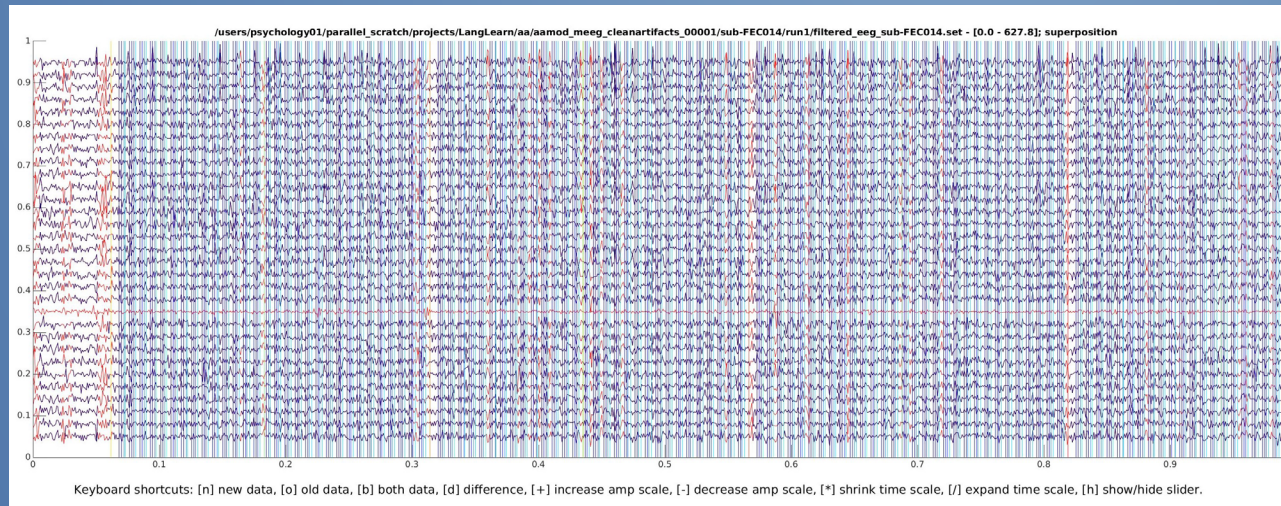
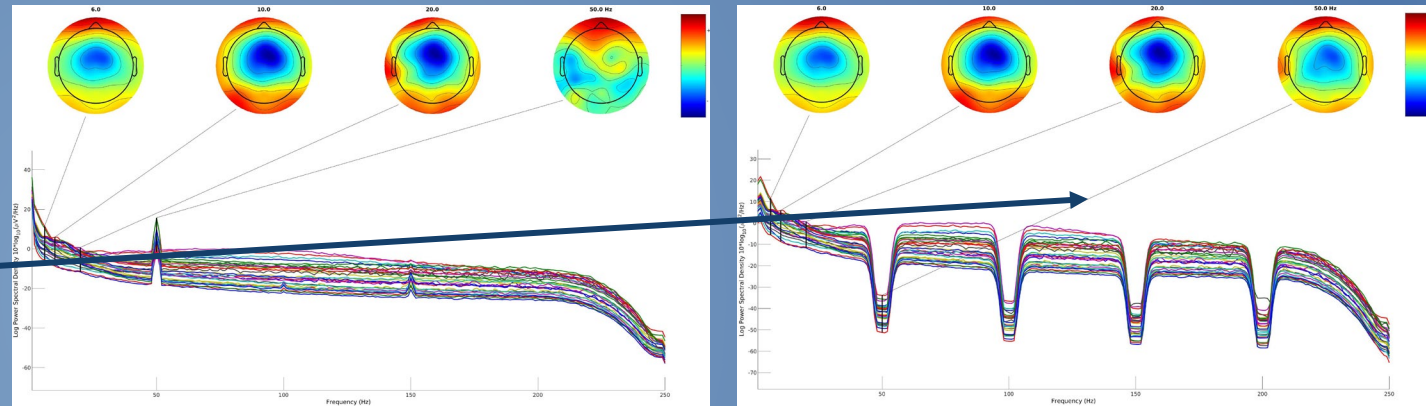
- Which tool for what → main data format
- **Conversion** ([automaticanalysis - eeglab2fieldtripER.m](#))!!!

- **Options**

- Configuration options
- Intuition, convenience
- Documentation
- E.g. [aamod_meeg_cleanartifacts](#), [aamod_meeg_icclassification](#)

Preprocessing – EEGLAB

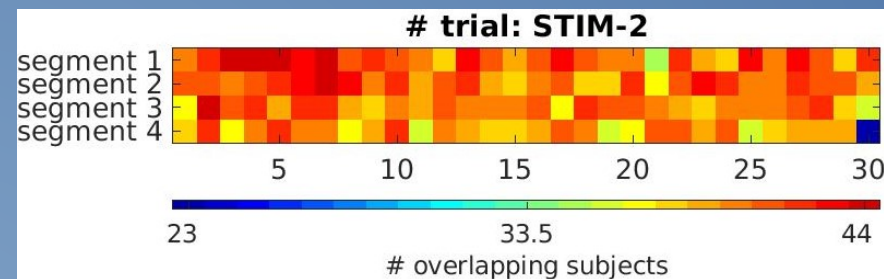
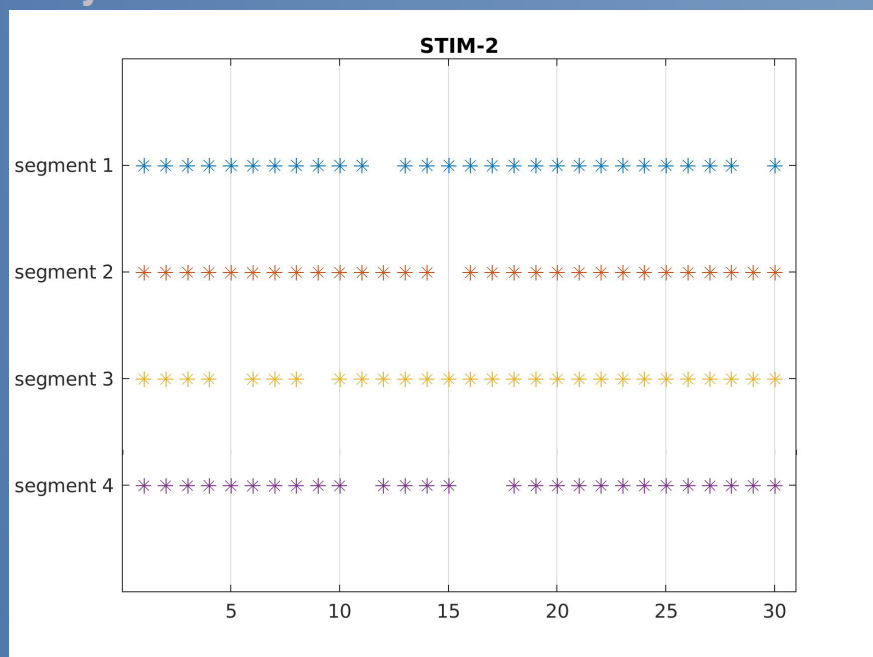
- Makoto's pipeline
 - Data format is EEGLAB's dataset
 - Configurable diagnostics after each step
 - Filtering is with FieldTrip



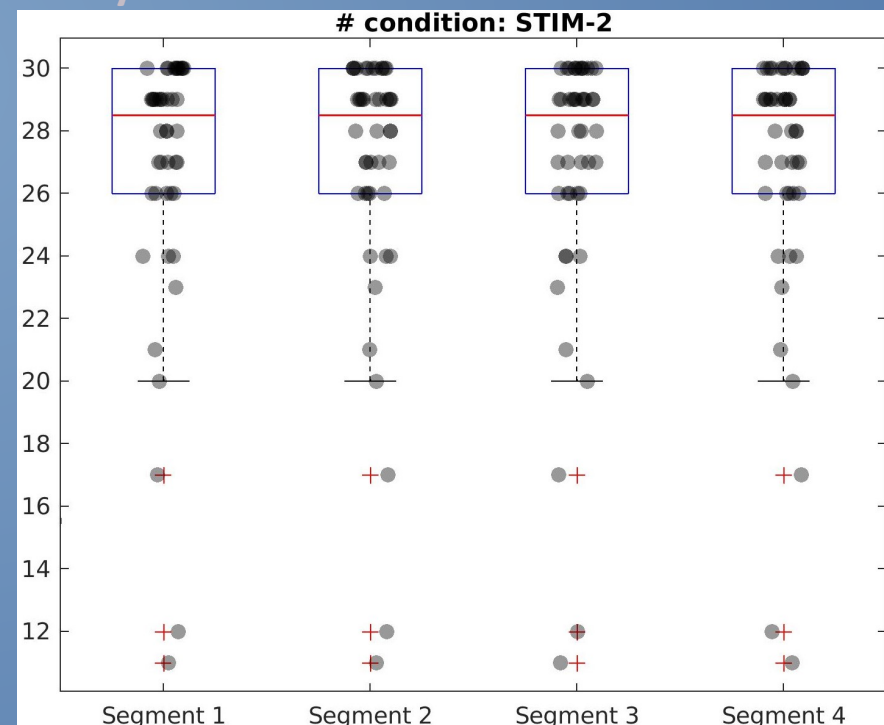
Preprocessing – EEGLAB

- Epoching
 - Extended diagnostics

- Subject domain

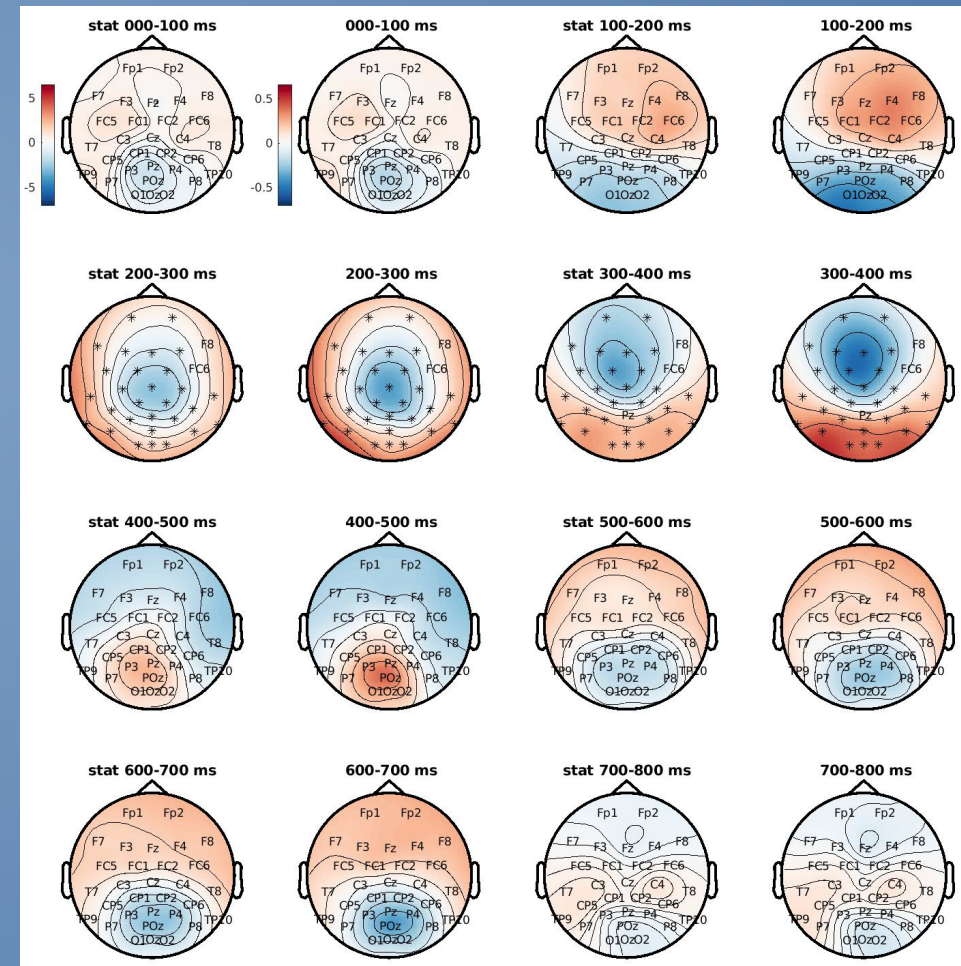
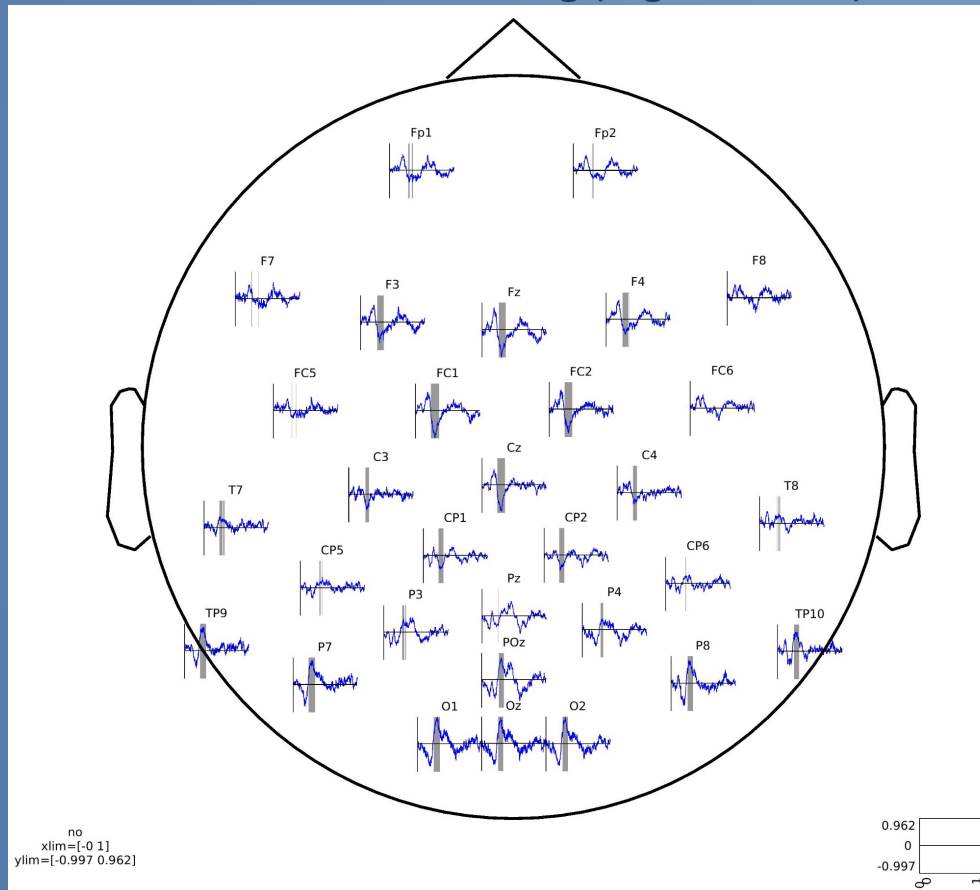


- Study domain



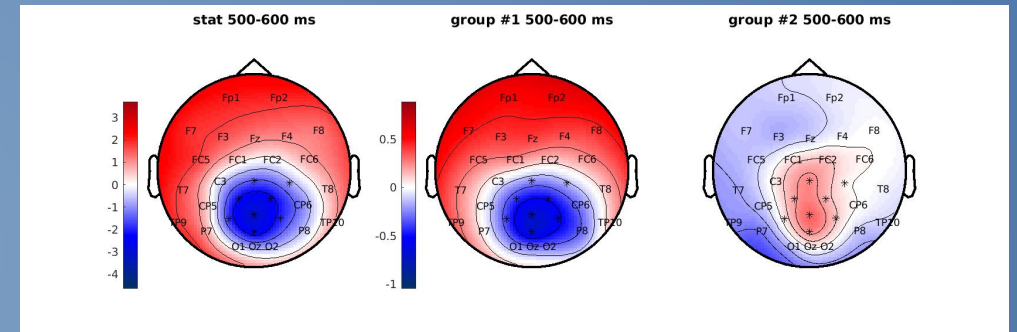
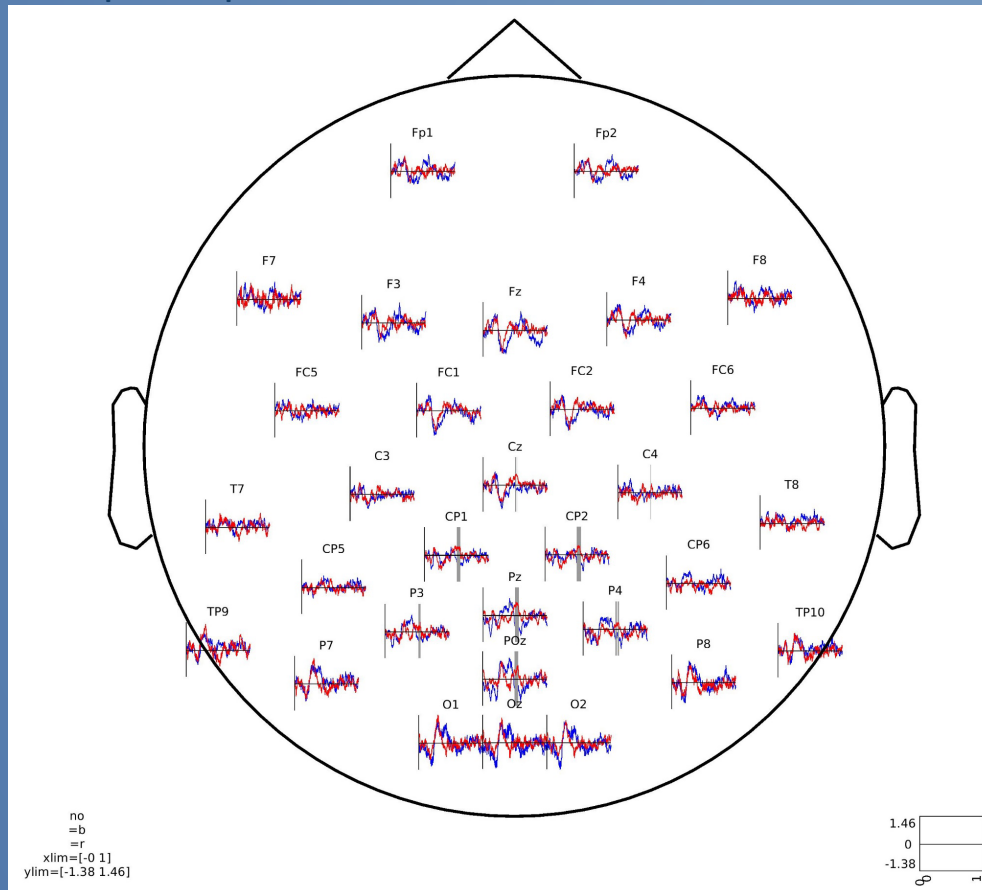
Analysis – FieldTrip

- Time-locked analysis (ERPs)
 - USP: Between-trial modelling (e.g. increase)



Analysis – FieldTrip

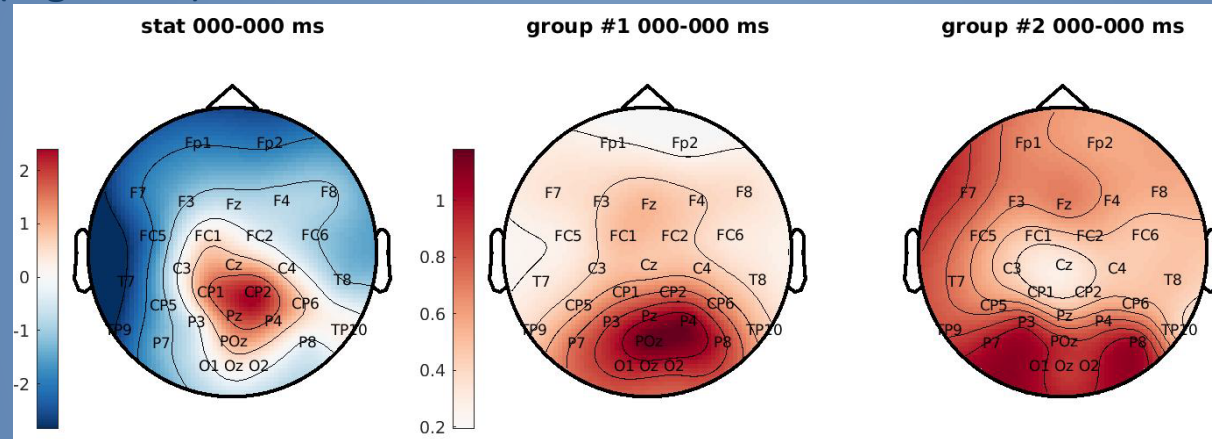
- Time-locked analysis (ERPs)
 - Group comparison



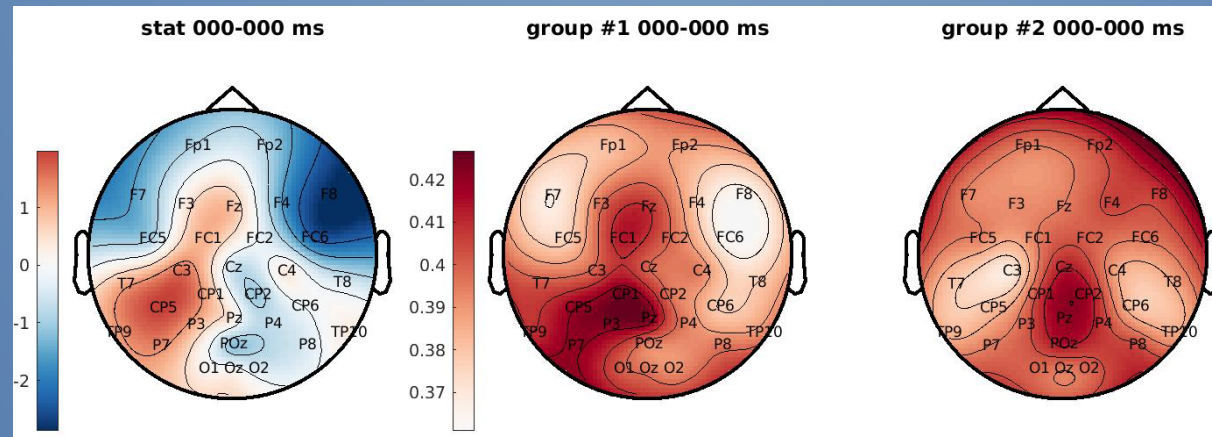
Analysis – FieldTrip

- Time-locked analysis (ERPs)
 - Peak analysis (e.g. P300)

■ Amplitude

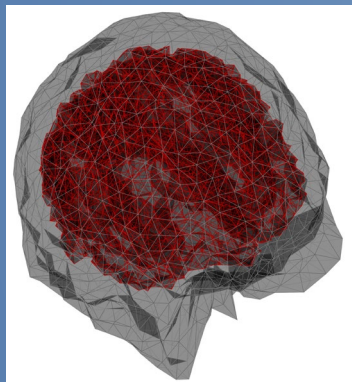


■ Latency

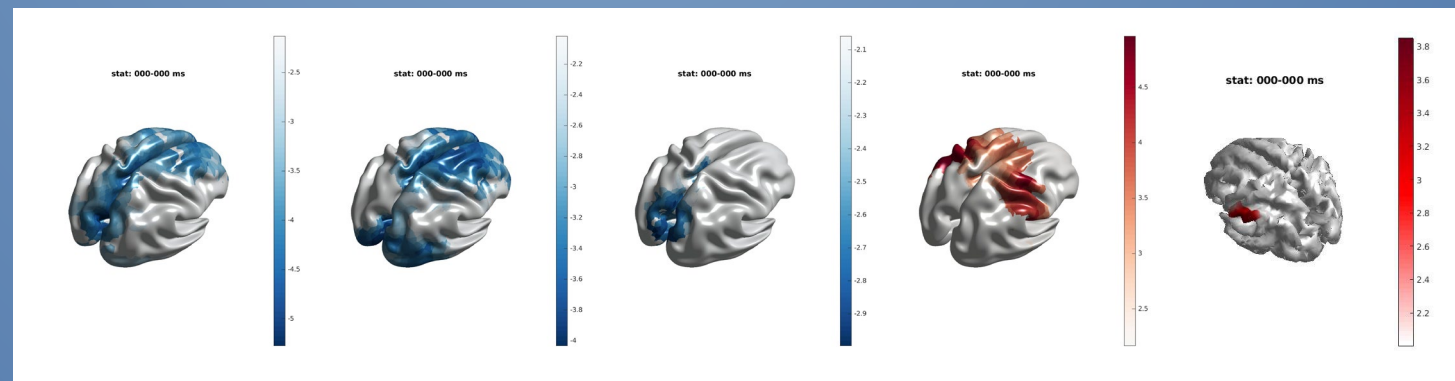
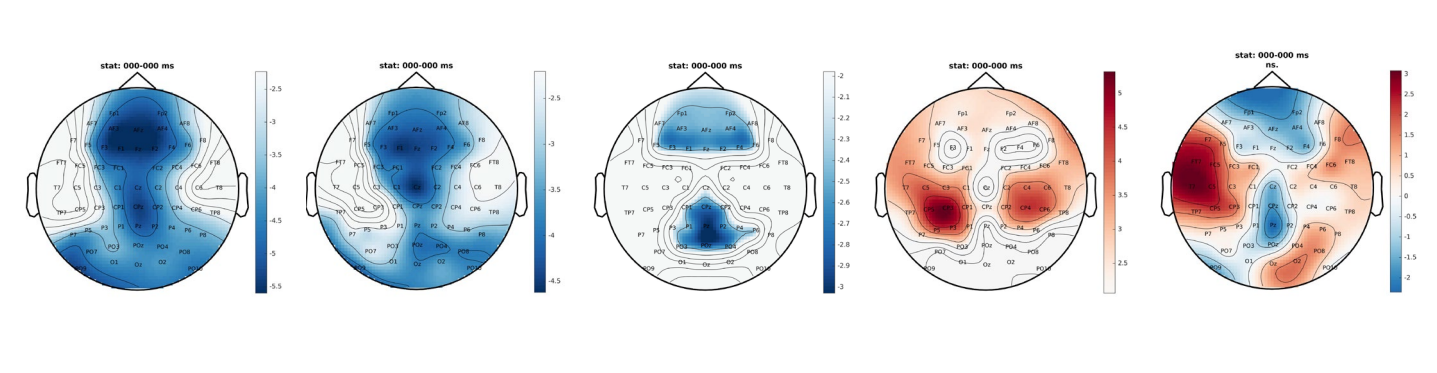


Analysis – FieldTrip

- Time-frequency analysis (TFRs)
 - Topoplots of band averages (configurable)
 - Sensor- and source-level (grid and cortical sheet) analysis

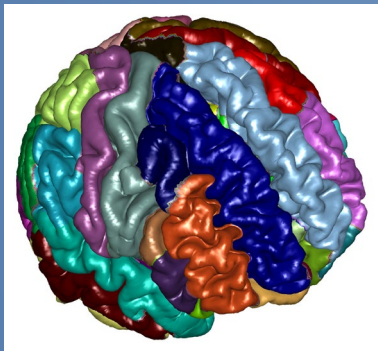


Delta (1-3Hz) Theta (4-7Hz) Alpha (8-13Hz) Beta (14-32Hz) Gamma (33-80Hz)



Analysis – FieldTrip

- Cross-frequency analysis (e.g. PAC)
 - Source-level signal reconstruction (virtual channels)
 - Atlasing e.g. according to Freesurfer's Desikan-Killiany-Tourville atlas (32 regions per hemisphere)

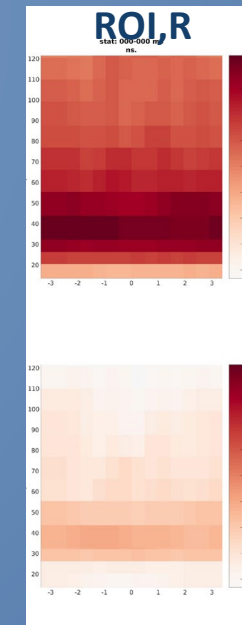
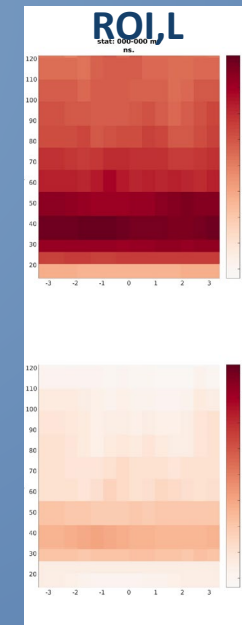
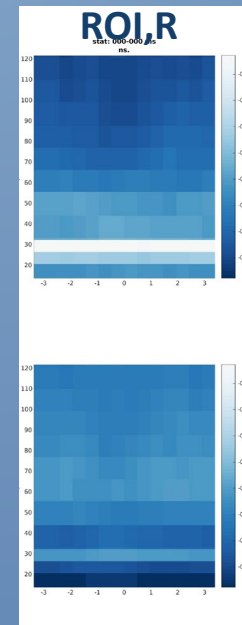
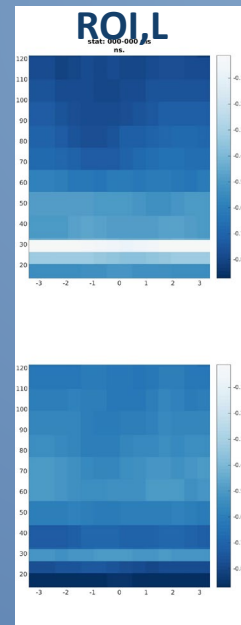


Phase: Theta (4-7Hz)

Group #1

Group #2

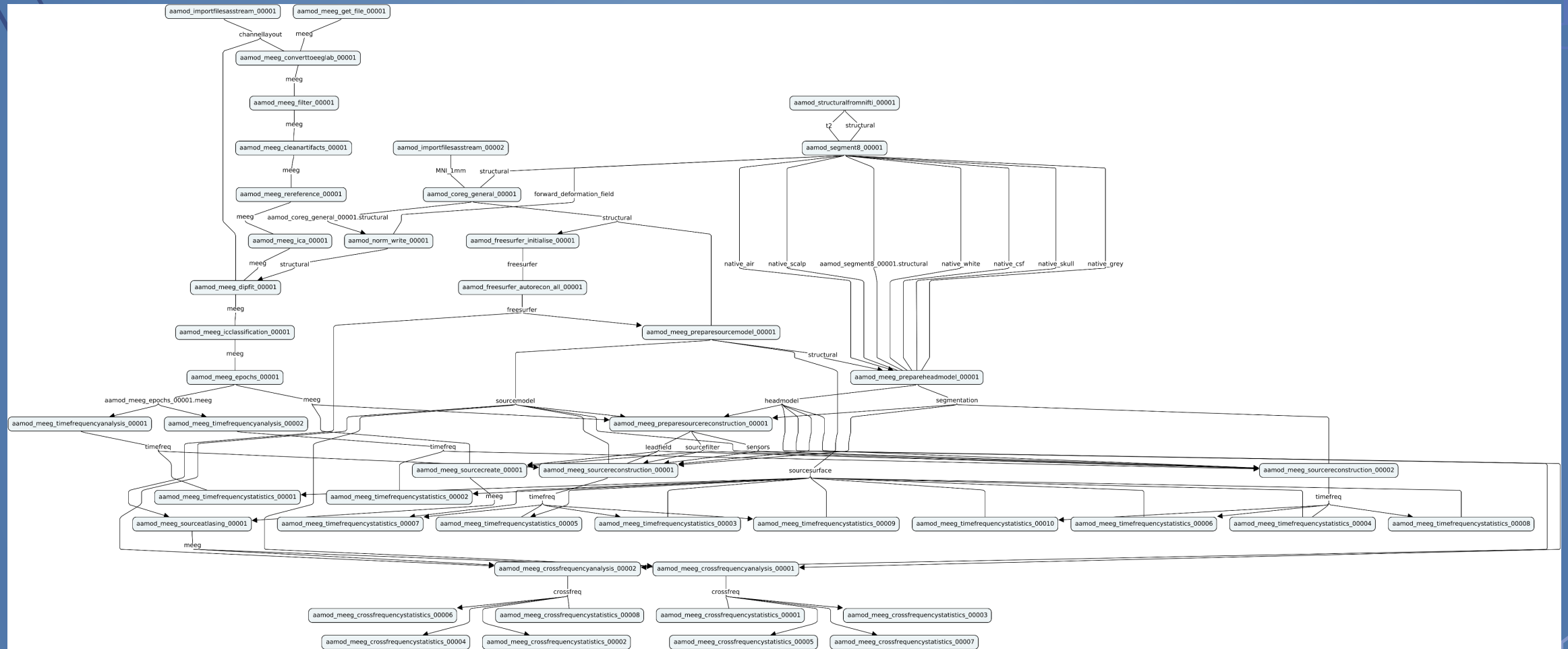
ROI, L



Amplitude

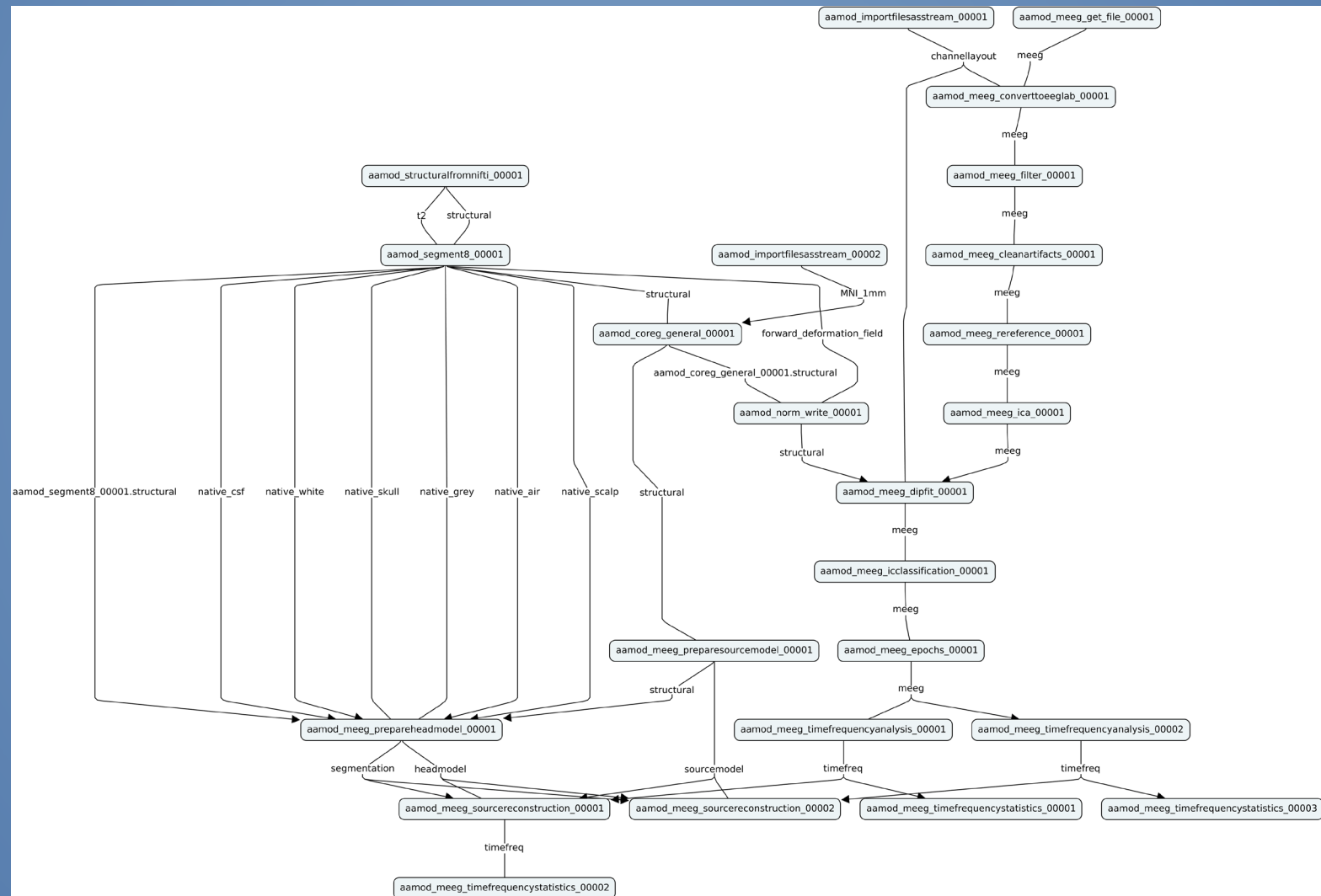
ROI, R

Example



Example

- Example tasklist
- Example UMS



- Running – aa intro

Current Folder

Name

aa

aamod_importfilesasstream_00001

aamod_meeg_cleanartifacts_00001

aamod_meeg_converttoeeglab_00001

aamod_meeg_dipfit_00001

aamod_meeg_filter_00001

aamod_meeg_get_file_00001

aamod_meeg_ica_00001

aamod_meeg_icclassification_00001

aamod_meeg_reference_00001

TECHNOLOGY REPORT ARTICLE

Front. Neuroinform., 15 January 2015 | <http://dx.doi.org/10.3389/fninf.2014.00090>

Command Window

New to MATLAB? See resources for [Getting Started](#).

>> load_tools

Please wait a moment, adding to the path

Welcome to aa version 5.4.0 (7e567b2aa6668bc3e800bd7606b264f200bbbb02) Aug 2020

If you publish work that has used aa, please cite our manuscript:

[Cusack R, Vicente-Grabovetsky A, Mitchell DJ, Wild CJ, Auer T, Linke AC, Peelle JE \(2015\) Automatic analysis \(aa\): Efficient neuroimaging workflows and parallel processing using Matlab and XML Frontiers in Neuroinformatics 8:90](#)

Please visit [The aa website](#) for more information!

automatic analysis

a MATLAB pipeline

Home About Getting started News

Definitions: (aa) means the automatic analysis software package and any associated documentation whether electronic or printed.

GitHub repo

automatic analysis wiki

aa is a pipeline system for neuroimaging written primarily in MATLAB. It supports SPM 12, as well as selected functions from other software packages (e.g., FSL, FreeSurfer). The goal is to facilitate automatic, flexible, and replicable neuroimaging analyses through a comprehensive pipeline system.

Recent Posts

Wiki

© less than 1 minute read

Old wiki

FEED

© 2021 automatic analysis. Powered by jekyll & Minimal Mistakes.

Automatic analysis (aa): efficient neuroimaging workflows and parallel processing using Matlab and XML

Rhodri Cusack^{1*}, Alejandro Vicente-Grabovetsky², Daniel J. Mitchell³, Conor J. Wild¹, Tibor Auer³, Annika C. Linke¹ and Jonathan E. Peelle⁴

¹Brain and Mind Institute, Western University, London, ON, Canada
²Donders Institute for Brain, Cognition and Behaviour, Nijmegen, Netherlands
³MRC Cognition and Brain Sciences Unit, Cambridge, UK
⁴Department of Otolaryngology, Washington University in St. Louis, St. Louis, MO, USA

Info/Support

- Running – aa intro

The image displays three screenshots of the MATLAB interface, showing the 'Current Folder' and 'Command Window' panels.

Top Screenshot:

- Current Folder:** Shows a folder named 'aa' containing subfolders like 'aamod_importfilesasstream_00001', 'aamod_meeg_cleanartifacts_00001', 'aamod_meeg_converttoeeglab_00001', 'aamod_meeg_dipfit_00001', 'aamod_meeg_filter_00001', 'aamod_meeg_get_file_00001', 'aamod_meeg_ica_00001', 'aamod_meeg_icclassification_00001', 'aamod_meeg_rereference_00001', 'aamod_segment8_00001', and 'aamod_structuralfromnifti_00001'.
- Command Window:** Shows the command `>> load_tools` and the following text:
Please wait a moment, adding to the path
Welcome to aa version 5.4.0 (7e567b2aa6668bc3e800bd7606b264f200bbbb02) Aug 2020
If you publish work that has used aa, please cite our manuscript:
[Cusack R, Vicente-Grabovetsky A, Mitchell DJ, Wild CJ, Auer T, Linke AC, Peelle JE \(2015\) Automatic analysis \(aa\): Efficient neuroimaging workflows and parallel processing using Matlab and XML Frontiers in Neuroinformatics 8:90](#)
Please visit [The aa website](#) for more information!
Here you can find example [parameter sets](#) and [examples](#).

Bottom Left Screenshot:

- Current Folder:** Shows a folder named 'aap_parameters_defaults' containing files like 'aap_parameters_defaults.xml', 'aap_parameters_defaults_AKK.xml', 'aap_parameters_defaults_CBSU.xml', 'aap_parameters_defaults_CUSACKLAB.xml', 'aap_parameters_defaults_RHUL.xml', 'aap_parameters_defaults_UEA.xml', and 'aap_parameters_defaults_UoS.xml'.
- Command Window:** Shows the command `>> load_tools` and the following text:
Please wait a moment, adding
Welcome to aa version 5.4.0 (7
If you publish work that has
[Cusack R, Vicente-Grabovetsky Automatic analysis \(aa\): Effi Frontiers in Neuroinformatics](#)
Please visit [The aa website](#) fo
Here you can find example [para](#)
Ready.
`fx >>`

Bottom Right Screenshot:

- Current Folder:** Shows a folder named 'cbu' containing files like 'aa_downloaddemo.m', 'aa_user_bids_ds000114.m', 'aa_user_demo.m', 'aa_user_demo_branching1.m', 'aa_user_demo_branching2.m', 'aa_user_meeg.m', 'aamod_template_session.m', 'aamod_template_session.xml', 'aap_tasklist_bids_ds000114.xml', 'aap_tasklist_demo.xml', 'aap_tasklist_demo_branching1.xml', 'aap_tasklist_demo_branching2.xml', and 'aap tasklist meeg.xml'.
- Command Window:** Shows the command `>> load_tools` and the following text:
Please wait a moment, adding
Welcome to aa version 5.4.0 (7
If you publish work that has
[Cusack R, Vicente-Grabovetsky Automatic analysis \(aa\): Effi Frontiers in Neuroinformatics](#)
Please visit [The aa website](#) fo
Here you can find example [para](#)
Ready.
`fx >>`

Info/Support

• GitHub

automaticanalysis / automaticanalysis

Unwatch 19

Unstar 55

Fork 32

<> Code

Issues 8

Pull requests 2

Discussions

Actions

Projects

Wiki

Security

Insights

Settings

Filters

is:issue is:open

Labels 6

Milestones 0

New issue

<input type="checkbox"/>	8 Open	✓ 159 Closed	Author	Label	Projects	Milestones	Assignee	Sort
<input type="checkbox"/>	aap.spm can no longer be modified in user script	#208 opened on Nov 27 2019 by jooh						1
<input type="checkbox"/>	Refactor CBU-specific examples to use open data	#193 opened on Feb 25 2019 by jooh						
<input type="checkbox"/>	aas_processBIDS: fmap.hdr.IntendedFor	#187 opened on Feb 1 2019 by jpeelle		bug question				1
<input type="checkbox"/>	fmap undefined in aas_processBIDS.m	#186 opened on Jan 27 2019 by jpeelle						2
<input type="checkbox"/>	Incorrect documentation in aamod_compSignal	#179 opened on Nov 28 2018 by jooh						
<input type="checkbox"/>	PCA output option in aamod_compSignal	#177 opened on Nov 6 2018 by jooh		enhancement				2
<input type="checkbox"/>	Inconsistent stream outputs between segment8 and dartel_normmni	#176 opened on Nov 6 2018 by jooh						4
<input type="checkbox"/>	aa user group	#162 opened on Aug 15 2018 by jooh		good first issue question				5

automaticanalysis / automaticanalysis

Unwatch 19

Unstar 55

Fork 32

<> Code

Issues 8

Pull requests 2

Discussions

Actions

Projects

Wiki

Security

Insights

Settings

Search all discussions

New

Top: All

Answered

Unanswered

New discussion

Categories

View all

General

Ideas

Q&A

Show and tell

Most helpful

Code of conduct

automaticanalysis.github.io

Beta Give feedback

Website	tiborauer started on Jun 24 2020 in General	3
processBIDS for MEG	ethanknights started on Feb 25 in Ideas	1
FSL/Matlab	jpeelle started on Feb 15 2019 in Ideas	13
Welcome to automaticanalysis Discussions!	tiborauer started on Feb 12 in General	0
Module naming conventions	tiborauer started on Apr 14 2015 in Ideas	7
Hyperalignment	tiborauer started on Jul 27 2018 in Ideas	6
Which tools should we provide modules for in core AA?	jooh started on Jul 26 2018 in Ideas	10
Diagnostics	tiborauer started on Dec 11 2013 in Ideas	3
qsub time and memory	tiborauer started on Jul 28 2015 in Ideas	0
Naming of structural streams	rhodricusack started on Jan 24 2014 in Ideas	4

Take home message

