aa5.8.0

Automatic analysis 5.8.0: demonstration of integrated and responsive open-source development

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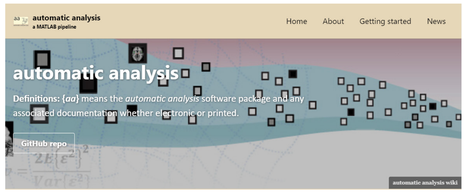


Introduction

Challenge

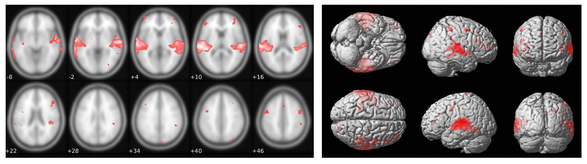
- Increasingly large cohort sizes: ~10 (2005) → hundreds (2020)
- Multimodality: a more integrated view of the brain

↓

- Requires integration of different tools → *Efficiency*
- Difficult documentation and increased risk of error → *Reproducibility*
- Harder to detect errors → *Transparency*

Solution - Automatic analysis (aa)

- Flexible construction of complex workflows in MATLAB
- Convenient integration of tools
- Parallel execution → *Efficiency*

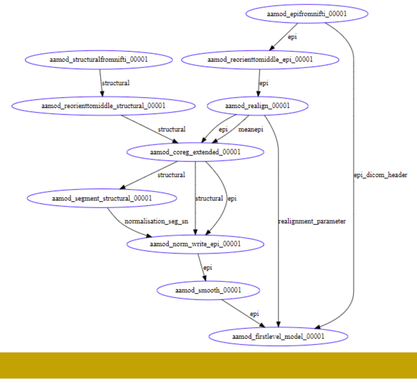


- Replicable high-level workflow description → *Reproducibility*

```
<?xml version="1.0" encoding="utf-8"?>
<aap>
    <tasklist>
        <initialisation>
            <module><name>aamod_study_init</name></module>
        </initialisation>

        <main>
            <!-- preprocessing -->
            <module><name>aamod_structuralfromnifti</name></module>
            <module><name>aamod_reorienttomiddle_structural</name></module>
            <module><name>aamod_epifromnifti</name></module>
            <module><name>aamod_reorienttomiddle_epi</name></module>
            <module><name>aamod_realign</name></module>
            <module><name>aamod_coreg_extended</name></module>
            <module><name>aamod_segment_structural</name></module>
            <module><name>aamod_norm_write_epi</name></module>
            <module><name>aamod_smooth</name></module>

            <!-- modeling -->
            <module><name>aamod_firstlevel_model</name></module>
            <module><name>aamod_firstlevel_contrasts</name></module>
            <module><name>aamod_firstlevel_threshold</name></module>
        </main>
    </tasklist>
</aap>
```

```
aa_ver5;
aap = aarecipe('tutorial_2_SPM_CH30.xml');

aap.directory_conventions.analysisid = 'SPM_CH30_MoAEpilot';
aap.directory_conventions.reportname='report.htm';

FULLDATAPATH = fullfile(aap.directory_conventions.rawdatadir, 'MoAEpilot');
aap.directory_conventions.rawdatadir = FULLDATAPATH;
aa_downloaddemo(aap, 'MoAEpilot');

aap.options.autoidentifystructural_choosefirst = 1;
aap.options.autoidentifystructural_chooselast = 0;
aap.options.NIFTI4D = 1;

aap.acq_details.numdummies = 0;
aap.acq_details.input.correctEVfordummies = 0;

aap.tasksettings.aamod_smooth.FWHM = 8;
aap.tasksettings.aamod_firstlevel_model.xBF.UNITS = 'secs';

aap = aas_processBIDS(aap);

aap = aas_addcontrast(aap, 'aamod_firstlevel_contrasts',...
    '*', 'sameforallsessions', 1, 'L_G_R','T');

aa_doprocessing(aap);
aa_report(fullfile(aas_getstudypath(aap),aap.directory_conventions.analysisid));
```

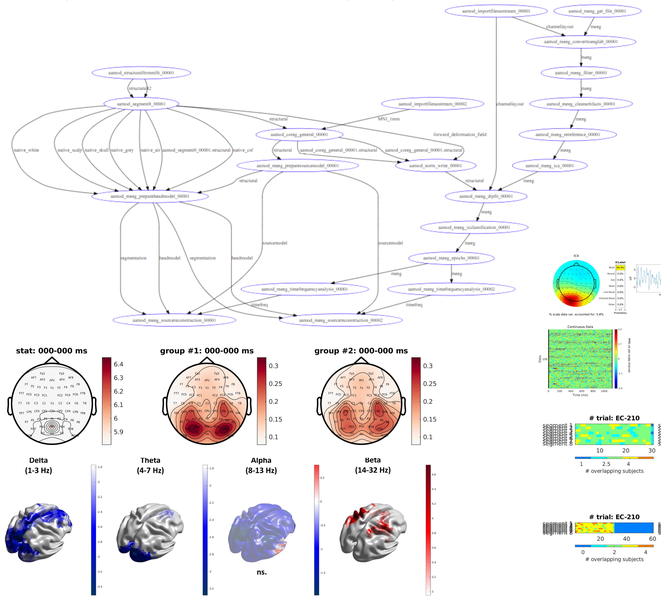
- Provenance information
- Relevant diagnostics for quality assurance → *Transparency*



Methods

New use-case - M/EEG

- Integration of EEGLAB and FieldTrip toolboxes with a new sets of modules
- Example workflow based on an openly available dataset



New environment - Windows

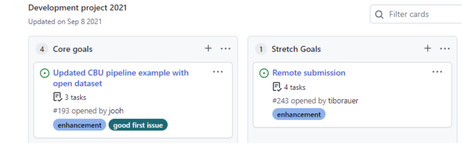
- MATLAB is a platform-dependent environment
- Platform-dependen engine: iterative testing of components

Lorem ipsum

Github as development framework

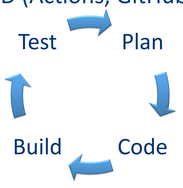
- Program development
- Wesite (Pages)

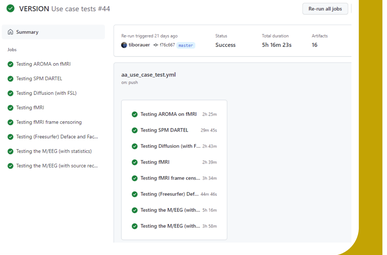
- Version control with audit
- Project managment (Projects)



- User support (Issues, Discussions)

- CI/CD (Actions, GitHub-hoster)





- Multiplatform testing

Results

The implemented changes improve aa's robustness and offer its benefits for a more diverse community. The improved transparency in the development and the application allows more agile and responsive development while it also reduces the technical debt for contribution and application.

Highlights

- *aa* improves reproducibility and supports a wide range of use cases.
- GitHub provides a powerful collaborative coding environment.

Track record

Mature platform

- 15 years old, under active development by an international team
- 100+ researchers in 100s of studies, comprising 1000s of participants.

Well suited to the analysis of large, multimodal datasets, such as Cambridge Centre for Aging and Neuroscience (www.cam-can.org)

References

1. Cusack, R., Vicente-Grabovetsky, A., Mitchell, D. J., Wild, C. J., Auer, T., et al. (2015). Frontiers in Neuroinformatics
2. Gorgolewski, K. J., Alfaro-Almagro, F., Auer, T., et al. (2017). PLoS Computational Biology
3. Auer T. (2020). F1000Research