aa4.2

Automatic analysis (aa):
newest features for efficient multimodal neuroimaging workflows

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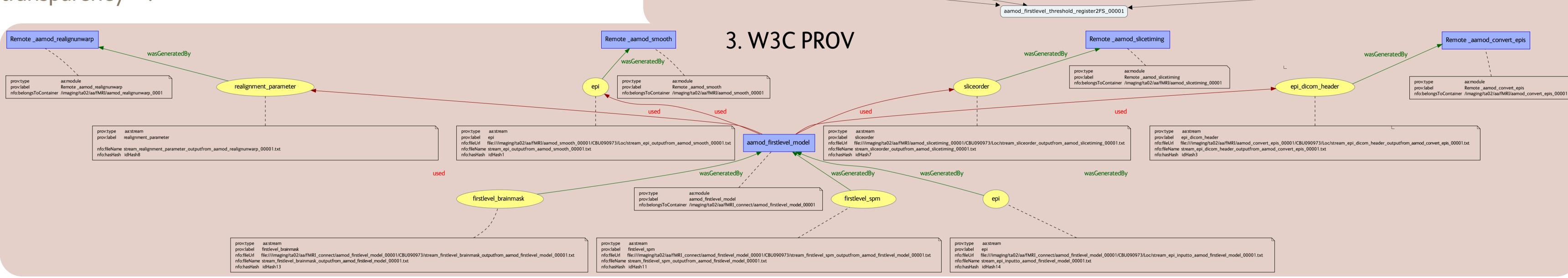
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Automatic analysis (aa) is an open-source, high-level framework written in MATLAB, that provides an efficient solution[1,2] to integrate neuroimaging analysis methods and results. It is beneficial even for simple, single subject studies, and especially useful for large, multimodal studies[3]. Flexibility and workflow integration is strongly supported by pipeline branching and connection.

Provenance

It relies on pipelines described by XML tasklists and run with a short user script. Together, these provide an accurate, easy-to-read, distributable summary of the methods. They not only allow re-creation of the whole analysis, but also serve as Supplementary Material for publication, facilitating transparency[4,5].

1. Tasklist

2. Concept map

3. W3C PROV

Robustness and versatility

Pipeline connection
- Improved flexibility
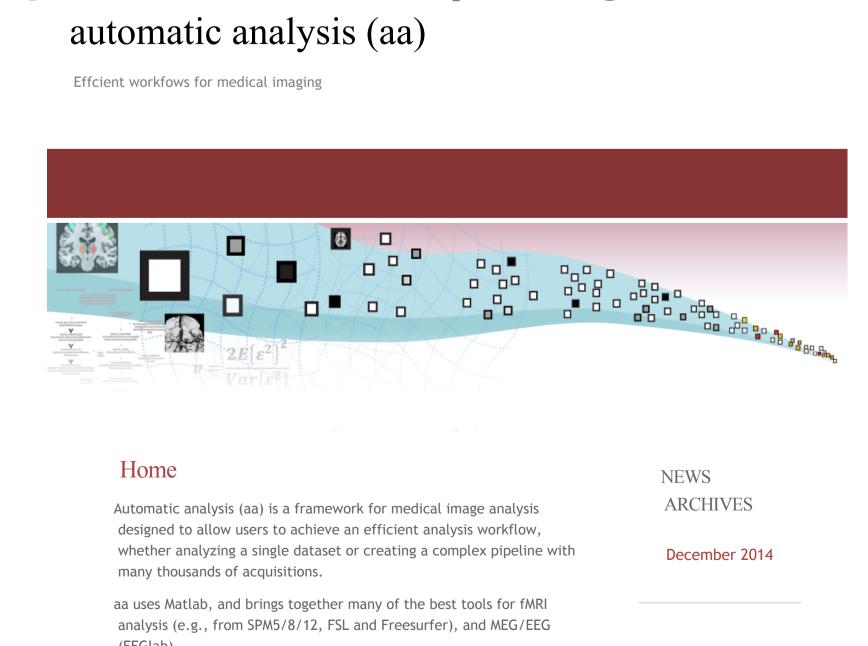- Improved control via fully specified stream names

Configuration
- Improved flexibility and robustness of redefinition of parameter subset via XML inheritance.

Parallel computing
- Improved accessibility via MATLAB's Parallel Computing Toolbox
- Improved control via explicit declariation of local execution for individual modules
- Improved job diagnostics via global "taskqueue"

http://automaticanalysis.org/

automatic analysis (aa)

Efficient workflows for medical imaging

Home
Automatic analysis (aa) is a framework for medical image analysis designed to allow users to achieve an efficient analysis workflow, whether analyzing a single dataset or creating a complex pipeline with many thousands of acquisitions.

aa uses MatLab, and brings together many of the best tools for fMRI analysis (e.g., from SPM5/8/12, FSL and Freesurfer), and MEG/EEG (EEGlab).

NEWS
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References

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New modules and solutions

fMRI
- Modeling noise
  - Spike detection
  - Global GM, WM, CSF signal extraction
  - GLMDenoise[6]
  - Motion Fingerprint[7]
- Fractional masking threshold for first-level masking (SPM12)
- Automatic slice time detection from DICOM header
- Easy temporal modulation
- Easy PPI
- Save first-level residual (SPM12)
- GIFT[8]
- Overlay onto FreeSurfer surface

Structural and registration
- Easy access to DARTEL[9] features
  - Excluding subjects from template creation
  - Using external template
- Integrating DARTEL into other modalities' workflow (see above)

- Three-stage registration via intermediate volume (~FSL)
- Registering only the first-level contrast images (~FSL)

Diffusion
- Nonlinear fitting for DTI[10]
- Fitting diffusion kurtosis[11] and estimating orientation distribution function
- Summaries for FSL probabilistic tractography

MEG
- Maxfilter (Elekta Neuromag)
- ICA denoise[10]

Code available (on GitHub)

Poster available