

Tibor Auer¹, Alejandro Vicente-Grabovetsky², Daniel J. Mitchell¹, Conor Wild³, Annika C. Linke³, Jonathan E. Peelle⁴, Rhodri Cusack³

- 1. MRC Cognition and Brain Sciences Unit, Cambridge United Kingdom
- 2. Donders Institute for Brain, Cognition and Behaviour, The Netherlands
- 3. Brain and Mind Institute, Western University, Canada.
- 4. Department of Otolaryngology, Washington University in St. Louis, United States

Challenge

Multimodality offers a more integrated view of the brain; however, it also requires a more integrated way of analysis:

- Multimodal acquisitions (e.g.): fMRI, DWI, anatomy(T1, T2)
- Diverse range of methods/softwares (e.g.):
 - SPM for fMRI
 - FSL for DWI
 - FreeSurfer for anatomy
- Software packages have heterogeneity in (e.g.):
 - Platforms
 - Concepts
 - Data formats

Increasingly large cohort sizes



Difficult integration of methods
Harder documentation.
Increased risk of human error
Errors harder to detect

Solution - Automatic analysis (aa)¹

Open-source → Availability, Transparency

High-level → Code sharing, Resuable code, Provenance
Pipelines described by tasklists Execution with User Master Script

```
<xml version="1.0" encoding="utf-8"?>
<aap>
<tasklist>
  <initialisation>
    <module><name>aamod_checkparameters</name></module>
    <module><name>aamod_evaluatesubjectnames</name></module>
    <module><name>aamod_study_init</name></module>
    <module><name>aamod_newsubj_init</name></module>
  </initialisation>
  <main>
    <module><name>aamod_automodifyseries_tlimprio</name></module>
    <module><name>aamod_get_dicom_structural</name></module>
    <module><name>aamod_get_dicom_epi</name></module>
    <module><name>aamod_get_dicom_fieldmap</name></module>
    <module><name>aamod_copystructural</name></module>
    <module><name>aamod_convert_epsi</name></module>
    <module><name>aamod_convertfieldmaps</name></module>
    <module><name>aamod_tsdfifana</name></module>
    <module><name>aamod_tsdfifunwarp</name></module>
    <module><name>aamod_slicetimeing</name></module>
    <module><name>aamod_cored_noss</name></module>
    <module><name>aamod_norm_noss</name></module>
    <module><name>aamod_norm_write</name></module>
    <module><name>aamod_smooth</name></module>
    <module><name>aamod_firstlevel_model</name></module>
    <module><name>aamod_firstlevel_contrasts</name></module>
    <module><name>aamod_firstlevel_threshold</name></module>
    <module><name>aamod_secondlevel_model</name></module>
  </main>
</tasklist>
<aap>
```

Modular - For each processing steps

- Encapsulated execution --> Independence
- Expandable



Parallel processing on cluster or cloud computing resources.

Tracks processes → No redundancy in execution

Track record

Mature platform

- 10 years old, under active development by an international team (GitHub: github.com/rhodricusack/automaticanalysis)
- 100+ researchers in 100s of studies, comprising 1000s of subjects.

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

New features

New modules to further support multimodal studies.

- Surface-based morphometry using FreeSurfer
- Analyzing DWI data using FSL tools
- Computational neuroanatomy using Advanced Normalization Tools

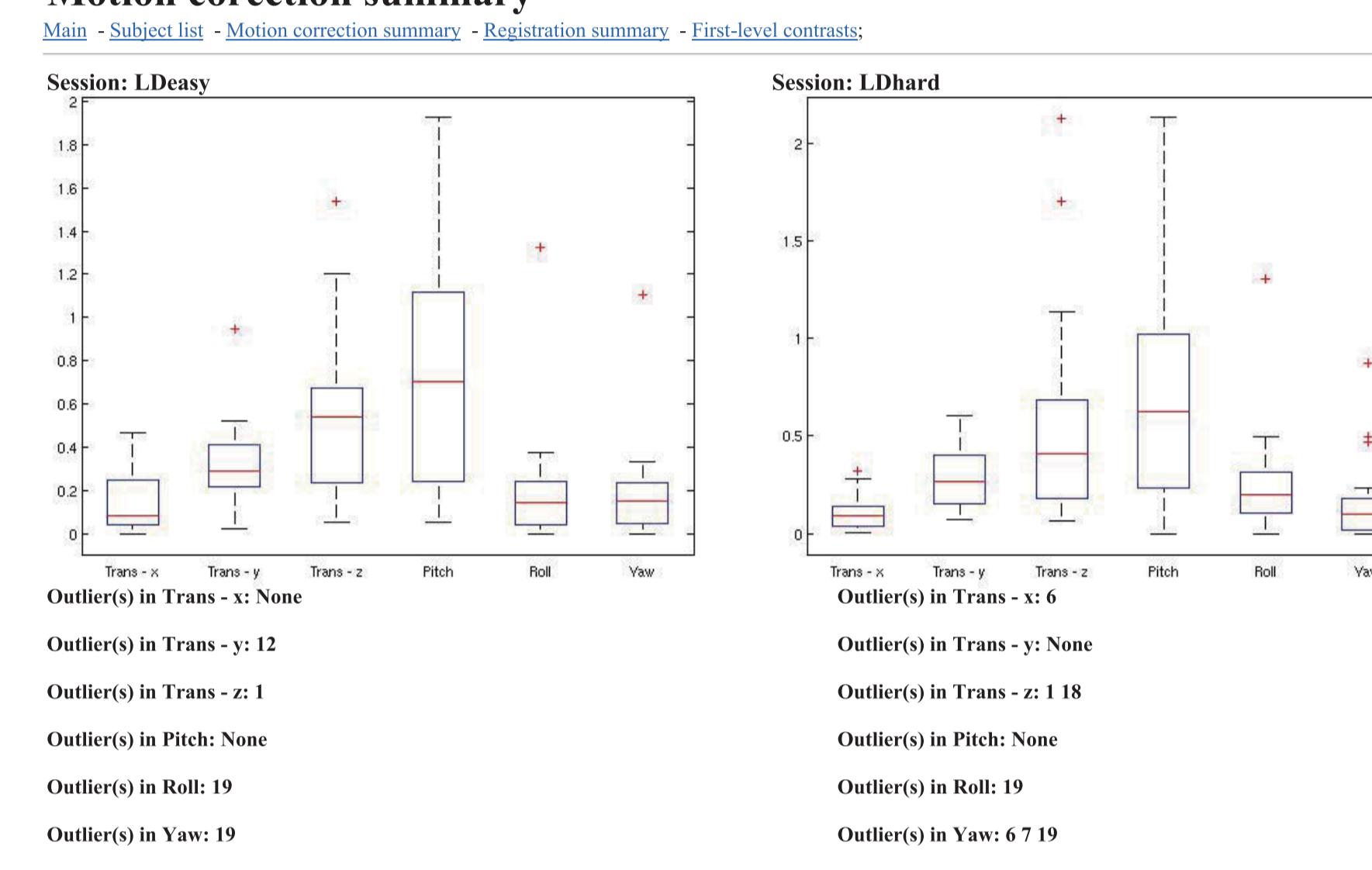
Diagnostics

- Module-specific at various stages
- Help to detect errors.
- Facilitate a better understanding of the results.

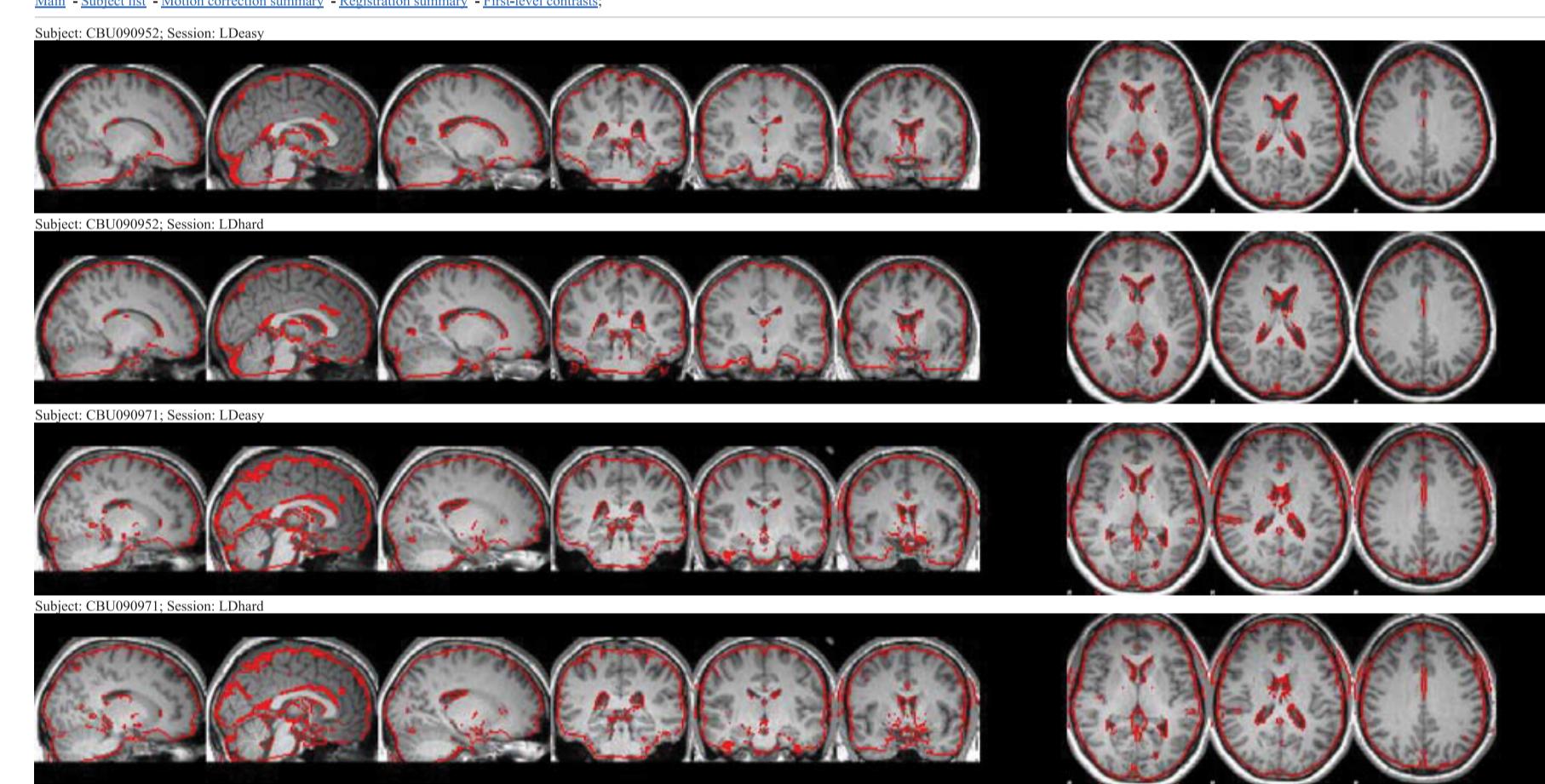
- Collected into a multi-level interlinked HTML report **AA Report**

Between-subject to identify outliers

Motion correction summary



Registration summary



Pipeline

“Branches”

- Serialisation: separation within the pipeline
 - Modalities (e.g. structural, fMRI, DWI)
 - Approaches (e.g. PPI, ICA, MVPA, fconn)
- Parallelisation: analysis with various
 - Parameters (e.g. smoothing kernel width)
 - Analysis strategies (e.g. +/- slice-timing)

Connection (*aas_connectAAPipelines*): direct aa streams from a common pipeline (e.g., common preprocessing stages)

- Keeps dependency: pipeline aware of source changes
- From remote repository to a local machine
- From multiple repository (to combine them locally)
- Can select only a subset of subjects and sessions

Data maintenance

- 4D NIFTI format also for SPM-based modules

Other “large study” features

- Site-/study-specific configuration defaults
- Multiple raw data (DICOM) sources
- Specification of subjects and statistics by means of a text file

```
<module>
  <!-- First fork: realign or slice timing first? -->
  <branch>
    <analysisid_suffix>.realign_then_slicetime</analysisid_suffix>
    <module><name>aamod_realign</name></module>
    <module><name>aamod_slicetimeing</name></module>
    <module><name>aamod_smooth</name></module>
  </branch>
  <branch>
    <analysisid_suffix>.slicetime_then_realign</analysisid_suffix>
    <module><name>aamod_slicetimeing</name></module>
    <module><name>aamod_realign</name></module>
    <module><name>aamod_smooth</name></module>
  </branch>
  <branch>
    <analysisid_suffix>.regularsmoothing</analysisid_suffix>
    <module><name>aamod_smooth</name></module>
    <branch>
      <!-- Now specifying smoothing -->
      <extraparameters>
        <aap><tasklist><currenttask><settings>
          <FWHM>16</FWHM>
        </settings></currenttask></tasklist></aap>
      </extraparameters>
    </branch>
  </branch>
</module>
```



aa-dvantages

aa efficiency

- Reduces both the amount of analyses time and errors.
- Helps to integrate methods and results.

aa versatility

- For simple, single subject studies
- Especially for large, multi-modal studies

aa provenance

- Allows re-creation of the whole analysis.
- Provides Supplementary Material for publication thus facilitating transparency.

References

- Cusack R. et al. (2012), ‘aa: Parallel Processing and Efficient Workflows in Matlab on your Cluster or in the Cloud’, 18th Annual Meeting of the Organization for Human Brain Mapping, Beijing, China.