



aa:
**the standardised pipeline
for analysing (f)MRI data**

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Challenge

Increasingly large cohort sizes

- 2004: <10
- 2014: hundreds

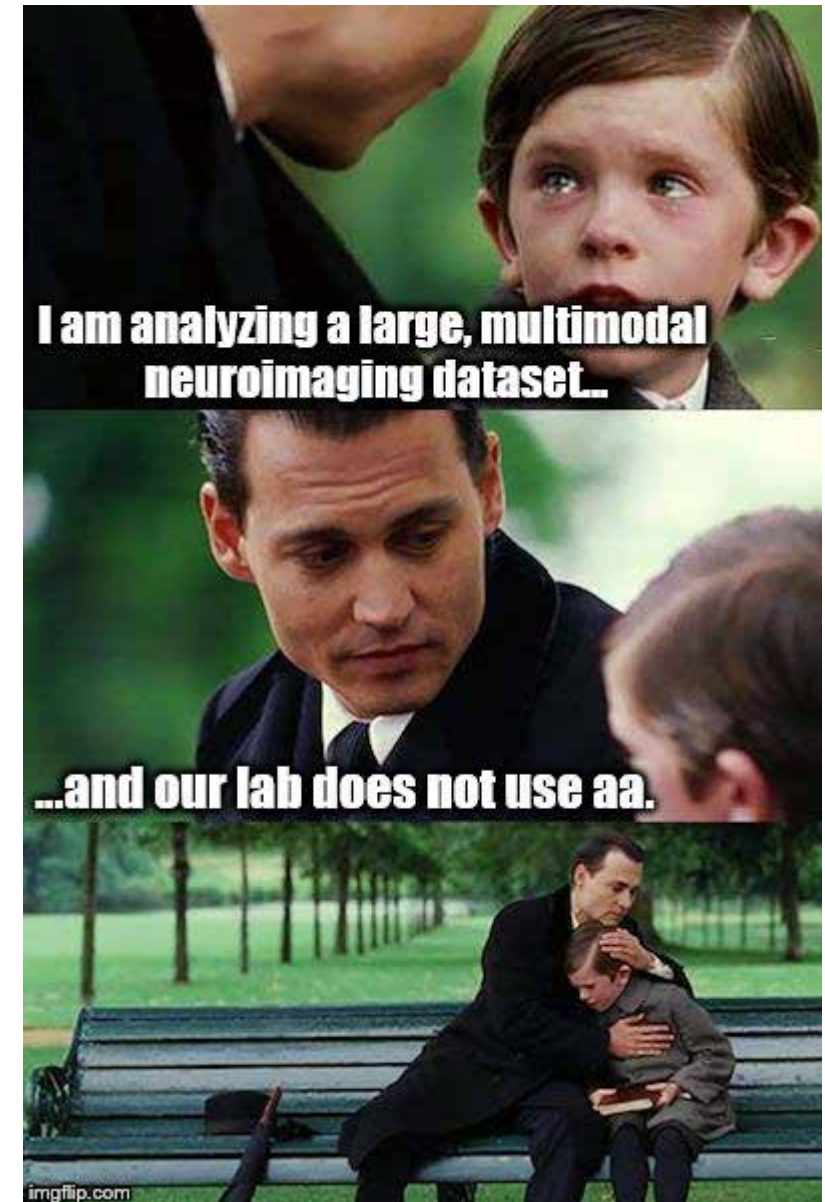
Multimodality: fMRI, DWI, anatomy(T1, T2), MTI

- Offers a more integrated view of the brain
- Requires integration of different methods



Issues:

- Difficult integration of methods
 - Difficult documentation → Reproducibility
 - Increased risk of human error
 - Harder to detect errors
- } Transparency





Solution – Automatic analysis (aa)

Description

- A pipeline system for neuroimaging written in Matlab
 - MRI: structural, fMRI, DTI/DKI, MTI
 - MEG/EEG
- Supports SPM 5/8/12¹ and some functions from FSL and Freesurfer ...
- Proprietary code from contributors and external scientists
- <http://automaticanalysis.org>
- <https://github.com/rhodricusack/automaticanalysis/blob/v5-stable/README.md>
- <http://imaging.mrc-cbu.cam.ac.uk/imaging/AA>

Availability

- GitHub (branch “v5-stable”)
- *MRC-CBSU – /imaging/local/software/AA/release-5.1.0*

Solution – Automatic analysis (aa)

Properties

- High-level based on standardised recipes
 - Automatic, transparent, replicable
 - Capture provenance
 - Code recycling/sharing/publishing
- Tracks processes à Restartable
- Notifies via e-mail
- Record keeping à Diagnostics¹
- NiFTI-4D support à “Economic”

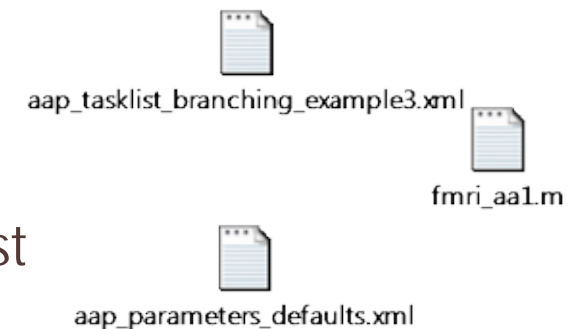


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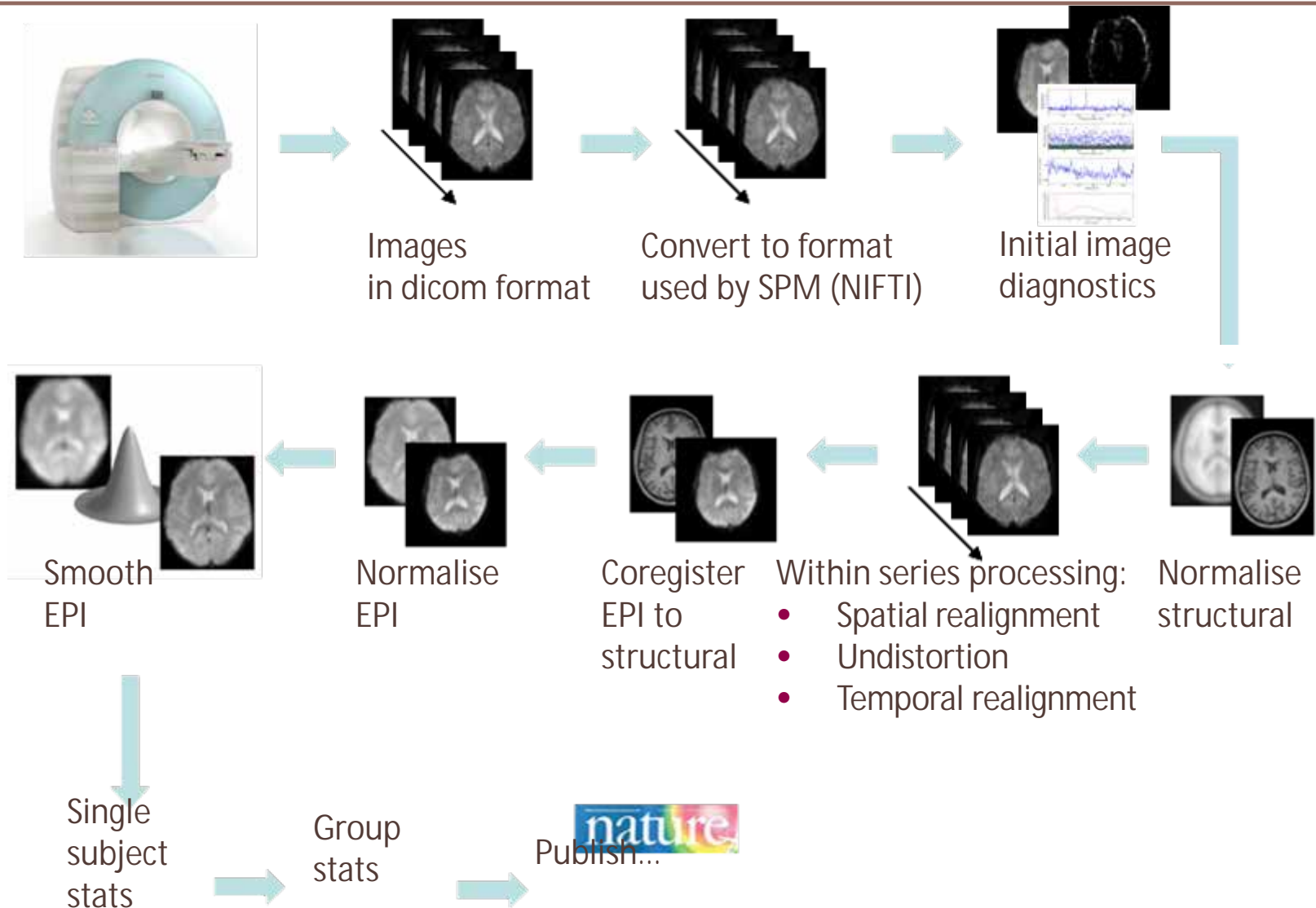
High-level scripting (examples also bundled)

- Automatic, Replicable, Transparent
- Code sharing/recycling, Provenance, Publishing
- **Tasklists:** pipelines describing a series of modules to be executed
 - Easy reading
 - Easy reordering
 - Branching
- **User Master Script:** specifies the analysis⁰
 - Loads in: default parameters and the tasklist
 - Customises: parameters and tasks
 - Specifies¹: data and model
 - Generates³: report
 - Cleans up⁴: garbage (from data encapsulation)



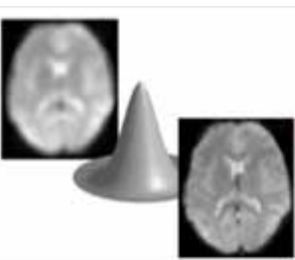
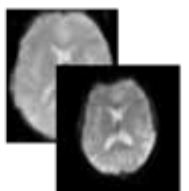
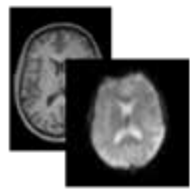
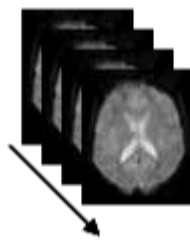
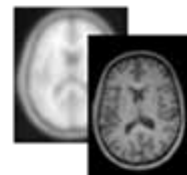
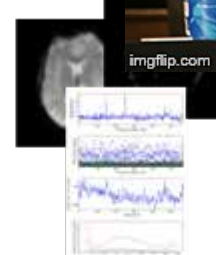
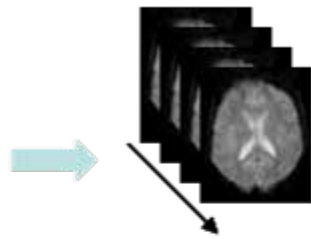
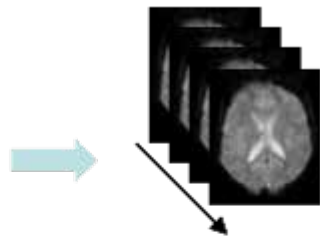
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Automatic analysis (aa)

aa-natomy



autoidentifyseries_timtrio
get_dicom_structural
get_dicom_epi
get_dicom_fieldmap

convert_structural
convert_epis
convert_fieldmaps
fieldmap2VDM

tsdiffana

smooth

norm_write_dartel
norm_write_meanepi_dartel

coreg_extended_2epi

realignunwarp
slicetiming

biascorrect_structural
coreg_extended_1
segment8_multichan
dartel_createtemplate
dartel_norm_write
+
freesurfer_initialise
freesurfer_autorecon_all

firstlevel_model
firstlevel_contrasts
firstlevel_threshold
+

secondlevel_model
secondlevel_contrasts
secondlevel_threshold



paper_maker ???

firstlevel_threshold_register2FS

secondlevel_threshold_register2FS

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Modules

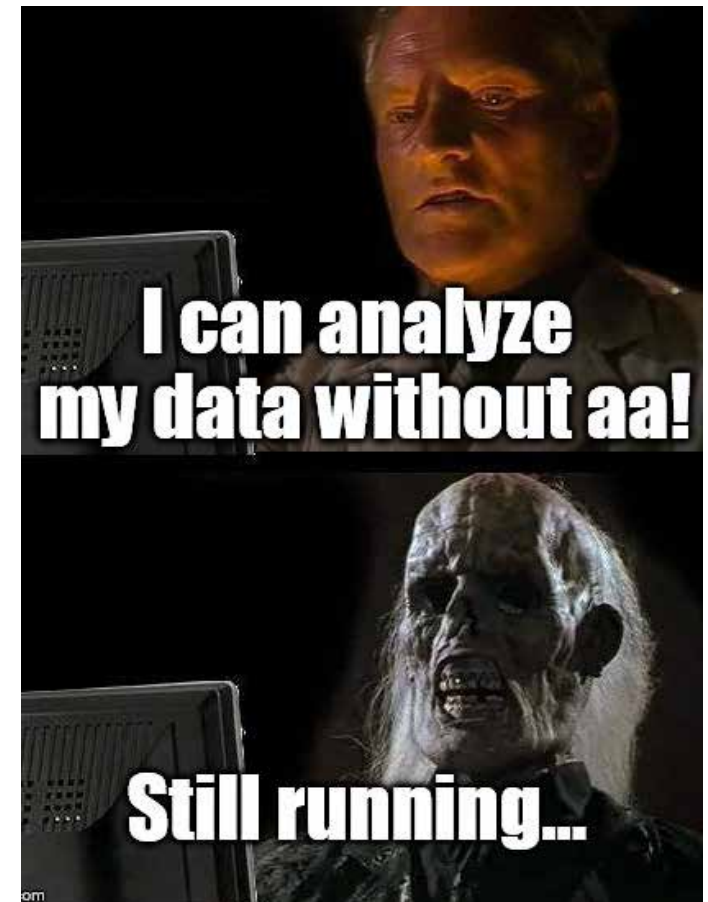
- Header¹ – Data encapsulation
 - Defines inputs and outputs (streams)
 - Defines domain (i.e. once per study/subject/session/scan)
 - Set parameter defaults²
 - Ensures independence → Parallel processing on cluster or cloud³
- Body⁴ – Code encapsulation
 - Low overhead, Expandable



aamod_realignunwarp.xml



aamod_realignunwarp.m



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Data streams¹

- Modules explicitly define their inputs and outputs.
e.g. (fragment from aamod_realignunwarp.xml)

```
<inputstreams>
```

```
  <stream>epi</stream>
```

à Takes a set of EPI volumes

```
  <stream>fieldmap</stream>
```

à and a fieldmap;

```
</inputstreams>
```

```
<outputstreams>
```

```
  <stream>realignment_parameter</stream>
```

à produces realignment parameters,

```
  <stream>epi</stream>
```

à another set of EPI volumes

```
  <stream>meanepi</stream>
```

à and a mean EPI volume

```
</outputstreams>
```

- Provenance (flow of data) à parallel computing, report generating
- Easy reordering of the modules without worrying for prefixes



diary.txt



aap_cmap.jpg

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“Study” features: Diagnostics

- Between-subject summaries with descriptive stats to identify outliers
 - Motion correction
 - Registration (Normalisation)
 - First-level activations
- Within-subject summary to localize the erroneous stage



aa_diag_moco.mht



aa_diag_reg.mht



aa_diag_C07.mht



aa_diag_S03.mht

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“Large Study” features:

- NiFTI-4D format also for SPM-based modules (data maintenance)
- Site-/study-specific configuration defaults
- Multiple raw data (DICOM) sources¹
- Pipeline connection: direct aa streams from a common pipeline
 - From remote repository to a local machine
 - From multiple repository (to combine them locally)
 - Can select only a subset of subjects and sessions
 - Keeps dependency: pipeline aware of source changes
 - E.g.:
 - Multimodal study: separate pipelines for each modality
 - Complex study: common preprocessing pipeline + multiple models



aap_parameters_defaults_CBSU.xml

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“Large Study” features:

- Specification of subjects, sessions and model by means of a text file
 - Inputfile (sCSV): Subjects and sessions
 - One file for more analysis
 - Selected sessions
 - Easy to add more subjects without coding
 - Reference Directory template for first-level model (SPM-format)
 - `condition_vol_ID-SessionName.mat`
 - E.g.:
 - `/imaging/ta02/ActionWords/Analysis/E-Prime/S1/condition_vol_S1-Loc.mat`
 - ↓
 - `referencedirectory_tmpl = /imaging/ta02/ActionWords/Analysis/E-Prime/*`
(“*” will be replaced with ID)



Input.txt



fmri_aa3.m

Info/Support

Website: <http://automaticanalysis.org>

GitHub: <https://github.com/rhodricusack/automaticanalysis/blob/v5-stable/README.md>

GitWiki: <https://github.com/rhodricusack/automaticanalysis/wiki>

Our Wiki: <http://imaging.mrc-cbu.cam.ac.uk/imaging/AA>

Maasters

