

aa:
magic explained
(MRI)

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Automatic analysis (aa)

aa-natomy



- **Modules**

- [Header](#)¹ – 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
- [Body](#)⁴ – Code encapsulation
 - Low overhead, Expandable



- Data streams¹

- Modules explicitly define their inputs and outputs and default parameters.

e.g. (fragment from [aamod_realignunwarp.xml](#))

```
<inputstreams>
```

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

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

```
</inputstreams>
```

```
<outputstreams>
```

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

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

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

```
</outputstreams>
```

→ Takes:

→ a set of EPI volumes

→ and a fieldmap;

→ Produces:

→ realignment parameters,

→ another set of EPI volumes

→ and a mean EPI volume

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

What you need

Tasklist – aa_demo_tasklist.xml



- Pipelines describing a series of modules to be executed

```
<?xml version="1.0" encoding="utf-8"?>
<!-- This is a tasklist to process BIDS multimodal NIfTI dataset ds114 (https://github.com/INCF/BIDS-examples/tree/master/ds114) -->
<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_autoidentifyseries_timtrio</name></module>
      <module><name>aamod_get_dicom_structural</name></module>
      <module><name>aamod_get_dicom_epi</name></module>
      <module><name>aamod_convert_structural</name></module>
      <module><name>aamod_convert_epis</name></module>
      <module><name>aamod_tsdiffana</name></module>
      ...
    </main>
  </tasklist>
</aap>
```

What you need

Tasklist – aa_demo_tasklist.xml



- Pipelines describing a series of modules to be executed

```
<module><name>aamod_coreg_extended_1</name></module>
<module><name>aamod_biascorrect_structural</name></module>
<module><name>aamod_segment8</name></module>

<module><name>aamod_realign</name></module>
<module><name>aamod_coreg_extended_2epi</name></module>
<module><name>aamod_coreg_extended_2meanepi</name></module>
<module><name>aamod_norm_write</name></module>
<module><name>aamod_norm_write_meanepi</name></module>
<module><name>aamod_smooth</name></module>
<module><name>aamod_tsdiffana</name></module>

<!-- Modelling. Now no need to make local copies of the first level model and contrasts -->
<module><name>aamod_firstlevel_model</name></module>
<module><name>aamod_firstlevel_contrasts</name></module>
<module><name>aamod_firstlevel_threshold</name></module>
</main>
</tasklist>
</aap>
```


What you need

UMS – aa_demo_script.xml



- **Specifies and runs the analysis**
 - Initialise: setup aa
 - Loads in: default parameters and the tasklist
 - Customises: parameters and tasks
 - Specifies: data and model
 - **Runs and cleans up: the main (p)art**
 - Generates: report

What you need

UMS – aa_demo_script.xml



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- Specifies and runs the analysis

- Initialise: setup aa

```
% Automatic analysis (aa) - user master script
%
% This example runs one session of one subject through a standard SPM-based
% fMRI analysis. After running, look at the results using SPM in
% aa_demo_results/auditory/aamod_firstlevel_contrasts_00001/2014_03_29_9001/stats
%
% v3: Johan Carlin, MRC CBU, 2018-08-06
% v2: Tibor Auer MRC Cognition and Brain Sciences Unit, 2016-02-17
% v1: Rhodri Cusack Brain and Mind Institute, Western University, 2014-12-15

%% INIT
clear
aa_ver5;
```

What you need

UMS – aa_demo_script.xml



- Specifies and runs the analysis
 - Loads in: default parameters and the tasklist

%% LOAD TASKLIST

```
aap = aarecipe('aap_parameters_defaults_RHUL.xml','aap_tasklist_demo.xml');
```

- Customises: parameters and tasks

%% DEFINE STUDY SPECIFIC PARAMETERS

```
aap.options.wheretoprocess = 'localsingle'; % running locally
```

```
aap.options.email = 'tibor.auer@rhul.ac.uk';
```

```
aap.tasksettings.aamod_norm_write.vox = [3 3 3];
```

```
aap.tasksettings.aamod_norm_write_meanepi.vox = [3 3 3];
```

What you need

UMS – aa_demo_script.xml



- Specifies and runs the analysis

- Specifies: data and model

%% DATA

```
aap.directory_conventions.rawdatadir = '/MRIRaw:/usr/local/apps/psycapps/automaticanalysis/aa_demo/aa_demo';
```

```
% Define how subject identifier (e.g. 2014_03_29_9001) is turned into
```

```
% subject foldername in rawdatadir
```

```
aap.directory_conventions.subjectoutputformat = '%s';
```

```
% This is name of the structural protocol, as typed into the scanner. If
```

```
% you're consistent with this, it can be found automatically in each new subject
```

```
aap.directory_conventions.protocol_structural = 'MPRAGE iPAT2_sag';
```

```
% Number of dummy scans at start of EPI runs
```

```
aap.acq_details.numdummies = 10;
```

%% STUDY

```
% Where to put the analyzed data
```

```
aap.acq_details.root = '/MRIWork/Training/mrtrain01';
```

```
aap.directory_conventions.analysisid = 'aa_demo';
```

What you need

UMS – aa_demo_script.xml



- Specifies and runs the analysis

- Specifies: data and model

```
% Add data
% Just one session
aap = aas_addsession(aap,'lullaby_task');
% Just one subject
aap = aas_addsubject(aap,'S1','2014_03_29_9001','functional',{6});

% Add model
% Just one regressor here ('Sound'): block onsets 0, 26, 52... 390 secs and duration 15 secs
aap = aas_addevent(aap,'aamod_firstlevel_model','*','*','Sound',0:26:390, 15);

% Specify contrast - just sound minus silence
aap = aas_addcontrast(aap, 'aamod_firstlevel_contrasts', '*', 'sameforallsessions', 1, 'sound-silence', 'T');
```

What you need

UMS – aa_demo_script.xml



- Specifies and runs the analysis
 - Runs and cleans up: the main (p)art

```
%% DO PROCESSING  
aa_doprocessing(aap);
```

- Generates: report

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

Congratulations!



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You have just analyzed a dataset...



...with aa!