MRC | Cognition and Brain Sciences Unit

aa:
magic explained
(MRI)

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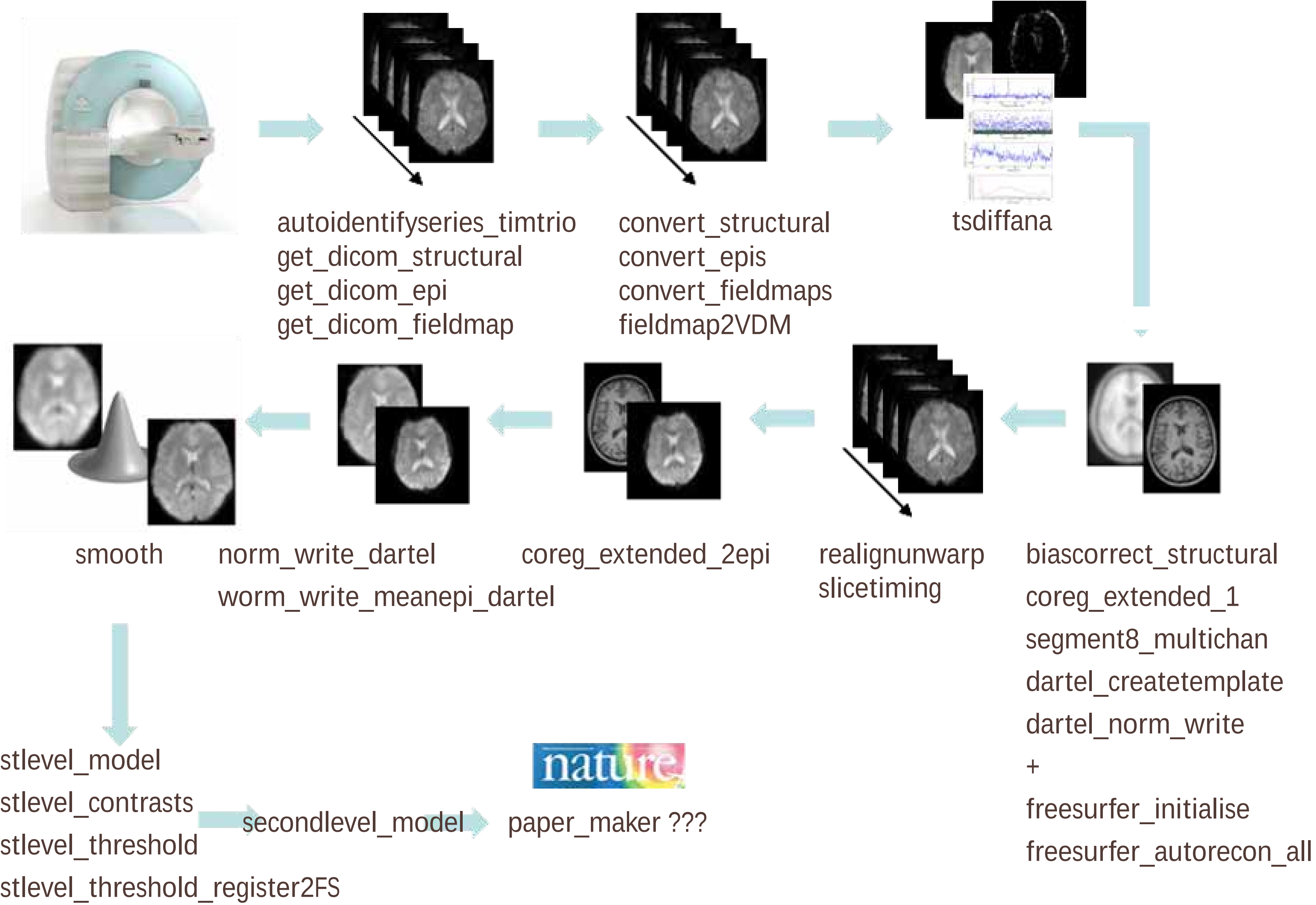
Recap

aa-natomy



autoidentifyseries_timtrio
get_dicom_structural
get_dicom_epi
get_dicom_fieldmap

convert_structural
convert_epis
convert_fieldmaps
fieldmap2VDM

tsdiffana

biascorrect_structural
coreg_extended_1
segment8_multichan
dartel_createtemplate
dartel_norm_write
+
freesurfer_initialise
freesurfer_autorecon_all

realignunwarp
slicetiming

coreg_extended_2epi

norm_write_dartel
worm_write_meanepi_dartel

smooth

firstlevel_model
firstlevel_contrasts
firstlevel_threshold
firstlevel_threshold_register2FS

secondlevel_model

paper_maker ???

Recap

aa-natomy

Modules

- Header[1] – Data encapsulation
  - Defines inputs and outputs (streams)
  - Defines domain (i.e. once per study/subject/session/scan)
  - Set parameter defaults[2]

  - Ensures independence à Parallel processing on cluster or cloud

- Body[1] – Code encapsulation
  - Low overhead, Expandable

aamod_realignunwarp.xml

aamod_realignunwarp.m

Recap

aa-natomy

Data streams[1]

- Modules explicitly define their inputs and outputs.

  e.g. (fragment from aamod_realignunwarp.xml)

```
<inputstreams>
        <stream>epi</stream>                          → Takes a set of EPI volumes
        <stream>fieldmap</stream>                     → and a fieldmap;
</inputstreams>
<outputstreams>
        <stream>realignment_parameter</stream>        → produces realignment parameters,
        <stream>epi</stream>                          → another set of EPI volumes
        <stream>meanepi</stream>                      → and a mean EPI volume
</outputstreams>
```

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

diary.txt aap_cmap.jpg

What you need

Tasklist

- **Pipelines describing a series of modules to be executed**

fmri_takslist.xml

```xml
<?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>
      <!-- Data -->
      <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_get_dicom_fieldmap</name></module>
      <module><name>aamod_convert_structural</name></module>
      <module><name>aamod_convert_epis</name></module>
      <module><name>aamod_convert_fieldmaps</name></module>
      …
    </main>
  </tasklist>
</aap>
```

What you need

Tasklist

- **Pipelines describing a series of modules to be executed**

```
<main>
  ...
  <!-- Structural -->
  <module><name>aamod_biascorrect_structural</name></module>
  <module><name>aamod_coreg_extended_1</name></module>

  <module><name>aamod_freesurfer_initialise</name></module>
  <module><name>aamod_freesurfer_autorecon_all</name></module>

  <module><name>aamod_segment8_multichan</name></module>
  <module><name>aamod_structuralstats</name></module>
  <module><name>aamod_dartel_createtemplate</name></module>
  <module><name>aamod_dartel_normmni</name></module>
  <module><name>aamod_normalisebytotalgrey</name></module>
  <module><name>aamod_roi_extract</name></module>
  <module><name>aamod_roi_valid_structural</name></module>

  <module><name>aamod_dartel_norm_write</name></module>
  ...
</main>
```

What you need

Tasklist

- **Pipelines describing a series of modules to be executed**

```
<main>
  ...
  <!-- Functional -->
  <module><name>aamod_fieldmap2VDM</name></module>
  <module><name>aamod_tsdiffana</name></module>
  <module><name>aamod_realignunwarp</name></module>
  <module><name>aamod_slicetiming</name></module>
  <module><name>aamod_tsdiffana</name></module>
  <module><name>aamod_coreg_extended_2epi</name></module>
  <module><name>aamod_norm_write_dartel</name></module>
  <module><name>aamod_norm_write_meanepi_dartel</name></module>
  <module><name>aamod_tsdiffana</name></module>
  <module><name>aamod_smooth</name></module>
  <module><name>aamod_tsdiffana</name></module>

  <!-- Modelling -->
  <module><name>aamod_firstlevel_model</name></module>
  <module><name>aamod_firstlevel_contrasts</name></module>
  <module><name>aamod_firstlevel_threshold</name></module>
  <module><name>aamod_firstlevel_threshold_register2FS</name></module>

  <module><name>aamod_secondlevel_model</name></module>

  <module><name>aamod_rois_dartel_denormepi</name></module>
</main>
```

What you need

User Master Script (UMS)

- **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

User Master Script (UMS)

- **Specifies and runs the analysis**
    - Initialise: setup aa

```
% Automatic analysis
% User master script example (aa version 5.*.*) - c.a. 2.5h
%
% Tibor Auer, MRC-CBSU
% 01-02-2016

clear

aa_ver5
```

What you need

User Master Script (UMS)

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

```
%% DEFINE SPECIFIC PARAMETERS
%  Default recipe with model
aap = aarecipe('aap_parameters_defaults_CBSU.xml','/imaging/xy01/Workshop/Material/4_aa/fmri_takslist.xml');
aap = aas_configforSPM12(aap);
```

What you need

User Master Script (UMS)

- **Specifies and runs the analysis**
    - Customises: parameters and tasks

```
% Modify standard recipe module selection here if you'd like
aap.options.wheretoprocess = 'qsub'; % queuing system                 % OPTIONS: 'localsingle'|'qsub' for aa engine, typical value 'qsub'
aap.options.email = 'xy01@mrc-cbu.cam.ac.uk';
aap.options.autoidentifyfieldmaps = 1;
aap.tasksettings.aamod_roi_extract_structural.ROIfile = '/imaging/camcan/templates/Juelich-maxprob-thr25-2mm.nii';
aap.tasksettings.aamod_realignunwarp.mfp.run = 1;                      % Motion FingerPrint, typical value 0
% Set slice order for slice timing correction
aap.tasksettings.aamod_slicetiming.autodetectSO = 1;
aap.tasksettings.aamod_slicetiming.refslice = 16;                      % reference slice (first acquired)
aap.tasksettings.aamod_smooth.FWHM = 5;                                % smoothing kernel size, typical value 10
aap.tasksettings.aamod_roi_extract_epi.ROIfile = '/imaging/camcan/templates/Juelich-maxprob-thr25-2mm.nii';
aap.tasksettings.aamod_firstlevel_model.xBF.name = 'hrf (with time and dispersion derivatives)';
aap.tasksettings.aamod_firstlevel_model.xBF.UNITS = 'secs';            % OPTIONS: 'scans'|'secs' for onsets and durations, typical value 'secs'
aap.tasksettings.aamod_firstlevel_model.includemovementpars = 1; % Include/exclude Moco params in/from DM, typical value 1
aap.tasksettings.aamod_firstlevel_threshold.threshold.correction = 'FWE';
aap.tasksettings.aamod_firstlevel_threshold.threshold.p = 0.05;
aap.tasksettings.aamod_secondlevel_threshold.threshold.correction = 'none';
aap.tasksettings.aamod_secondlevel_threshold.threshold.p = 0.1;
aap.tasksettings.aamod_secondlevel_threshold.threshold.extent = 1000;
```

What you need

User Master Script (UMS)

- **Specifies and runs the analysis**
  - Specifies: data

```
% Directory for analysed data
aap.acq_details.root = '/imaging/xy01/Workshop';
aap.directory_conventions.analysisid = 'aa_fMRI1';
aap.directory_conventions.subject_directory_format = 3;

% Add data
aap = aas_addsession(aap,'Loc');
aap = aas_addsubject(aap,'S1',90973,'structural',2,'functional',{7});
aap = aas_addsubject(aap,'S2',90979,'structural',2,'functional',{7});

aap = aas_addinitialstream(aap,'rois',{...
   '/imaging/xy01/Workshop/Material/4_aa/SMC_L.nii',...
   '/imaging/xy01/Workshop/Material/4_aa/SMC_R.nii',...
   '/imaging/xy01/Workshop/Material/4_aa/SSC_L.nii',...
   '/imaging/xy01/Workshop/Material/4_aa/SSC_R.nii'...
   });
```

What you need

User Master Script (UMS)

- **Specifies and runs the analysis**
  - Specifies: model

```
% Add model
% Obtain TR from the first session
h = dicominfo(mri_finddcm(aap, 90973,7));
TR = h.RepetitionTime/1000; % in seconds
% The "hard"(-coded) way
aap = aas_addevent(aap,'aamod_firstlevel_model','S1','*',...
    'REST',...                                                                             % name
    [30.0560 100.1620 160.2800 200.3700 280.5340 340.6670]-aap.acq_details.numdummies*TR,... % onsets
    [10.0070  10.0230  10.0230  10.0220  10.0210  10.0230]);                               % durations
aap = aas_addevent(aap, 'aamod_firstlevel_model','S1','*',...
    'RIGHTFINGER',...                                                                      % name
    [70.0960 140.2360 170.3030 240.4600 320.6220 350.6890]-aap.acq_details.numdummies*TR,... % onsets
    [10.0220  10.0220  10.0220  10.0220  10.0230  10.0230]);                               % durations

aap = aas_addevent(aap, 'aamod_firstlevel_model','S2','*',...
    'REST',...                                                                             % name
    [30.0570 100.1310 160.1990 200.2380 270.3610 330.4300]-aap.acq_details.numdummies*TR,... % onsets
    [10.0070  10.0220  10.0060  10.0220  10.0070  10.0220]);                               % durations
aap = aas_addevent(aap, 'aamod_firstlevel_model','S2','*',...
    'RIGHTFINGER',...                                                                      % name
    [70.0970 140.1860 170.2050 240.3110 310.4020 340.4510]-aap.acq_details.numdummies*TR,... % onsets
    [10.0060  10.0070  10.0210  10.0220  10.0210  10.0220]);                               % durations

aap = aas_addcontrast(aap,'aamod_firstlevel_contrasts','*','singlesession:Loc','+1xRIGHTFINGER|-1xREST','Loc_RightFinger-Rest','T');
```

What you need

User Master Script (UMS)

- **Specifies and runs the analysis**
  - Specifies: model (alternative way)
    - Prerequisite: condition files in “SPM format“[1]
      - One per subject and per session[2]

```
for s = 1:numel(aap.acq_details.subjects)                    % for each subject
   load(['/imaging/xy01/Workshop/Material/4_aa/condition_vol_' aas_getsubjname(aap,s) '-Loc.mat']);
   for ev = 1:numel(names)                                   % for each EV
      aap = aas_addevent(aap,'aamod_firstlevel_model',aas_getsubjname(aap,s),'*',...
         names{ev},...                                       % name
         onsets{ev}-aap.acq_details.numdummies*TR,...        % onsets
         durations{ev});                                     % durations
   end
end
```

What you need

User Master Script (UMS)

- **Specifies and runs the analysis**
  - Specifies: data and model (alternative way – aa-specific)
    - Prerequisite:
      - “Input list”: CSV-file[1]
      - Condition files
        - *‘condition_vol_<subject name>-<session name>.mat’*
        - “SPM format“

Input.txt

```
aap.acq_details.input.list = '/imaging/xy01/Workshop/Material/4_aa/Input.txt';
aap.acq_details.input.selected_sessions = 1; % Only session "Loc"
aap.acq_details.input.referencedirectory_tmpl = '/imaging/xy01/Workshop/Material/4_aa';
aap = aas_processinput(aap);
```

What you need

User Master Script (UMS)

- **Specifies and runs the analysis**
  - Specifies: data and model (alternative way – standard)
    - Prerequisite: dataset in BIDS-format

```
aap.directory_conventions.rawdatadir = '/imaging/xy01/Workshop/Material/4_aa/BIDS';
aap.acq_details.numdummies = 0;
aap = aas_processBIDS(aap);
```

What you need

User Master Script (UMS)

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

```
aa_doprocessing(aap);
```

What you need

User Master Script (UMS)

- **Specifies and runs the analysis**
    - Generates: report

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

Congratulations!