

GTT connectivité

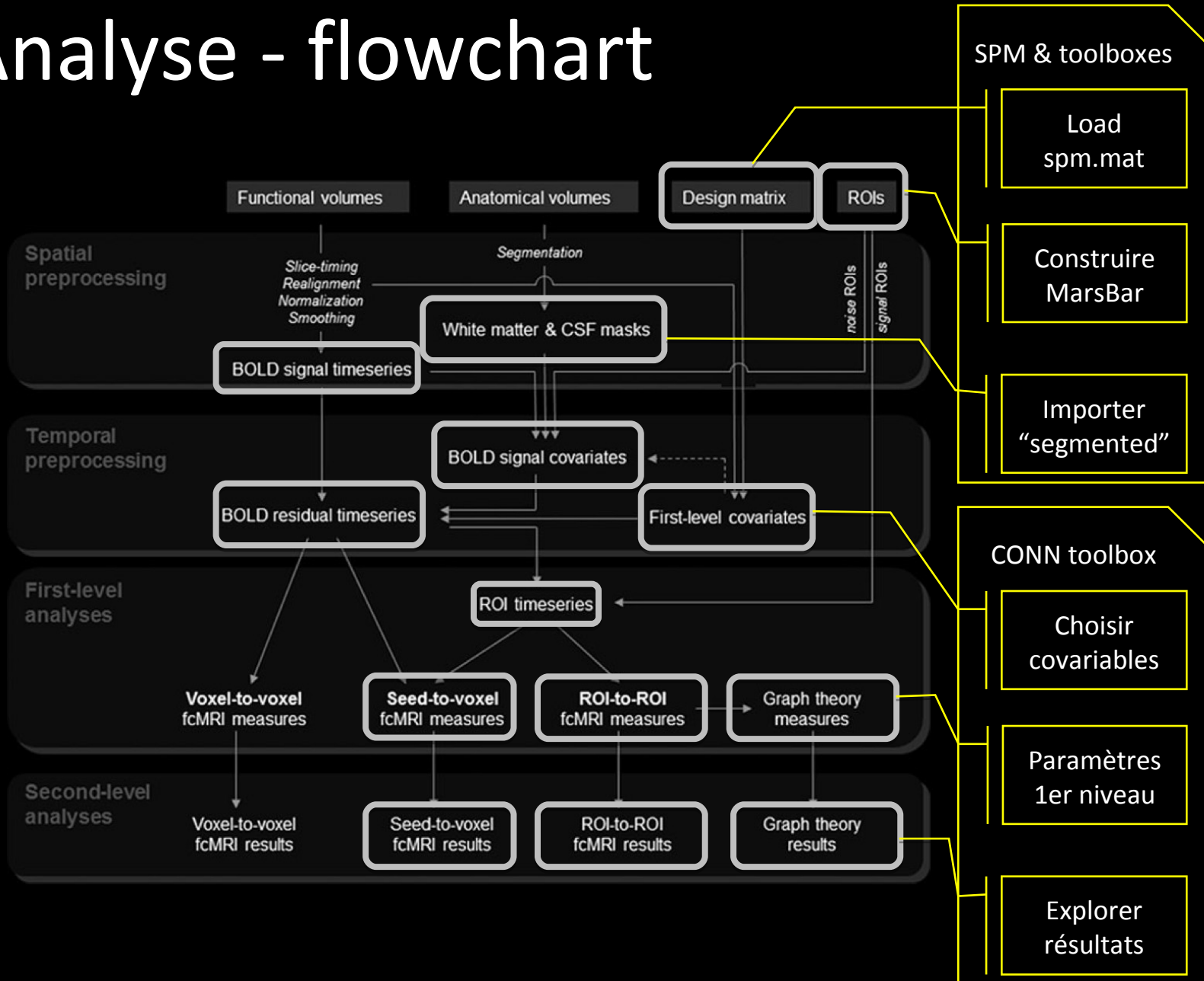
CONN toolbox

Analyse de connectivité

Connectivité fonctionnelle – Régions d'intérêt

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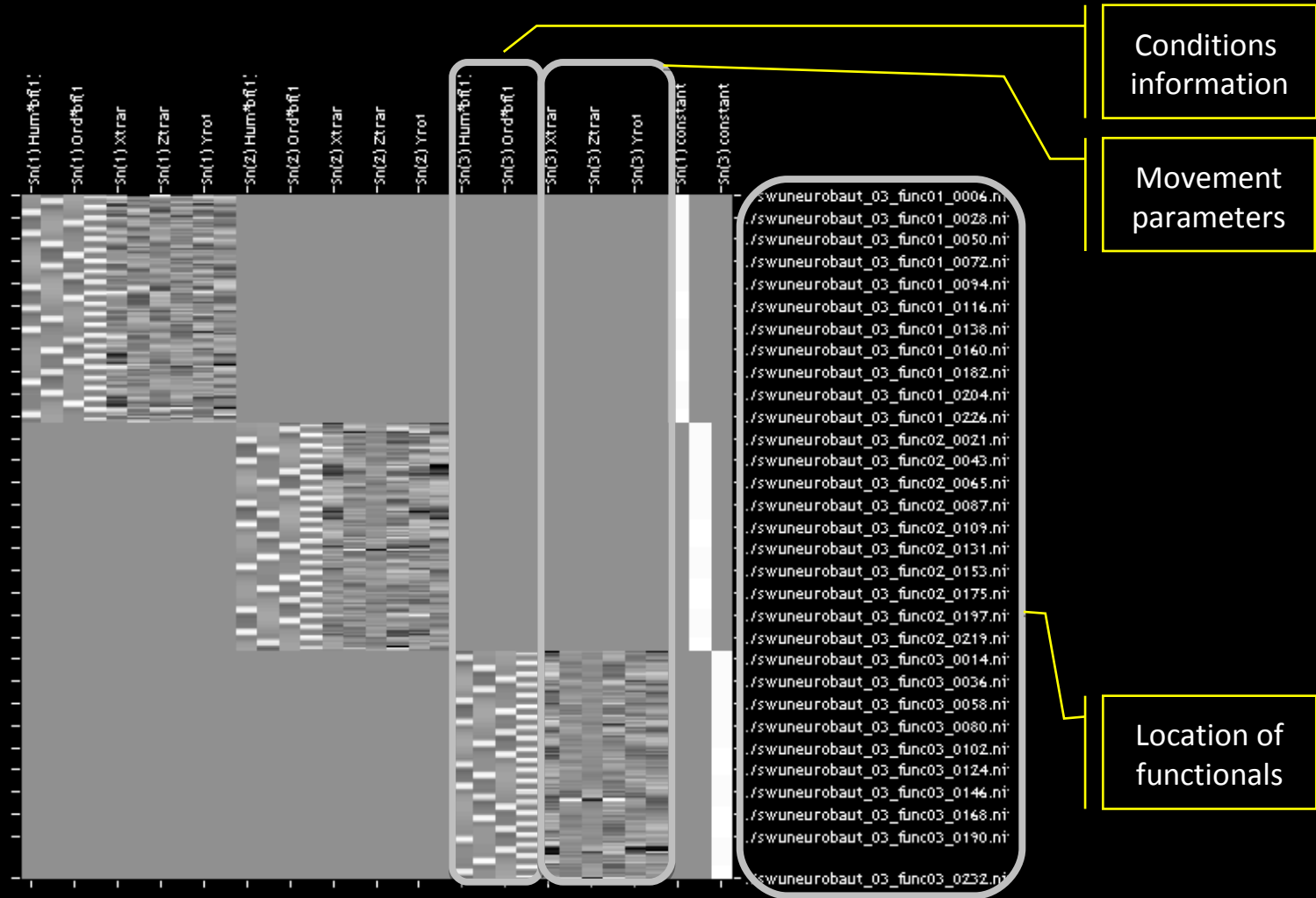
Analyse - flowchart



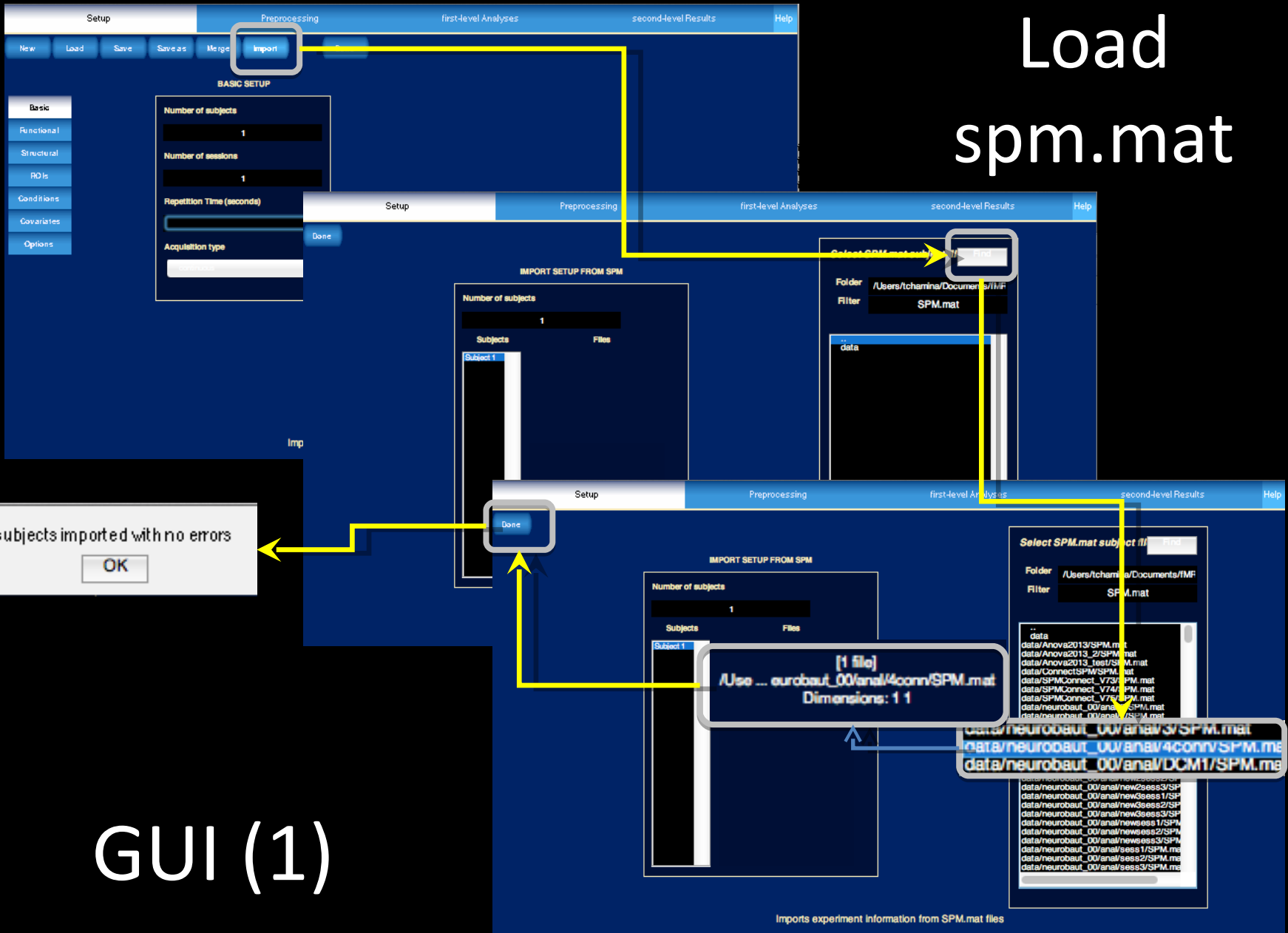
Utiliser spm.mat

- Utiliser spm.mat permet de rentrer
 1. Conditions onset and durations
 2. Movement covariates
 3. Location of preprocessed functional time-series
 4. Other within-subject covariates
- ① Obligation de mettre le mouvement en covariable
- ① spm.mat issus de scripts automatisés: le nom des conditions doit être exactement le même (casse et accents compris) entre les différents sujets
- ① il existe un problème avec certaines versions qd spm.mat stocke les fonctionelles 'swuaXXXXX.img,1'

Load spm.mat



Load spm.mat



GUI (1)

New Load Save Save as Merge Import Done

BASIC SETUP

Number of subjects: 1

Number of sessions: 3

Repetition Time (seconds): 2.4

Acquisition type: continuous

Basic
Functional
Structural
FDs
Conditions
Covariates
Options

FUNCTIONAL DATA SETUP

Subjects	Sessions	File
Subject 1	Session 1 Session 2 Session 3	[216 files] Firs ... wuneurobasf_00_func01_0006.nii Last ... wuneurobasf_00_func01_0221.nii Dimensions: 121 145 121

EXPERIMENTAL CONDITIONS SETUP

Conditions	Subjects	Sessions
Hum Rob Ord Vid	Subject 1	Session 1 Session 2 Session 3

condition name: Hum

onset: 27.56 77.584 202.829 252.753 3

duration: 15

Basic
Functional
Structural
FDs
Condition
Covariate
Options

FIRST-LEVEL COVARIATES SETUP

Covariates	Subjects	Sessions
SPM covari	Subject 1	Session 1

covariate name: SPM covariates

Files

Load spm.mat batch

BATCH.Setup.spmfiles

“Specifies the location of SPM.mat files (cell array, one file path per subject pointing to the subject-level SPM.mat file) from which the toolbox may extract the location of the functional volumes, design specification, as well as subject motion parameters.”

```
RootDir=('/Users/tchamina/Documents/fMRI_Studies/NeuRobAut/data/');
```

```
Cont=[0 1 2 3 6 8 10 12 14 22];
```

```
Aspi=[15 16 17 20 21 24 25 26 27 29];
```

```
batch.filename = [RootDir 'Conn_v1'];
```

```
batch.Setup.RT = 2.4;
```

```
batch.Setup.isnew=1;
```

```
batch.Setup.nsubjects=20;
```

```
for Sub=[Cont Aspi]
```

```
Spms{i}=fullfile(RootDir, ['neurobaut_' num2str(Sub,'%02.0f')'],'/analysis/', 'spm.mat');
```

```
end;
```

```
batch.Setup.spmfiles=spms;
```

Anatomies

- 2 possibilités
 - Soit entrer les anatomies, CONN fait la segmentation lui-même
 - Soit entrer les images segmentées WM/GM/CSF
- ① Dans tous les cas: les images anatomiques sont déjà “coregistered” avec la série fonctionnelle
- ① Ségmentation VBM8 meilleure que celle utilisée dans CONN
- ① Pour moi, aussi couplé avec DARTEL et les images anatomiques ne sont pas originales, mais “DARTELisées” ET ont été utilisées pour normaliser les fonctionnelles → très bon alignement anat/fonctionnel

Anatomies (GUI)

The screenshot displays the SPM12 GUI with the 'STRUCTURAL DATA SETUP' window. The 'Covariates' section is set to 'First level'. A file selection dialog is open, showing a list of anatomical files. A yellow arrow points from the selected file in the dialog to the 'Subjects' list in the main window.

STRUCTURAL DATA SETUP

Subjects	Files
Subject 1	[1 file] /Joo ... nat01/wneurobaut_01_anat01.nii Dimensions: 79 95 68

Select structural data files

Folder: NeuRobAut/data/Neurobaut_01/e
Filter: *.img; *.nii

- c1neurobaut_01_anat01.nii
- c1wneurobaut_01_anat01.nii
- c2neurobaut_01_anat01.nii
- c2wneurobaut_01_anat01.nii
- c3wneurobaut_01_anat01.nii
- ec2wneurobaut_01_anat01.nii
- ec3wneurobaut_01_anat01.nii
- ly_neurobaut_01_anat01.nii
- mneurobaut_01_anat01.nii
- neurobaut_01_anat01.nii
- rc1neurobaut_01_anat01.nii
- rc2neurobaut_01_anat01.nii
- rc1neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc2neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc3neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc4neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc5neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc6neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc7neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc8neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc9neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc10neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc11neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc12neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc13neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc14neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc15neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc16neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc17neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc18neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc19neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc20neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc21neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc22neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc23neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc24neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc25neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc26neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc27neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc28neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc29neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc30neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc31neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc32neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc33neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc34neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc35neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc36neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc37neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc38neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc39neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc40neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc41neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc42neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc43neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc44neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc45neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc46neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc47neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc48neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc49neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc50neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc51neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc52neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc53neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc54neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc55neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc56neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc57neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc58neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc59neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc60neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc61neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc62neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc63neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc64neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc65neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc66neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc67neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc68neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc69neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc70neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc71neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc72neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc73neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc74neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc75neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc76neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc77neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc78neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc79neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc80neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc81neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc82neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc83neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc84neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc85neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc86neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc87neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc88neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc89neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc90neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc91neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc92neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc93neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc94neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc95neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc96neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc97neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc98neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc99neurobaut_01_anat01_Neurobaut_01_anat01.nii
- rc100neurobaut_01_anat01_Neurobaut_01_anat01.nii

Defines first or second level covariates

Segmented anatomies (GUI)

The screenshot displays the 'ROI DATA SETUP' window. On the left is a vertical menu with options: Basic, Functional, Structural, **ROIs**, Conditions, Covariates, and Options. The main area is divided into three columns: ROIs, Subjects, and ROI name/dimensions. The 'ROIs' column lists 'Grey Matter', 'White Matter', 'CSF', and 'hypothalamus'. The 'Subjects' column lists 'Subject 1' through 'Subject 34'. The 'ROI name' column shows 'Grey Matter' and '1'. Below this, there are three checkboxes: 'multiple ROIs', 'mask with Grey Matter', and 'regress out covariates'. A 'Files' section shows '[1 file]' with the path '/Use ... EL/c1swneuroabout_00_anat01.nii' and dimensions '121 145 121'. A brain slice image is shown below the file list. A yellow arrow points from the 'ROIs' menu to the 'Grey Matter' ROI. Another yellow arrow points from the 'regress out covariates' checkbox to a file selection dialog on the right. The dialog shows 'Select ROI definition files', 'Folder: /Users/chamina/Documents/fmf', 'Filter: *.img; *.nii; *.tal', and a list containing 'data'.

- ① Reserved ROI names (“Grey Matter”, “White Matter”, “CSF”) (à vérifier)
- ① Regress out covariates: default “yes”, 16 dimensions for WM and CSF, “no” for GM

Load anatomies (batch)

BATCH.Setup.structurals

Description: Specifies the source anatomical volumes for connectivity analyses. This field contains a cell array ranging over each subject, where the BATCH.Setup.structural{nsup} element contains a char array pointing to the source anatomical volume for subject nsup.

```
j=1
for Sub=[Cont Aspi]
anats{j}=fullfile(RootDir, 'DARTEL', ['swneurobaut_' num2str(Sub,'%02.0f') '_anat01.nii']);
j=j+1
end;

batch.Setup.structurals = anats;
```

Load segmented anatomies (batch)

`BATCH.Setup.masks. [Grey/White/CSF]`

Each of these three fields is characterized as a structure with sub-fields `files` and `dimensions`, characterizing the Grey matter, White matter, and CSF masks, respectively, for each subject.

`BATCH.Setup.masks.[Grey/White/CSF].files`

This field contains a cell array ranging over each subject, where the `BATCH.Setup.masks.Grey.files{nsub}` element contains a char array pointing to the grey matter mask for subject `nsub` (typically a `c1.img` file obtained from segmentation of the anatomical volumes), the `BATCH.Setup.masks.White.files{nsub}` element contains a char array pointing to the white matter mask for subject `nsub` (typically a `c2*.img` file obtained from segmentation of the anatomical volumes), and the `BATCH.Setup.masks.CSF.files{nsub}` element contains a char array pointing to the CSF mask for subject `nsub` (typically a `c3*.img` file obtained from segmentation of the anatomical volumes).*

`BATCH.Setup.masks.[Grey/White/CSF].dimensions`

This field contains a single number specifying the number of component dimensions to extract from each mask area. By default the toolbox will extract 1 component (the mean BOLD signal) from the Grey matter area, and 16 components (PCA decomposition) from the White and CSF areas.

`BATCH.Setup.masks.Grey.files{1}='mypath/subject1/anatomical/c1foo.img';`

`BATCH.Setup.masks.Grey.files{2}='mypath/subject2/anatomical/c1foo.img';`

`BATCH.Setup.masks.Grey.dimensions=32;`

Load segmented anatomies (batch)

```
j=1
for Sub=[Cont Aspi]
grey{j}=fullfile(RootDir, 'DARTEL', ['c1swneurobaut_' num2str(Sub,'%02.0f') '_anat01.nii']);
white{j}=fullfile(RootDir, 'DARTEL', ['c2swneurobaut_' num2str(Sub,'%02.0f') '_anat01.nii']);
csf{j}=fullfile(RootDir, 'DARTEL', ['c3swneurobaut_' num2str(Sub,'%02.0f') '_anat01.nii']);
j=j+1;
end;
```

```
batch.Setup.masks.Grey.files = grey;
batch.Setup.masks.Grey.dimensions=1;
```

```
batch.Setup.masks.White.files = white;
batch.Setup.masks.White.dimensions=16;
```

```
batch.Setup.masks.CSF.files = csf;
batch.Setup.masks.CSF.dimensions=16;
```

ROIs

- Les ROI sont des images (analyze/niftii) dans le même espace soit binaire (1/0), soit avec plusieurs valeurs entières (e.g. la liste des aires de Brodmann fournie dans la distribution CONN)
- Pour ma part, ROIs contruites avec MarsBAR soit à partir du fonctionnel (“Get SPM clusters”), soit construites à partir de coordonnées MNI
- Possibilités d’avoir différentes ROI pour différents sujets (BW)

Load ROI (GUI)

The screenshot displays the 'ROI DATA SETUP' interface. On the left, a vertical menu contains options: Basic, Functional, Structural, **ROIs**, Conditions, Covariates, and Options. The main window is divided into several sections:

- ROIs:** A list of ROI categories including Grey Matter, White Matter, CSF, and hypothalamu.
- Subjects:** A list of subjects from Subject 1 to Subject 34. Subject 1 is highlighted.
- ROI name:** A text field containing 'hypothalamu'.
- dimensions:** A text field containing '1'.
- Options:** A group of checkboxes for 'multiple ROIs', 'mask with Grey Matter', and 'regress out covariates'.
- File:** A section showing '[1 file]' with the path '/Use ... uRobAut/data/Hypothalamus2.img' and dimensions '121 145 121'. A red circle highlights a small icon in this section.

Yellow arrows indicate the workflow: from the 'ROIs' menu to the 'hypothalamu' ROI, from 'Subject 1' to the 'ROI name' field, and from the 'File' section to a 'Select ROI definition files' dialog box. The dialog box shows the folder path '/Users/tchamina/Documents/IMF' and a filter '*.img; *.nii; *.tal'. A file named 'data' is visible in the file list.

Load ROI (batch)

BATCH.Setup.rois

Specifies the ROI files for connectivity analyses. If unset the toolbox will by default use all files in the rois directory.

BATCH.Setup.rois.names

This field contains a cell array ranging over each ROI, where the BATCH.Setup.rois.names{nroi} element contains a char array with the name of the ROI nroi.

BATCH.Setup.rois.files

This field contains a cell array ranging over each ROI, where the BATCH.Setup.rois.files{nroi} element contains a char array pointing to the ROI file for the nroi ROI.

Alternatively, if subject-specific ROIs are being used, the BATCH.Setup.rois.files{nroi}{nsub} element contains a char array pointing to the subject-specific ROI file for the nroi ROI for subject nsub.

BATCH.Setup.rois.dimensions

This field contains a cell array ranging over each ROI, where the BATCH.Setup.rois.dimensions{nroi} element contains an integer describing the number of component time-series to be extracted from each ROI. This value, if unspecified, defaults to the value of 1 for every ROI (where only the mean timeseries is extracted from each ROI).

BATCH.Setup.rois.names={'ROI1','ROI2'};

BATCH.Setup.rois.dimensions={1,1}

BATCH.Setup.rois.files{1}='mypath/rois/roifile1.img'

BATCH.Setup.rois.files{2}='mypath/rois/roifile2.img'

Load Roi (batch)

```
for Sub=[Cont Aspi]
ROIfiles=spm_select('list',char(fullfile(RootDir, , ['neurobaut_' num2str(Sub,'%02.0f')], 'ROI')), ['^.*\.nii$']);

    for i=1:size(ROIfiles,1)
        tmpname=regexp(ROIfiles(i,:),['_'],'split');
        ROInames{i}=char(strcat(tmpname(1), tmpname(2)));
        ROI dims{i}=1;
        ROIaddress{i}{Sub}=fullfile(RootDir, 'ROI', ROIfiles(i,:))
    end;

end;

batch.Setup.rois.names=ROInames;
batch.Setup.rois.dimensions=ROI dims;
batch.Setup.rois.files=ROIaddress;
```

- ① Dimensions=1 défaut, sinon chaque dim est indépendante (comme dérivées dans SPM)...
- ① Masquer avec GM: selon autres facteurs (ie type de structure, type de normalisation, taille ROI, qté de WM...)
- ① Regress out: Non (pour garder variation)

Fin du setup

- Second-level (between subjects) covariates

SECOND-LEVEL COVARIATES SETUP

Covariate

ctl	coveriate name
asp	
	ctl
	values
	11111111111111111111111111111111

`BATCH.Setup.subjects`

Specifies the second-level covariates (subject-level variables, such as behavioral or demographic measures as well as subject group definitions). Note that second-level covariates can be redundant as different subsets of second-level covariates can be used in different second-level analyses

`BATCH.Setup.subjects.effect_names`

The `BATCH.Setup.subjects.effect_names{ncovariate}` element contains a char array with the name of the second-level covariate `ncovariate`.

`BATCH.Setup.subjects.effects`

The `BATCH.Setup.subjects.effects{ncovariate}` element contains a column vector (with one element per subject) characterizing the second-level covariate `ncovariate`.

```
batch.Setup.subjects.effects{1} = [ones(1,30) zeros(1,30)]';  
batch.Setup.subjects.effects{2} = [zeros(1,30) ones(1,30)]';  
batch.Setup.subjects.effect_names = {'ctl', 'asp'};
```

Fin du setup (GUI)

PROCESSING OPTIONS SETUP

Planned analyses

- ROI-to-ROI
- Seed-to-Voxel
- Voxel-to-Voxel

Spatial resolution (voxel-level)

Same as functional

Analysis mask (voxel-level)

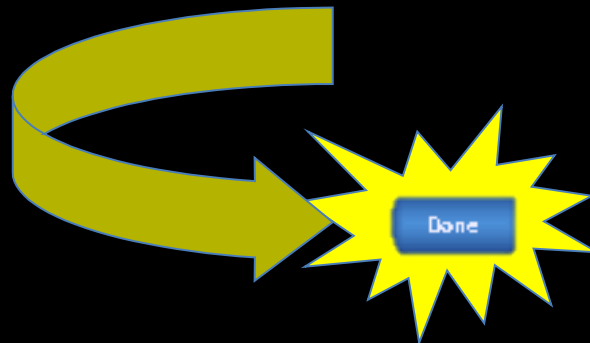
Explicit

Analysis units

% signal change

Optional output files

- Create confound effects beta-maps
- Create confound-corrected time-series
- Create first-level seed-to-voxel r-maps
- Create first-level seed-to-voxel p-maps
- Create first-level seed-to-voxel FDR-...



Fin du setup (Batch)

```
batch.filename = [RootDir 'Conn_XXX'];
```

```
batch.Setup.RT = 2.4;
```

```
batch.Setup.isnew=1 (or not!)
```

Définir tous les paramètres discutés précédemment: spm.mat, anat, GM/WM/CSF, ROIs

```
batch.Setup.analyses = [1 2];
```

1 for ROI-to-ROI analyses, 2 for seed-to-voxel analyses, and 3 for voxel-to-voxel analyses

```
batch.Setup.voxelmask = 1;
```

1 for using a fixed template mask (brainmask.nii), or 2 for using a subject-specific analysis mask

```
batch.Setup.voxelresolution = 2;
```

1 for using a fixed template resolution (with 2mm isotropic voxels), 2 for using the same resolution/registration as the structural volumes, or 3 for using the same resolution/registration as the functional volumes.

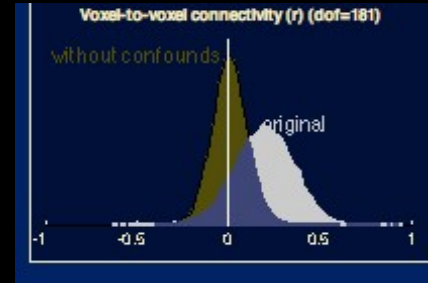
```
batch.Setup.outputfiles=[0,0,0];
```

```
batch.Setup.done=1;
```

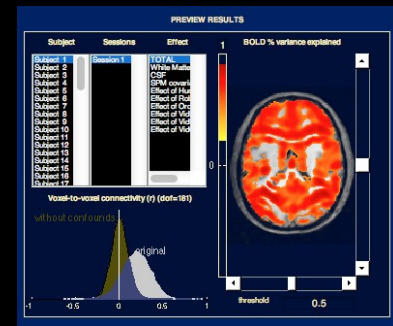
```
conn_batch(batch)
```

Preprocessing

- Choix perso:
 - Mêmes setup pour tous les sujets (ie pas adapté en fonction de →)
 - Pas de dérivées (sauf éventuellement pour mvt)
 - Effets principaux (1 dimension) pour
 - Conditions
 - GM
 - Mvt,
 - WM, CSF: 5 dimensions (empirique!!!)
 - Filtre passe-bande: en général par défaut, mais à rectifier dans le cas d'événement très long en particulier?)
 - ① Lorsqu'on a déjà vérifié le nettoyage des données en fonction des confound (J-L A) et choisit ses valeurs, on peut sauter l'étape *preprocessing* dans la GUI



Preprocessing (batch)



Définir les confound

```
batch.Preprocessing.confounds.names = {'White Matter','Grey Matter','CSF','motion','Condition'};
```

```
batch.Preprocessing.confounds.dimensions={5,1,5,6,1};
```

```
batch.Preprocessing.confounds.deriv={0,0,0,1,0};
```

Filtre passe-bande

```
batch.Preprocessing.filter=[.01,.1];
```

BATCH.Preprocessing.done

1/0 variable specifying whether to run the data preprocessing steps (the steps performed in the gui when pressing 'Done' on the 'Preprocessing' window). These steps include: a) removal of confounding effects from the BOLD signal at each voxel and for each ROI; and b) frequency filtering of the residual BOLD signal.

```
batch.Preprocessing.done=1;
```

```
batch.Preprocessing.overwrite='Yes';
```

```
conn_batch(batch);
```

1st level analysis (GUI)

The screenshot displays the SPM12 software interface for first-level analysis, specifically the 'GLM CONNECTIVITY - DEFINE SOURCES' and 'PREVIEW RESULTS' sections.

GLM CONNECTIVITY - DEFINE SOURCES

- Measure:** Regression
- Weights:** HRF
- Analysis:** all
- derivatives order:** 0
- dimensions:** 1
- Sources:** Two columns labeled 'hypo' and 'hypo' are shown, each with a vertical bar representing a source. A double-headed arrow indicates a relationship between them.
- Graph:** A line graph showing a green signal fluctuating around a red horizontal line at 0, with a y-axis ranging from -1.5 to 1.

PREVIEW RESULTS

- Subject List:**

Subject	Conditions	Sources
Subject 1	Hum	TOTAL
Subject 2	Rob	hypo
Subject 3	Ord	
Subject 4	Vid-Hum	
Subject 5	Vid-Rob	
Subject 6	VidOrd	
Subject 7		
Subject 8		
Subject 9		
Subject 10		
Subject 11		
Subject 12		
Subject 13		
Subject 14		
Subject 15		
Subject 16		
Subject 17		
Subject 18		
Subject 19		
Subject 20		
Subject 21		
Subject 22		
Subject 23		
Subject 24		
Subject 25		
Subject 26		
Subject 27		
Subject 28		
- Connectivity Map:** A brain slice showing connectivity values. A color scale on the left ranges from 0 (blue) to 1 (red). A threshold of 0.5 is indicated at the bottom.

Util pour vérifier processing → self-connectivity

1st level analysis (batch)

```
batch.Analysis.sources.names={'hypothalamus'};  
batch.Analysis.sources.dimensions={1}; la quantité de dimensions par ROI dépend de batch.Setup.rois.dimensions  
batch.Analysis.sources.deriv={0};
```

```
batch.Analysis.measure =3
```

- 1 – Correlation (bivariate) [default]
- 2 – Correlation (semipartial)
- 3 – Regression (bivariate)
- 4 – Regression (multivariate)

```
batch.Analysis.weight =2
```

- 1 – none
- 2 – hrf [default]
- 3 – hanning

```
batch.Analysis.type = 3;
```

Specifies the type of analyses to be performed . Use 1 for ROI-to-ROI analysis, 2 for seed-to-voxel analyses, or 3 for both ROI-to-ROI and seed-to-voxel analyses.

① Pas le même code que batch.setup.analyses

```
batch.Analysis.done=1;
```

```
batch.Analysis.override='Yes';
```

```
conn_batch(batch);
```

Identique à preprocessing (faire l'analyse, overwrite, et run batch).