A (quick) introduction to Magnetic Resonance Imagery (MRI) preprocessing and analysis

Stephen Larroque
Coma Science Group, GIGA research
University of Liège

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Outline

- MRI preprocessing with SPM (long!)
- VBM analysis
- Functional MRI analysis with CONN
- Graph Theory analysis,
  by Rajanikant Panda
- Diffusion MRI (DTI),
  by Stephen Larroque
- Parcellation and Freesurfer,
  by Jitka Annen

MRI modalities

- 3 main types of MRI:

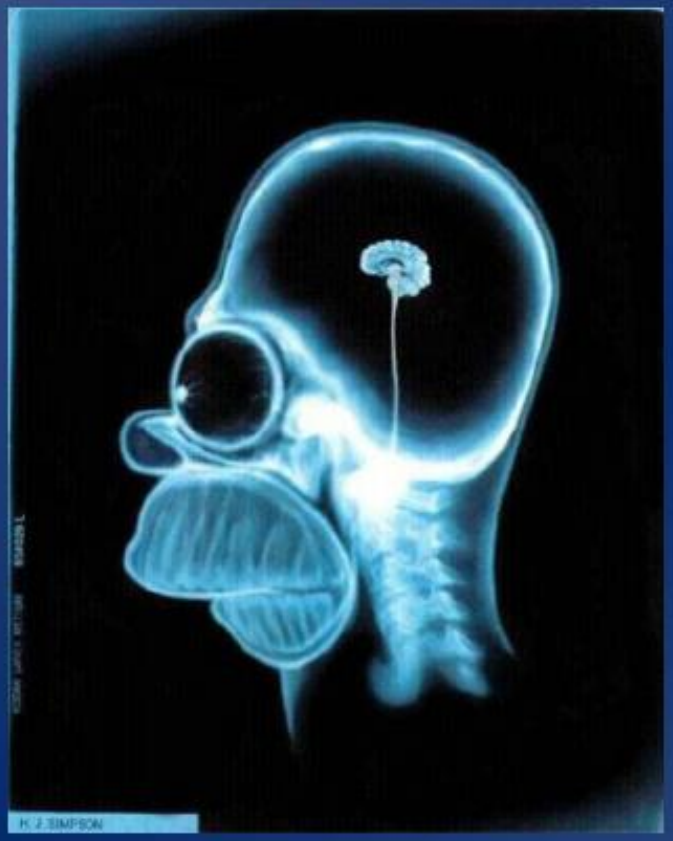
1. Structural (T1) = **structure** of grey and white matters

2. Functional (T2 or EPI) = ***functional* connectivity**

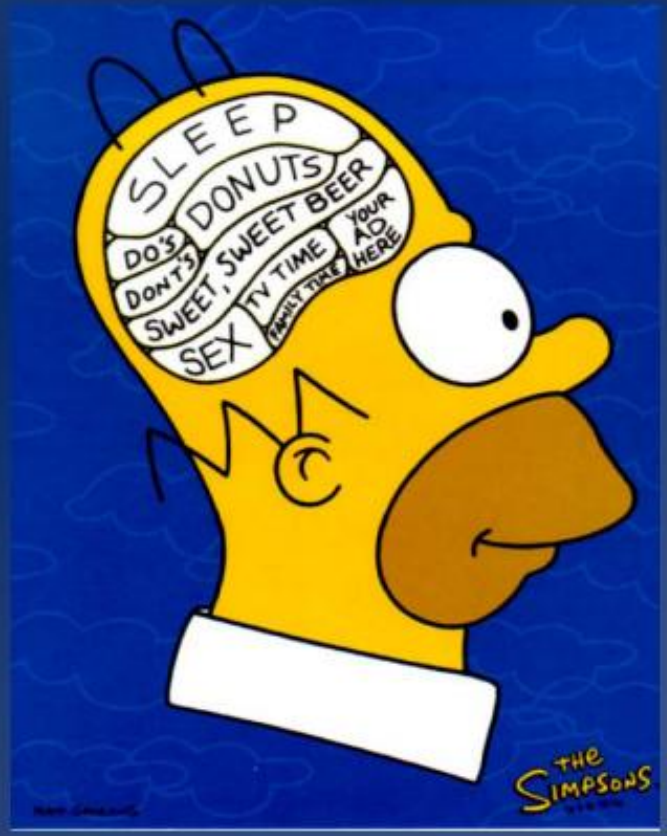
3. Diffusion (DTI/DWI) = ***structural* connectivity**

MRI vs fMRI

MRI studies brain anatomy



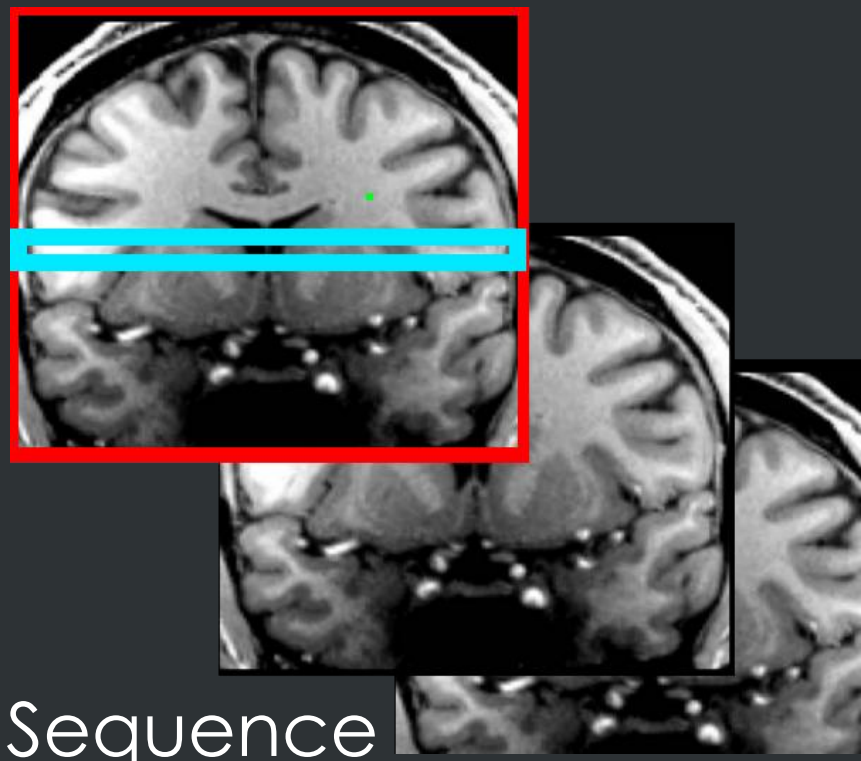
Functional MRI (fMRI) studies brain function



From Christophe Phillips course

Nomenclatura

- Sequence = multiple volumes of same brain
- **Volume** = one image of brain
- **Slice** = one plane slice of one volume
- **Voxel** = 3D pixel

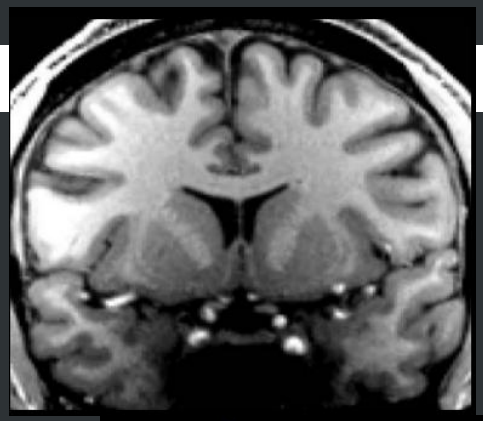


→Voxel < Slice < Volume < Sequence

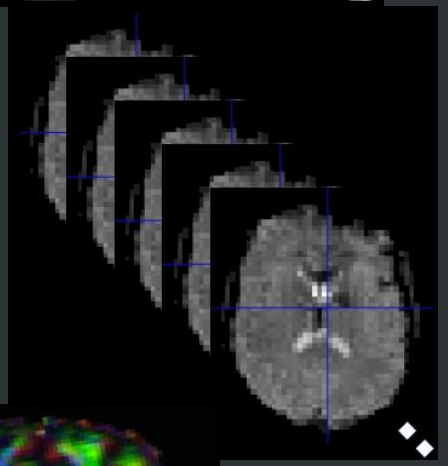
MRI modalities

- 3 types of MRI:

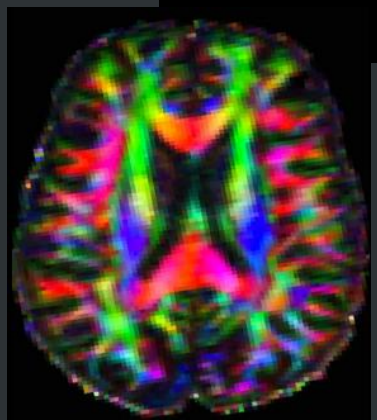
1. Structural (T1) = **1** volume **high-resolution**



2. Functional (T2 or EPI) = sequence of volumes (low-res)

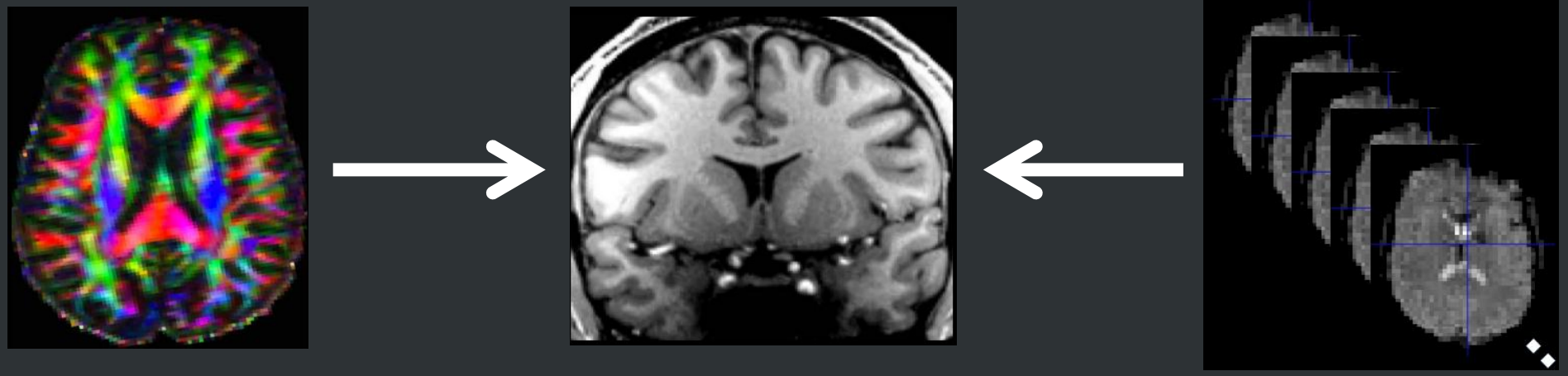


3. Diffusion (DTI/DWI) = 1 volume but with lots of vectors
   (ie, as if there were cameras all around the subject shooting all at once)



MRI modalities: T1 always needed

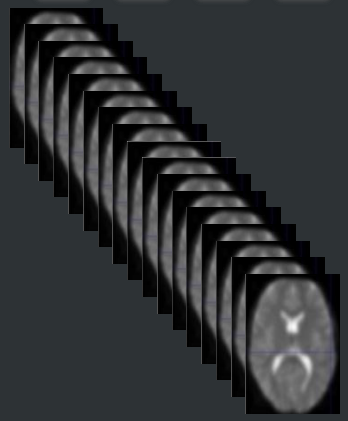
- fMRI and dMRI are **too low resolution** to do anything.
- Solution: **use T1 as a reference** = (intra-subject) **coregistration**

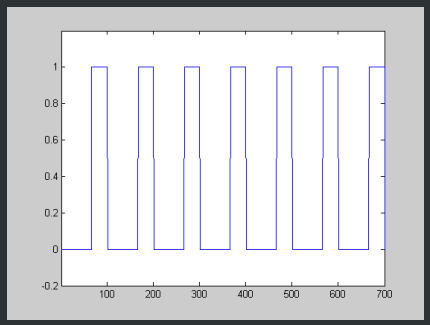


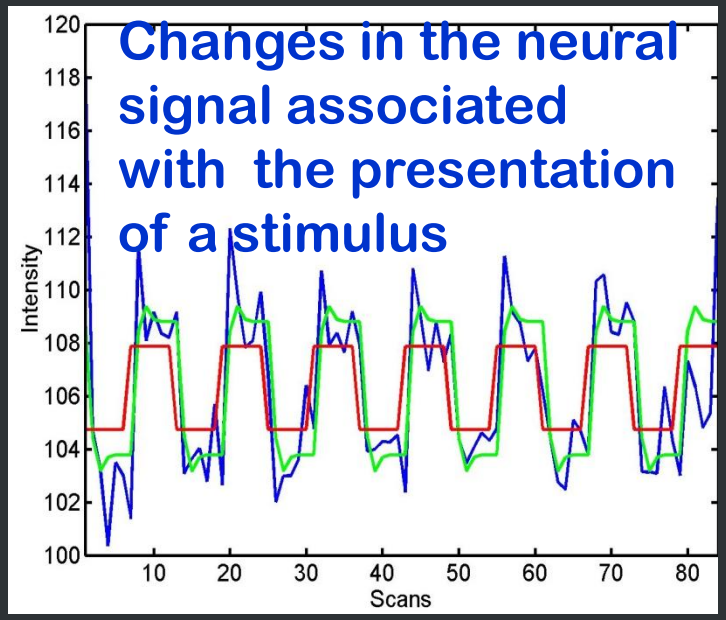
About SPM

- SPM = Statistical Parametric Modelling
- Both a software and a methodology
- Freely downloadable from www.fil.ion.ucl.ac.uk/spm/
- See also documentations, articles and (video) tutorials
- We use SPM for MRI preprocessing (but can also do analysis)
- Alternatives: FSL, AFNI, BrainVoyager, Broccoli, etc.

SPM model for functional MRI

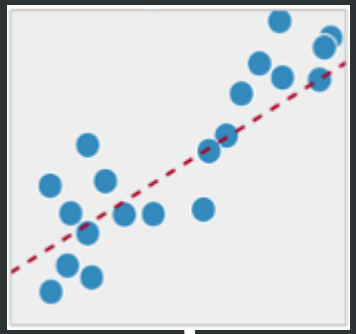






Design matrix

Generalized Linear Model

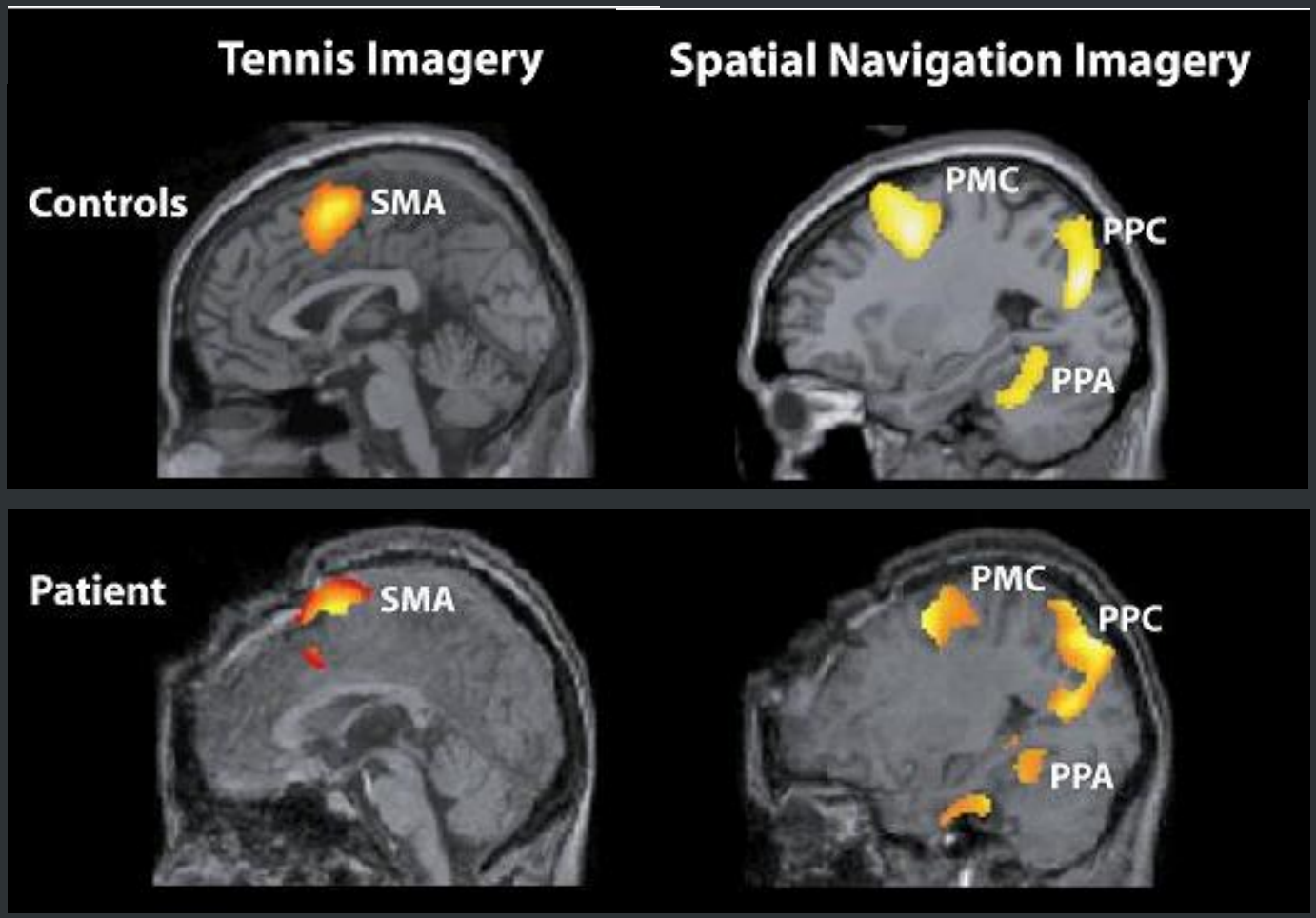


$$Y = X \times \beta + \varepsilon$$

Model and predictions!

Adapted from "Methods for dummies 2011-12"
Hikaru Tsujimura and Hsuan-Chen Wu

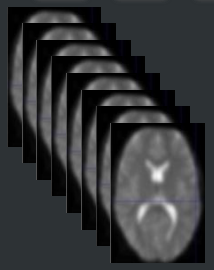
Result of SPM

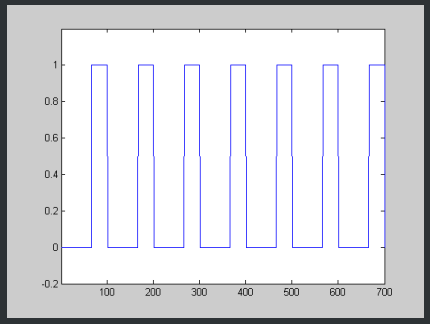


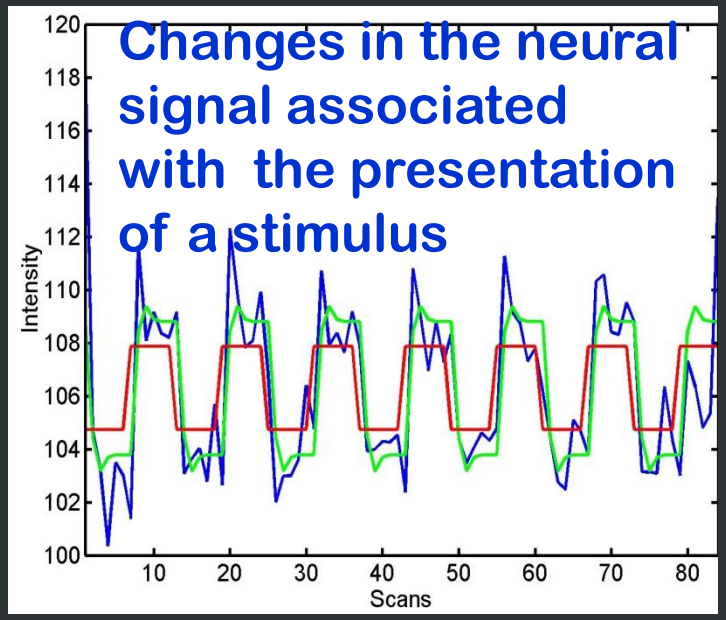
Boly et al, NeuroImage 2007

Owen, Coleman, Boly, Davis, Laureys and Pickard, Science, 2006

SPM model for functional MRI







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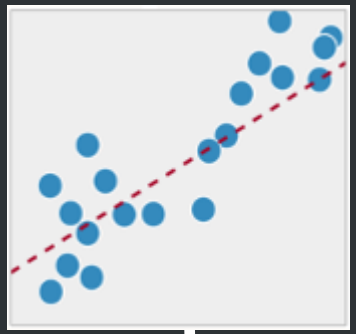

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Model and predictions!

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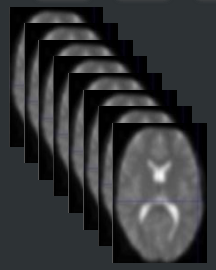
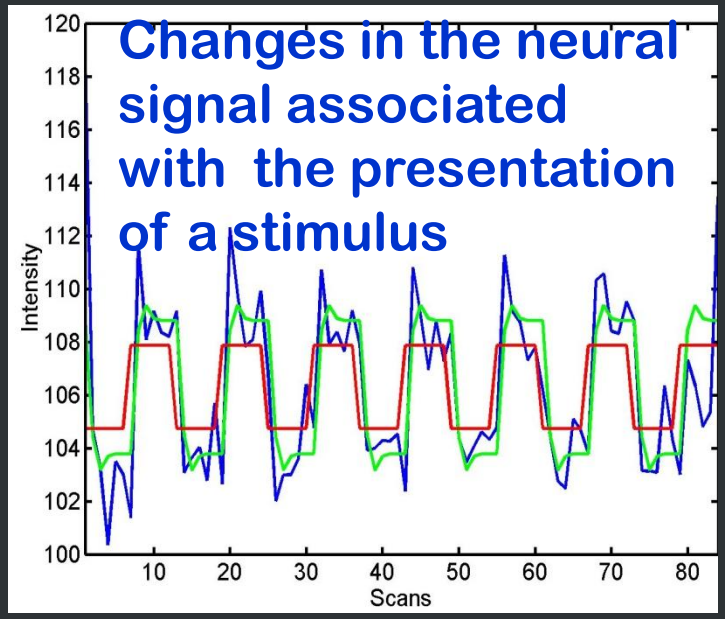
SPM model for functional MRI

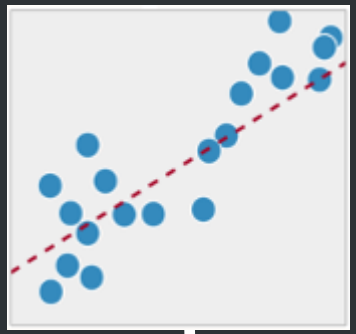


PRE-PROCESSING!



Design matrix

Generalized Linear Model



$$Y = X \times \beta + \varepsilon$$

Model and predictions!

Adapted from "Methods for dummies 2011-12"
Hikaru Tsujimura and Hsuan-Chen Wu

SPM Preprocessing

- Convert from DICOM to NIfTI
- Exclude bad subjects (too much motion, artifacts, brain surgery, metallic prosthesis, etc)
- T1 reorient
- EPI & DTI manual coregistration

Manual preproc

- Slice timing correction
- Realignment (motion correction)
- Auto coregistration
- Segmentation + Normalization (MNI 152)
- Smoothing
- Movement correction/rejection
- aCompCorr

Auto Preproc (parameters MUST be identical for all subjects of 1 experiment)

Manual Preprocessing

- Why? Automatic reorientation and coregistration are **convex** problems →Multiple **local optimums**
- In practice: if brain is upside-down or difficult to read, automatic algorithms will fail (but without any error! You just **get false results**…)
- **Solution: Manually reorient** and **coregister**, then use automatic coregistering
- Technically, this provides a better starting point for algorithms to explore the solutions landscape (because these algos are sensitive to initialization)

Manual Preprocessing - Tips

- Cumbersome, but can be done as the **very first step** (thus you don't lose time waiting for automatic steps to compute)
- **Keep** the manually preprocessed nifti files, you can **reuse** for another analysis!

DICOM vs NIfTI

- DICOM = **medical format**, contains all sequences + patient's medical records
- Generated automatically by MRI scanner
- DICOM is old, cumbersome and not shareable. Not standard fields (each scanner produce different fields, volumes have different encoding and orientations, etc)
- NIfTI newer format for **neuroimagery processing** with a **standard** format (somewhat)
- NIfTI contains ONLY volumes, not patient's records

→With NIfTI, you need **demographics** (age, gender, left handedness, etc)

DICOM vs NIfTI - 2

- Shortcomings: NIfTI strips too much info!
- DICOM → NIfTI always possible, but NIfTI →DICOM often impossible
- **An error in conversion is unrecoverable without DICOM**
- See https://openfmri.org/dataset-orientation-issues/
- Another example: MRIConvert will round DTI gradients values, so bad results. Prefer mrconvert from MRTRIX3.

From DICOM to NIfTI

- There are two NIfTI formats: **3D** (1 .nii file **per volume**) or **4D** (1 .nii file **per sequence**). They are equivalent.
- Use **MRConvert** or dcm2niix for structural and fMRI
- Use MRTRIX3 mrconvert for DTI (can also be used for structural and functional)
- Or use SPM (but does not support DTI)

Exclude bad subjects

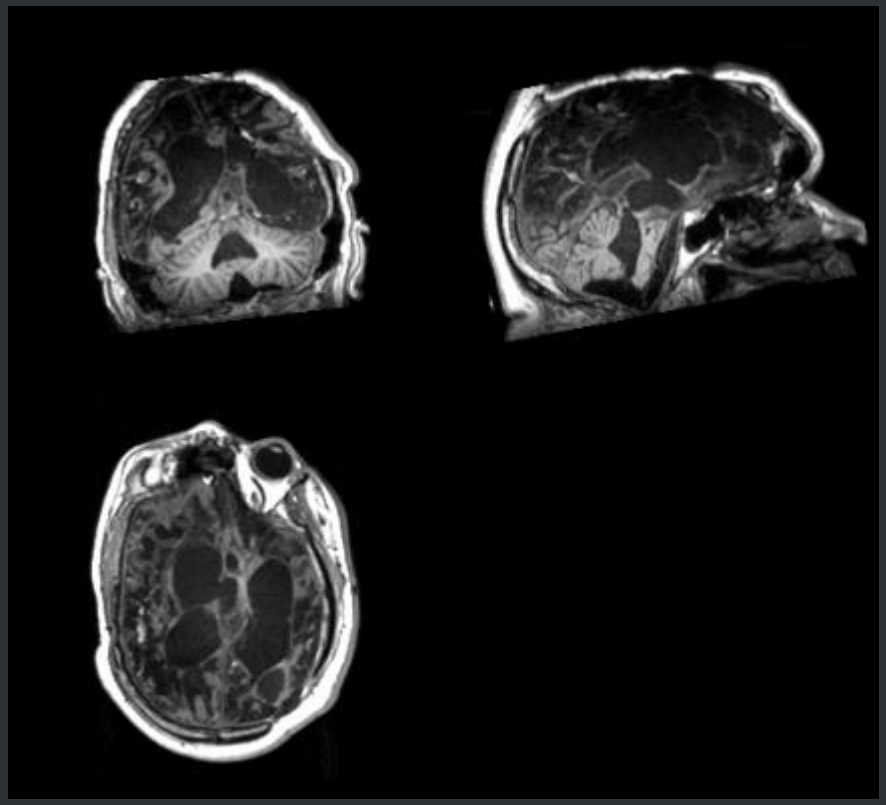
Rejection is CRITICAL: defines what you will get. If you don't reject, you will get false or no results. This cannot be automated.

Criteria of rejection:

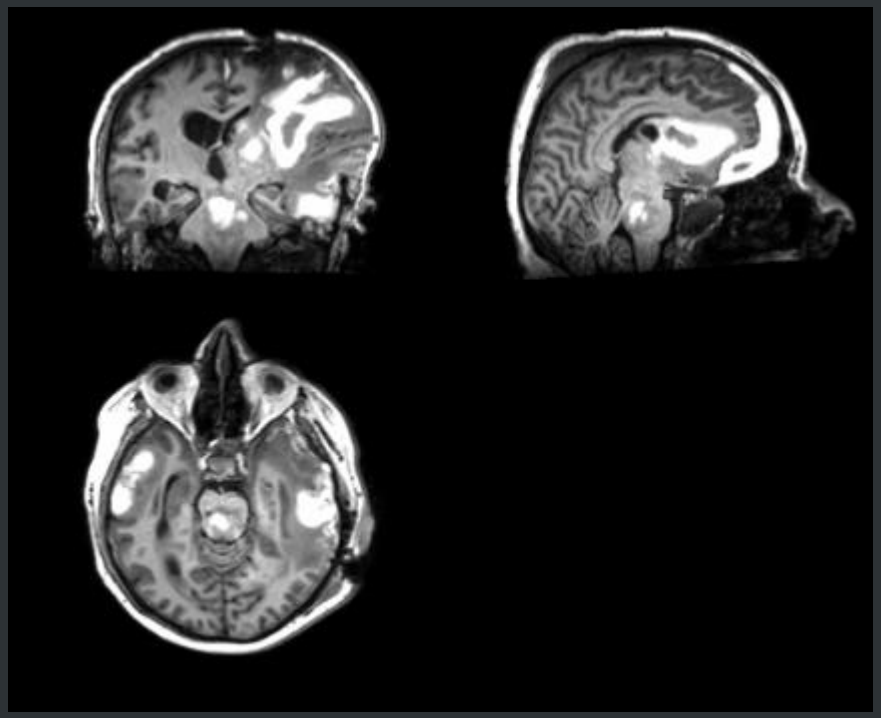
- Demographics (underage, overage, only representant of one gender, sedation, etc.)
- Bad volumes (metal implants, acquisition artifacts due to motion, too different brain, too much damage, …)
- Bad segmentation (after preprocessing)
- Too much movements (might show activity where there's none!) – use ART results with LRQ3000/movvis.m

Exclude bad subjects

Bad volumes (T1 here but check also functional and DTI)



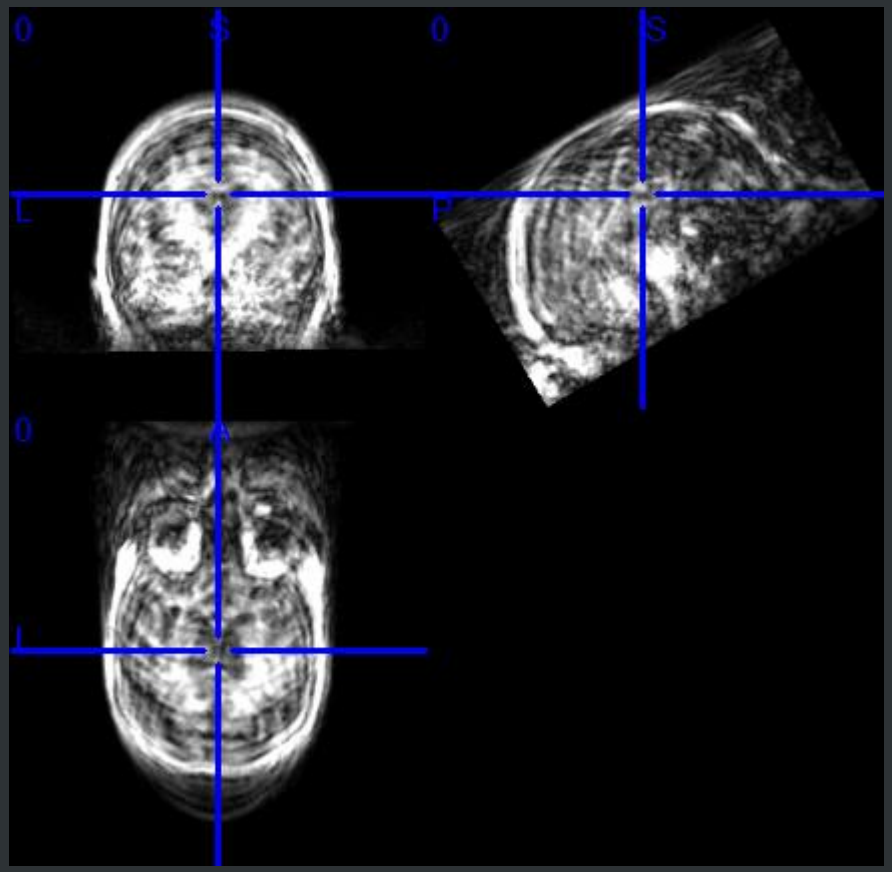
Too much damages,
Will be too different from other brains



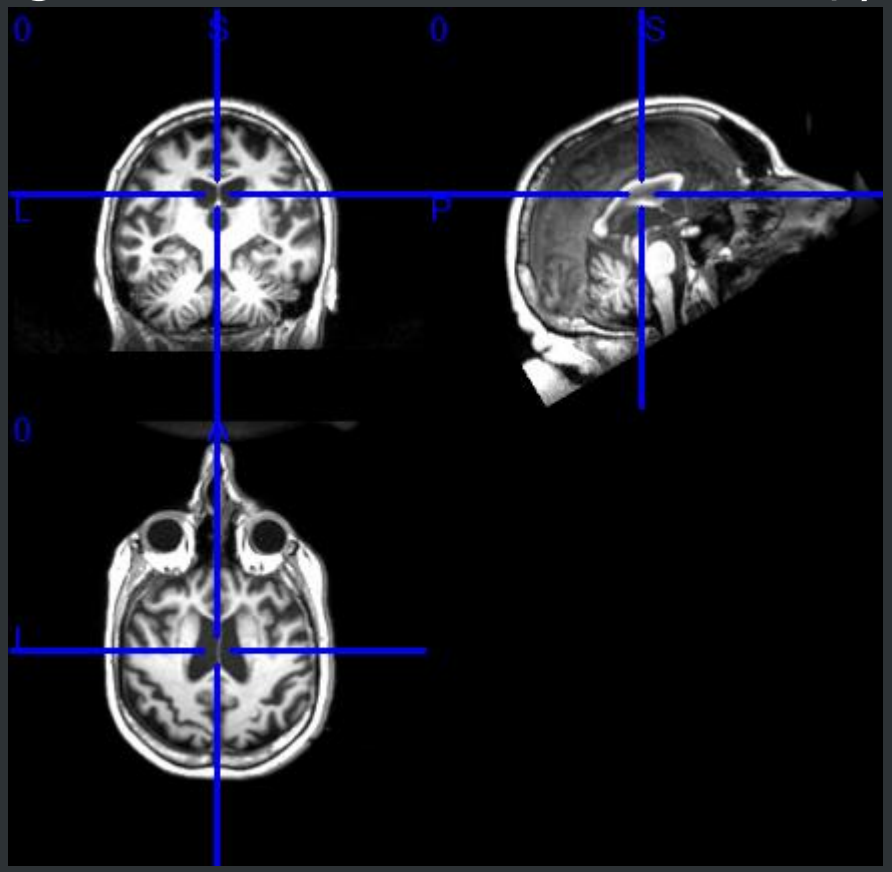
Metal implants makes MRI go crazy

Exclude bad subjects

If multiple sequences, use the latest/best one (but might be sedated – sedation changes functional connectivity)



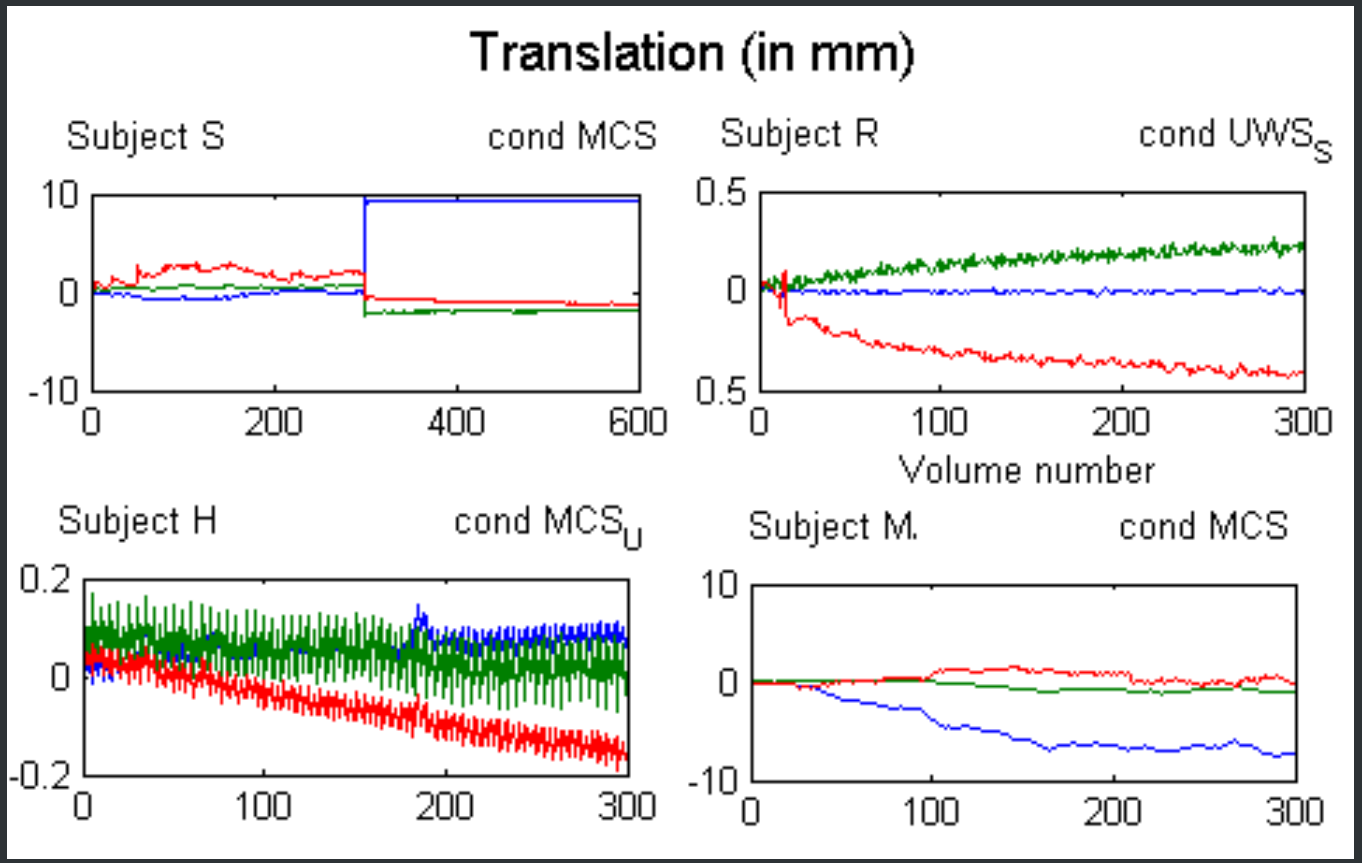
1st scan, patient moved



2nd scan, patient sedated

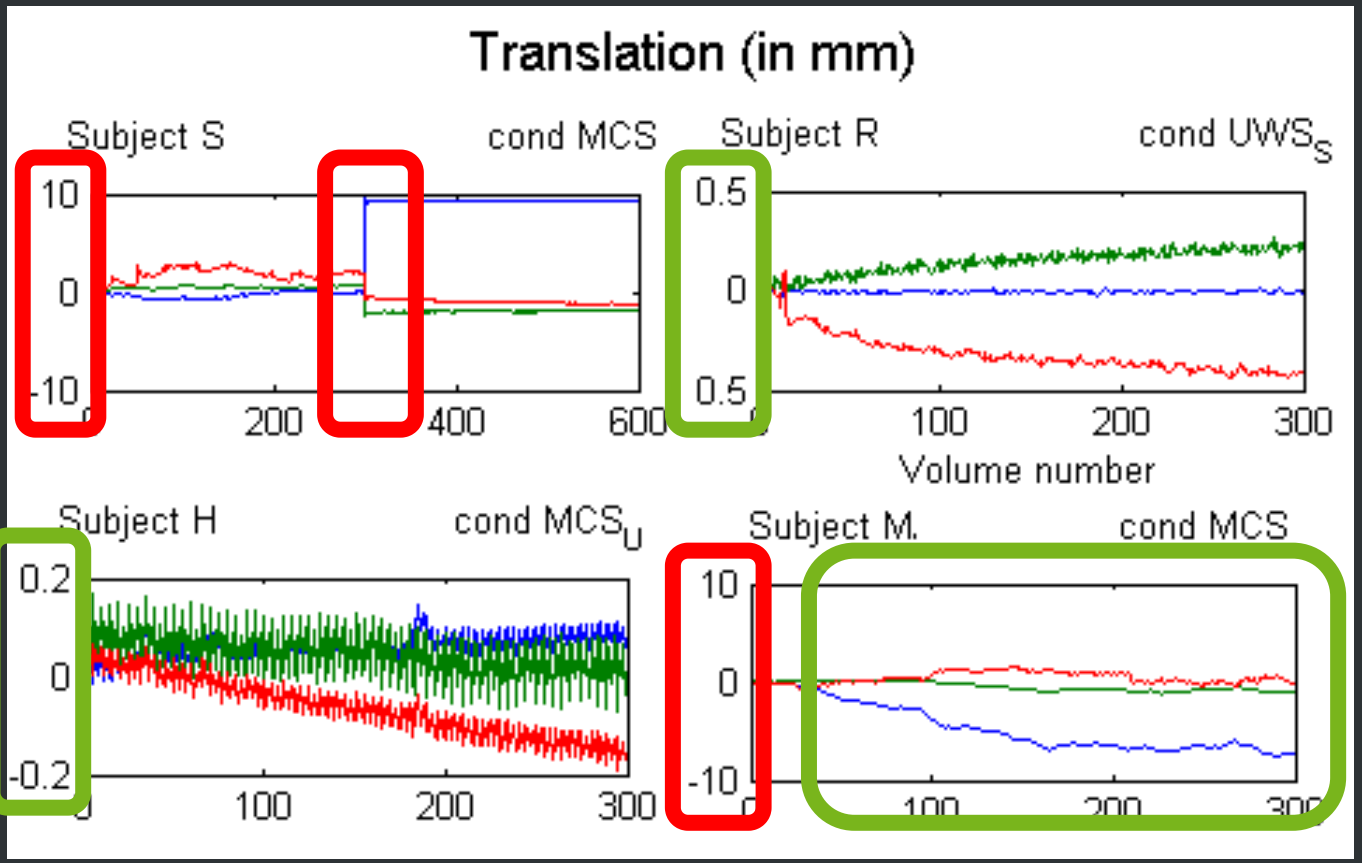
Exclude bad subjects

Too much movement



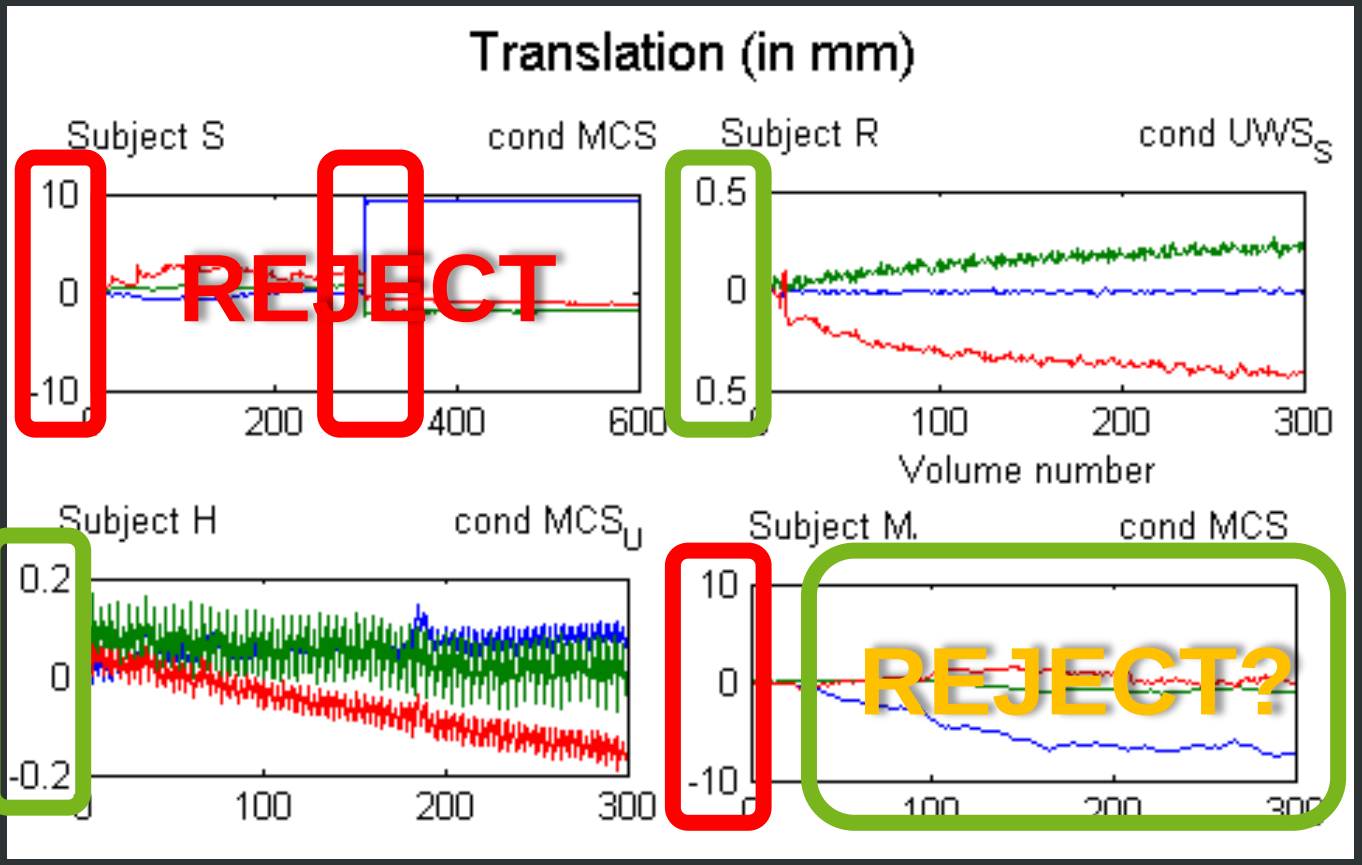
Exclude bad subjects

Too much movement



Exclude bad subjects

Too much movement



SPM Preprocessing

- Convert from DICOM to NIfTI
- Exclude bad subjects (too much motion, artifacts, brain surgery, metallic prosthesis, etc)
- **T1 reorient** ← we are here
- EPI & DTI manual coregistration

Manual preproc

- Slice timing correction
- Realignment (motion correction)
- Auto coregistration
- Segmentation + Normalization (MNI 152)
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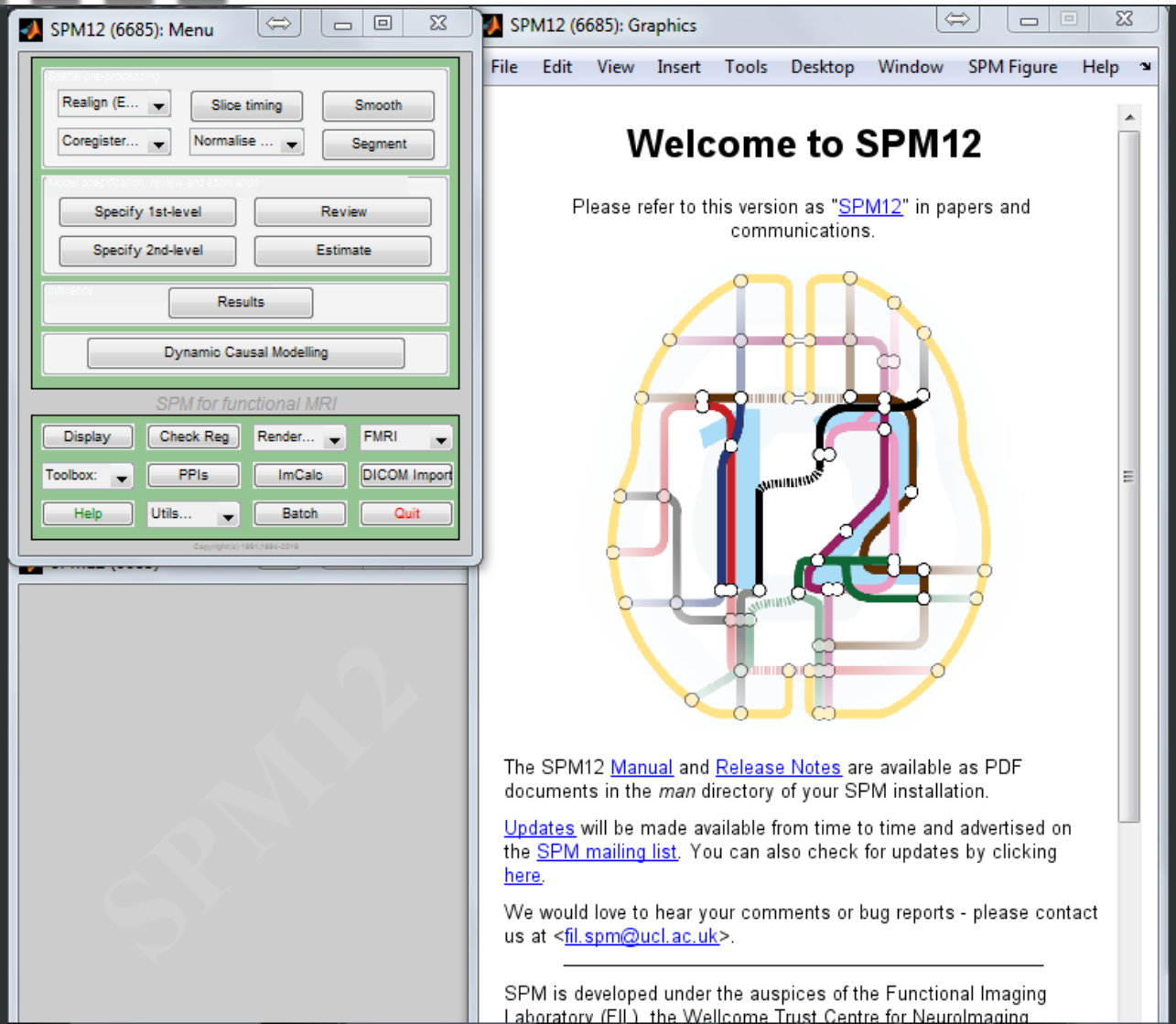
Auto Preproc (parameters MUST be identical for all subjects of 1 experiment)

SPM interface

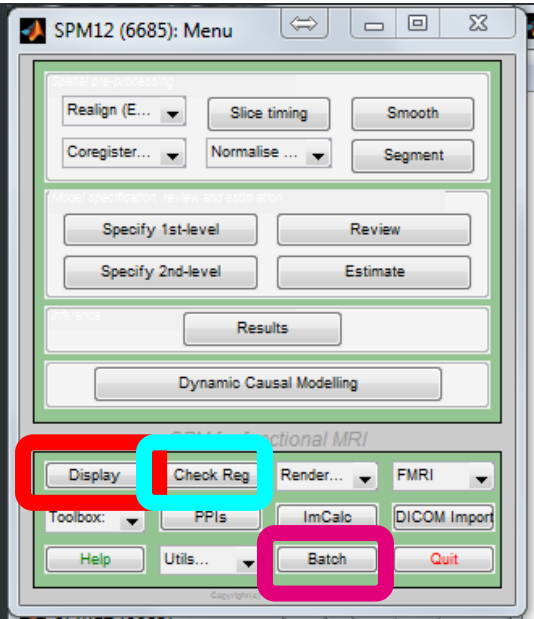


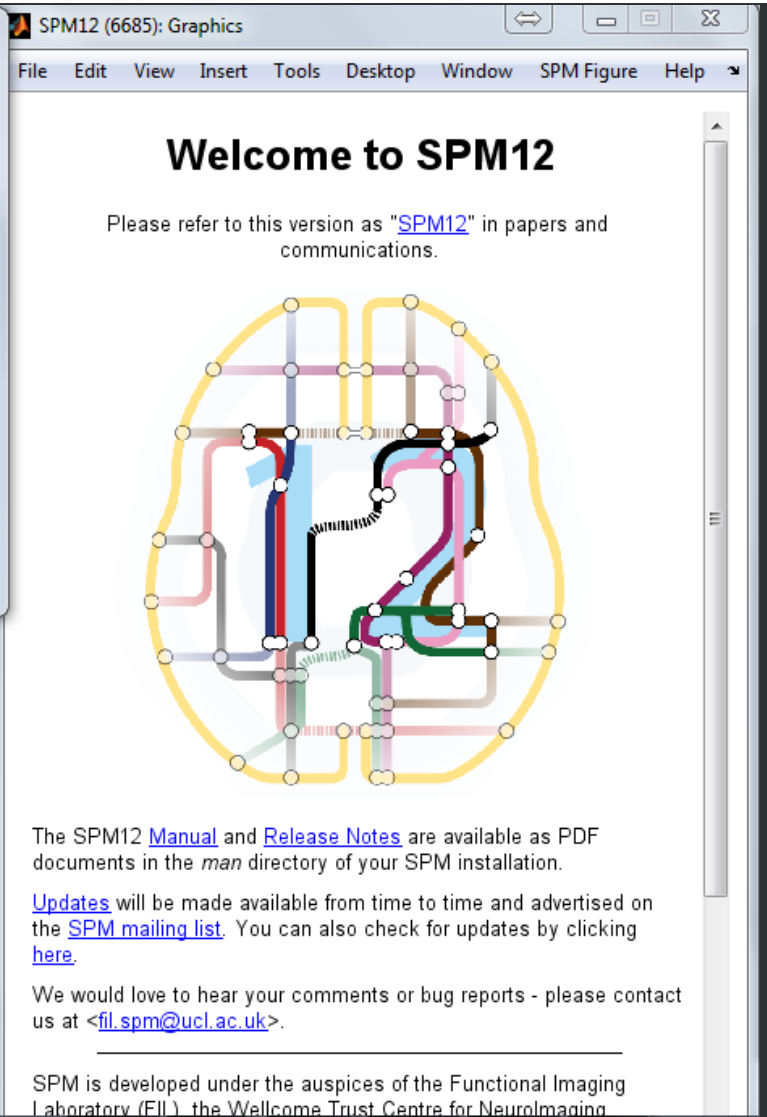
SPM interface

- Display: T1 reorient
- Check Reg: Manual coregistration
- Batch: all the rest

Processing progress: here → and in console

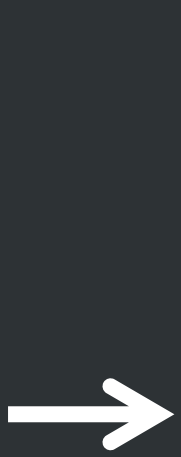
Also **check console** for **detailed errors!**

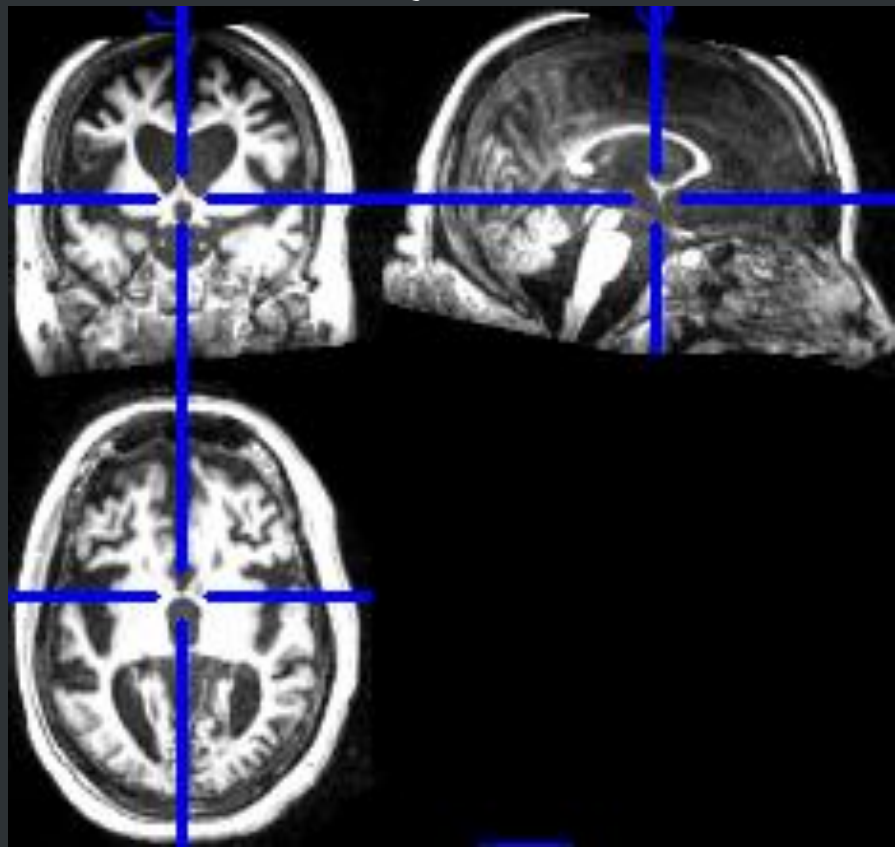




T1 reorient - 1

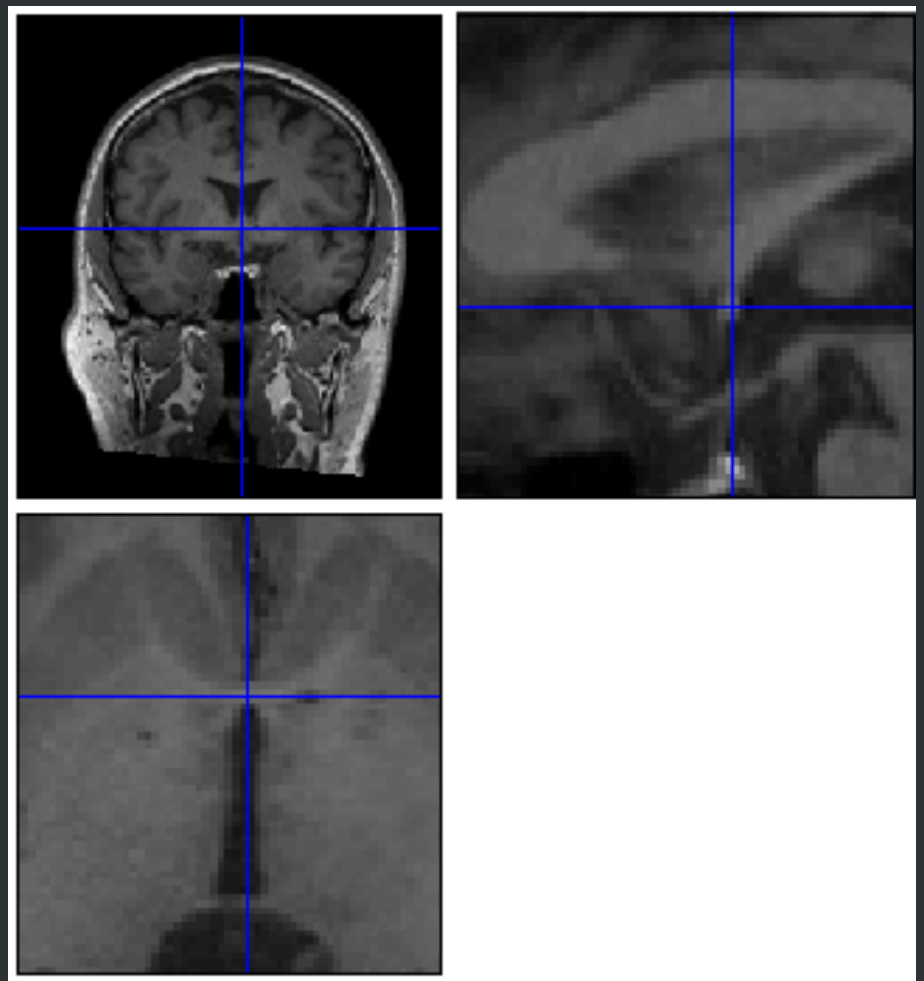
- Why? To help intra and inter-subjects comparison/co-registration.
- Provide a standard orientation for all subjects





T1 reorient - 2

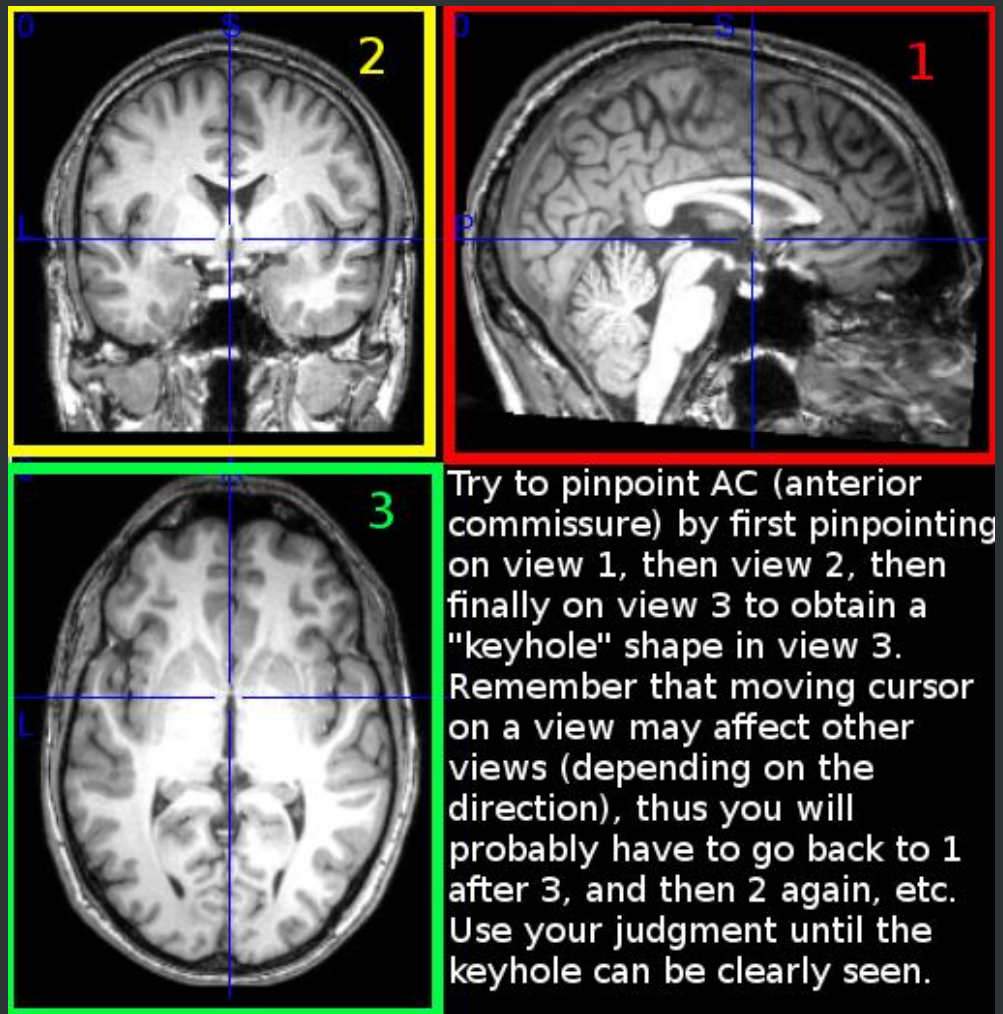
- Our method: internal reference point **AC-PC alignment**



Estimated time:
< 3 min per subject

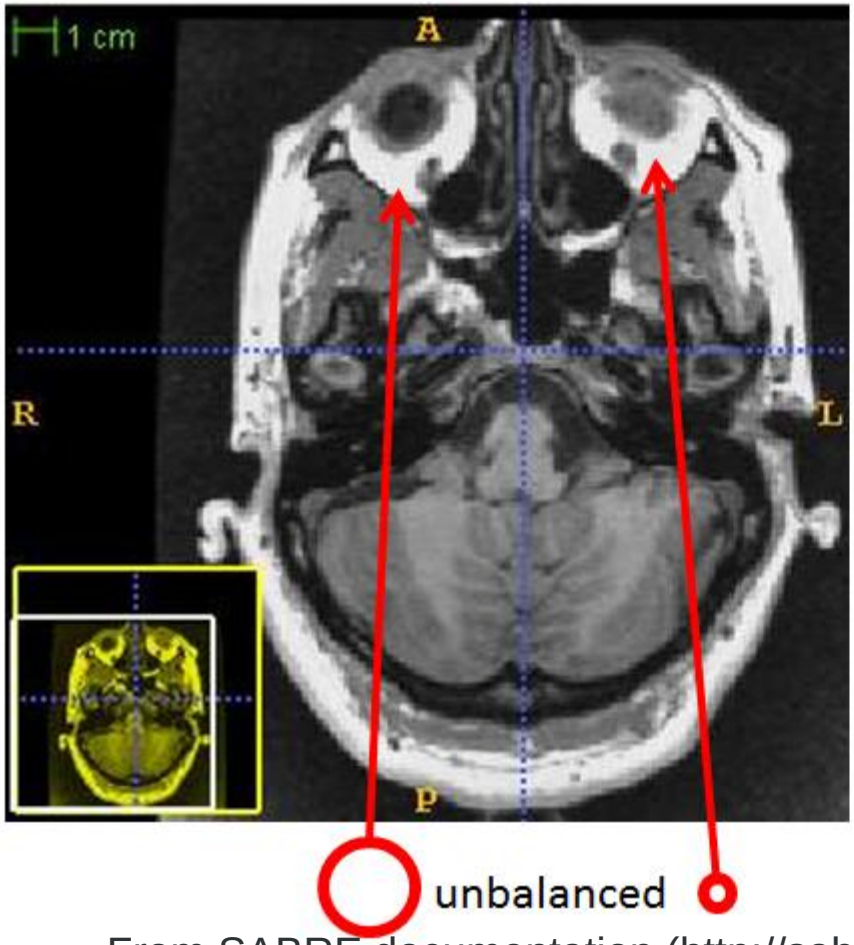
T1 reorient – Recipe - 1

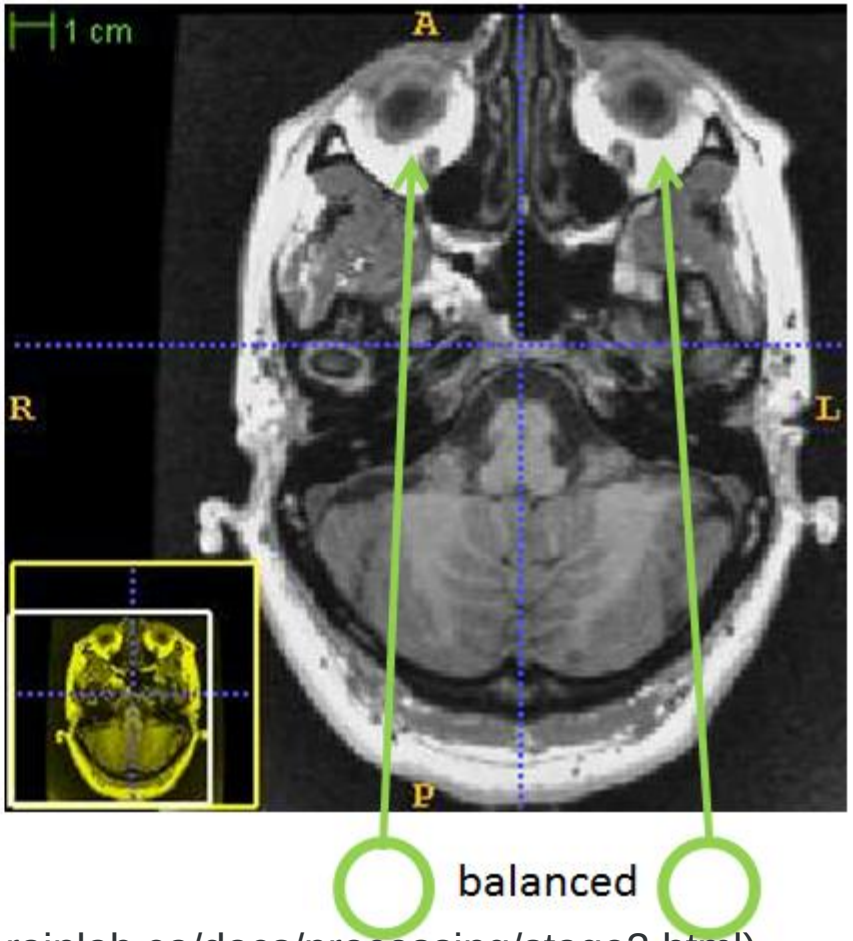
- Nomenclatura



T1 reorient – Recipe - 2

1. **Balance eyes** on view 2 & 3 for respectively yaw & roll

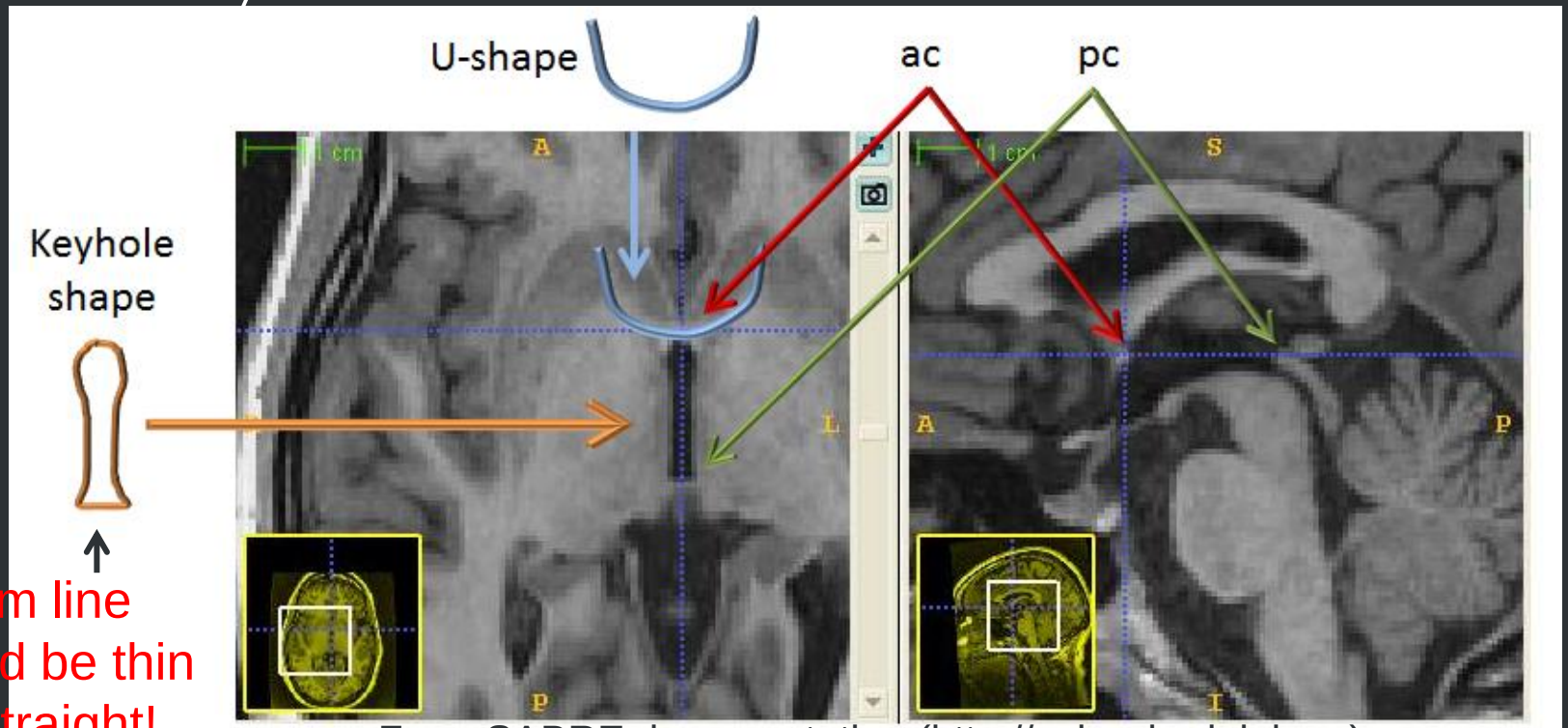




From SABRE documentation (http://sabre.brainlab.ca/docs/processing/stage3.html)

T1 reorient – Recipe - 3

2. **Adjust pitch & cursor** watching view 1 and 3 to get:
   - A winged keyhole shape in View 3
   - A extruded ball in View 1. Cursor must be on ball and top of keyhole.



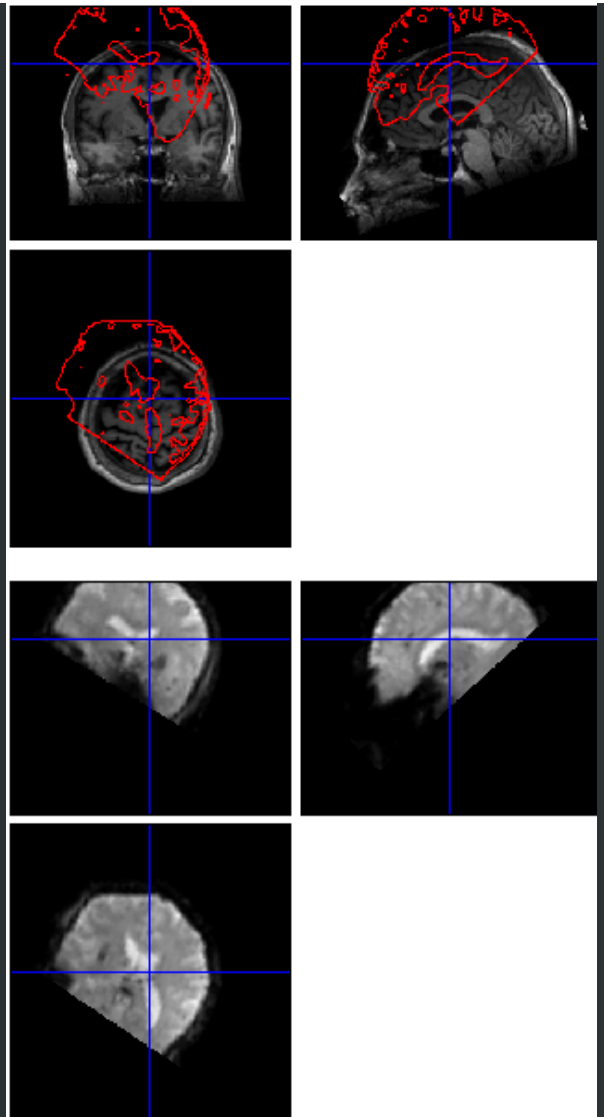
Bottom line should be thin and straight!

From SABRE documentation (http://sabre.brainlab.ca)

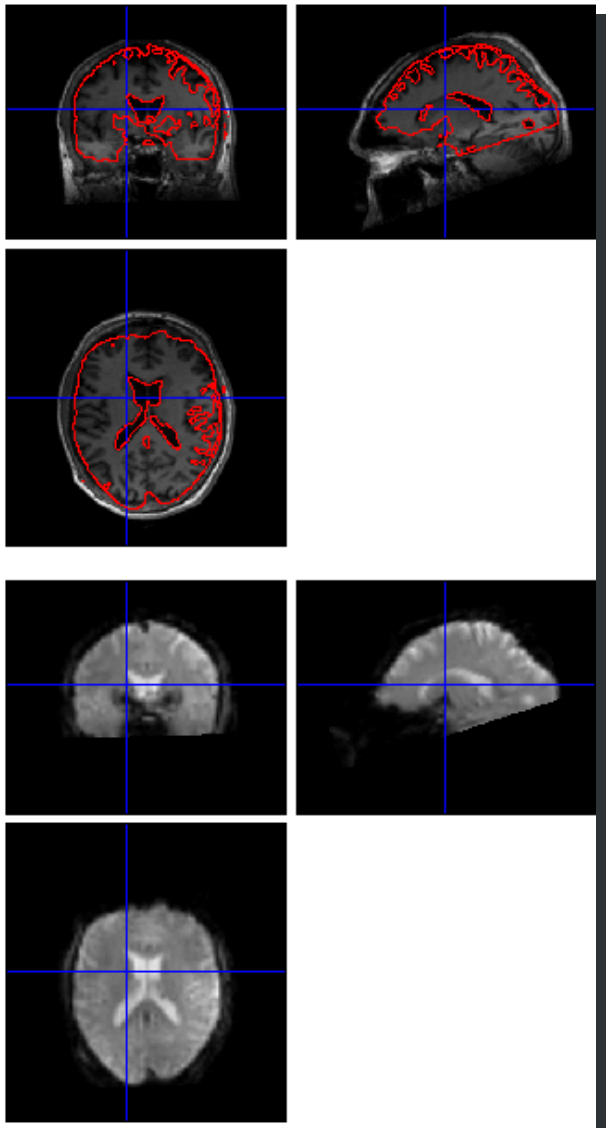
fMRI coregistration on T1

- Why? To ensure good start for auto-coregistration. A precise coregistration ensures **activity** is attributed to **correct region**!
- Estimated time: < 10 min per subject

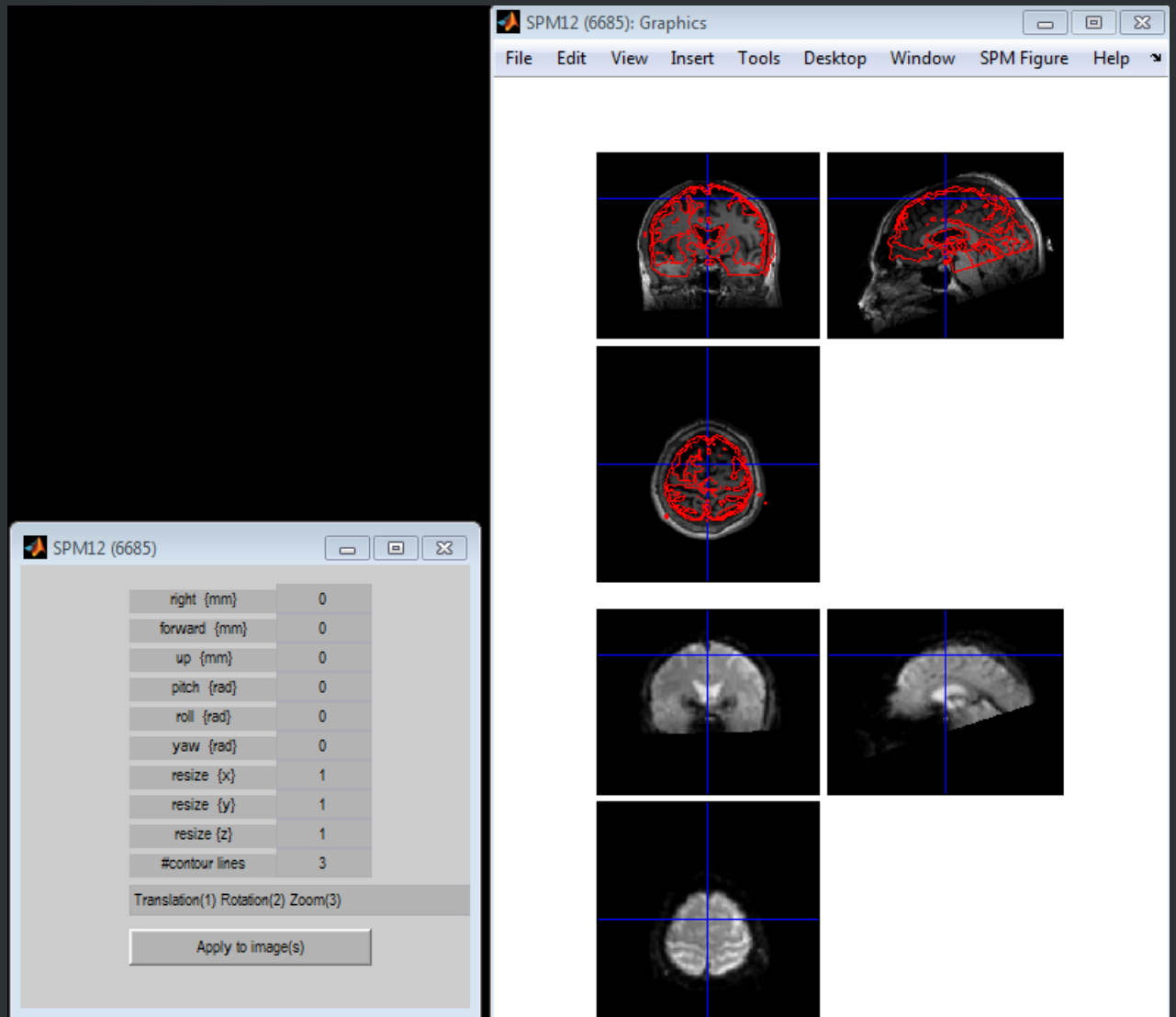
fMRI coregistration on T1



Perfect coreg = internal ventricules aligned (but not always possible, particularly with inhomogenous scans)



fMRI coregistration on T1 using SPM



fMRI coregistration on T1 - Method

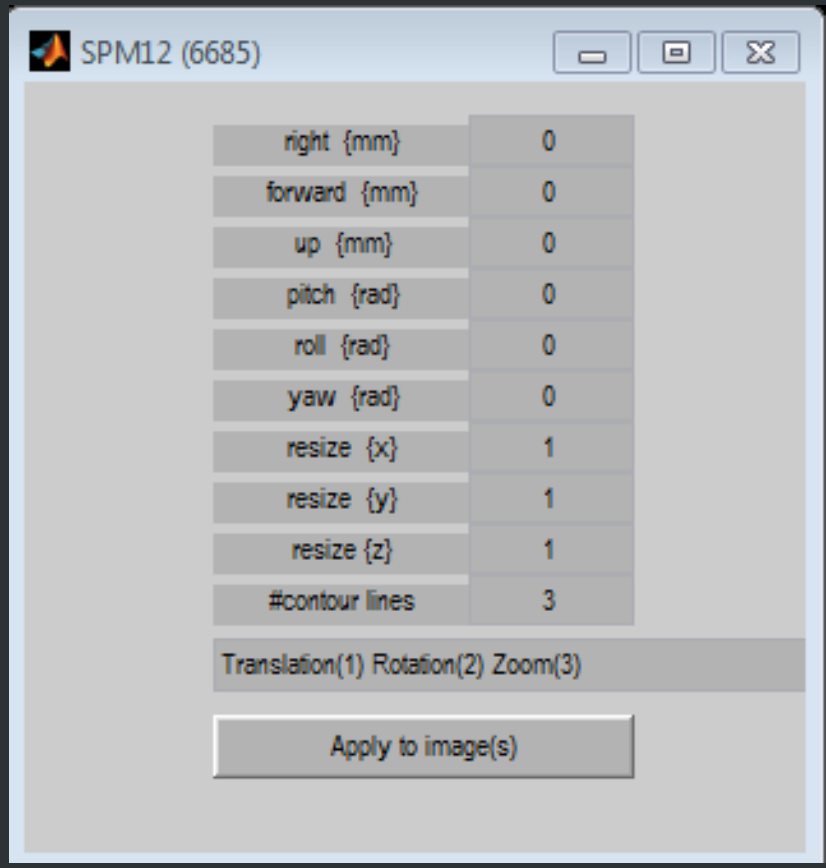
- Use **ventricles** as the guiding line to **overlay T2 on T1**, as ventricles are what is the closest to an internal structure.

fMRI coregistration on T1 - Recipe

1. SPM fmri > CheckReg, then select T1 and one T2 volume
2. T2 right-click > Reorient images > Current image
3. Translate to roughly overlay T2 on T1 (right, forward, up)
4. Save (click on Reorient Images button > deselect current image > right-click on image list and Select All > OK – Warning: if you don't select all, only one image will be coregistered! And it will be considered as movement noise).
5. Rotate (pitch, roll, yaw) and adjust translation, until you get ventricles nicely aligned on all views.
6. Save again.
7. Check first and last T2 volumes: T2 right-click > [name] > change image, select the last volume and check if also aligned. (Else the subject moved too much OR you are looking at two different acquisitions mixed in one)

fMRI coregistration on T1 - Tips

- Try to set **#contours to 2** (instead of 3), usually ventricles are more easy to see
- If T1 intensity is too low: T1 right click > Image > Intensity Mapping > Local > Equalised squared-histogram
- To zoom: T2 Right-click > Zoom > Bbox, this image nonzero OR Bbox, this image > 100
- Check ventricles alignment not only at 1 point but over the whole brain. **Slide cursor** to **animate** the brain, very useful to estimate rotation params.



SPM Preprocessing

DONE

- Convert from DICOM to NIfTI
- Exclude bad subjects (too much motion, artifacts, brain surgery, metallic prosthesis, etc)
- T1 reorient
- EPI & DTI manual coregistration

Manual preproc

- Slice timing correction
- Realignment (motion correction)
- Auto coregistration
- Segmentation + Normalization (MNI 152)
- Smoothing
- Movement correction/rejection
- aCompCorr

Auto Preproc (parameters MUST be identical for all subjects of 1 experiment)

Automated preprocessing - 1

- **Slice timing correction** = interpolate slices to represent activity at **identical time point**. Indeed, slices are NOT acquired at same time, so in reality a volume is composed of several slices of slightly different time points, thus of different activity. Slice timing correction tries to fix this.
- **Realignment (motion correction)** = correct slight motion artifacts **between slices**. Do NOT confuse with movement correction (correct bigger motion **between volumes**).
- Problem: doing one first will affect the other step. Thus, neuroscientists debate (fight) about what is best.
- Future solution: calculate both at the same time using a joint optimization cost function.
- **Field maps** = optional step just after realignment to correct magnetic fields bias. Need to acquire a field map.

Precision: Slice Timing & Repetition time

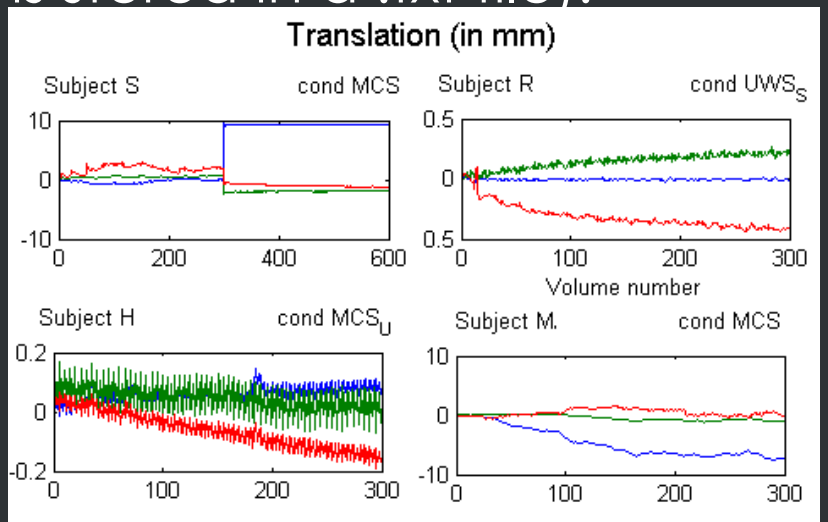
- **Repetition time, slice scheme & order** are critical infos (often not stored in DICOMs) needed for slice timing correction. The scanning crew define them, ask them to be sure!
  E.g. TR=2.0s , slice scheme=72 slices singleband, slice order=ascending interleaved.
- Repetition time = time between two full volumes. In other words: this is the time it takes to acquire all slices for one volume.
- → **Repetition time is NOT a pause**, it is the **cumulative sum** of the **delay** between each slice acquisition.
- → Leads to a **paradox**: **Last slice** of volume X is the **closest** slice (in time and neural activity) to the **first slice of next** volume X+1! Hence the need for **slice timing correction**!

Automated preprocessing - 2

- **Automatic coregistration** = like manual coreg but better at fine-tuning (but worse than human to roughly overlay).
- **Segmentation** = separating grey matter (GM), white matter (WM) and cerebro-spinal fluid (CSF = ventricles). Tips: CSF can be used as exclusion mask, GM mask will be used by VBM and CONN. Always done on T1. NB: **Skull-stripping** is done here implicitly.
- **Normalization (to MNI)** = transform brain's shape (affine or non-linear) to overlay subjects between groups. For this, we use a template generated on lots of subjects, usually MNI (152 subjects). Always done on T1 (same transform will be applied to T2 thanks to coregistration, with no loss of precision – if coregistration was done right ☺).
- Segmentation and normalization are very close processes mathematically, thus there are two main approaches:
  - SPM "Unified segmentation", using Tissue Probability Maps (TPM). Most modern, using bayesian inference. But hard to adapt on brain damaged patients.
  - Old segmentation using a "study-template", generated on your own dataset (or if healthy subjects, can use SPM T1.nii template).

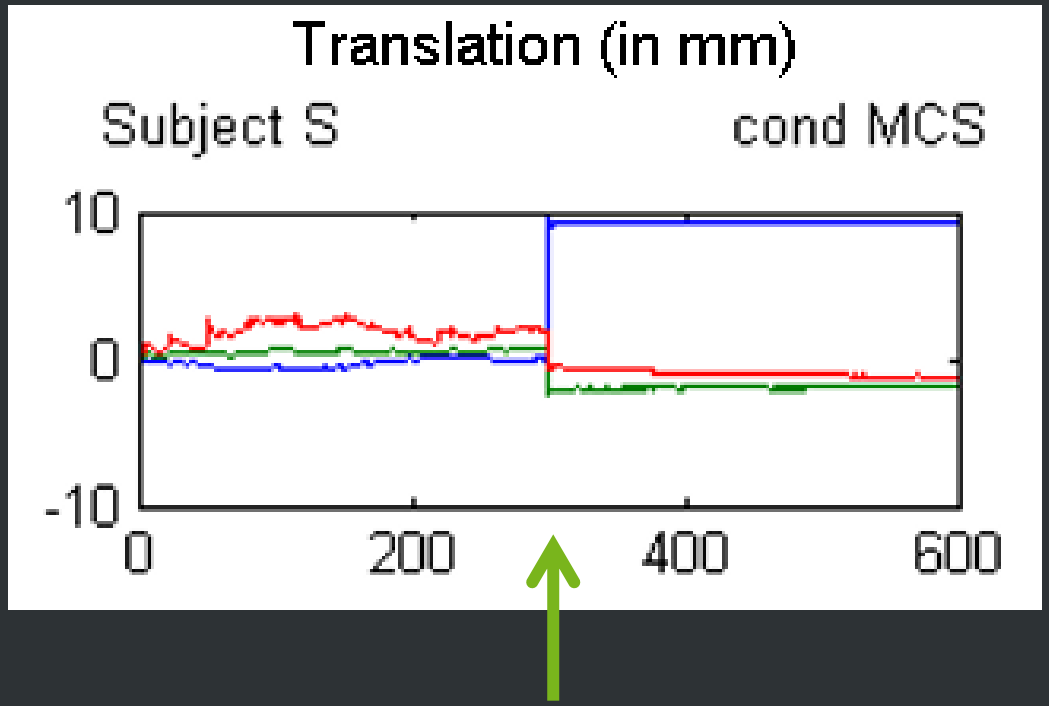
Automated preprocessing - 3

- **Smoothing** = "blurring" final normalized T1 & T2 images to increase SNR (signal-to-noise ratio), at the expense of specifity → More significance, but less precise localization of activity and correlations.
  Usually: 8^3 FWHM for healthy, 12^3 for brain damage patients.
- **Movement correction/rejection** = detect **big** motion **between volumes**. Use NITRC ART toolbox. Use movvis.m to visualize (all is stored in a .txt file).



Automated preprocessing - 4

- Can also delete just the volumes where too much movement (if still got enough volumes, above threshold for statistical correctness: add ref, eg, for TR 2.0: 5 minutes mini).



Can cut here (either before or after)

Automated preprocessing - 5

- **aCompCor** (Component Based Noise Reduction, Behzadi et al, 2007) = alternative to signal regression, useful to get meaningful anticorrelations (negative connectivity = increase of anti-synchronized connectivity) in contrasts. Indeed, anticorrelations produced after signal regression can be due to noise (Muschelli et al, 2014).
  Included in CONN "denoise" step.

SPM Preprocessing

DONE

- Convert from DICOM to NIfTI
- Exclude bad subjects (too much motion, artifacts, brain surgery, metallic prosthesis, etc)
- T1 reorient
- EPI & DTI manual coregistration

Manual preproc

DONE

- Slice timing correction
- Realignment (motion correction)
- Auto coregistration
- Segmentation + Normalization (MNI 152)
- Smoothing
- Movement correction/rejection
- aCompCorr

Auto Preproc (parameters MUST be identical for all subjects of 1 experiment)

Always CHECK

- Bad T1
- Movement records by ART
- Segmented images (GM is correctly segmented away from WM?)
- Normalized images (not too deformed compared to original T1?)
- Etc.

WARNING: Last point of rejection

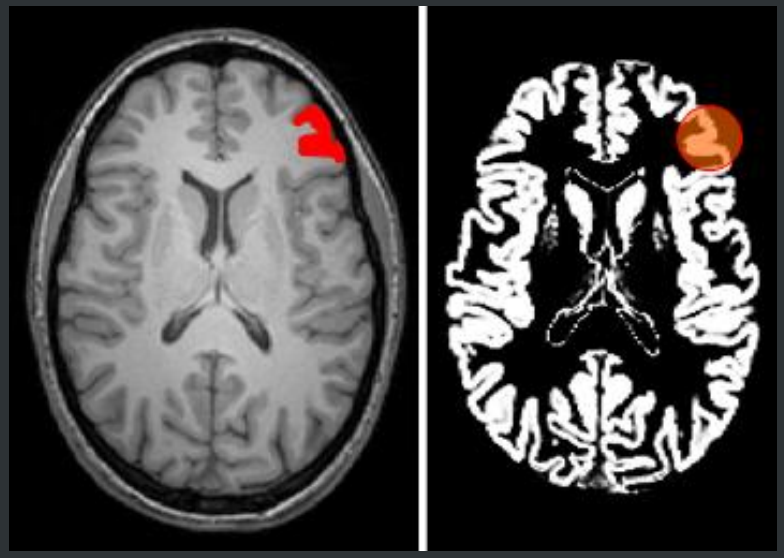
- **After automated preprocessing** is the **last point** where you can still **reject subjects**.
- After this point, you begin **analysis**, and you **can NOT reject** any subject anymore, else you are **p-hacking**.
- You can reject one or two subjects to match gender and age (ie, no significance in T-Test) to avoid using regressors (to decrease degrees of flexibility and thus increase significance), but only BEFORE analysis, NOT AFTER!

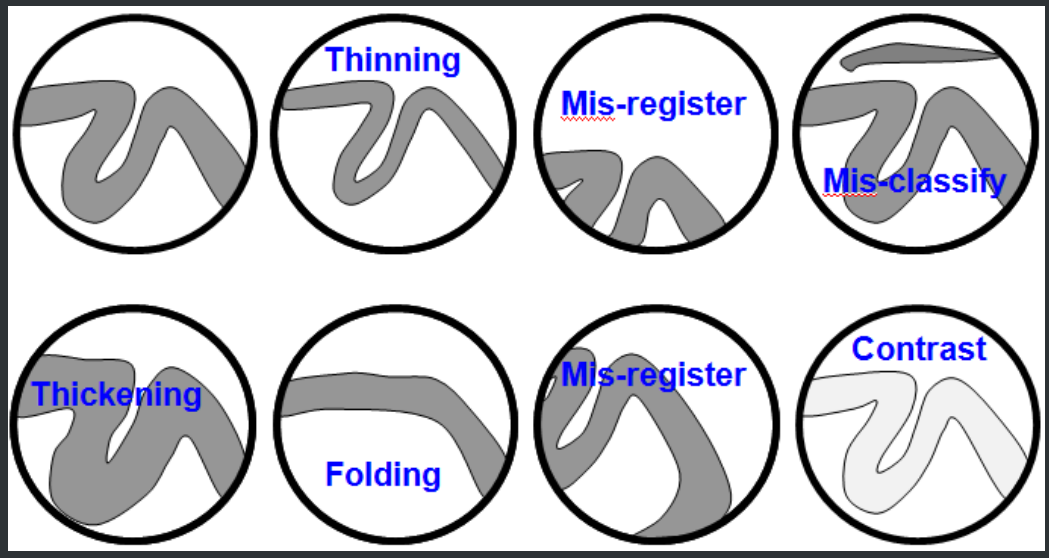
VBM analysis

- **Voxel-based morphometry (VBM)** = **compare** increases/decreases of **brain tissue** between two groups.

→We compare the voxels of T1, while respecting shape of GM.

- Whole-brain analysis (no seed).
- Need only T1 (manual and auto preprocessing).





From Zurich SPM Course 2015 by **Ged Ridgway (Oxford & UCL)**

Functional analysis

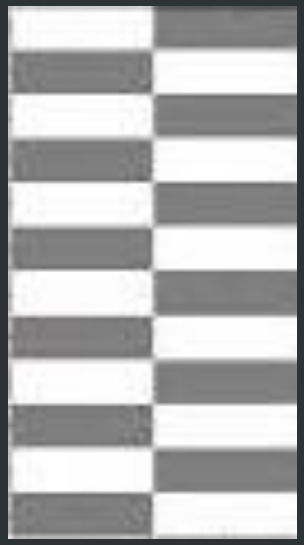
- Functional analysis = studying **functional connectivity**
- Infer from neural signal (brain "activity") functional connectivity by looking at correlations of activity between brain regions (ie, synchronized activity).
- Capture temporality (but low-resolution).
- Limitations: **BOLD** (Blood-Oxygen-Level Dependent) signal, **not neural signal**:
  → BOLD = convol(haemodynamic response , neural signal)
- SPM can model and regress haemodynamic response (up to an extent). Always think about haemodynamic response impact in your results!
- Compare with:
  - M/EEG: capture neural signal directly (change of potential) with high temporal resolution (but low spatial).
  - PET: capture radioactive emissions of a biomarker (eg, glucose).

Functional analysis: paradigms & design matrix

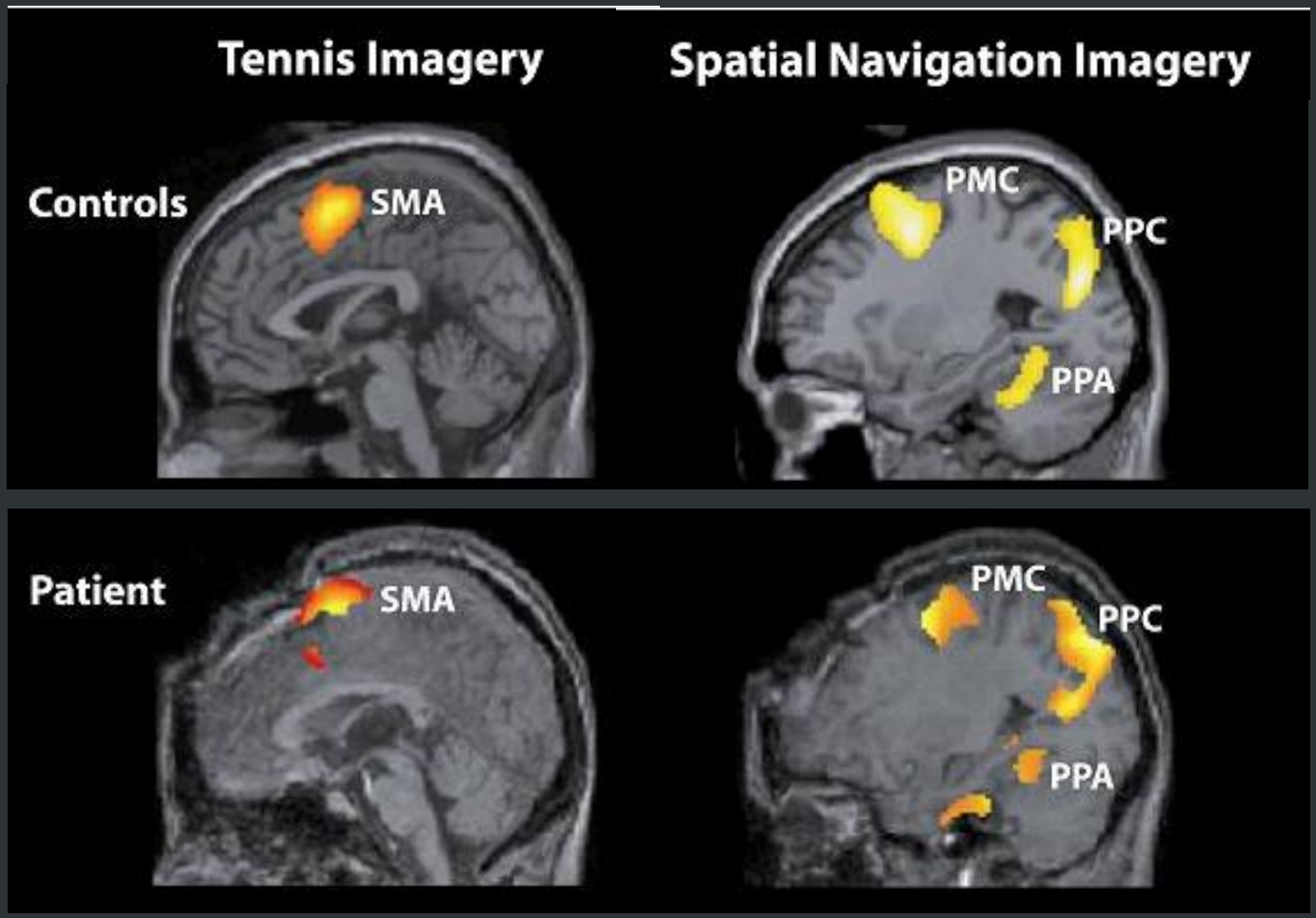
- 1st-level analysis: Look at the activity of each voxel for each time points for one subject.
- 2nd-level analysis: Either:
  - Inter-subjects (or between-subjects): compare between two groups (need normalization) → two-tailed t-test.
  - Intra-subject (or within-subject): compare across sessions for same subject (eg, before and after drug administration) → paired t-test.
- 3rd-level: both intra and inter-subjects (multiple groups and multiple sessions per subject). SPM does NOT support this, use CONN or manual scripts.
- Task-based vs resting-state (rsfMRI) paradigms define design matrix:
  - **Task-based**: subject is acquired in at least **two sessions**: one without doing anything (resting-state) and one doing the required task. Use 2nd-level **intra**-subject analysis or 3rd-level.
  - **Resting-state**: subject is acquired **5 to 10 min doing nothing**, with eyes either closed or open (need to fix this in protocol, changes results). Use 2nd-level **inter**-subjects on 3rd-level.

Functional analysis: paradigms & design matrix

- Design matrix for n subjects doing task (two sessions):



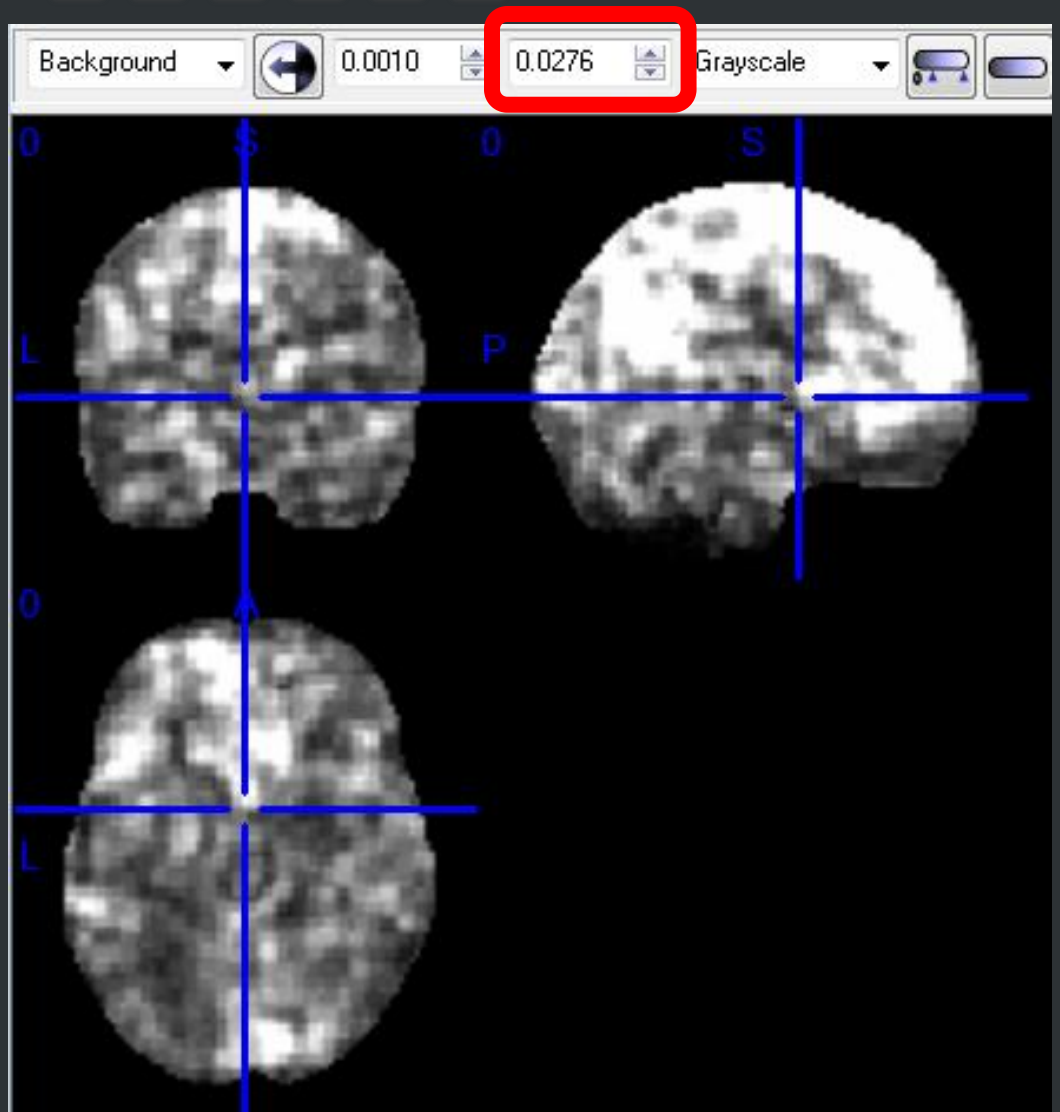
Result of SPM



Boly et al, NeuroImage 2007

Owen, Coleman, Boly, Davis, Laureys and Pickard, Science, 2006

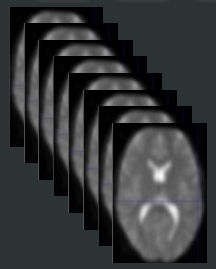
Model error in ResMS.nii



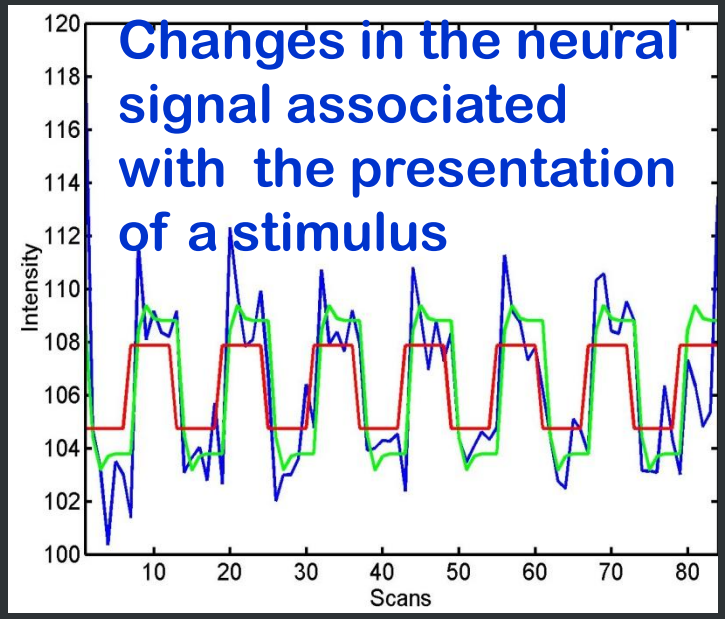
Residual error = residual activity which **cannot be explained** by the model (check the design matrix!)

Note the max value is very low (so we are OK).

SPM model = learning to predict neural stimuli

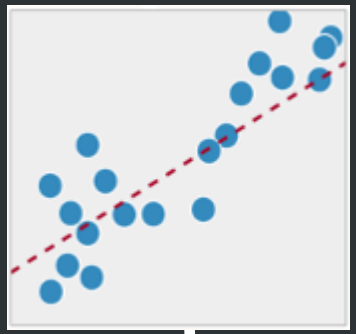


PRE-PROCESSING!



Design matrix

Generalized Linear Model

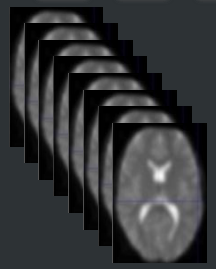


$$Y = X \times \beta + \varepsilon$$

Model and predictions!

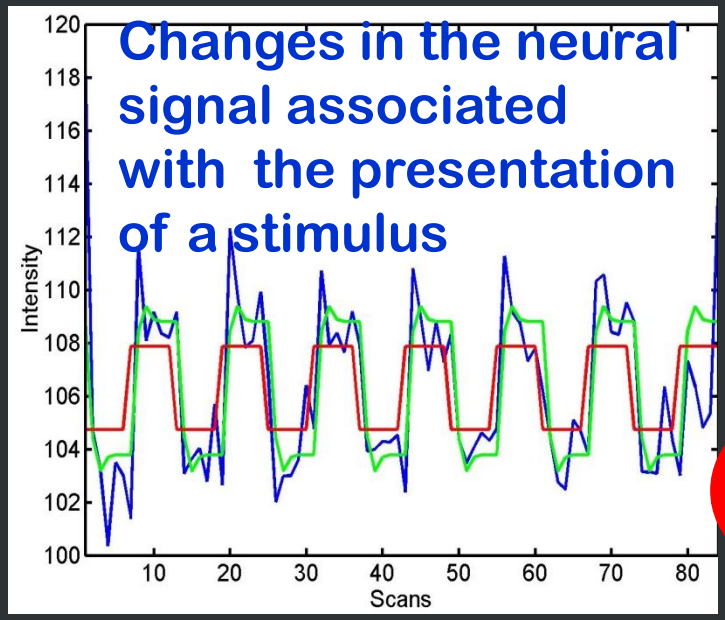
Adapted from "Methods for dummies 2011-12"
Hikaru Tsujimura and Hsuan-Chen Wu

SPM model = learning to predict neural stimuli



PRE-PROCESSING!

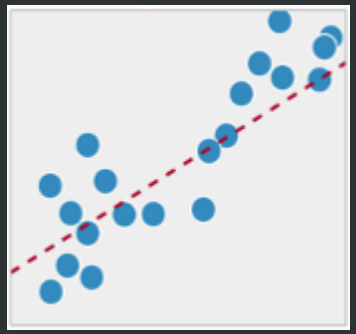
Y



Design matrix

X

Generalized Linear Model



β

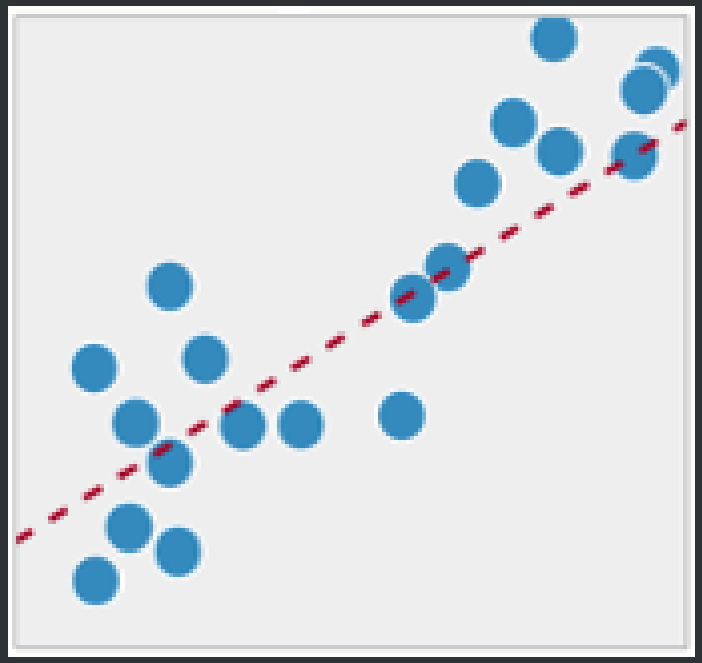
$$Y = X \times \beta + \varepsilon$$

Adapted from "Methods for dummies 2011-12"
Hikaru Tsujimura and Hsuan-Chen Wu

Learn (Betas, GLM) to predict Y (neural signal) using X (design matrix).
→Map design matrix (stimuli) to neural signal changes!

Linear model v. Generalized Linear Model

$Y = x0 + x1*\beta1 + x2*\beta2 + \ldots$

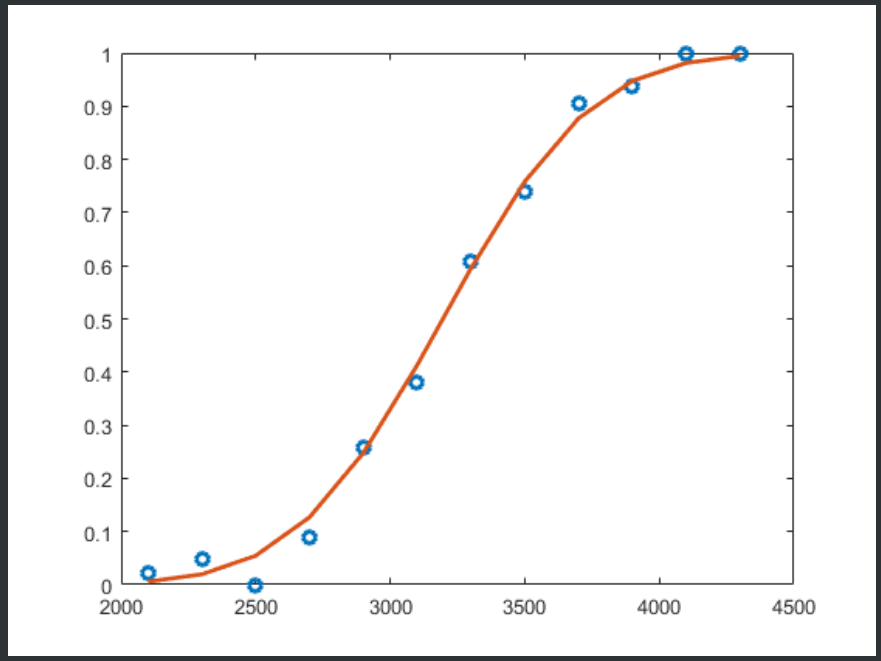


Noise ~ **Normal** distribution

How to know noise distribution?

$Y = f'(x0 + x1*\beta1 + x2*\beta2 + \ldots)$

where f() is the **link function**



Noise ~ **Link function** distribution

Visualize data and use descriptive stats!

SPM model: Why?

- Neural brain activity = high dimensional data (1 voxel = 1 feature, eg if 1 volume you have 30x30x30 = 27K! And that's just for 1 volume, count for a whole sequence!)
- Classical statistics (hypothesis testing, contrasts, etc) can only work when n > p (~5p <= n, where p is number of features and n number of samples, so you need at least 5 samples per dimension).
- Machine learning statistics is better fit to high dimension data (sparsity with L1, etc.)

→SPM uses ML (regression) to reduce dimensionality

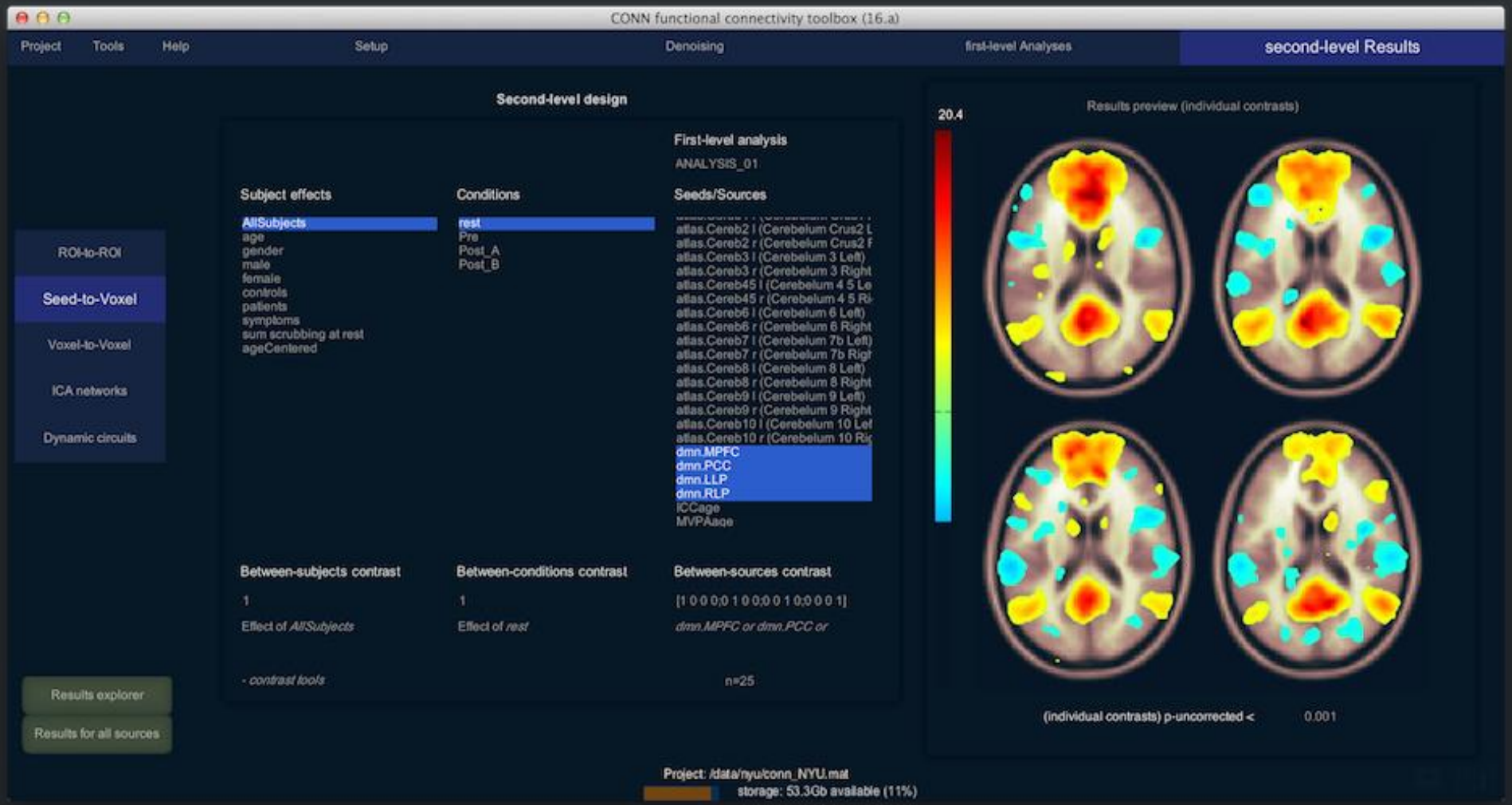
→Then can use classical statistics

→Contrasts are comparing models parameters (Betas), NOT brain activity

SPM model: Going further

- SPM uses Generalized Linear Model to reduce dimensionality, but you can use other machine learning models (see **ICA**, SearchLight, nilearn, scikit-learn, etc.).
- We use **CONN** (GabLab's Connectivity Toolbox) for functional analysis, as it streamlines SPM analysis and can go further (voxel-to-voxel, dynamic functional connectivity, graph theory, etc.) with more ergonomic interface.

CONN toolbox



Functional connectivity analyses

- ROI = Region of Interest = a defined group of voxels that you consider to be stable across all subjects.
- **From intensity to connectivity: Pearson correlation** is done on voxels **activity across time** to find regions **activating together** (and thus are parts of a network).

3 main types of analysis:

- **Seed-to-Seed** (ROI-to-ROI) = analysis of connectivity between two ROIs across time.
- **Seed-to-Voxel** = connectivity between one ROI and all voxels
- **Voxel-to-Voxel** = connectivity between each voxel and every other voxels of the brain.

Functional connectivity analyses - 2

- 1st and 2nd (& 3rd) level analyses are both possible with functional connectivity
- **1st level** = correlation of brain regions activity across time
- **2nd level** = difference of 1st level between conditions (groups/sessions) = difference in the correlations of brain regions activity
- **Correlation** = positive/synchronous/**within-network connectivity**
- **Anticorrelation** = negative/alternately sync/**between-network connectivity**.
  → **Anticorrelation is still a correlation**! Just that when one network turns on, the other one turns off, and inversely. This is not necessarily inhibition, it's just indirect communication! Warning: need to use **aCompCor** (CONN denoise) to ensure anticorrelations are not due to noise!

Correlations/anticorrelations

- **Correlation** = positive/synchronous/within-network connectivity
- **Anticorrelation** = negative/alternatively synchronized/between-network connectivity. NB: Anticorrelation is still a correlation! Just that when one network turns on, the other one turns off, and inversely. This is not necessarily inhibition, it's just indirect communication!

WARNING: Good practices

- Reminder: no p-hacking, no rejection after analysis!
- **Multiple comparison problem**: use **voxel-wise FDR** or FWE or **cluster-wise FWE** (not C-FDR) or permutation test, but **nothing below**!
  Indeed, without multiple comparison correction (p-uncorrected), you will ALWAYS find something!
- Multiple comparison problem (again): **FDR/FEW correction does NOT PROTECT against multiple comparison!** If you test lots/all seeds, you also do multiple comparison!
  →Define **beforehand max 4/5 seeds** to explore, and **STICK TO IT!**
  →Or apply multiple comparison at seed level: FWE = simply dividing p-values by number of seeds explored.

WARNING: Good practices - 2

- Exploring multiple seeds being bad practice might seem counter-intuitive
- Why clicking to explore results that have already been computed would skew the validity?
- Because clicking **generates** new results: **clicking is like launching a coin**:

I win if with 1 launch, I get tails:
→50% chances

vs

I win if, **with as many launches I want**, I get tails:

- 1st launch: 50% chances
- 2nd launch: 50+25=75% chances
- 3rd launch: 87.5% chances
- 5th launch: 96% chances
- 7th launch: 99% chances of winning

Exploring multiple seeds increases chances of getting results just by chance!

WARNING: Good practices - 3

- **Statistical validity** might seem a daunting task
- In case of doubt, **ask a statistician**…
- … and look for seminars to learn **statistical literacy**
- Statistical literacy is the ability to **understand statistics** (ie, when one tool should be used, what are the limitations, etc.) → in other words, to develop **intuition**
- Noone would write in a language without understanding its words, but **no need to be an expert** writer
- Statistics are the same: it is possible to understand and get intuition without mastering statistics: the goal is not to be able to derive calculations manually nor to prevent any issue (honest mistakes happen), but just the **most common ones**

At the end of analysis

- Check **ResMS.nii max value**: your model is as good as low your error is. If error is high, your model can be meaningless!
- Check **standard functional connectivity results**: check that controls show DMN, or other network of interest. Compare to literature. If not, either your preprocessing/analysis is buggy, or your MRI scanner has vibrational artifacts or worse (then call MRI IT guys to fix that).
- **Ensure reproducibility: Archive (zip)** your progress at at least 3 points:
  - **Original DICOM files** (non anonymized if possible – anonymization might lose critical info).
  - **After manual preprocessing** and before auto preprocessing.
  - **After whole analysis**: zip both auto preprocessed files + SPM/CONN projects + **scripts/jobs used** (with all the parameters you used!).

Thank you for your attention

Resources:

- Andy's brain blog & youtube channel
- SPM advanced video tutorials (2011): http://www.fil.ion.ucl.ac.uk/spm/course/video/
- SPM annotated bibliography
- CONN manual (explains very well seed-to-voxel and voxel-to-voxel approaches and measures
- Consult **community forums/mailing-list** (mrtrix, spm, conn) and ask if necessary!

Courses at Ulg (try to find similar ones close to your university):

- SPM course by Christophe Phillips
- Multivariate statistics by Gentiane Haesbroeck
- Learning the CONN toolbox by GabLab
- Neuroimagery course (about MRI technical inner workings etc)

BONUS SLIDES

Field maps resources

- Field maps tutorials:
  - https://en.wikibooks.org/wiki/Neuroimaging_Data_Processing/Field_map_correction#SPM
  - http://www.fil.ion.ucl.ac.uk/spm/data/fieldmap/
  - Essentially: after realignment, use field map toolbox to generate a vdm file, and use "Apply VDM" to apply it on functional volumes. Alternative way is, instead of using "Apply VDM", to supply the vdm file in realignment so you can do it at the same time, but this does not support dynamic correction (more complex acquisition schemes) like R→L, high field fMRI (ie, above 3.5T), etc.

Neuroimagery analyses outline