



## fMRI Preprocessing & Noise Modeling An SPM Tutorial

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September 25<sup>th</sup>/ October 17<sup>th</sup>, 2015

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## **Tutorial: Code and Data**

- S
- Download example code and data presented in this talk:
  - http://www.tnu-zurich.org/team/lars-kasper/
  - Section: Talk and Lecture Materials
- SPM12 (Statistical Parametric Mapping)
  - http://www.fil.ion.ucl.ac.uk/spm/software/spm12/
  - developed by the Functional Imaging Lab, UCL, London
- TAPAS PhysIO Toolbox (SPM or Matlab standalone)
  - <u>http://www.translationalneuromodeling.org/tapas/</u>
  - Documentation & Example Data (Philips/Siemens/GE):
    - <u>http://www.translationalneuromodeling.org/software/documentation/</u>
    - <u>http://www.translationalneuromodeling.org/software/tapas-data/</u>

 Setting up a Preprocessing Pipeline in SPM: The Batch Editor

Setup Pipeline DEMO 1

- Monitoring and Comparing Pipelines: Quality Assurance
- Multi-subject Pipelines: Automatisation

Quality Monitoring DEMO 2

> Multi-Subject DEMO 3

Integrating Own Code and Toolboxes:
 Physiological Noise Modeling and Evaluation

Noise Modeling DEMO 4

## The SPM GUI





## The Batch Editor in SPM



Setup Pipeline	Quality Monitoring	Multi-Subject Noise Modeling
<ul> <li>Develope</li> </ul>	er: V. Glauche	Student Version> : SPM12 (6225): Menu
<ul> <li>Command line usage: spm_jobman</li> </ul>		Realign ‡     Slice timing     Smooth       Coregis ‡     Normali ‡     Segment
	Batch Editor	
File Edit View SPM BasiclO		Creatify tet level
Image: Segment       Current Module: Realign & Unwarp         Segment       Coregister: Estimate DEP         Normalise: Write       DEP         Smooth       DEP         Separation       Separation         Smooth       Separation         Seguing       Wrapping         Weighting       Unwarp Estimation Options         Stimation Options       Interpolation         Wrapping       Weighting         Unwarp Estimation Options       Basis Functions         Regularisation       Regularisation         Surgers/kasperla/Dropbox/C       //sers/kasperla/Dropbox/C         /Users/kasperla/Dropbox/C       //sers/kasperla/Dropbox/C         /Users/kasperla/Dropbox/C       //sers/kasperla/Dropbox/C	Current Module: Realign & Unwarp Help on: Realign & Unwarp Data . Session . Images . Phase map (vdm* file) Estimation Options . Quality . Separation . Smoothing (FWHM) . Num Passes . Interpolation . Wrapping . Weighting Unwarp Estimation Options . Basis Functions . Regularisation . Reg. Factor . Jacobian deformations Current Item: Images /Users/kasperla/Dropbox/Conferences/SPMZuric /Users/kasperla/Dropbox/Conferences/SPMZuric /Users/kasperla/Dropbox/Conferences/SPMZuric /Users/kasperla/Dropbox/Conferences/SPMZuric /Users/kasperla/Dropbox/Conferences/SPMZuric /Users/kasperla/Dropbox/Conferences/SPMZuric /Users/kasperla/Dropbox/Conferences/SPMZuric	Specify 2nd-level       Estimate         Specify 2nd-level       Estimate         Results       Dynamic Causal Modelling         Dynamic Causal Modelling       SPM for functional MRI         Display       Check Reg       Rend ‡         Tool ‡       PPIs       ImCalc         Help       Utils ‡       Batch       Quit
	Specify	Copyright (c) 1991,1994-2014

## **SPM Preprocessing Pipeline**



Lars Kasper: fMRI Preprocessing & Noise Modeling in SPM

Input

## **From Pipelines to Batches**



3.

## Demo 0

**Setup Pipeline** 



Setting up the data for all demos & checking it

Quality Monitoring

Source: Social Learning (A. Diaconescu<sup>[1]</sup>, TNU Zurich, Philips 3T)

- After download:
  - 1. Unzip archive examples\_physio\_short.zip
  - 2. Open Matlab, run code/init\_reset\_example.m
    - subject01-folder created, Batches filled with right data (filenames and path) already
  - 3. Inspect raw functional and structural data carefully
    - Required for each subject
    - Preferred viewer: SPM CheckReg

# Demo 0: CheckReg-Magic



Quality Monitoring

Multi-Subject

- Recommended Plotting: Check Reg
  - via Batch Editor: SPM => Util => Check Reg.
  - Matlab command line: spm\_check\_registration(`img1.nii', `img2.nii', ...)
  - 4D NIFTI files:
    - show individual image tiles: spm\_check\_registration(`fmri.nii,1', `fmri.nii,2', ...)
    - show movie (NEW! SPM12):
      spm\_check\_registration(`fmri.nii')
  - Right click reveals amazing features (edges, anatomic labels, header info, contrast, add blobs) bels





Save As...

# Demo 1

**Setup Pipeline** 



- Simple preprocessing pipeline for fMRI (G. Ridgway)
  - Based on spm12/batches/preproc\_fmri\_simplified.m
- Run via:
  - 1. Load subject01/batches/demo01\_simple\_batch\_preproc/ batch\_spm\_preproc\_fmri\_simplified.m in Batch Editor

Multi-Subject

```
Either via GUI or
spm_jobman(`initcfg');
spm_jobman(`interactive',...
`batch_spm_preproc_fmri_simplified.m');
```

Quality Monitoring

- 2. Run Batch (Press Play)
- Exercise: Draw Pipeline Diagram (Modules/Dependencies/Data)

## Demo 1 – GUI Batch Editor



Setup Pipeline	Quality Monitoring	Multi-Subject Noise Modeling
Eile Edit View SPM BasiclO	Batch Editor	
Module List          Realign & Unwarp         Segment         Coregister: Estimate       DEP         Normalise: Write       DEP         Smooth       DEP	Current Module: Realign & Unwarp Data . Session . Images . Phase map (vdm* file) Estimation Options . Quality . Separation . Smoothing (FWHM) . Num Passes . Interpolation . Wrapping Unwarp Estimation Options . Basis Functions . Basis Functions . Regularisation . Reg. Factor . Jacobian deformations . Reg. Factor . Jacobian deformations . Current Item: Images	100 files 0 files 0.9 4 5 Register to first 2nd Degree B-spline No wrap 0 files 12x12x* 1 Medium No 2 2 2 2 2 2 2 2 2 2 2 2 2

## **Demo 1 - Dependencies**

Setup Pipeline	Quality Monitoring	Multi-Subject	Noise Modeling
Setup Pipeline File Edit View SPM BasiclO Coregister: Estimate DEP Normalise: Write DEP Smooth DEP	Current line:: Source Image	DEP Segment DEP Realign & Unwarp: Unwarp Realign & Unwarp: Unwarp Normalised	t: Bias Corrected (1) warped Mean Image bed Images (Sess 1) d Mutual Information [4 2] 1x12 double [7 7]
	Current Item: Source Imege		
	Reference from Realign & Unwarp: Unwarped	Mean Image	Dependency

Source Image

## Demo 1 - Results

Setup Pipeline

#### Quality Monitoring



#### Multi-Subject

## Automatic status plots saved in spm\_<date>.ps

Image realignment

1 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces 2 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces 3 4 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces 5 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces 7 8 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces 9 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces 10 11 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces 12 /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreproces ..... etc





#### **Normalised Mutual Information Coregistration**





# Outline

**Setup Pipeline** 



 Setting up a Preprocessing Pipeline in SPM: The Batch Editor

Quality Monitoring

- Monitoring and Comparing Pipelines
  - Performance Measures: Mean/SD/SNR/Diff Image

- SPM Plotting Routines and Automatic Reporting
- Spotting Failed Pipelines
- Comparing Alternative Pipelines
- Multi-subject Pipelines
- Integrating Own Code and Toolboxes:
   Physiological Noise Modeling and Evaluation

# **Pipeline Monitoring**



Pipelines

**Setup Pipeline** 



Automatisation of Preprocessing

Multi-Subject

- When something goes wrong...how do we even notice?
  - Monitoring, but: cumbersome, when lots of data
  - Thus: Automatise quality monitoring as well via pipelines
- Required: Suitable performance measures

Quality Monitoring

- Single image: visual inspection geometry/contrast/noise/SNR
  - structural image
- Time series: Statistical Images (Mean, SD, tSNR, max(abs(diff)))
  - functional images

Welvaert (2013), PLoS One

Friedman/Glover (2006), JMRI

# **Statistical Images**

## Setup Pipeline

## Quality Monitoring

- Structural Image: visual inspection geometry/ contrast/noise/SNR
- Functional Time Series:
  - => Artifact levels Mean (localization)
    - => Fluctuation levels SD
  - tSNR = Mean/SD=> sensitivity for BOLD signal changes Diff  $= \max(abs(diff))$  or odd – even
    - => outlier detection, image noise



vs Even





**fMRI** 









Max Abs Diff n vs n+1

Lars Kasper: fMRI Pre

## Demo 2

Setup Pipeline

Noise Modeling

- Complete preprocessing & monitoring pipeline for fMRI
  - Based on spm12/batches/preproc\_fmri

Quality Monitoring

 Includes batch\_report\_quality.m to visualize and save quality measures after each preprocessing step

- Run via
  - Cleanup processed data of subject01: init\_reset\_example(2)
  - 2. Load subject01/batches/demo02\_simple\_batch\_preproc/ batch\_preproc\_fmri\_report\_quality.m
  - 3. Either via GUI or spm\_jobman(`interactive', `batch\_preproc\_fmri\_report\_quality.m' );
    - Alternative: Run batch directly from command line: spm\_jobman(`run', `batch\_preproc\_fmri\_report\_quality.m' );

## Demo 2 - GUI

Noise Modeling

**Quality Monitoring** Setup Pipeline Multi-Subject Batch Editor File Edit View SPM BasiclO D 🚔 Module List Current Module: Run Batch Jobs Named File Selector Help on: Run Batch Jobs Named File Selector ..demo02\_compare\_batch\_quality/batch\_report\_quality.m Job File(s) Realign & Unwarp DEP Runs DEP . Job Inputs Seament Get Pathnames DEP . . Directory DEP Make Directory: Make Directory 'report\_guality' Image Calculator DEP . . String 00 raw ... NIfTI Images DEP Move/Delete Files: Moved/Copied Files Coregister: Estimate DEP Normalise: Write DEP . . NIfTI Images DEP Named File Selector: Structural Image(1) - Files . Job Inputs Smooth DEP Normalise: Write DEP DEP Make Directory: Make Directory 'report\_guality' . . Directory . . String 01 realigned Make Directory DEP . . NIfTI Images DEP Realign & Unwarp: Unwarped Images (Sess 1) Change Directory Move/Delete Files DEP Named File Selector: Structural Image(1) - Files DEP . . NIfTI Images Run Batch Jobs DEP . Job Inputs DEP Make Directory: Make Directory 'report guality' . . Directory 02 coregistered . . String DEP Coregister: Estimate: Coregistered Images . . NIfTI Images DEP Named File Selector: Structural Image(1) - Files . . NIfTI Images . Job Inputs . . Directory DEP Make Directory: Make Directory 'report\_quality' Current Item: Job File(s) /Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysIOPreprocessing/exa

Specify...

## Demo 2 - Output



## • Output:

Setup Pipeline

- subject01/report\_quality/report\_quality.ps
  - PostScript file with all output plots, generated from the following nifti image files
- report\_quality/00\_raw/

mean.nii

sd.nii

snr.nii

diffOddEven.nii

Quality Monitoring

maxAbsDiff

subject01/01\_realigned

=> mean of time series (per pixel)

=> standard deviation (per pixel)

=> raw time series statistics

=> mean/sd (per pixel)

Multi-Subject

- => SumOddImages SumEvenImages
- => maximum delta image (vol n vs n+1)
- => realigned time series stats

subject01/04 smoothed

=> smoothed time series stats

...

# **Plotting Example**

Setup Pipeline

Noise Modeling

Example: Comparing temporal SNR throughout preprocessing

Quality Monitoring

 Temporal SNR per pixel in functional image time series after each preprocessing step

Multi-Subject

Command line code:

```
dirs = {'00_raw', '01_realigned',
'02_coregistered', '03_normalized',
'04_smoothed'}';
files = 'snr.nii';
fpFiles = strcat(dirs, '/', files);
spm_check_registration(fpFiles{:})
```

# **Plotting Example**

## Setup Pipeline

Quality Monitoring

- Example: Temporal SNR
   per pixel in functional
   image time series after
   each preprocessing step
- Right click reveals amazing features
- Result: Increased SNR through realignment and smoothing



2015-09-25

## Quiz...

# Noise Modeling

- Setup Pipeline
- Quality Monitoring

- Task: Spotting unusual quality report images
  - run demo02.../batch\_run\_artefact\_subjects.m
    - executes code/create\_artefact\_subjects.m
    - then: executes demo02-preprocessing batch for each subject
  - View for individual subjects: report\_quality.ps
- What went wrong here?
  - subjectA1
  - subjectA2
  - subjectA3

## Quiz...



# Quiz...



### Setup Pipeline

Quality Monitoring

- Task: Spotting unusual quality report images
- What went wrong here?
  - subjectA1
    - realignment failed
    - one volume rotated (30 degrees around x-axis)
  - subjectA2
    - segmentation failed
    - structural mirrored compared to template
  - subjectA3
    - co-registration failed
    - functional image shifted by 10 cm (x, y, and z) compared to structural

# **Comparing Pipelines**

Noise Modeling

When running different preprocessing pipelines on the same subject:

Multi-Subject

- Always start from raw nifti data (structural and functional)
- Copy it to new processing folder, e.g.

Quality Monitoring

subject01/preproc\_alternative/fmri/

## /struct/

- Alter original batch file and save it under new name
- Swapping preprocessing steps is not simple in the batch editor
  - Solution: save as .m-file and edit in Matlab
  - helper script (code folder):
    - reorder\_matlabbatch(fileBatch, indicesBefore, indicesAfter)
- Run different batch files via run\_job

**Setup Pipeline** 

# **Comparing Pipelines**



Setup Pipeline

Quality Monitoring

- Example: When to use Slice timing correction?
- Run:
  - demo02\_compare\_batch\_quality/batch\_compare\_preproc
- this executes:
  - batch\_compare\_template\_stc\_realign
    - slice timing correction before realignment
  - batch\_compare\_template\_realign\_stc
    - realignment before slice timing
- Note: Proper Assessment only after statistical analysis possible

# Outline

**Setup Pipeline** 



 Setting up a Preprocessing Pipeline in SPM: The Batch Editor

Quality Monitoring

- Monitoring and Comparing Pipelines
- Multi-subject Pipelines
  - Staying on Top: Organisation of Data
  - Looping Pipelines over Subjects' Data
  - Tips for Efficient Performance Monitoring
- Integrating Own Code and Toolboxes:
   Physiological Noise Modeling and Evaluation

## **Data Organisation**



## Demo 3 – Example Loop Script

```
Quality Monitoring
                                                            Multi-Subject
                                                                                        Noise Modeling
Setup Pipeline
         % List of open inputs
         % Named File Selector: File Set - cfg files
         % Named File Selector: File Set - cfg_files
         % Make Directory: Parent Directory - cfg_files
         pathStudy
                         = '/Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysI0Prepr
         dirSubjectArray = {
             'subject10'
             'subject11'
             }:
         fileFunctional = 'fmri/fmri.nii';
         fileStructural = 'struct/struct.nii';
         nrun = 2; % enter the number of runs here
         jobfile = {'/Users/kasperla/Dropbox/Conferences/SPMZurich15/PracticalsPhysI0Preprocessir
         jobs = repmat(jobfile, 1, nrun);
         inputs = cell(3, nrun);
       □ for crun = 1:nrun
             pathSubject = fullfile(pathStudy, dirSubjectArray{nrun});
             fullpathFunctional = fullfile(pathSubject, fileFunctional);
             fullpathStructural = fullfile(pathSubject, fileStructural);
             % functional file
             inputs{1, crun} = {fullpathFunctional}; % Named File Selector: File Set - cfg_files
             % structural file
             inputs{2, crun} = {fullpathStructural}; % Named File Selector: File Set - cfg_files
             % subject folder
             inputs{3, crun} = {pathSubject}; % Make Directory: Parent Directory - cfg_files
         end
         som('defaults', 'FMRI');
         spm jobman('run', jobs, inputs{:});
```

## Demo 3

Setup Pipeline

Quality Monitoring



- Performs Demo 2 (complete preproc + quality report) for multiple subjects (subject10 and subject11)
  - create subject folders: Run code/create\_multi\_subject\_data.m
  - Run via
    - 1. Load "job":
       subject10/batches/demo03\_multi\_subject/batch\_prepro
       c\_fmri\_report\_quality\_job.m Inspect!
    - 2. Load & Run batch\_preproc\_fmri\_report\_quality\_gui.m
    - 3. Alternative: Open in *Matlab* Editor, inspect construction of subject dependent file names, run in Matlab GUI: batch\_preproc\_fmri\_report\_quality\_run.m

# Outline

**Setup Pipeline** 



 Setting up a Preprocessing Pipeline in SPM: The Batch Editor

Quality Monitoring

- Monitoring and Comparing Pipelines
- Multi-subject Pipelines
- Integrating Own Code and Toolboxes:
   Physiological Noise Modeling and Evaluation

- Executing Custom Matlab Code within the Pipeline
- The TAPAS PhysIO Toolbox
- Automatic (Noise) Modeling and Contrast Reporting

## Demo 4

Setup Pipeline

Quality Monitoring



- Performs whole single-subject analysis except preprocessing
  - creates behavioral regressors (visual stimuli/button responses)
    >multiple\_conditions.mat
  - creates nuisance regressors, including RETROICOR via the TAPAS PhysIO Toolbox
    - >multiple\_regressors.mat
  - Sets up 1<sup>st</sup> level analysis GLM & estimates it
  - Estimates F-contrasts of interests and plots them to .ps file
- Run via
  - 1. spm\_jobman(`interactive',
     subject01/batches/demo04\_stats\_physio/batch\_physio\_
     glm\_contrasts.m)

## Demo 4

Setup Pipeline	Quality Monitoring	Multi-Subject	Noise Modeling
	Batch Ed	ditor	
Module List	Current Module: TAPAS PhysiO Toolbox		
Named File Selector Named File Selector Named File Selector Make Directory Named File Selector Call MATLAB function DEP TAPAS PhysIO Toolbox DEP fMRI model specification DEP Model estimation DEP Contrast Manager DEP Results Report DEP	Help on: TAPAS PhysIO Too save_dir log_files . vendor . log_cardiac . log_respiration . log_scan_timing . sampling_interval . relative_start_acquisition . align_scan sqpar (Sequence timing para . Nslices . NslicesPerBeat . TR . Ndummies . Nscans . onset_slice . time_slice_to_slice . Nprep thresh (Thresholding parame Current Item: save_dir Reference from Make Directory: Make Direct	ameters) eters for de-noising and timing tory 'first_level_2BF'	Directory 'first_level_2BF'         Philips        siological Logfile(1) - Files        siological Logfile(1) - Files         0         first         37         1         2.5         5         100         19         6

# Pipeline Noise Modeling/Report

Setup Pipeline

Quality Monitoring

Multi-Subject

**Noise Modeling** 

- Model physiological noise as nuisance regressors
- Check noise correction via explained variance (F-contrasts)
  - Automatic contrast creation and report (glass brain): Batch Editor
     SPM => Stats => Contrast Manager/Results Report
  - With underlays: tapas\_physio\_report\_contrasts



## Conclusion

Setup Pipeline



 Setting up a Preprocessing Pipeline in SPM: The Batch Editor

Quality Monitoring

... best way for reproducible, documented preprocessing

- Monitoring and Comparing Pipelines
   ...within Batch Editor, CheckReg Tool, Stat Images per step
- Multi-subject Pipelines
  - ...via template batch, same sub-folders & Matlab script (subj.-loop)
- Integrating Own Code & Physiological Noise Correction
   ... by calling Matlab functions within Batch Editor, e.g. PhysIO Toolbox