Data Processing of Resting-State fMRI: DPARSF

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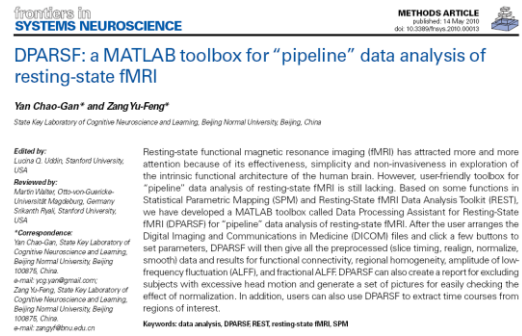
DPARSF



frontiers in SYSTEMS NEUROSCIENCE

METHODS ARTICLE
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DPARSF: a MATLAB toolbox for "pipeline" data analysis of resting-state fMRI

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Resting-state functional magnetic resonance imaging (fMRI) has attracted more and more attention because of its effectiveness, simplicity and non-invasiveness in exploration of the intrinsic functional architecture of the human brain. However, user-friendly toolbox for "pipeline" data analysis of resting-state fMRI is still lacking. Based on some functions in Statistical Parametric Mapping (SPM) and Resting-State fMRI Data Analysis Toolkit (REST), we have developed a MATLAB toolbox called Data Processing Assistant for Resting-State fMRI (DPARSF) for "pipeline" data analysis of resting-state fMRI. After the user arranges the Digital Imaging and Communications in Medicine (DICOM) files and click a few buttons to set parameters, DPARSF will then give all the preprocessed (slice timing, realign, normalize, smooth) data and results for functional connectivity, regional homogeneity, amplitude of low-frequency fluctuation (ALFF), and fractional ALFF. DPARSF can also create a report for excluding subjects with excessive head motion and generate a set of pictures for easily checking the effect of normalization. In addition, users can also use DPARSF to extract time courses from regions of interest.

Keywords: data analysis, DPARSF, REST, resting-state fMRI, SPM

(Yan and Zang, 2010)

DPARSF

Data Processing Assistant for Resting-State fMRI (DPARSF)

Yan and Zang, 2010. Front Syst Neurosci.

http://rfmri.org/DPARSF

DPABI

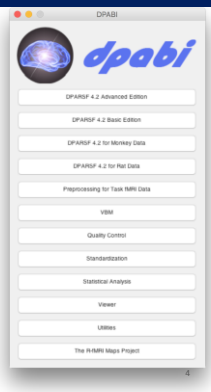
DPABI: a toolbox for Data Processing & Analysis of Brain Imaging

License: GNU GPL

Chao-Gan Yan
Programmer
Initiator

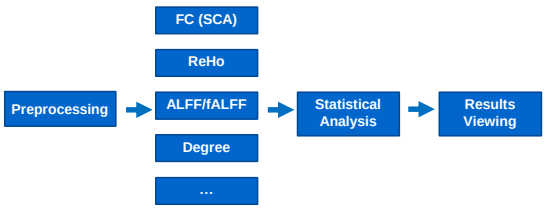
Xin-Di Wang
Programmer

http://rfmri.org/dpabi
http://dpabi.org



DPABI

Resting State fMRI Data Processing



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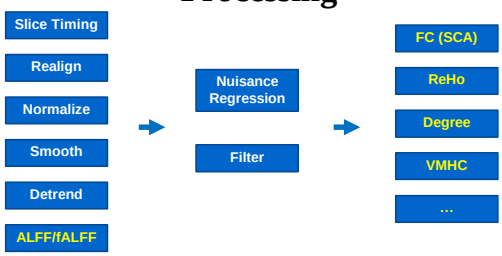
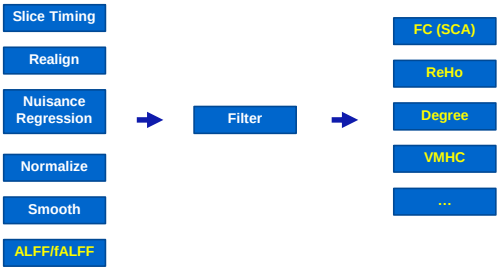
Resting State fMRI Data Processing



Calculate in MNI Space: TRADITIONAL order

DPABI

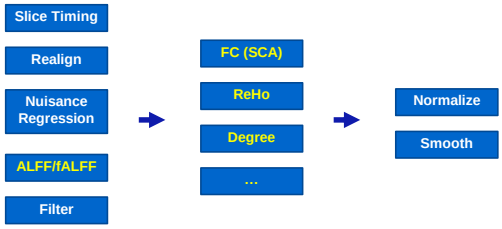
Resting State fMRI Data Processing



Calculate in MNI Space: alternative order

DPABI

Resting State fMRI Data Processing



Calculate in Original Space

Resting State fMRI Data Processing

Template Parameters

Data Organization

ProcessingDemoData.zip

FunRaw

- Sub_001
- Sub_002
- Sub_003

Functional DICOM data

T1Raw

- Sub_001
- Sub_002
- Sub_003

Structural DICOM data

http://rfmri.org/DemoData

Data Organization

ProcessingDemoData.zip

FunImg

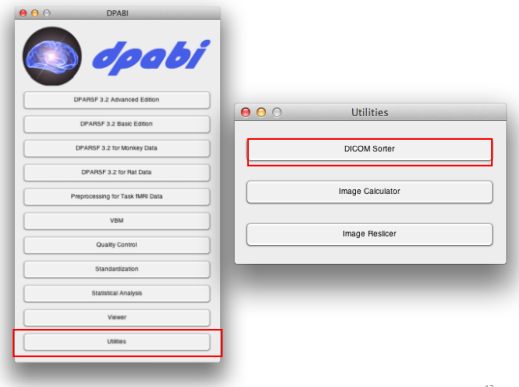
- Sub_001
- Sub_002
- Sub_003

Functional NIfTI data (.nii.gz., .nii or .img)

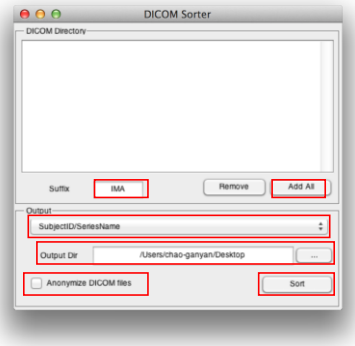
T1Img

- Sub_001
- Sub_002
- Sub_003

Structural NIfTI data (.nii.gz., .nii or .img)



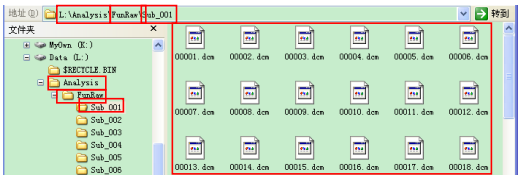
IMA
dcm
none



13

Data preparation

Arrange each subject's fMRI DICOM images in one directory, and then put them in "FunRaw" directory under the working directory.



SubjectSubjectDICOMFilesDirectory, please name as this Working directory

14

Data preparation

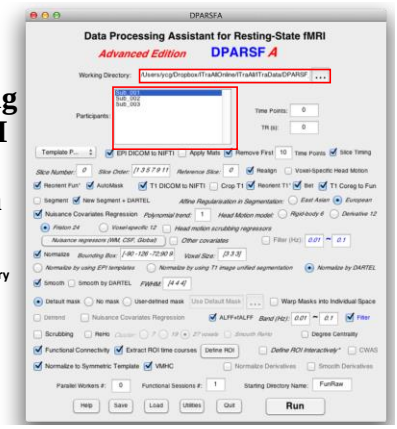
Arrange each subject's T1 DICOM images in one directory, and then put them in "T1Raw" directory under the working directory.

SubjectSubjectDICOMFilesDirectory, please name as this Working directory

15

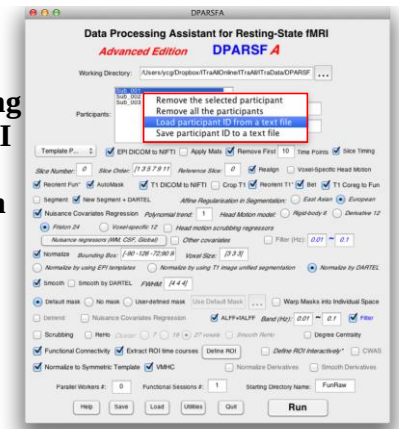
Preprocessing and R-fMRI measures Calculation

Working Dir where stored Starting Directory (e.g., FunRaw)
Detected participants



Preprocessing and R-fMRI measures Calculation

Detected participants



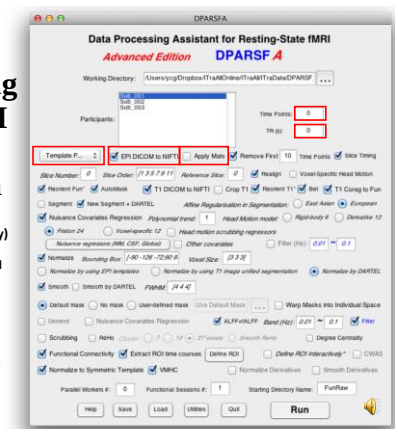
Preprocessing and R-fMRI measures Calculation

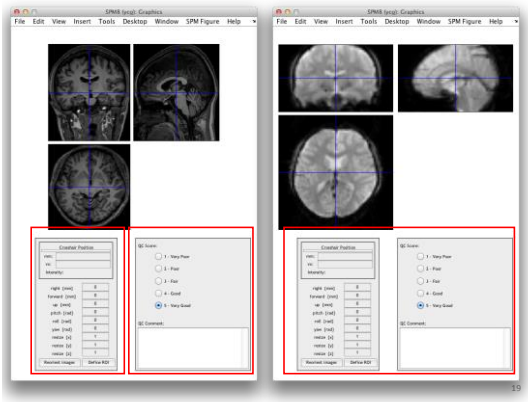
Number of time points (if 0, detect automatically)
TR
(if 0, detect from NifTI header)

Template Parameters

DICOM to NifTI, based on MRIcroN's dcm2nii

Apply reorientation matrices





19

Preprocessing and R-fMRI measures Calculation

Apply reorientation matrices:

ReorientMats

Rename to:

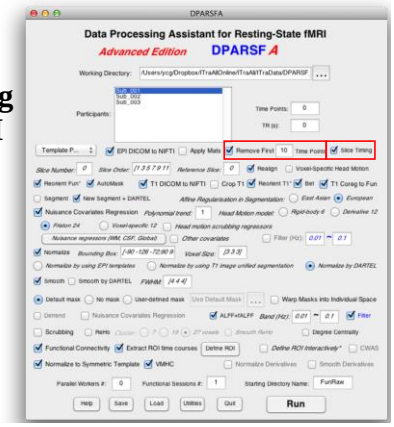
DownloadedReorientMats

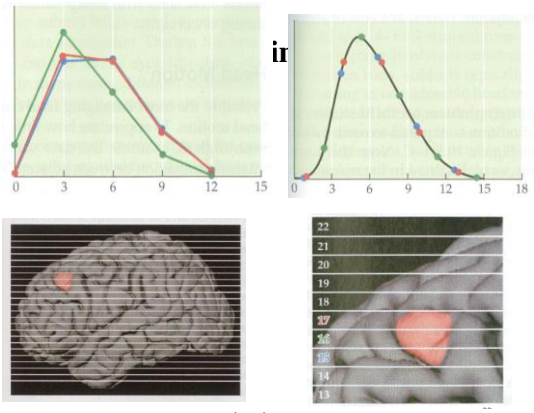
20

Preprocessing and R-fMRI measures Calculation

Remove several first time points

Slice Timing





Huettel et al., 2004

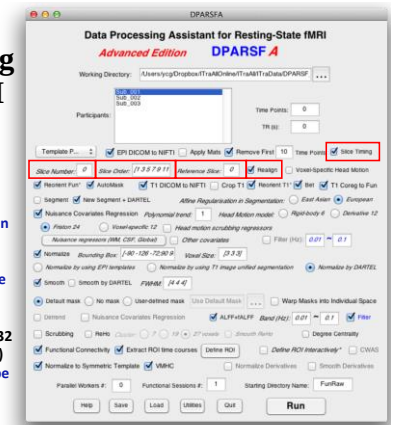
Preprocessing and R-fMRI measures Calculation

Total slice number

(if 0, The slice order is then assumed as interleaved scanning: [1:2:SliceNumber,2:2:SliceNumber]. The reference slice is set to the slice acquired at the middle time of each TR (i.e., SHOULD BE CAUTIOUS!!!)

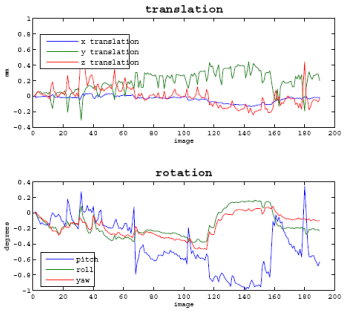
Slice order: 1:2:33,2:2:32 (Interleaved scanning)

Slice acquired at the middle time of each TR



Realign

Why?



24

Realign

Check head motion:

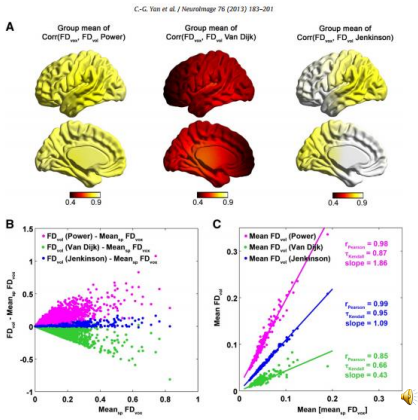
{WorkingDir}\RealignParameter\Sub_xxx:

rp_*.txt: realign parameters

FD_Power_*.txt: Frame-wise Displacement (Power et al., 2012)

FD_VanDijk_*.txt: Relative Displacement (Van Dijk et al., 2012)

FD_Jenkinson_*.txt: Relative RMS (Jenkinson et al., 2002)



(Yan et al., Neuroimage 2013)

Realign

Check hea

{WorkingD

ExcludeSu

Excluding Criteria: 2.5mm and 2.5 degree in max head motion
None

Excluding Criteria: 2.0mm and 2.0 degree in max head motion
Sub_013

Excluding Criteria: 1.5mm and 1.5 degree in max head motion
Sub_013

Excluding Criteria: 1.0mm and 1.0 degree in max head motion
Sub_007
Sub_012
Sub_013
Sub_017
Sub_018

Realign

Check head motion:

HeadMotion.csv: head motion characteristics for each subject (e.g., max or mean motion, mean FD, # or % of FD>0.2)

Threshold:

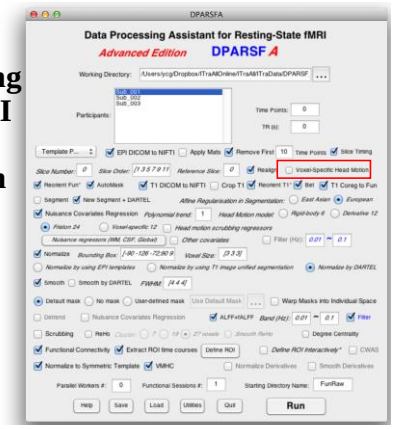
Group mean (mean FD) + 2 * Group SD (mean FD)

Yan et al., in press Neuroimage; Di Martino, in press, Mol Psychiatry

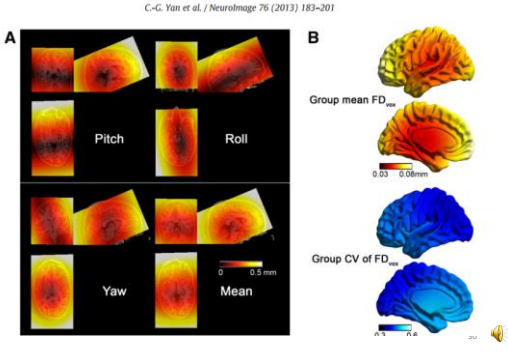
Preprocessing and R-fMRI measures Calculation

Voxel-Specific Head Motion Calculation

(Yan et al., Neuroimage 2013)



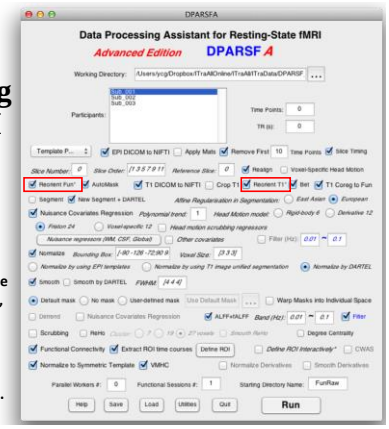
Voxel-Specific Head Motion Calculation

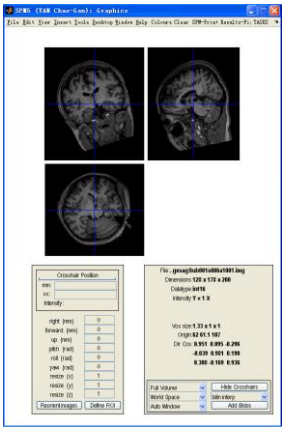


Preprocessing and R-fMRI measures Calculation

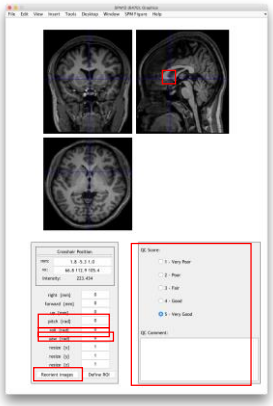
Reorient Interactively

This step could improve the accuracy in coregistration, segmentation and normalization, especially when images had a bad initial orientation. Also can take as a QC step.





32

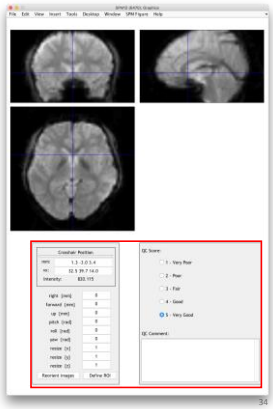


33

Display the mean image after realignment. (Could take this step as a QC procedure.)

The reorientation effects on and realigned functional images and voxel-specific head motion images.

QC scores and comments are stored at {WorkDir}/QC

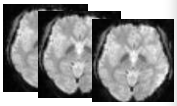


34

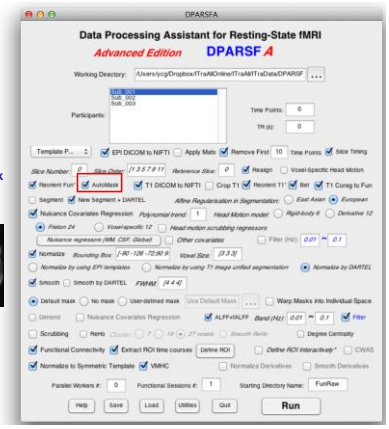
Automask generation

For checking EPI coverage and generating group mask

FunImgAR/Sub_001



Masks/AutoMasks/

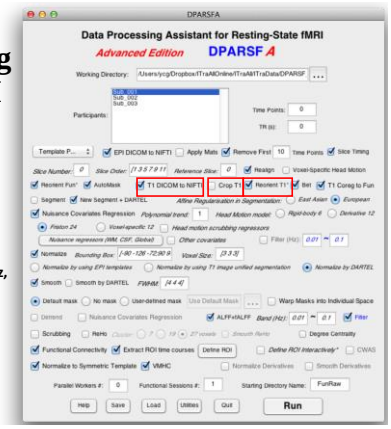


Preprocessing and R-fMRI measures Calculation

T1 DICOM files to NIfTI (based on MRIcroN's dcm2nii)

Crop T1 image (.nii, .nii.gz, .img) (based on MRIcroN's Dcm2nii)

Reorient T1 image Interactively

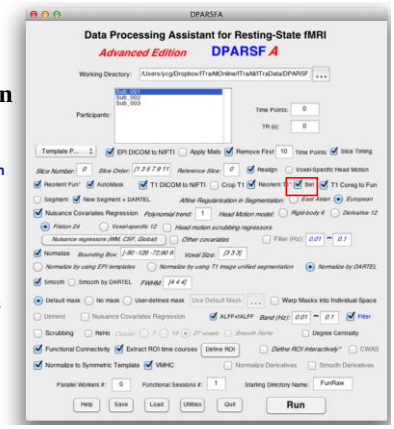


Brain extraction (Skullstrip)

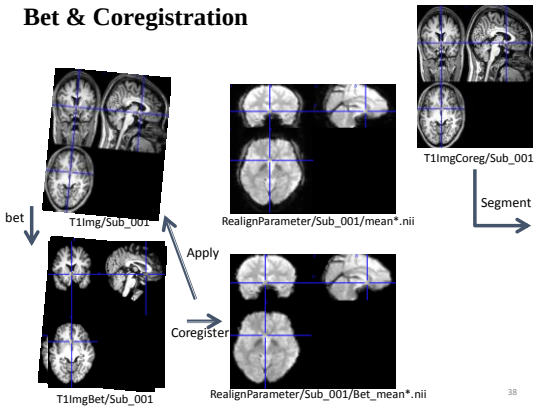
For better coregistration

For Linux and Mac:
Need to install FSL or dpabi docker.

For Windows:
Thanks to Chris Rorden's compiled version of bet in MRIcroN, our modified version can work on NIfTI images directly.



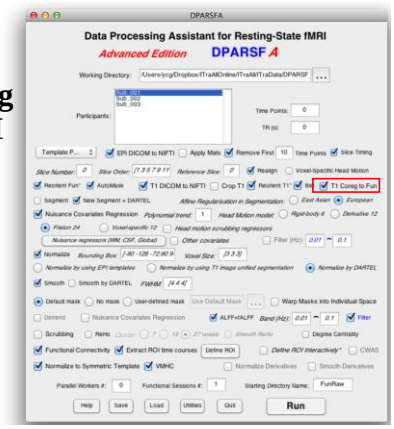
Bet & Coregistration



38

Preprocessing and R-fMRI measures Calculation

Coregister T1 image to functional space

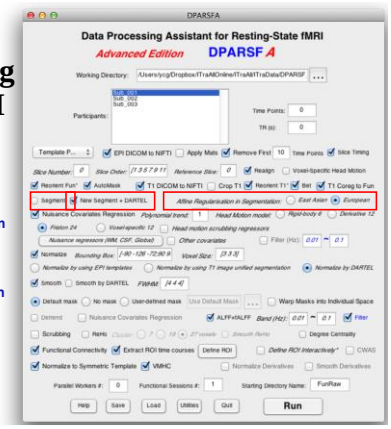


Preprocessing and R-fMRI measures Calculation

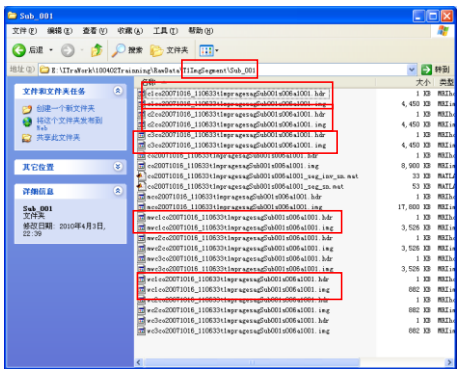
Unified Segmentation.
Information will be used in spatial normalization.
(In SPM12 only Segment)

New Segment and DARTEL.
Information will be used in spatial normalization.

Affine regularisation in segmentation



By-Product: VBM



GM in original space

WM in original space

CSF in original space

Modulated GM in normalized space

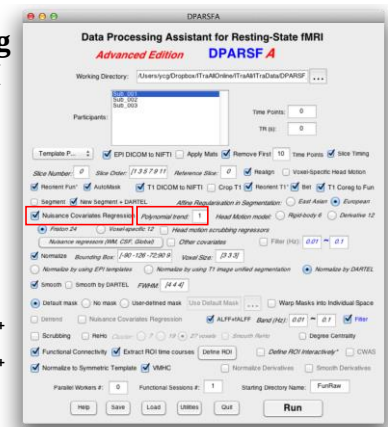
GM in normalized space

41

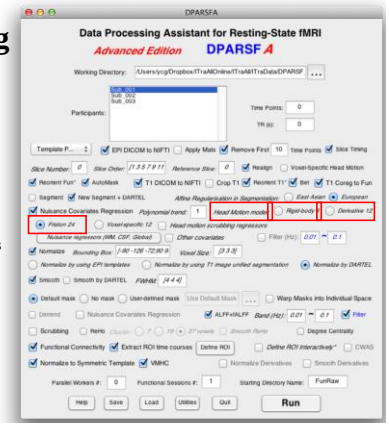
Preprocessing and R-fMRI measures Calculation

Nuisance Covariates Regression

Polynomial trends as regressors:
0: constant (no trends)
1: constant + linear trend (same as linear detrend)
2: constant + linear trend + quadratic trend
3: constant + linear trend + quadratic trend + cubic trend
...

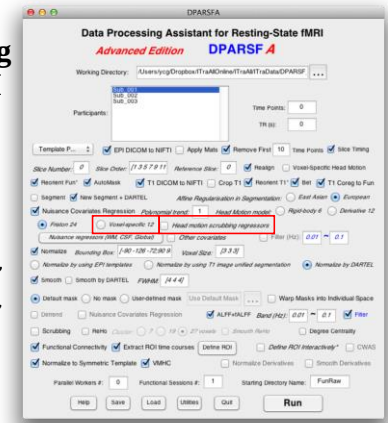


Preprocessing and R-fMRI measures Calculation



Head Motion regression model
6 head motion parameters
Friston 24-parameter model: 6 head motion parameters, 6 first derivatives, 6 head motion parameters one time point before, and the 12 corresponding squared items (Friston et al., 1996).

Preprocessing and R-fMRI measures Calculation



Voxel-specific 12-parameter model: the 3 voxel-specific translation motion parameters in x, y, z, the same 3 parameters for one time point before, and the 6 corresponding squared items

Head Motion Scrubbing Regressors

Each "bad" time point defined by FD will be used as a separate regressor.

45

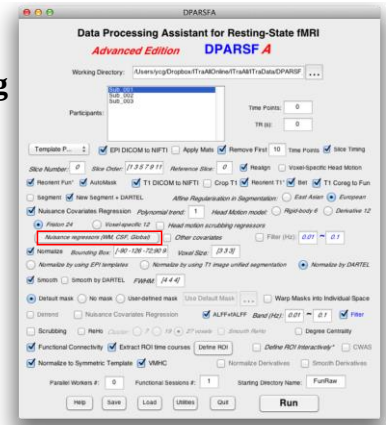
Yan et al., 2013, Neuroimage

Table 3
Summary recommendations.

Summary recommendation
• Individual-level correction with the Friston-24 model is recommended. • Additionally, group-level correction for mean FD is recommended, and removes the need for scrubbing. • If group-level correction for mean FD is contraindicated or not practical, then individual-level correction with scrubbing is recommended for PCC-FC, VMHC and ReHo (not ALFF[a], fALFF, DC[b]).
Additional considerations
• Inclusion of global signal regression at the individual-level produces robust reductions in the relationships between motion and R-fMRI measures across participants – particularly for measures without Z-standardization. The benefits of GSR need to be balanced against potential risks for introduction of artifact in the specific analyses employed. • For studies limited to low motion datasets, the utility of higher-order Friston 24 model decreases. In this case, we recommend consideration of lower-order (i.e., 6 or 12-parameter) models to minimize the potential for over-fitting, as noted in Satterthwaite et al. (2013). • fALFF appeared to be relatively insensitive to motion correction strategies in the present work. Prior work (Satterthwaite et al., 2012) has suggested greater sensitivity in higher motion populations; as such we recommend continued application of correction procedures at the present time.

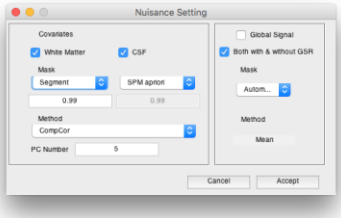
[a] Recommendations against scrubbing for ALFF and fALFF apply to commonly employed FFT-based implementations (see Limitations and future directions section for alternatives).
[b] Recommendations against scrubbing for DC were based on concerns regarding its ability to compromise graph construction (see The ability of motion correction strategies to decrease residual relationships between motion and R-fMRI metrics at group-level section for demonstration).

Preprocessing and R-fMRI measures Calculation



Nuisance Regressors (WM, CSF, Global)

Nuisance Regression

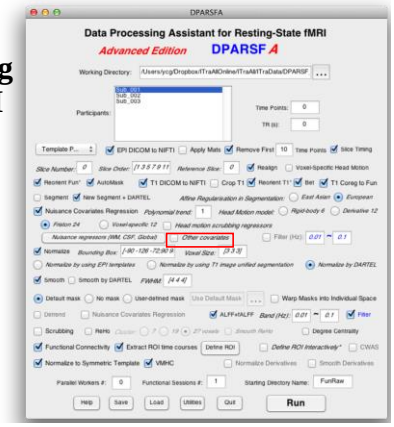


- Mask based on segmentation or SPM apriori
- CompCor or mean [note: for CompCor, detrend (demean) and variance normalization will be applied before PCA, according to Behzadi et al., 2007]
- Global Signal based on Automask

48

Preprocessing and R-fMRI measures Calculation

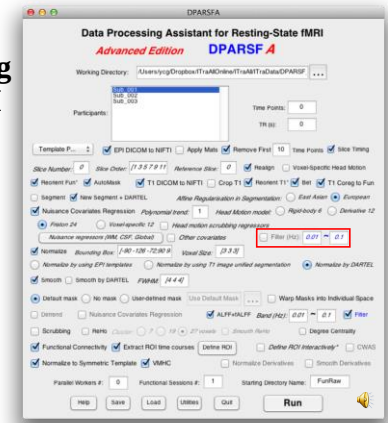
Define other covariates



Preprocessing and R-fMRI measures Calculation

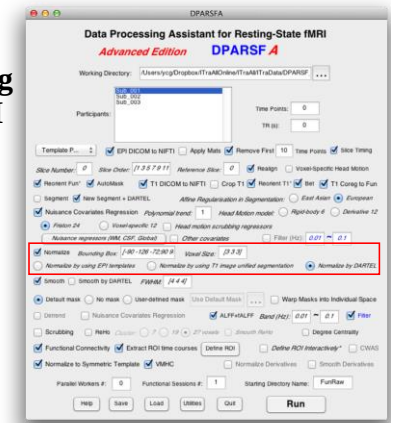
Filtering

The filtering parameters will be used later (Blue checkbox).

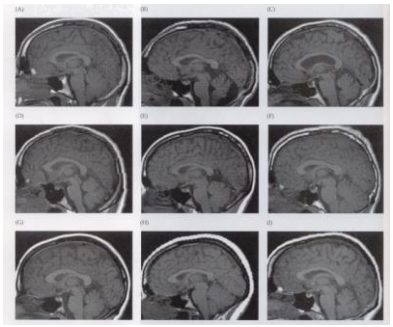


Preprocessing and R-fMRI measures Calculation

Spatial Normalization



Normalize



Huettel et al., 2004

52

Normalize

Methods:

I. Normalize by using EPI templates

II. Normalize by using T1 image unified segmentation

➡ III. Normalize by using DARTEL

IV. Normalize by using T1 templates (hidden)

53

Normalize

III. Normalize by using DARTEL

- Structural image was coregistered to the mean functional image after motion correction
- The transformed structural image was then segmented into gray matter, white matter, cerebrospinal fluid by using a unified segmentation algorithm (New Segment)
- DARTEL: create template
- DARTEL: Normalize to MNI space. The motion corrected functional volumes were spatially normalized to the MNI space using the normalization parameters estimated in DARTEL.

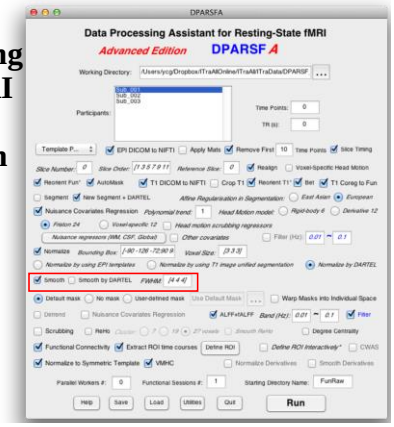
54

Preprocessing and R-fMRI measures Calculation

Smooth

For ReHo, Degree Centrality: don't smooth before calculation

FWHM kernel settings can be applied to later steps



Smooth

Why?

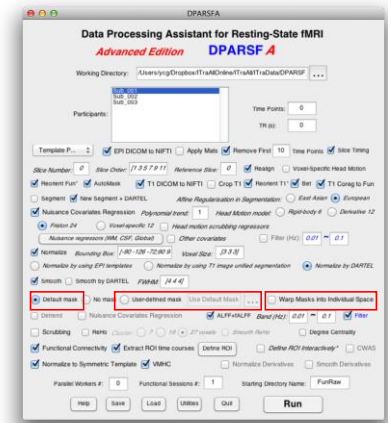
- **Reduce the effects of bad normalization**
- **Increase SNR**
- **…**

56

Mask

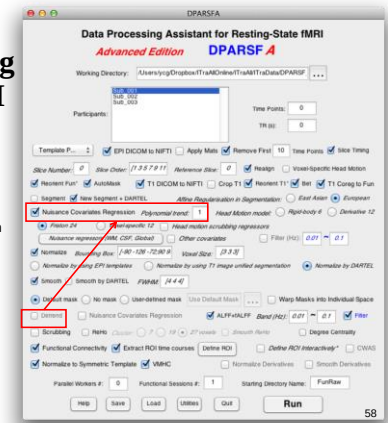
Default mask: SPM5 apriori mask (brainmask.nii) thresholded at 50%.
User-defined mask

Warp the masks into individual space by the information of DARTEL or unified segmentation.



Preprocessing and R-fMRI measures Calculation

Linear detrend (NO need since included in nuisance covariate regression)

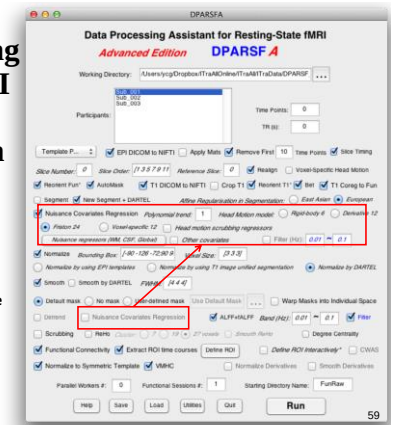


58

Preprocessing and R-fMRI measures Calculation

Nuisance Covariates Regression

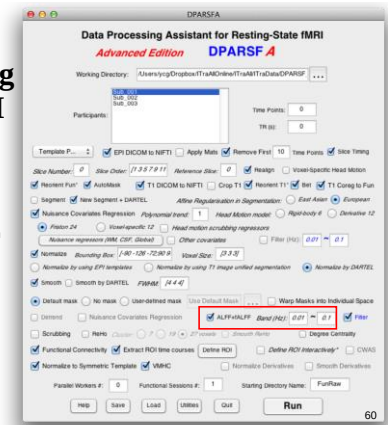
If needed, then use the parameters set in the upper section.



59

Preprocessing and R-fMRI measures Calculation

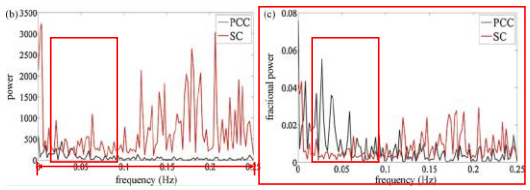
ALFF and fALFF calculation (Zang et al., 2007; Zou et al., 2008)



60

ALFF/fALFF

Amplitude of low frequency fluctuation / Fractional ALFF



PCC: posterior cingulate cortex

SC: suprasellar cistern

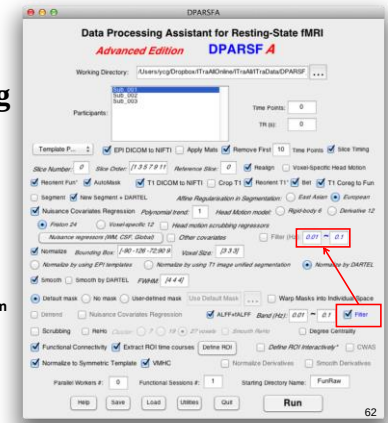
Zang et al., 2007; Zou et al., 2008

61

Preprocessing and R-fMRI measures Calculation

Filtering

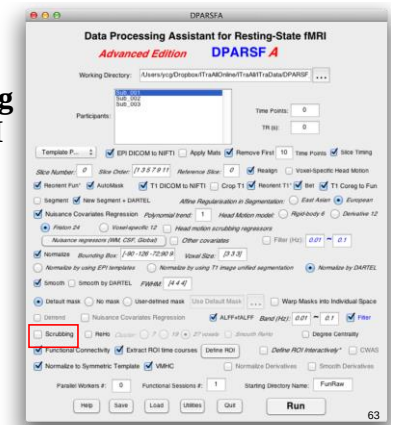
Use the parameters set in the blue edit boxes.



62

Preprocessing and R-fMRI measures Calculation

Scrubbing



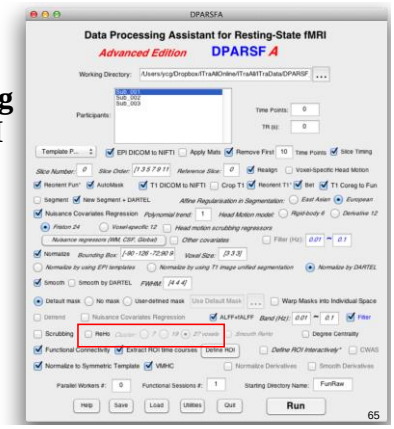
63

The "bad" time points defined by FD_Power (Power et al., 2012) will be interpolated or deleted as the specified method.

64

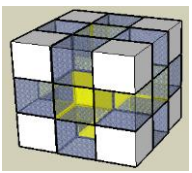
Preprocessing and R-fMRI measures Calculation

Regional Homogeneity (ReHo) Calculation (Zang et al., 2004)



65

ReHo (Regional Homogeneity)



$$W = \frac{\Sigma(R_i)^2 - n(\overline{R})^2}{\frac{1}{12}K^2(n^3 - n)}$$

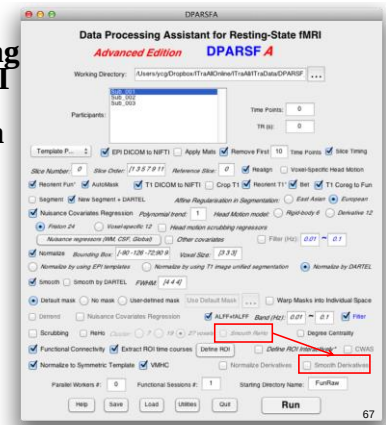
Zang et al., 2004

Zang YF, Jiang TZ, Lu YL, He Y, Tian LX (2004) Regional homogeneity approach to fMRI data analysis. Neuroimage 22: 394–400.

66

Preprocessing and R-fMRI measures Calculation

Regional Homogeneity (ReHo) Calculation (Zang et al., 2004)

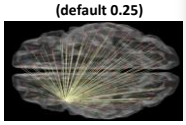


67

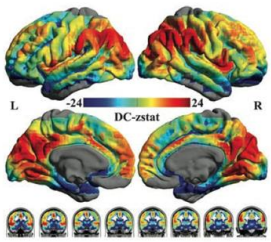
Preprocessing and R-fMRI measures Calculation

Degree Centrality Calculation (Buckner et al., 2009; Zuo et al, 2012)

> r Threshold (default 0.25)



68



Zuo et al., 2012

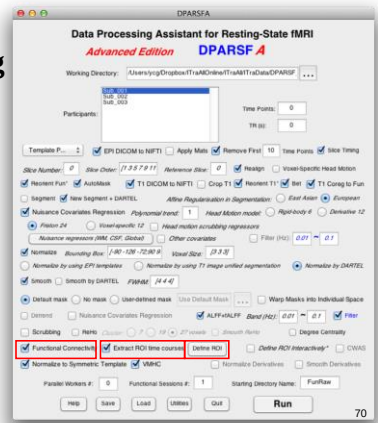
69

Preprocessing and R-fMRI measures Calculation

Functional Connectivity (voxel-wise seed based correlation analysis)

Extract ROI time courses (also for ROI-wise Functional Connectivity)

Define ROI



70

Define ROI

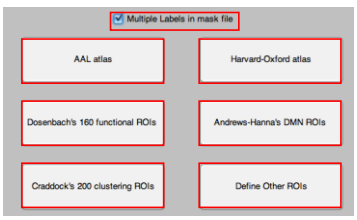
Multiple labels in mask file: each label is considered as one ROI

Dosenbach et al., 2010

Andrews-Hanna et al., 2010

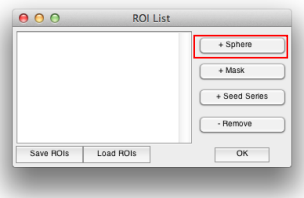
Craddock et al., 2011

Define other ROIs



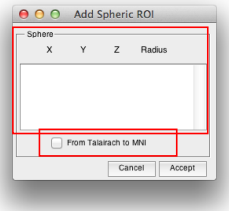
71

Define ROI



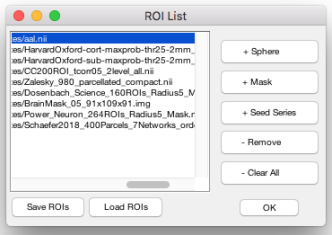
72

Define ROI



73

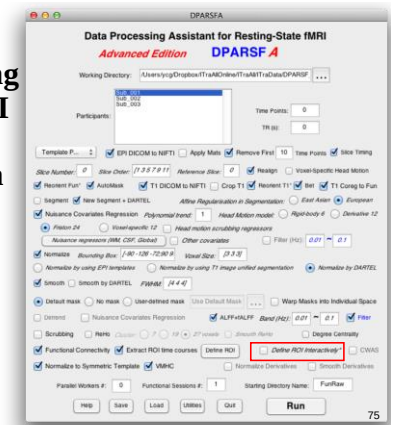
Define ROI



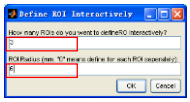
74

Preprocessing and R-fMRI measures Calculation

Define ROI Interactively



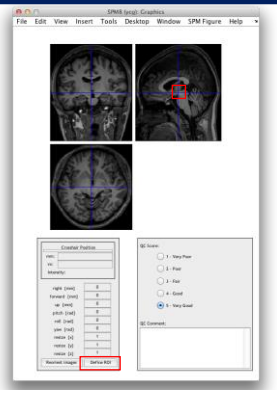
Define ROI



0 means define ROI Radius for each ROI seperately

76

Define ROI



77

Functional Connectivity

You will get the Voxel-wise functional connectivity results of each ROI in {working directory}\Results\FC:

zROI1FCMap_Sub_001.img

zROI2FCMap_Sub_001.img

For ROI-wise results, please see {working directory}\Results\FunImgARCW*_ROISignals.

78

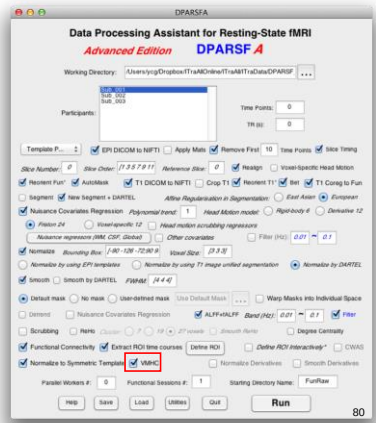
Preprocessing and R-fMRI measures Calculation

Voxel-mirrored homotopic connectivity (VMHC) (Zuo et al., 2010)

Prepare for VMHC: Further register to a symmetric template

Preprocessing and R-fMRI measures Calculation

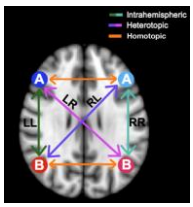
Voxel-mirrored homotopic connectivity (VMHC) (Zuo et al., 2010)



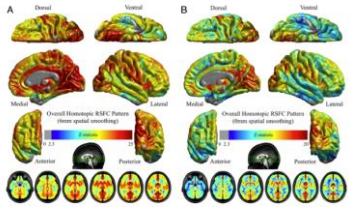
VMHC

1) Get the T1 images in MNI space (e.g., wco*.img or wco*.nii under T1ImgNewSegment or T1ImgSegment) for each subject, and then create a mean T1 image template (averaged across all the subjects).
2) Create a symmetric T1 template by averaging the mean T1 template (created in Step 1) with it's flipped version (flipped over x axis).
3) Normalize the T1 image in MNI space (e.g., wco*.img or wco*.nii under T1ImgNewSegment or T1ImgSegment) for each subject to the symmetric T1 template (created in Step 2), and apply the transformations to the functional data (which have been normalized to MNI space beforehand). Please see a reference from Zuo et al., 2010.

81



Gee et al., 2011



Zuo et al., 2010

82

Preprocessing and R-fMRI measures Calculation

Parallel Workers (if parallel computing toolbox is installed)

Each subject is distributed into a different worker. (Except DARTEL-Create Template)

Preprocessing and R-fMRI measures Calculation

Multiple functional sessions

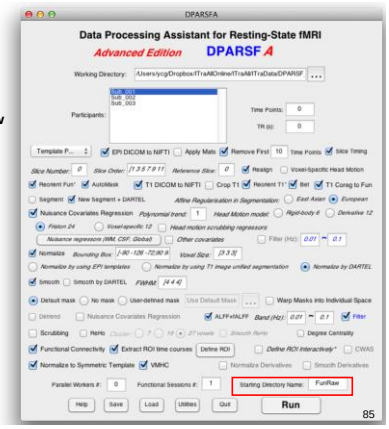
1st session: FunRaw
2nd session: S2_FunRaw
3rd session: S3_FunRaw
…

Starting Directory Name

If you do not start with raw DICOM images, you need to specify the Starting Directory Name.

E.g. "FunImgARW" means you start with images which have been slice timed, realigned and normalized.

Abbreviations:
A - Slice Timing
R - Realign
W - Normalize
S - Smooth
D - Detrend
F - Filter
C - Covariates Removed
B - ScruBBing



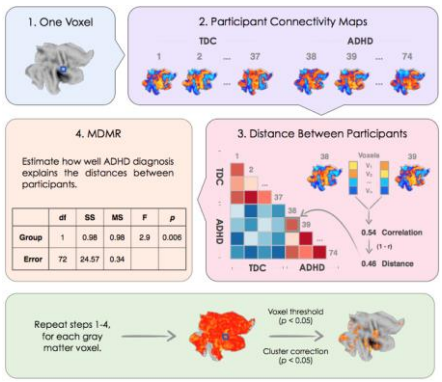
85

Preprocessing and R-fMRI measures Calculation

Connectome-wide association studies based on multivariate distance matrix regression (Shehzad et al., 2014)

Resource consuming as compared to other measures

86

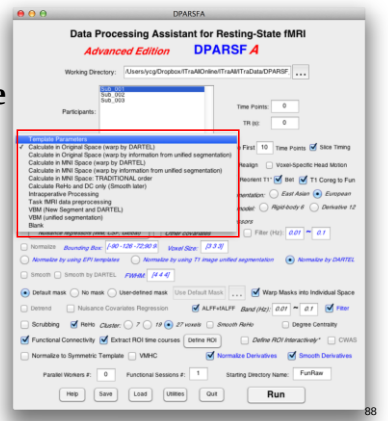


Shehzad et al., 2014. Neuroimage

87

Resting State fMRI Data Processing

Template Parameters

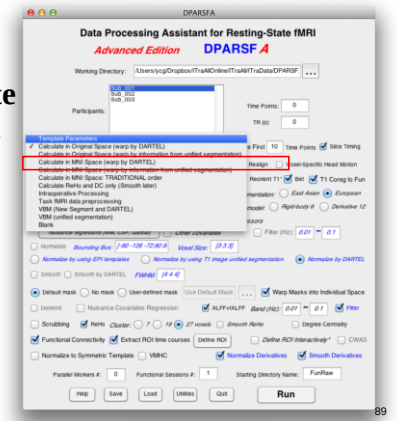


88

Resting State fMRI Data Processing

Calculate in MNI space

Calculate in Original space

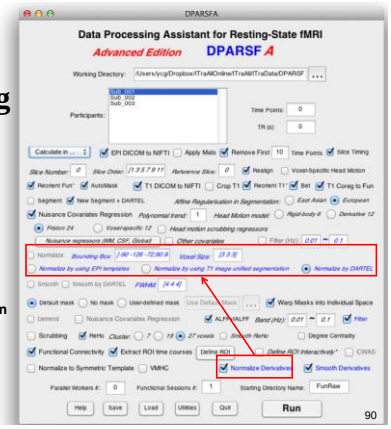


89

Preprocessing and R-fMRI measures Calculation

Normalize measures (derivatives) calculated in original space into MNI space

Use the parameters set in the upper section.

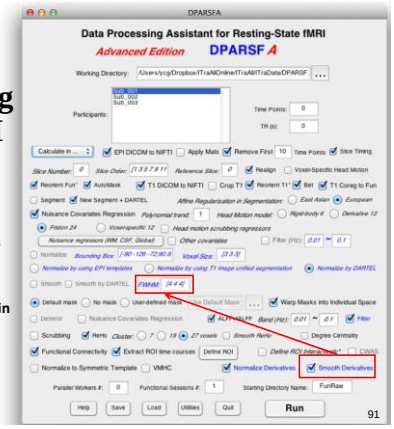


90

Preprocessing and R-fMRI measures Calculation

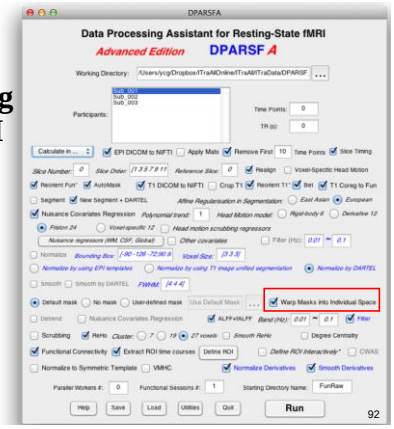
Smooth R-fMRI measures (derivatives)

Use the parameters set in the upper section.



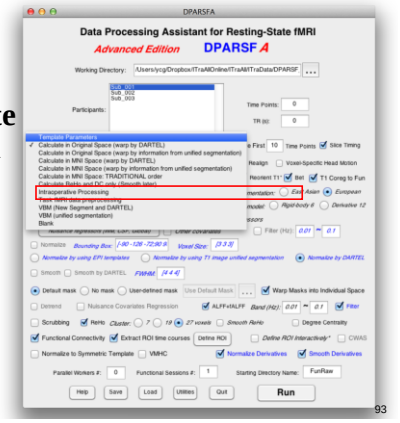
Preprocessing and R-fMRI measures Calculation

Warp masks into original space



Resting State fMRI Data Processing

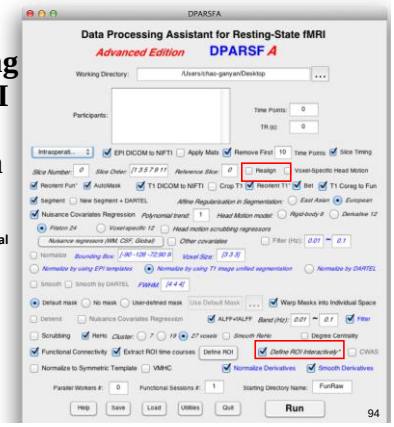
Intraoperative Processing



Preprocessing and R-fMRI measures Calculation

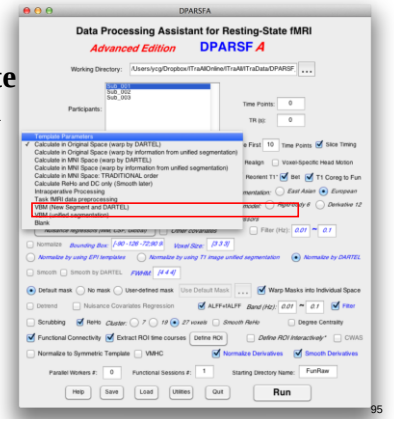
No realign since there is no head motion. DPARSFA will generate the mean functional images automatically.

Define ROI Interactively



Resting State fMRI Data Processing

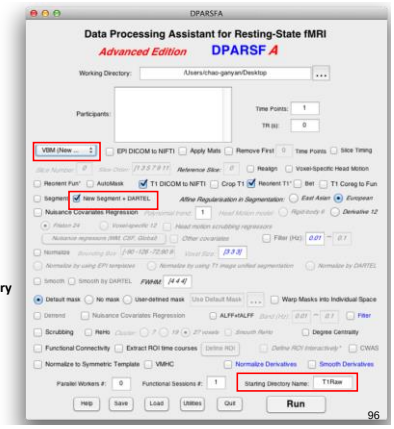
VBM



VBM

Only New Segment + DARTEL is checked

Define the Starting Directory Name as T1Raw



Resting State fMRI Data Processing

Blank

97

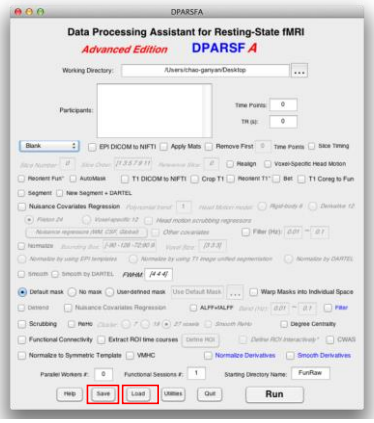
Blank

98

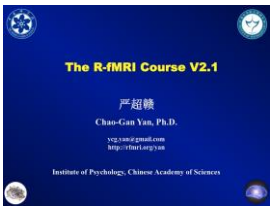
Save and Load Parameters

Save parameters to *.mat

Load parameters from *.mat



Further Help



http://rfmri.org/Course

http://wiki.rfmri.org

The R-fMRI Journal Club

Official Account: RFMRILab

100

Acknowledgments

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Child Mind Institute
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101

Thanks for your attention!

102