




心理统计

第二十七讲：脑影像统计2

——脑影像数据处理与DPARSF程序实践

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Outline

- 脑影像统计1：脑影像数据分析原理
- 脑影像统计2：脑影像数据处理与DPARSF程序实践
- 脑影像统计3：脑影像数据统计分析

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DPARSF

frontiers in SYSTEMS NEUROSCIENCE

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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)

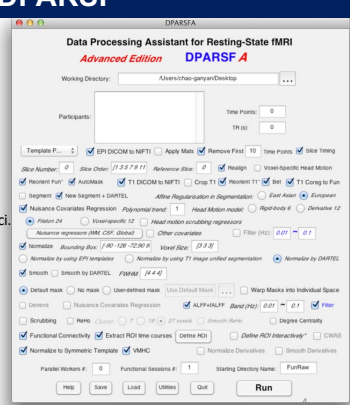
3

DPARSF

Data Processing Assistant for Resting-State fMRI (DPARSF)

Yan and Zang, 2010. Front Syst Neurosci.

<http://rfmri.org/DPARSF>



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DPABI

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

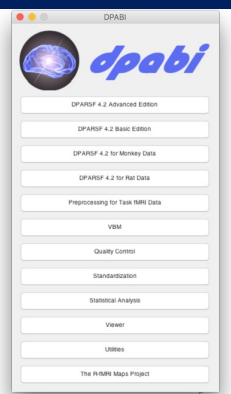
License: GNU GPL




Chao-Gan Yan
Programmer
Initiator

Xin-Di Wang
Programmer

<http://rfmri.org/dpabi>
<http://dpabi.org>



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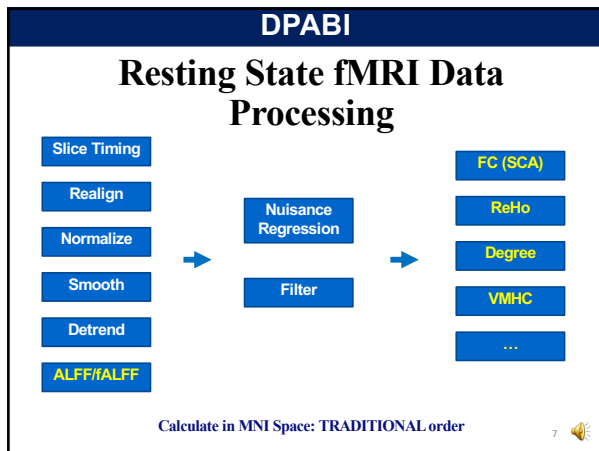
DPABI

Resting State fMRI Data Processing

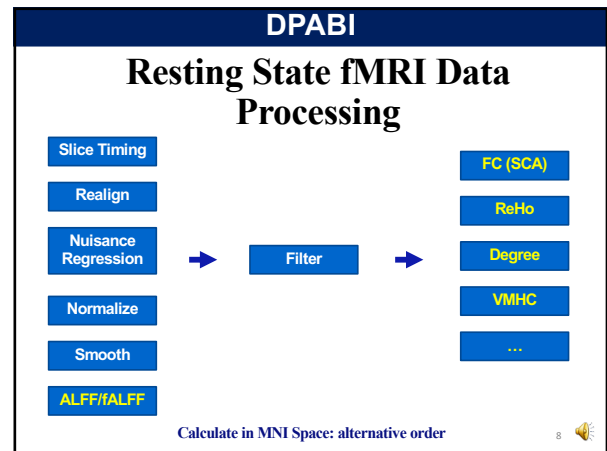
```

graph LR
    subgraph Preprocessing
        FC_SCA[FC (SCA)]
        ReHo[ReHo]
        ALFF_fALFF[ALFF/fALFF]
        Degree[Degree]
        Dots[...]
    end
    subgraph Statistical_Analysis
        FC_SCA
        ReHo
        ALFF_fALFF
        Degree
        Dots
    end
    subgraph Results_Viewing
        Results[Results Viewing]
    end
    Preprocessing --> Statistical_Analysis
    Statistical_Analysis --> Results_Viewing
  
```

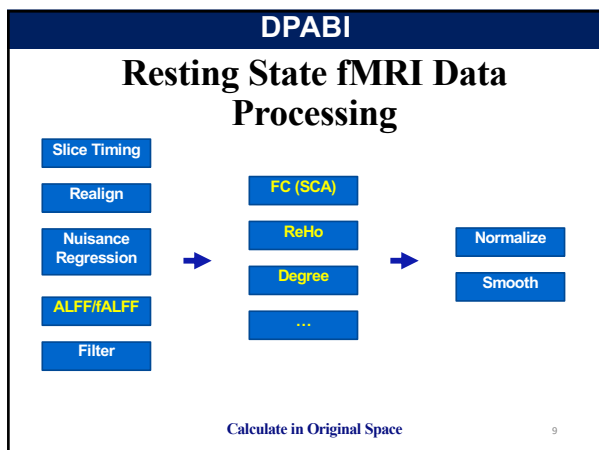
6



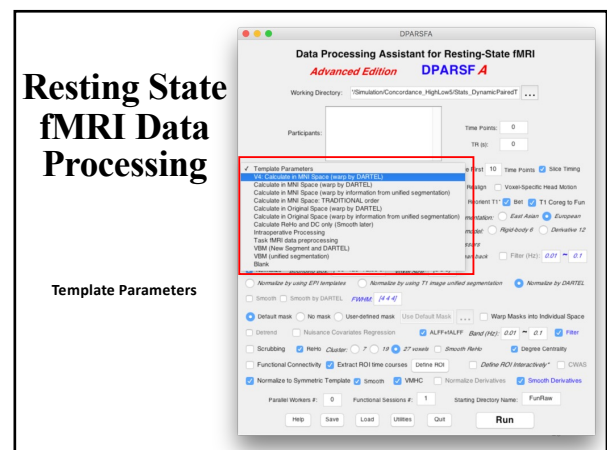
7



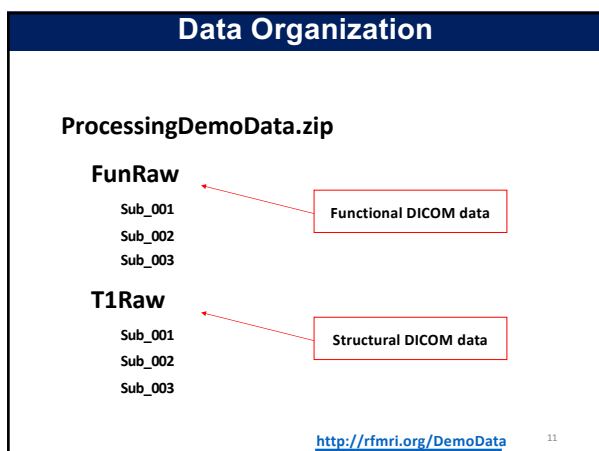
8



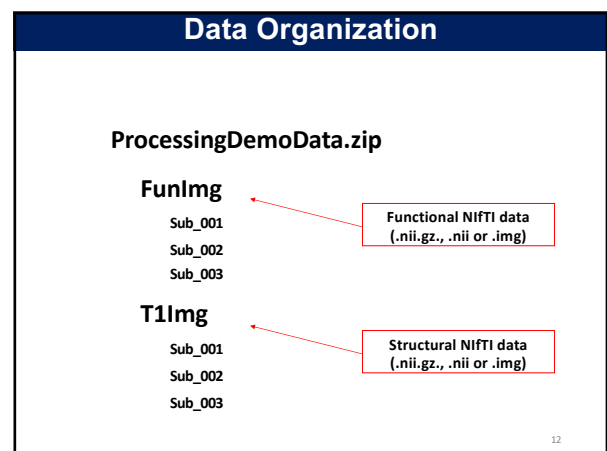
9



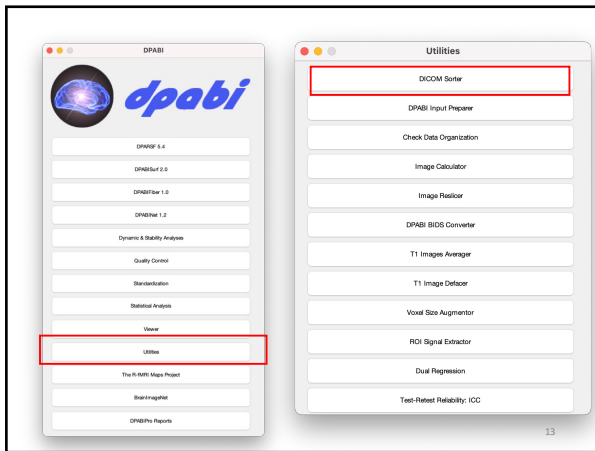
10



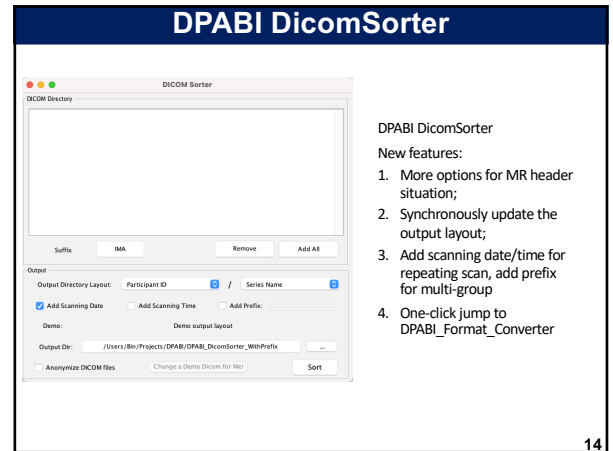
11



12

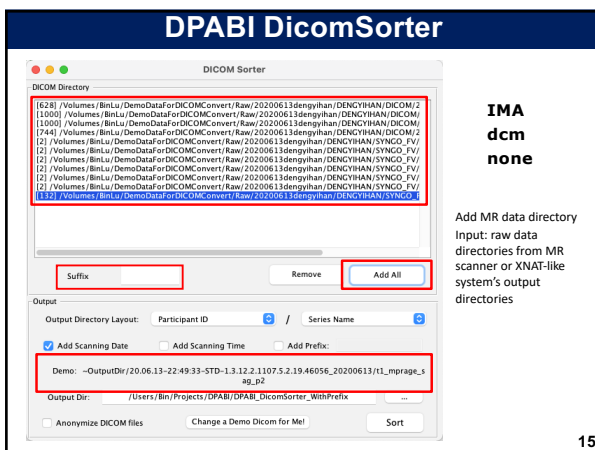


13



14

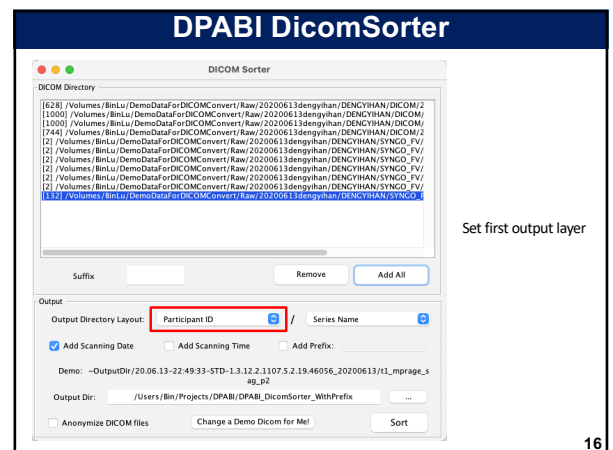
- DPABI DicomSorter
- New features:
1. More options for MR header situation;
 2. Synchronously update the output layout;
 3. Add scanning date/time for repeating scan, add prefix for multi-group
 4. One-click jump to DPABI_Format_Converter



15

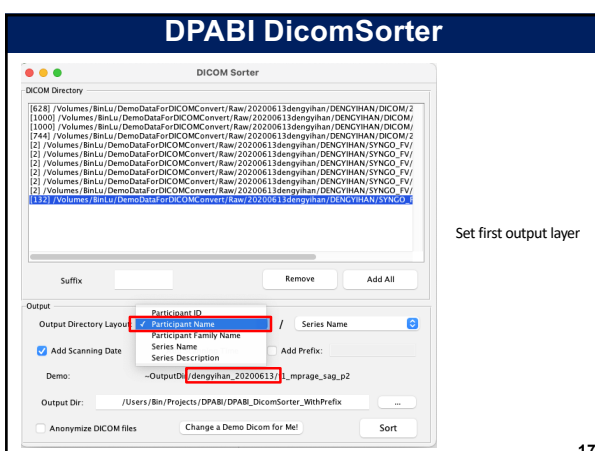
IMA
dcm
none

Add MR data directory
Input: raw data
directories from MR
scanner or XNAT-like
system's output
directories



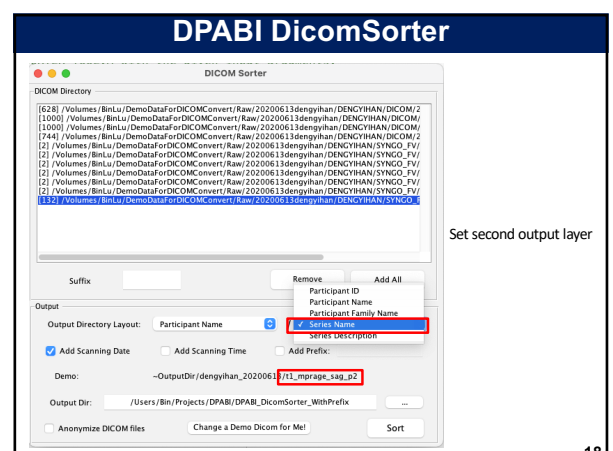
16

Set first output layer



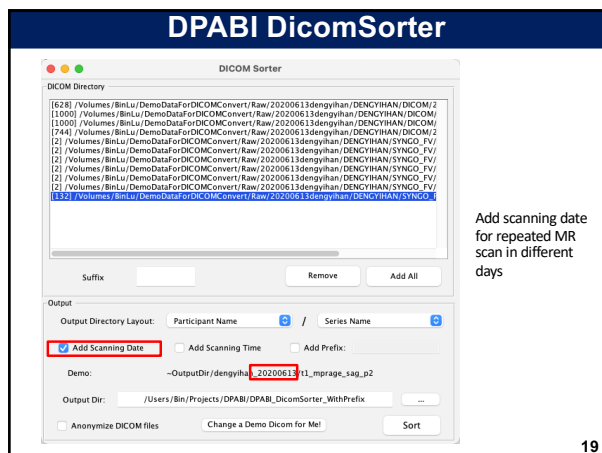
17

Set first output layer



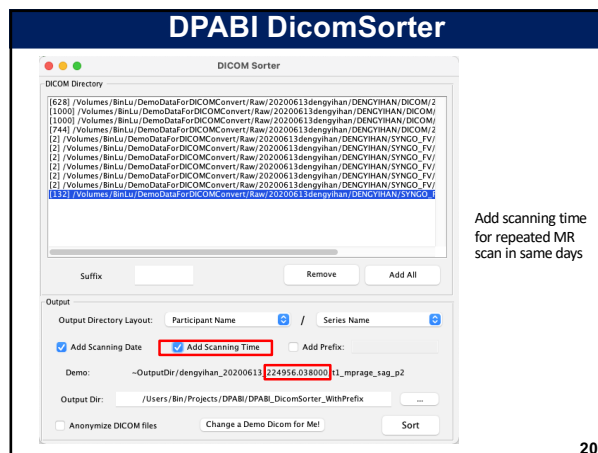
18

Set second output layer



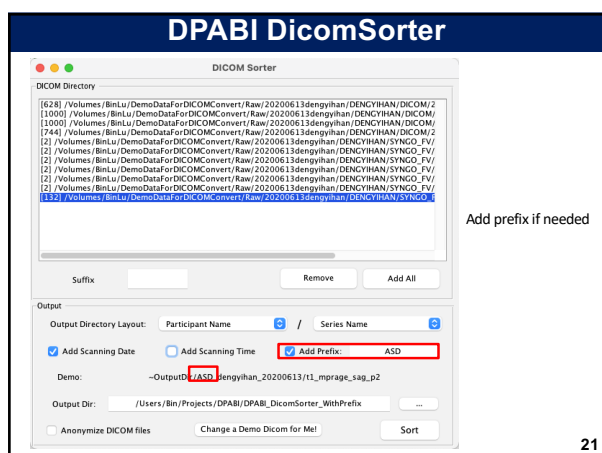
Add scanning date
for repeated MR
scan in different
days

19



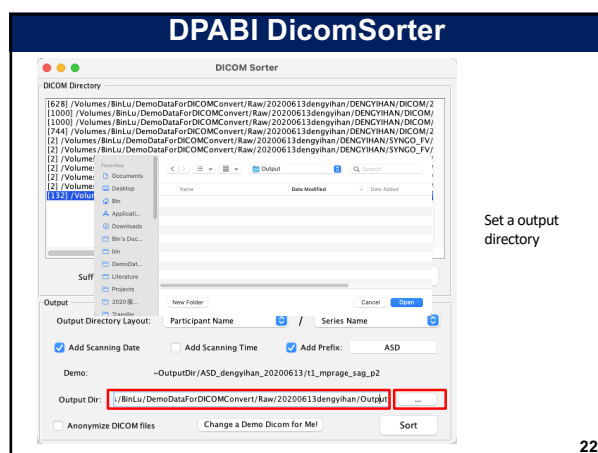
Add scanning time
for repeated MR
scan in same days

20



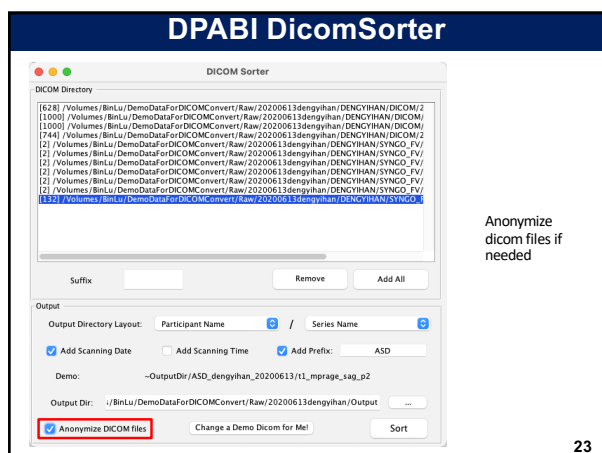
Add prefix if needed

21



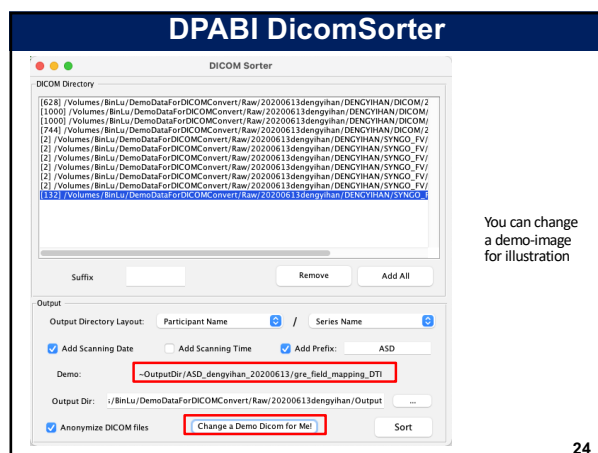
Set a output
directory

22



Anonymize
dicom files if
needed

23



You can change a demo-image for illustration

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DPABI DicomSorter

DICOM Sorter

DICOM Directory

(628) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\DICOM\Z
(1000) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\DICOM\Z
(1000) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\DICOM\Z
(744) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\DICOM\Z
(2) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\SYNGCO_FV
(2) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\SYNGCO_FV
(2) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\SYNGCO_FV
(2) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\SYNGCO_FV
(2) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\SYNGCO_FV
(2) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\SYNGCO_FV
(132) F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan\DENGYIHAN\SYNGCO_FV

Run!

Suffix Remove Add All

Output

Output Directory Layout: Participant Name / Series Name

☒ Add Scanning Date ☐ Add Scanning Time ☒ Add Prefix: ASD

Demo: -OutputDir\ASD_dengyihan_20200613\1_mrpage_sag_p2

Output Dir: F:\Volumes\BinLu\DemoDataForDICOMconvert\Raw\20200613dengyihan

☐ Anonymize DICOM files ☐ Change a Demo Dicom for Me! Sort

25

25

[illegible]

26

[illegible]

27

Coming soon...

```

ASD_RAL1dcm_20101224
0000_3_P171900E
0000_3_P171900E
0000_A01_cali3winim
0000_0a772f1a10
0000_0a772f1a10
0000_0a772f00P1L1R
0000_0a0d1a0a0t
0000_00a01f1a10
0000_Sag01r0a0t
0000_A01_cali3winim
0001_A01_3a1d_0a_REST
0001_0a_3a1d_0a_REST
0001_A01_d01r_0a0d
0001_3_P171900E
0000_A01_d01r_0a0d
0700_A01dcm01FunRawOffFaint(m02)
0700_C000001A01dcm01FunRawOffFaint
0000_M000000a0a0t
2000S_Screensave
ASD_RAL1dcm_20101229
0000_3_P171900E
0000_A01_cali3winim
0000_0a772f1a10
0000_0a772f1a10
0000_0a772f00P1L1R
0000_0a0d1a0a0t
0000_Sag01r0a0t
0000_A01_3a1d_0a_REST
0000_A01_cali3winim
0001_A01_3a1d_0a_REST
0000_A01_d01r_0a0d
0000_C000001A01dcm01FunRawOffFaint(m02)
0000_C000001A01dcm01FunRawOffFaint
0000_M000000a0a0t
0000_M000000a0a0t
2000S_Screensave
ASD_RAL1dcm_20101212
0000_3_P171900E
0000_A01_cali3winim
0000_0a772f1a10
0000_0a772f00P1L1R
0000_0a772f1a10
2000S_Screensave
ASD_Che0dcm_20100817
0000_3_P171900E
0000_A01_cali3winim

```

001.dcm

FunRaw

???

Data Organization

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DPABI Input Preparer

DPABI Input Preparer

InputDir: /Users/panzhang/Desktop/17112017/17112017/17112017/17112017/GoogleDrive/17112017/

OutputDir: /Users/panzhang/Desktop/17112017/17112017/17112017/17112017/GoogleDrive/17112017/

Input Layout: -Participants:MR_Series

Change Subject Name to: Sub001, Sub002, Sub003...

☒ Use Basic Series to Replace the incomplete BOLD Series

Organize BOLD Series to Fwhm 1

Organize DMG Series to Diffmap ☒ DICOM to NIFTI

T1raw

Select a MR series:

Phase select an appropriate input directory

Number of Files for a T1raw Series:

☒ Fixed Number of Files 0 (B/N)

Change Number of Files: No Less than 0 Files

Fwhm

Select a MR series:

FullFWHM

Phase select an appropriate input directory

Number of Files for a T1raw Series:

☒ Fixed Number of Files

Phase Number of Files: Change Number of Files

Diffraw

Select a MR series:

Phase select an appropriate input directory

Number of Files for a T1raw Series:

☒ Fixed Number of Files

Phase Number of Files: Change Number of Files

Change another Demo Subject

Get DPARSFA Get DPARSUT Run

DPABI Format Converter

Features:

1. One-click to convert output of DicomSorter or XNAT-like system's output directory
2. Build-in quality control, massively reduce errors for data sorting
3. Anat-only and multi-sessions compatible
4. One-click to begin DPARSFA/DPABISurf processing!

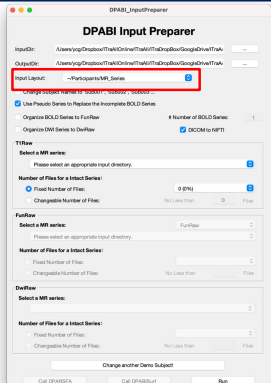
20

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DPABI Input Preparer

30

DPABI Input Preparer



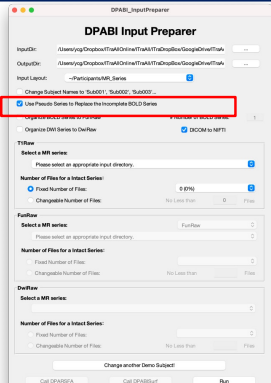
Set input directory layout:

- ~/Participants/MR_Series
- ~/Sub001
- ~/Sub001/0001_MPRAGE
- ~/Sub001/0002_Resting fMRI
- ...
- ~/Sub042
- ~/Sub042/0002_Resting fMRI
- ...
- ~/MR_Series/Participants
- ~/0001_MPRAGE
- ~/0001_MPRAGE/Sub001
- ~/0001_MPRAGE/Sub002
- ...
- ~/0003_MPRAGE
- ~/0003_MPRAGE/Sub042
- ...

- Automatically predicting layout.

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DPABI Input Preparer

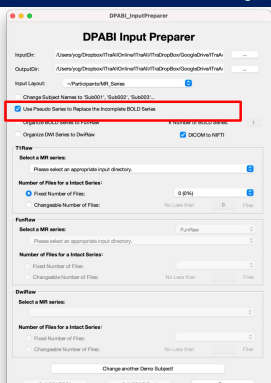


Change raw subject ID into anonymous ID

- The pairing info for raw subject ID and anonymous ID would be recorded in Report.csv in output folder

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DPABI Input Preparer

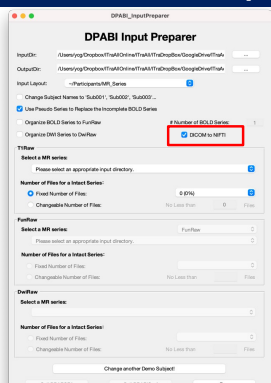


Use pseudo series to replace incomplete functional series

- e.g. Sub_013 didn't finished the task-fMRI series but finished T1-weighted series and resting-fMRI series. A pseudo series would be seemed as task-fMRI series for Sub_013, so that the structure series and resting-fMRI series would be wasted.
- The subject with pseudo series would be recorded in Report.csv in output folder.

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DPABI Input Preparer

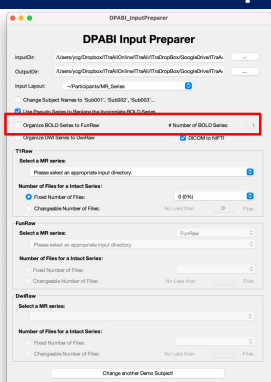


Whether convert dicom files into nifty files

- One of the most common error in running DPARSFA/DPABISurf is the empty FunImg/T1Img folders for sessions failed passing DCM2NII.
- If checked, the subjects with empty T1Img/Funimg folders would be delete to avoid errors.

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DPABI Input Preparer

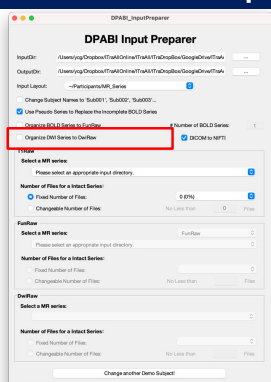


Organize FunRaw

Add more functional sessions for S2_FunRaw, S3_FunRaw ...

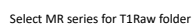
35

DPABI Input Preparer



Organize DwiRaw

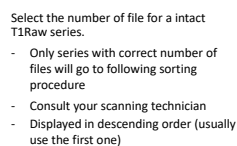
36



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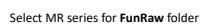


39

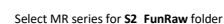


Structure image preprocessing only
(New feature of DPABI V6.0)

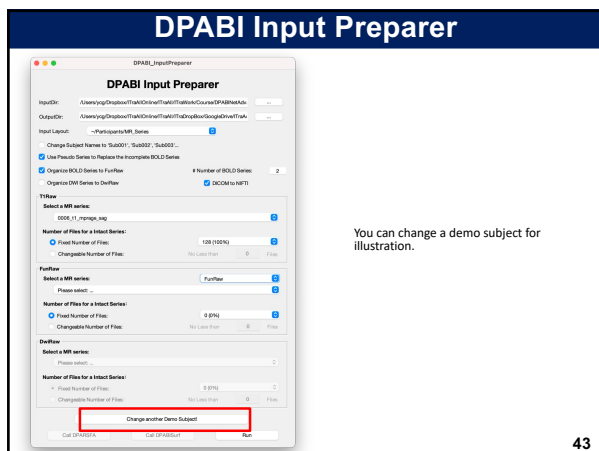
40



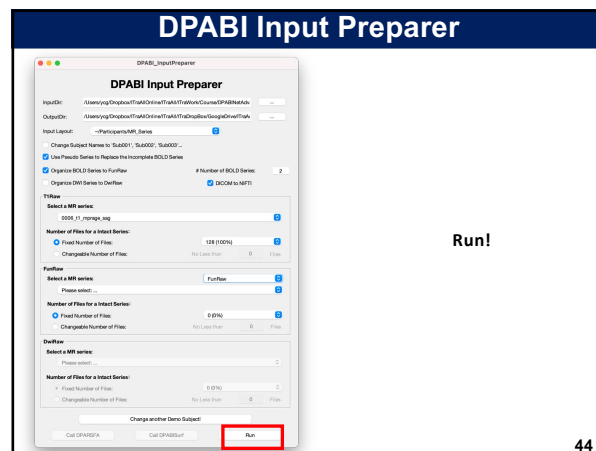
41



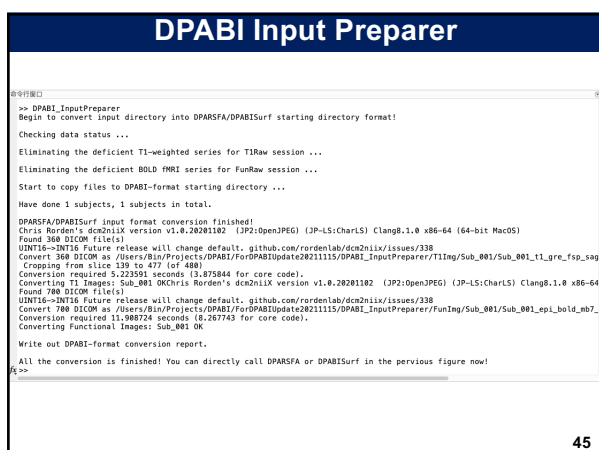
42



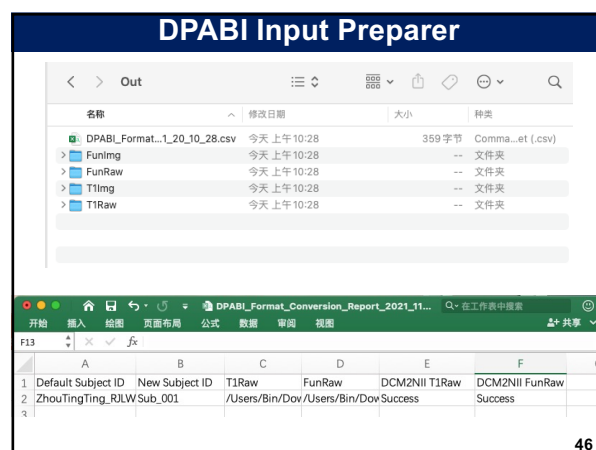
43



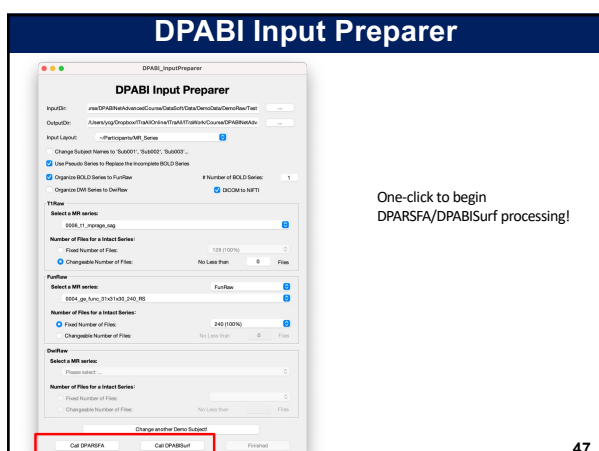
44



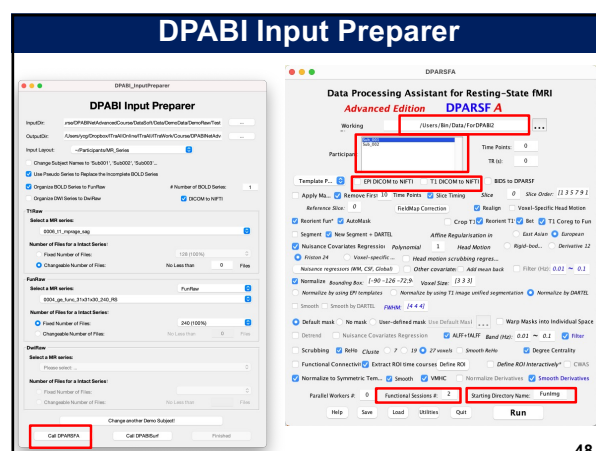
45



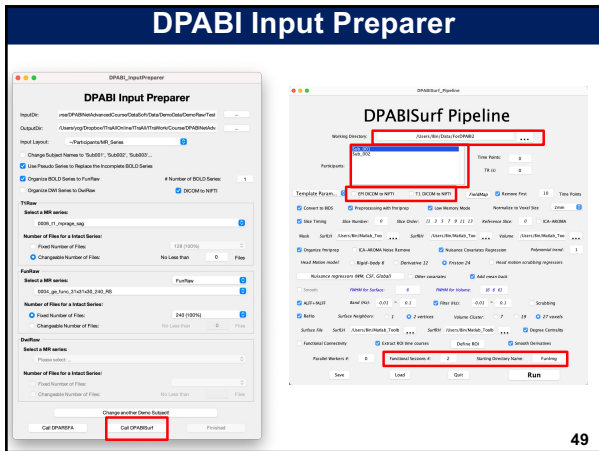
46



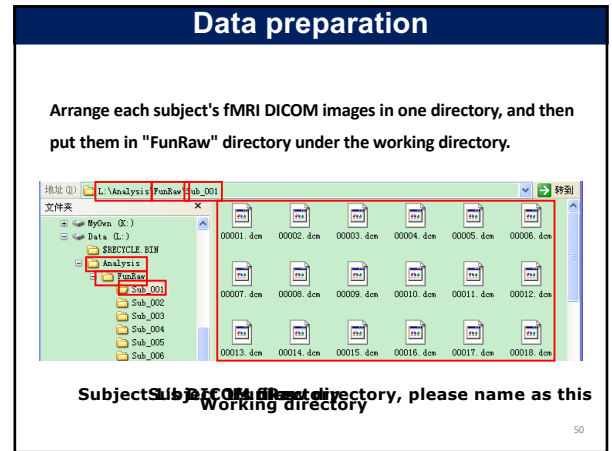
47



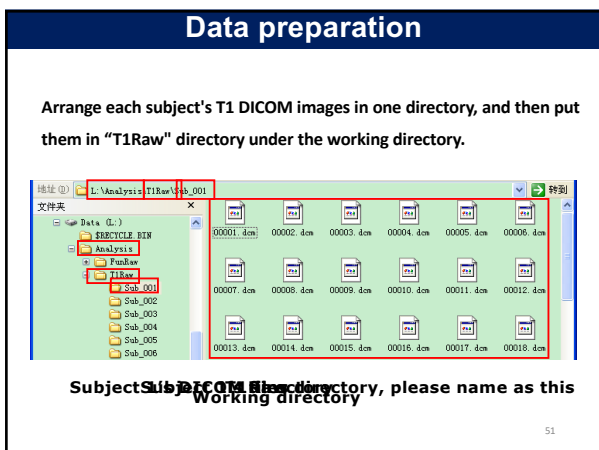
48



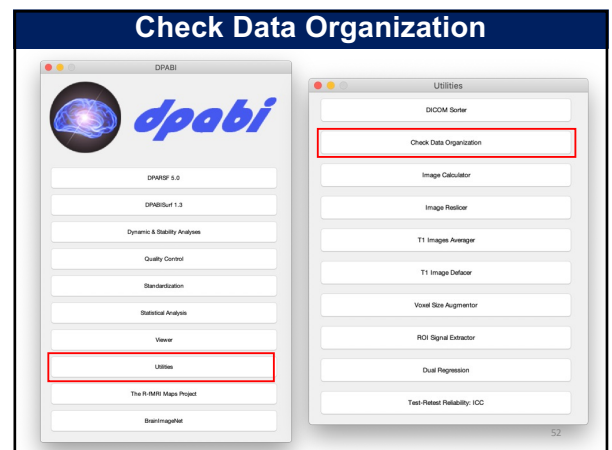
49



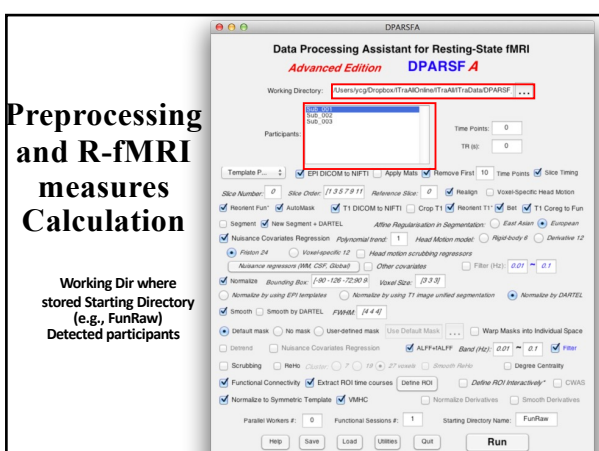
50



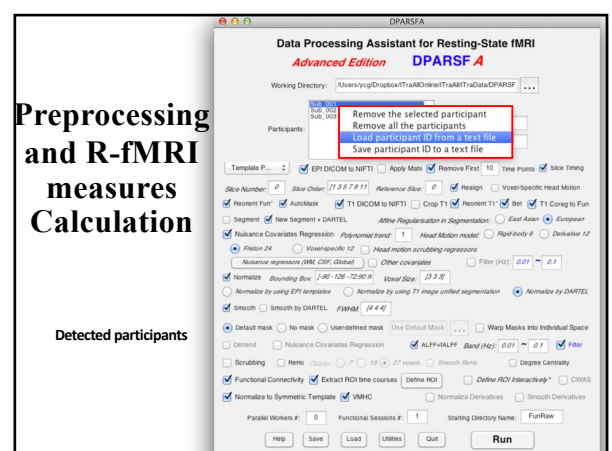
51



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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

If start from BIDS data

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Preprocessing and R-fMRI measures Calculation

Apply reorientation matrices

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Preprocessing and R-fMRI measures Calculation

Apply reorientation matrices:

ReorientMats

Rename to:

DownloadedReorientMats

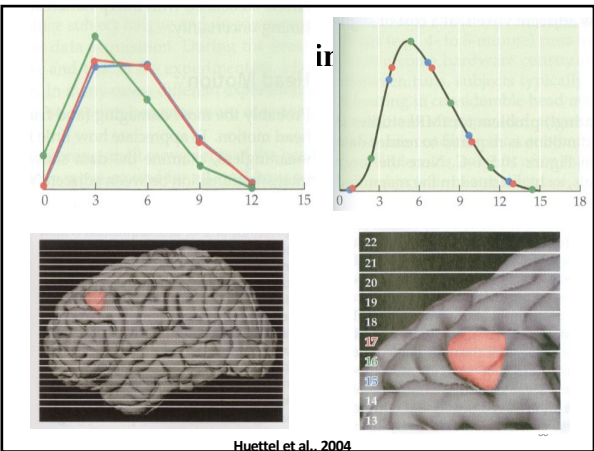
58

Preprocessing and R-fMRI measures Calculation

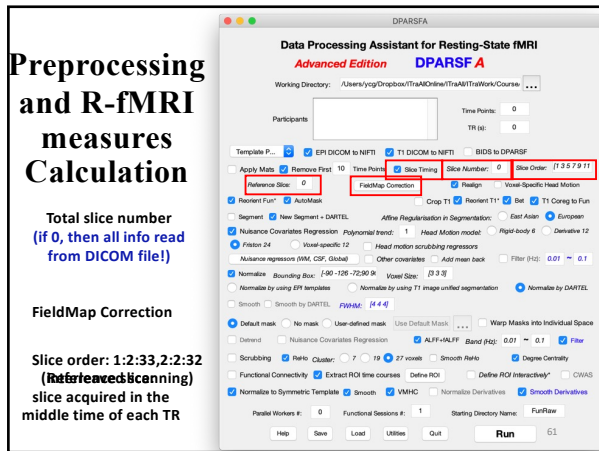
Remove several first time points

Slice Timing

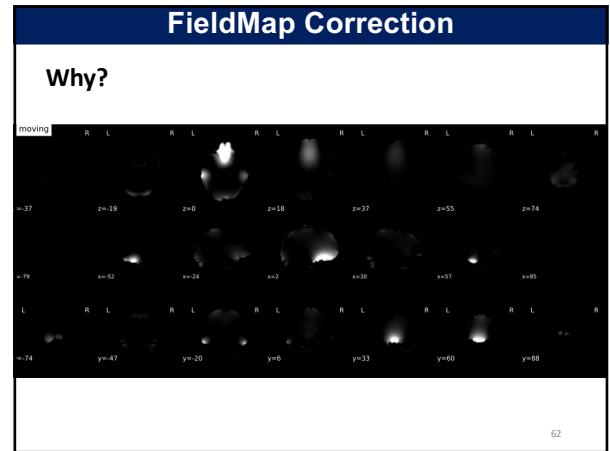
59



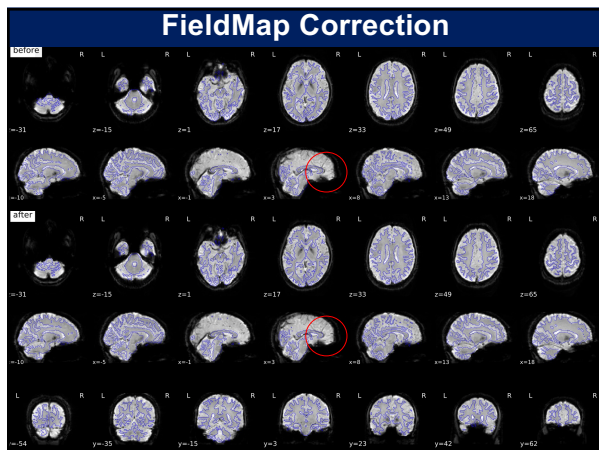
60



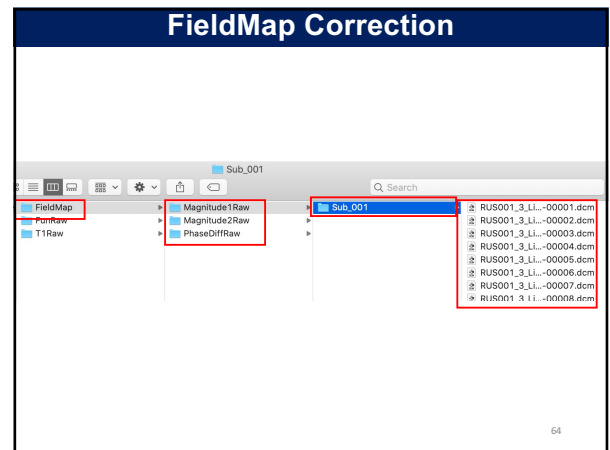
61



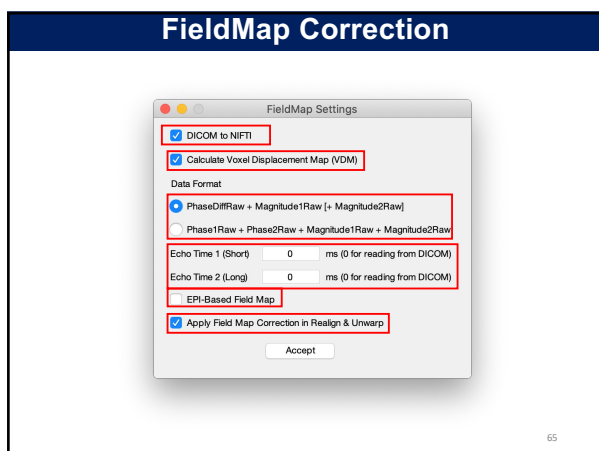
62



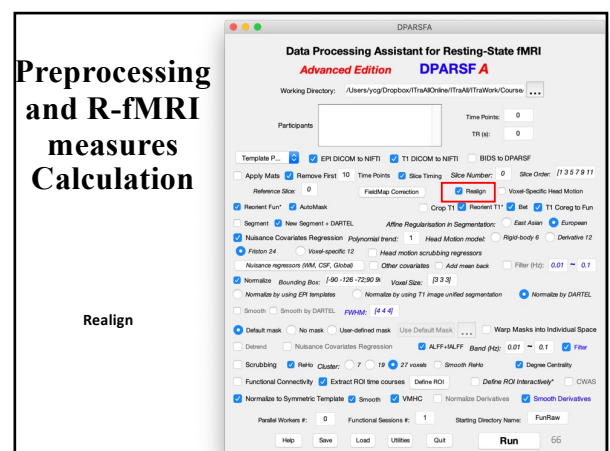
63



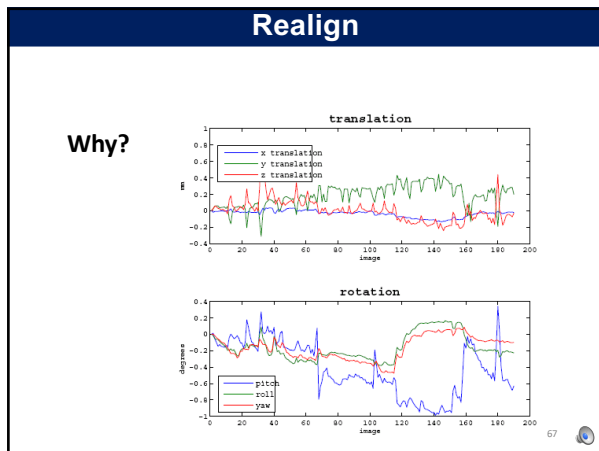
64



65



66



Realign

Check head motion:

{WorkingDir}\RealignParameter\Sub_000:

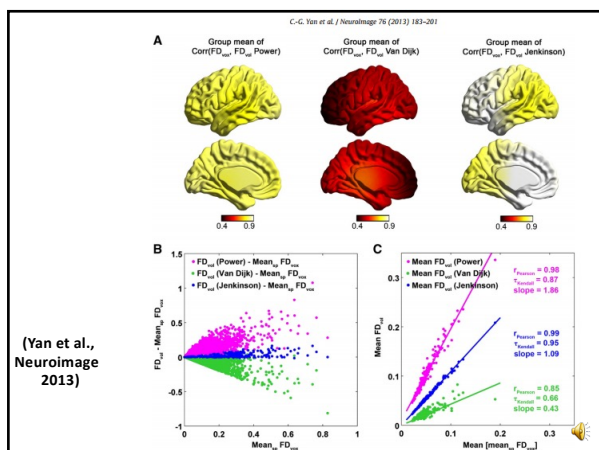
rp_*.txt: realign parameters

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)

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Realign

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

Check head motion: {WorkingDir}\RealignParameter\Sub_000:

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

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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

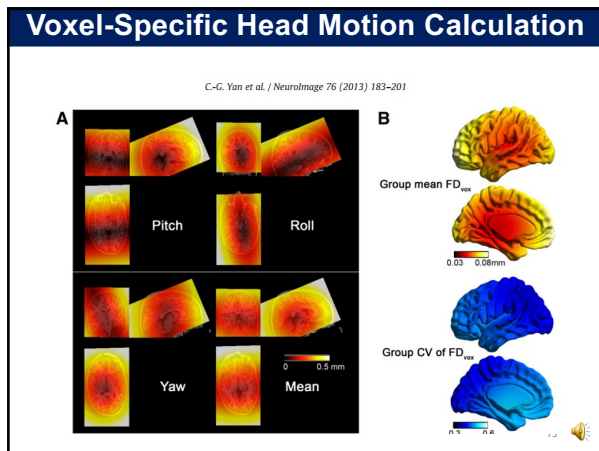
71

Preprocessing and R-fMRI measures Calculation

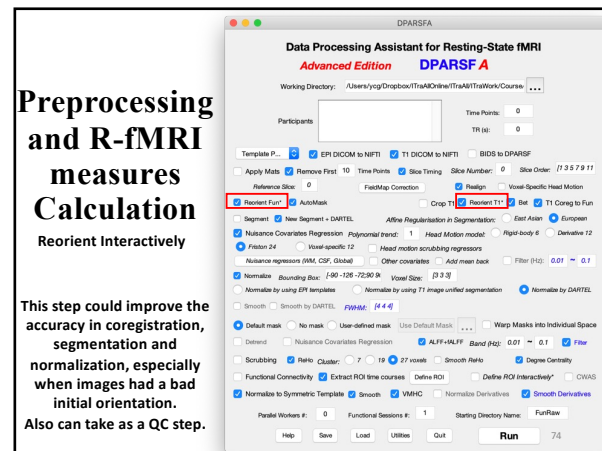
Voxel-Specific Head Motion Calculation

(Yan et al., Neuroimage 2013)

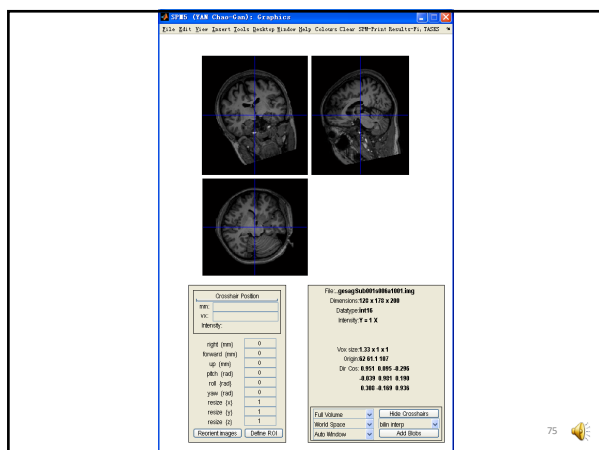
72



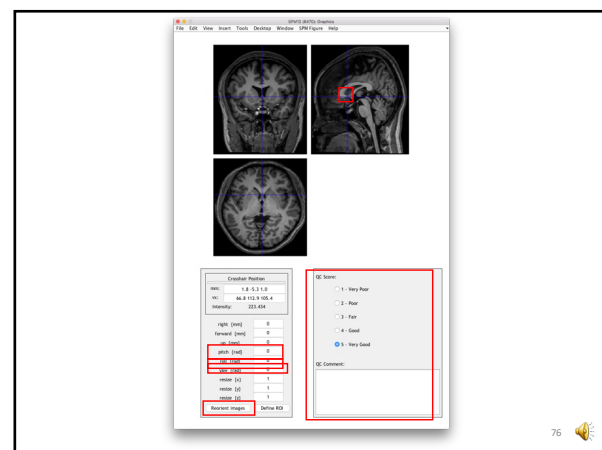
73



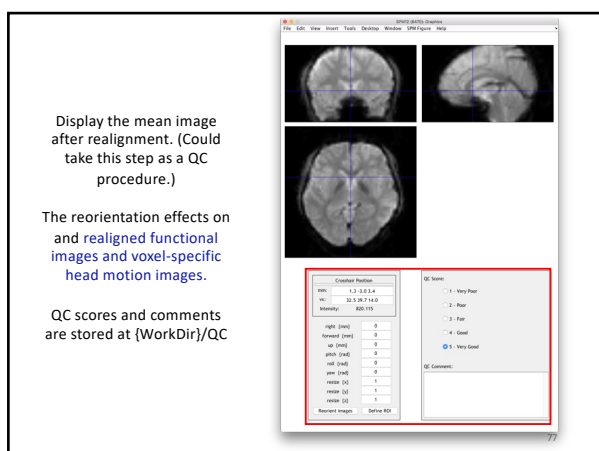
74



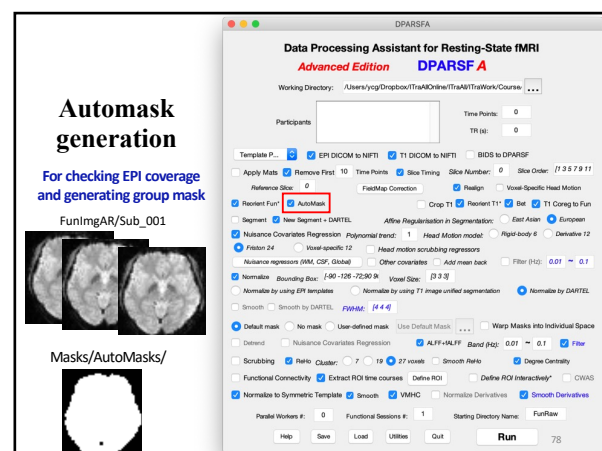
75



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77



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Crop T1 image (.nii, .nii.g
 .img)
 (based on MRIcron's
 Dcm2nii)
 Reorient T1 image
 Interactively



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



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Preprocessing and R-fMRI measures Calculation

Nuisance Covariates Polynomials 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
- ...

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Preprocessing and R-fMRI measures Calculation

Head Motion regression model

6 head motion parameters

Derivative 12: 6 head motion parameters

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

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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

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

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Preprocessing and R-fMRI measures Calculation

Nuisance Regressors (WM, CSF, Global)

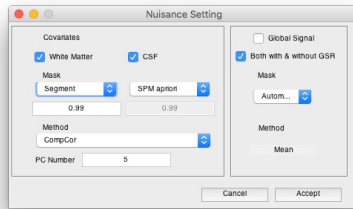
89

Preprocessing and R-fMRI measures Calculation

Nuisance Regressors (WM, CSF, Global)

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Nuisance Regression

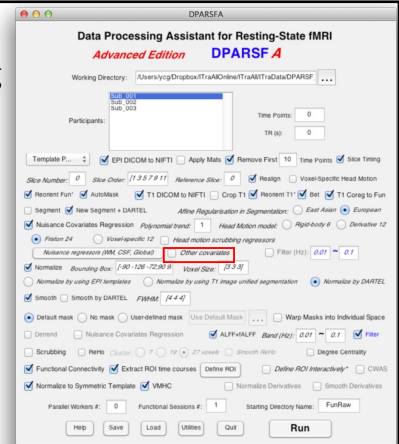


- Mask based on segmentation or SPM apriori
- CompCor or mean [note: for CompCor, detrend (demean) and variance normalization will be applied before PCA, according to Behzadi et al., 2007]
- Global Signal based on Automask

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Preprocessing and R-fMRI measures Calculation

Define other covariates

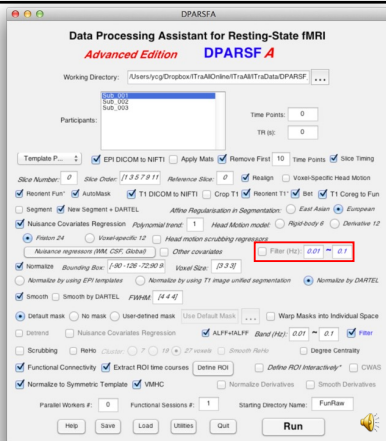


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Preprocessing and R-fMRI measures Calculation

Filtering

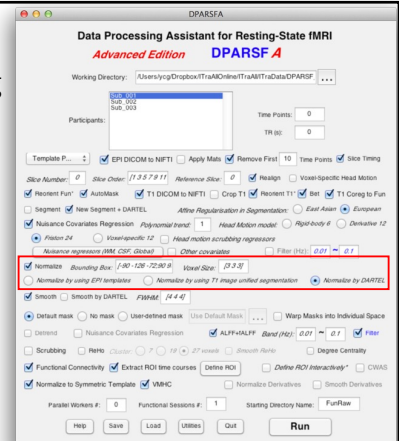
The filtering parameters will be used later (Blue checkbox).



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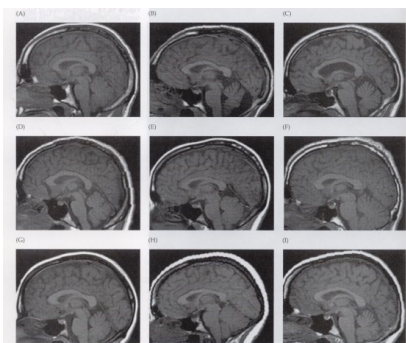
Preprocessing and R-fMRI measures Calculation

Spatial Normalization



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Normalize



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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)

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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.

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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

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Smooth

Why?

- Reduce the effects of bad normalization
- Increase SNR
- ...

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Mask

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

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

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Preprocessing and R-fMRI measures Calculation

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

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Preprocessing and R-fMRI measures Calculation

Nuisance Covariates Regression

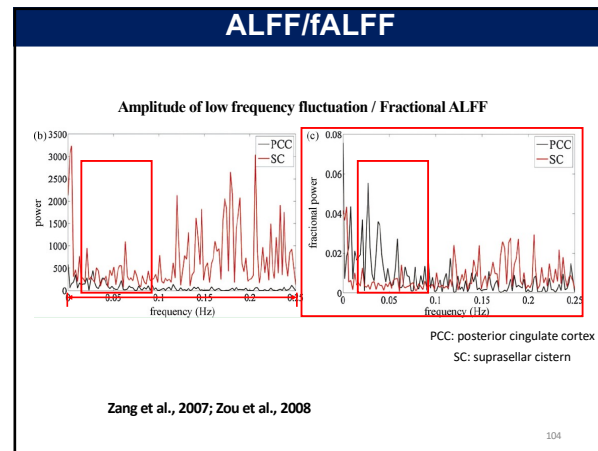
If needed, then use the parameters set in the upper section.

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Preprocessing and R-fMRI measures Calculation

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

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Preprocessing and R-fMRI measures Calculation

Filtering

Use the parameters set in the blue edit boxes.

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Preprocessing and R-fMRI measures Calculation

Scrubbing

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Preprocessing and R-fMRI measures Calculation

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

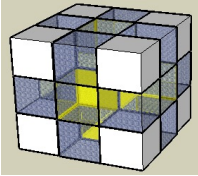
107

Preprocessing and R-fMRI measures Calculation

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

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ReHo (Regional Homogeneity)



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

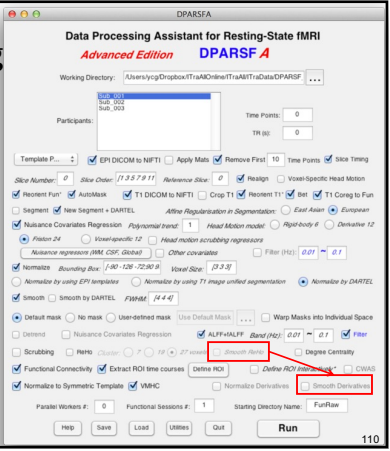
Zang et al., 2004

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

109

Preprocessing and R-fMRI measures Calculation

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

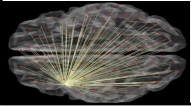


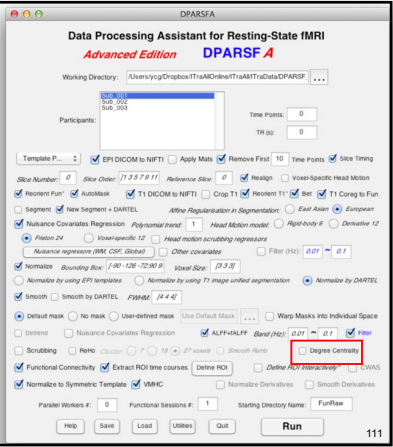
110

Preprocessing and R-fMRI measures Calculation

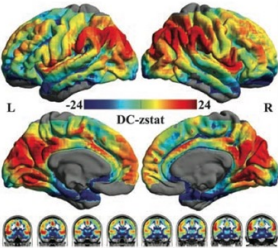
Degree Centrality Calculation (Buckner et al., 2009; Zuo et al, 2012)

> r Threshold (default 0.25)





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Zuo et al., 2012

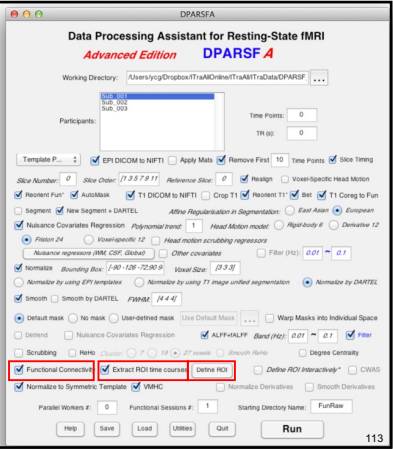
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Preprocessing and R-fMRI measures Calculation

Functional Connectivity (voxel-wise seed based correlation analysis)

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

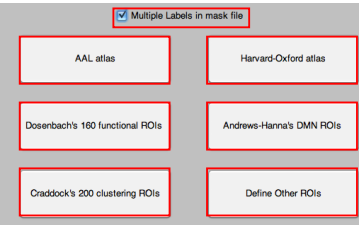
Define ROI



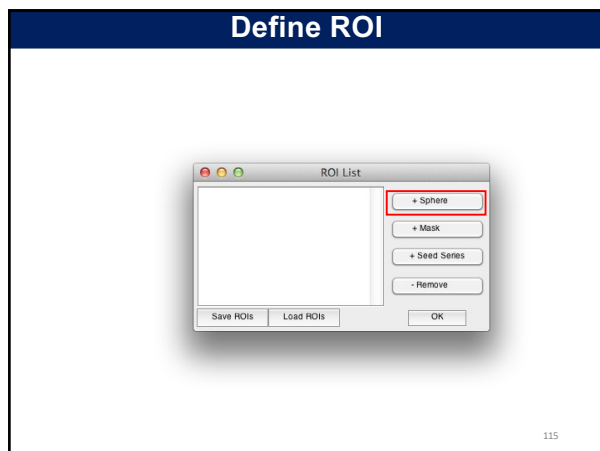
113

Define ROI

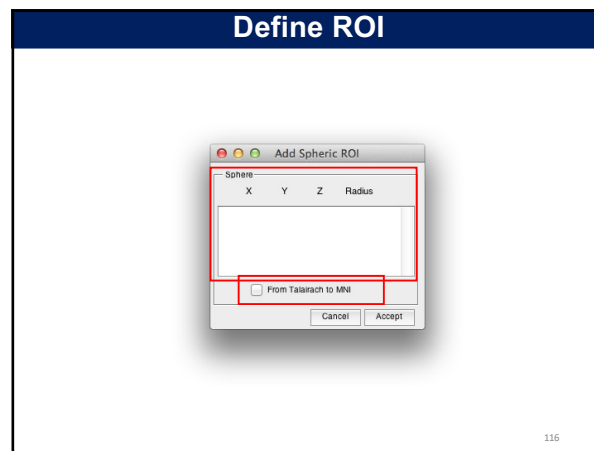
Multiple labels in mask file: each label is considered as one ROI



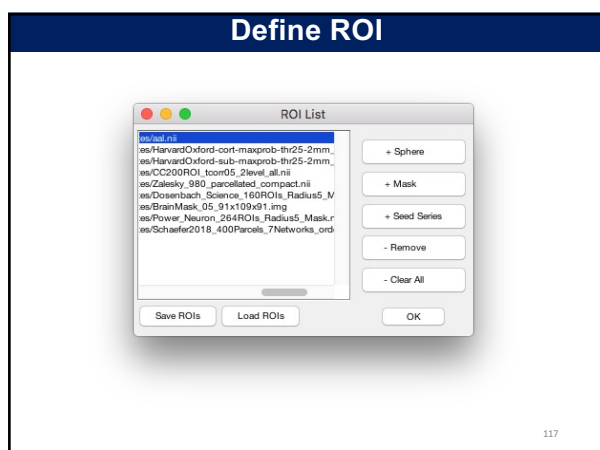
114



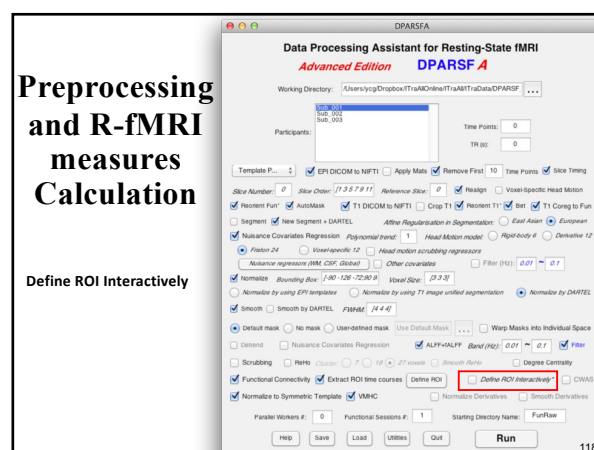
115



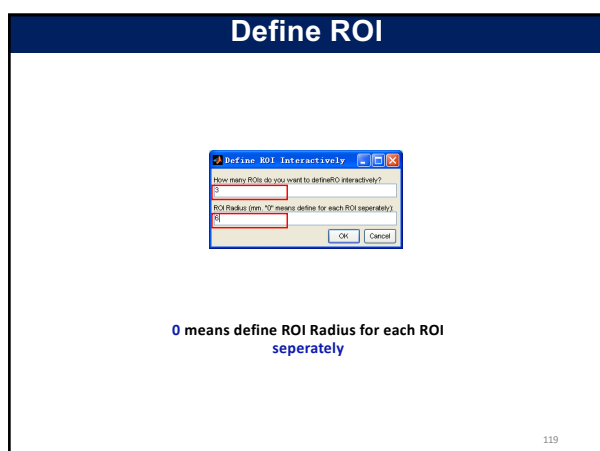
116



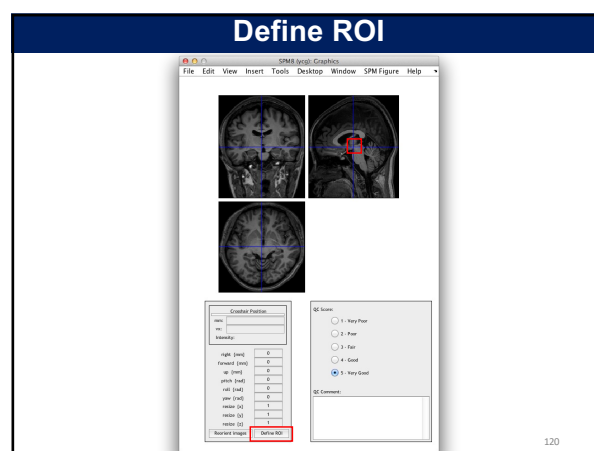
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Functional Connectivity

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.

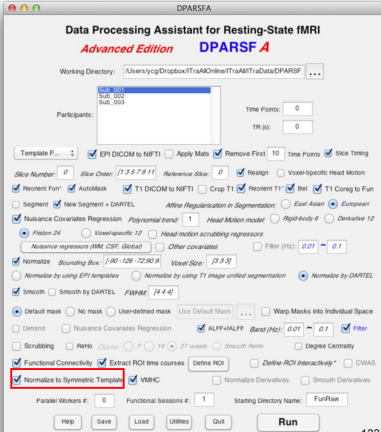
121

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Preprocessing and R-fMRI measures Calculation

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

Prepare for VMHC: Further register to a symmetric template

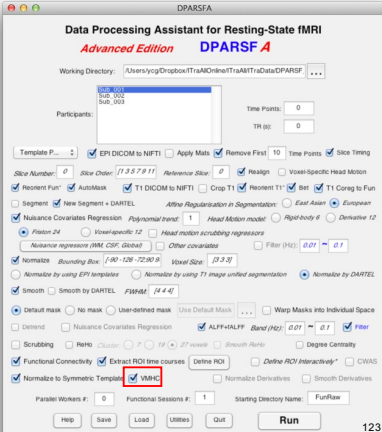


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Preprocessing and R-fMRI measures Calculation

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



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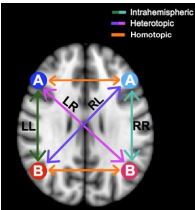
123

VMHC

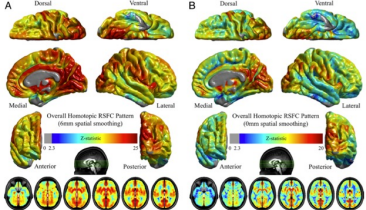
- 1) Get the T1 images in MNI space (e.g., wco*.img or wco*.nii under T1ImgNewSegment or T1ImgSegment) for each subject, and then create a mean T1 image template (averaged across all the subjects).
- 2) Create a symmetric T1 template by averaging the mean T1 template (created in Step 1) with it's flipped 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.

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Gee et al., 2011



Zuo et al., 2010

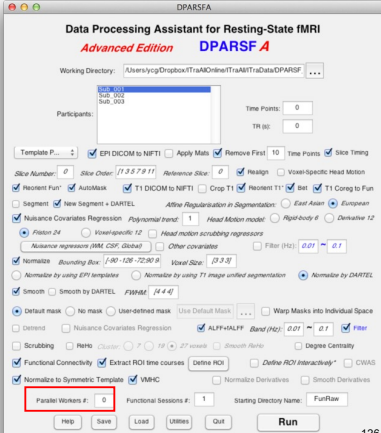
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Preprocessing and R-fMRI measures Calculation

Parallel Workers (if parallel computing toolbox is installed)

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



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Preprocessing and R-fMRI measures Calculation

Multiple functional sessions

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

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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 R-Resampled.

S - Smooth
D - Detrend
F - Filter
C - Covariates Removed
B - Scrubbing

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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

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1. One Voxel

2. Participant Connectivity Maps

3. Distance Between Participants

4. MDMR

Estimate how well ADHD diagnosis explains the distances between participants.

	df	SS	MS	F	p
Group	1	0.98	0.98	2.9	0.006
Error	72	24.57	0.34		

Repeat steps 1-4, for each gray matter voxel.

Voxel threshold ($p < 0.05$)

Cluster correction ($p < 0.05$)

Shehzad et al., 2014. Neuroimage

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Resting State fMRI Data Processing

Template Parameters

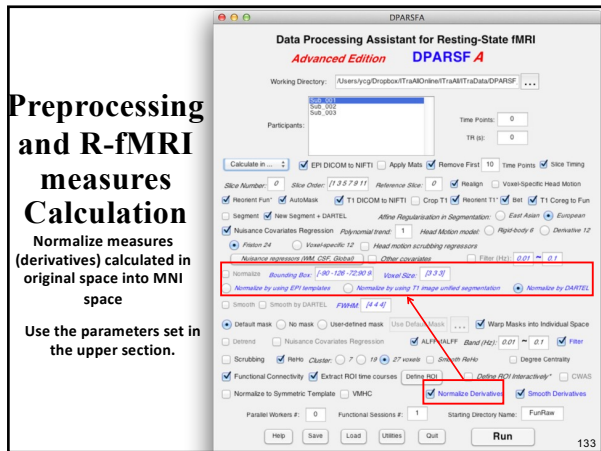
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Resting State fMRI Data Processing

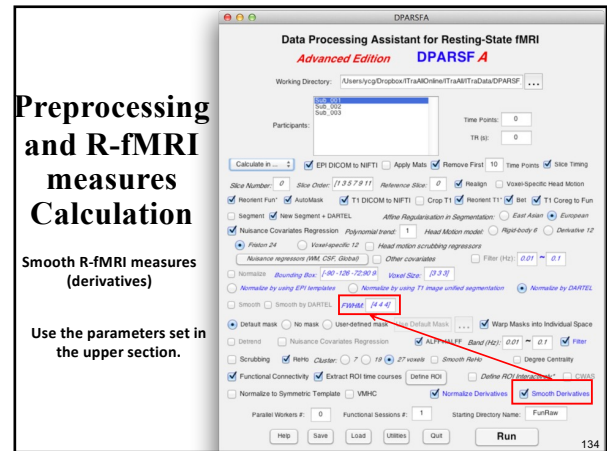
Calculate in MNI space

Calculate in Original space

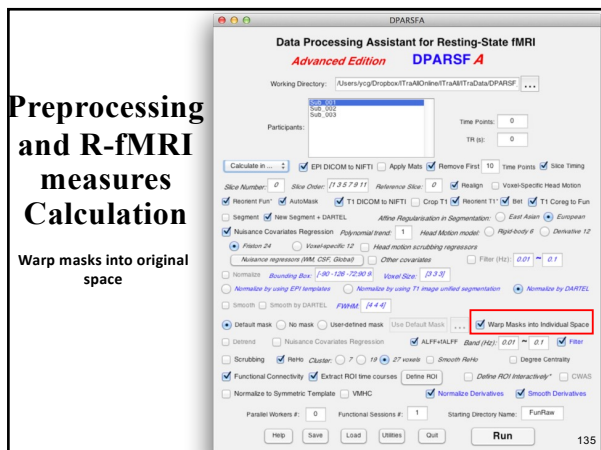
132



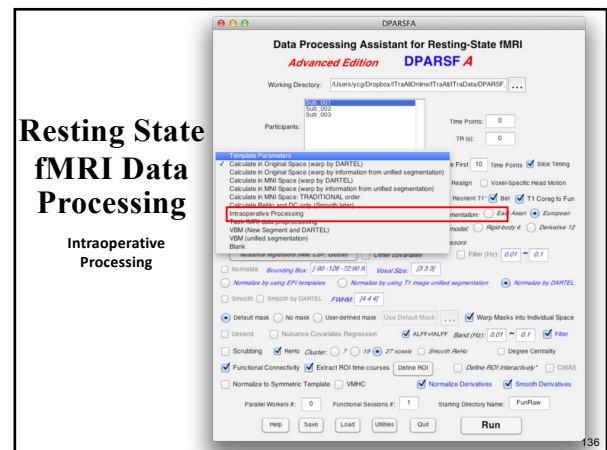
133



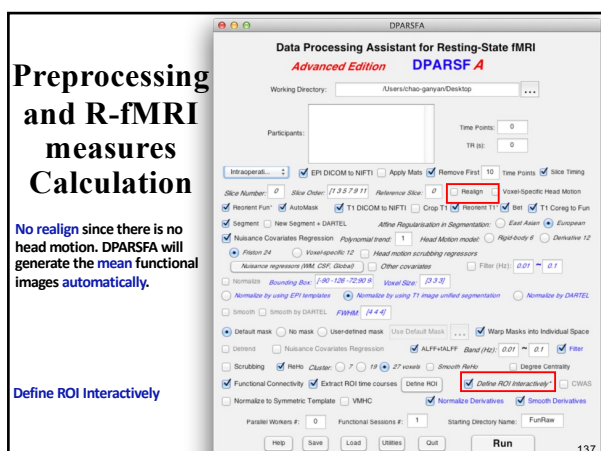
134



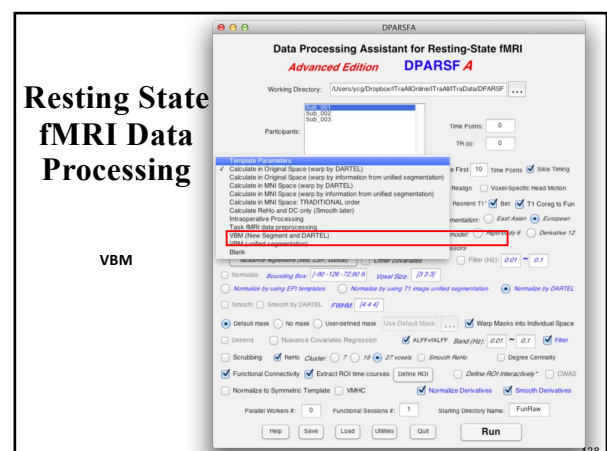
135



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VBM

Only New Segment +
DARTEL is checked

Define the Starting Directory
Name as T1Raw

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Resting State fMRI Data Processing

Blank

140

Blank

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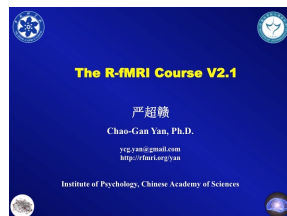
Save and Load Parameters

Save parameters to
*.mat

Load parameters
from *.mat

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Further Help



<http://rfmri.org/Course>



<http://wiki.rfmri.org>



The R-fMRI Journal Club



Official Account: RfMRIlab

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NYU Child Study Center
F. Xavier Castellanos

Child Mind Institute
Michael P. Milham

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- National Natural Science Foundation of China
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Thanks for your attention!

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