Advanced Analyses of Resting-State fMRI (rs-fMRI): PART I

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Download Demo Materials

心智科學腦研究推動網
心智影像研究(MRI)中心 @成大 活動網頁 → 實作資料

http://fmri.ncku.edu.tw/tw/download/20160528_29rsfMRI/adrsfMRIdata.zip

盧家鋒 個人網頁
進階fMRI資料分析理論與實作→ 實作資料

http://www.ym.edu.tw/~cflu/adrsfMRIdata.zip

Course Arrangement

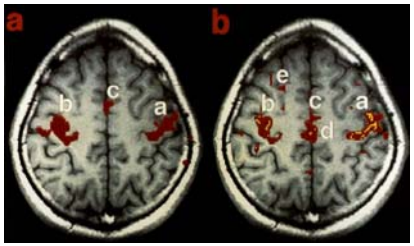
PART I (5/28)
- Preprocessing of rs-fMRI
- SPM preprocessing batch
- Modification of batch file
- Group independent component analysis (group ICA)

PART II (5/29)
- Seed-based functional connectivity
- Complex network analysis

First rs-fMRI Article (MRM 1995)

Functional Connectivity in the Motor Cortex of Resting Human Brain Using Echo-Planar MRI

Bharat Biswal, F. Zerrin Yetkin, Victor M. Haughton, James S. Hyde



a. Functional activation during tasking
b. rs-fMRI correlation maps
(red: positive, yellow: negative)

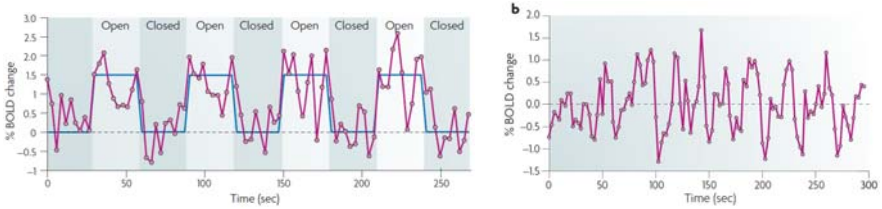
Spontaneous Fluctuation

Task-specific fMRI

- ✓ Model-based Analysis
- ✓ Model-free (data-driven) Analysis

Resting-state fMRI (rs-fMRI)

- ✓ Model-free (data-driven) Analysis



Nature Reviews Neuroscience 8.9 (2007): 700-711.

Rs-fMRI Analyses

1. Functional connectivity analysis

- Linear correlation analysis
- Independent component analysis (**GIFT-ICA**; Calhoun et al., NeuroImage 2001)
- Granger causality analysis (**GCA**), effective connectivity

2. Depicting local features of BOLD signal

http://www.ym.edu.tw/~cflu/CFLu_course_speech.html

- Regional homogeneity (**ReHo**; Zang et al., NeuroImage 2004)
- Amplitude of low-frequency fluctuation (**ALFF**; Zang et al., Brain & Development 2007)
- Fractional ALFF (**fALFF**; Zou et al., J Neurosci Methods 2008)

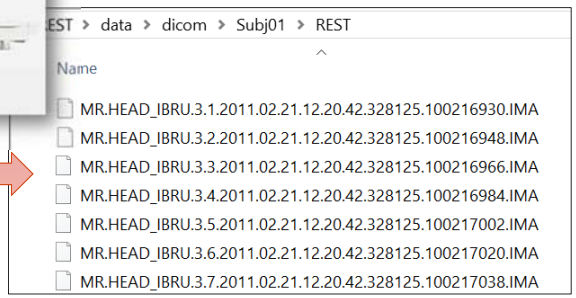
Functional Integration ⇔ Functional segregation

Employed Software/Package

1. **SPM** preprocessing
   - http://www.fil.ion.ucl.ac.uk/spm/
2. **REST** functional connectivity, ReHo, ALFF, fALFF, VMHC
   - http://restfmri.net/forum/index.php?q=rest
3. **GIFT (v3.0a), group ICA**
   - http://mialab.mrn.org/software/gift/#
4. **Brain Connectivity Toolbox/Network Based Statistic Toolbox**
   - https://sites.google.com/site/bctnet/

Let's Start from Very Beginning

DICOM format!! ⇔ NIfTI (.nii) or Analyze75 (*.hdr, *.img)



DICOM (1993)

- Digital Imaging and COmmunication in Medicine

DICOM
Digital Imaging and Communications in Medicine
http://dicom.nema.org/

NEMA, Suite 1752
1300 North 17th Street
Rosslyn, VA 22209
Ph: (703) 841-3285
http://dicom.nema.org

- ACR & NEMA formed a committee in 1983
  - American College of Radiology
  - National Electrical Manufacturers Association

"The Common Language of Medical Equipment"

DICOM format

Header + **Image data**

0008,0020,Study Date=20151204
0008,0021,Series Date=20151204
0008,0022,Acquisition Date=20151204
0008,0023,Image Date=20151204
0008,0030,Study Time=122630
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0008,0090,Refe
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0008,1070,Ope
0008,1090,Mar
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0018,0081,Echo Time [TE, ms]=127.948
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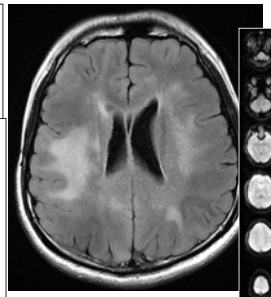
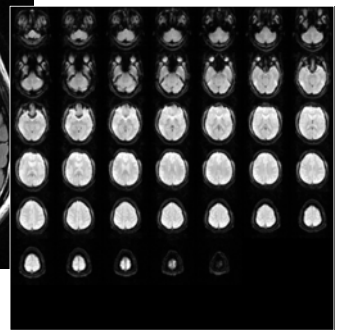
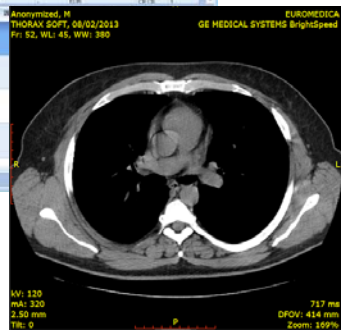
0018,0088,Spacing Between Slices=6
0018,0091,Echo Train Length=1



Mosaics



Retrieve of subject/imaging information.
Use with caution! Personal privacy!

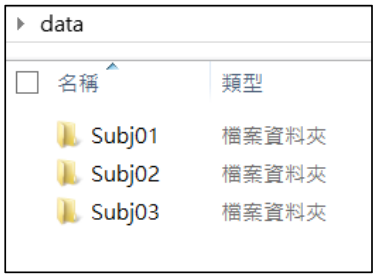


- Data query
- Image Information
- Communication

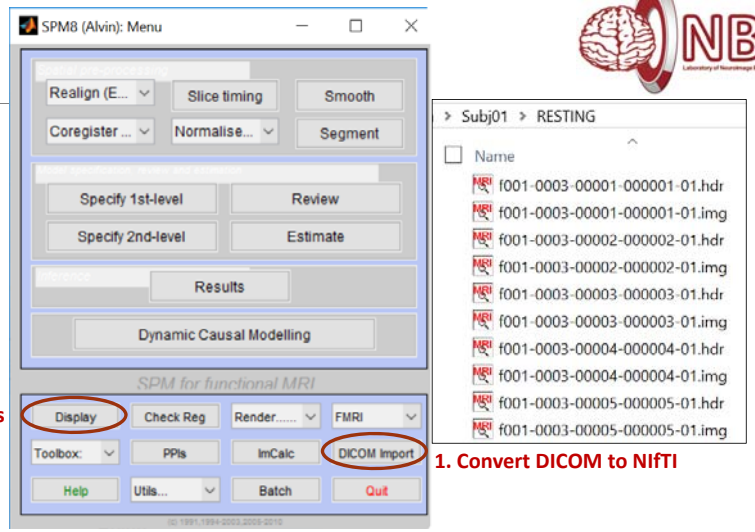
Switch current folder to data folder

More convenient to execute the subsequent processing steps….

Current Folder: C:\Users\Alvin\Desktop\data\data\Subj01



DICOM import

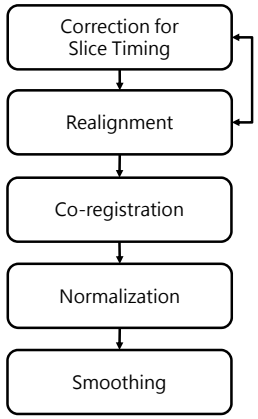


2. Check converted images

1. Convert DICOM to NIfTI

Preprocessing for rs-fMRI

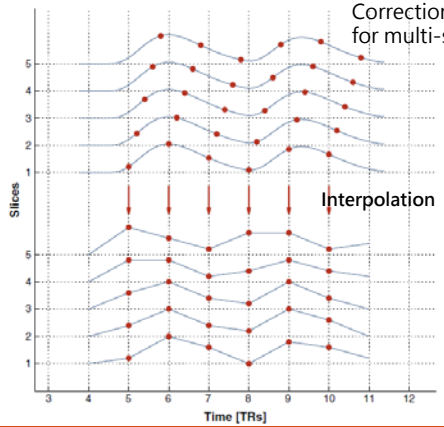
Similar to that used for task-specific fMRI analysis
- Slice timing
- Realignment
- Co-registration (with anatomical images)
- Normalization
- Smoothing
- Segment (tissue classification; optional)



Standard procedure for fMRI preprocessing

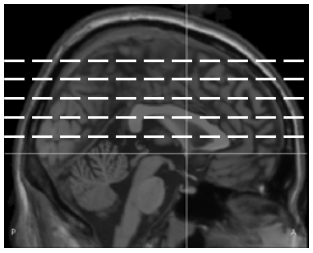
http://www.ym.edu.tw/~cflu/CFLu_course_mriprinp.html, Week 16

Correction for Slice Timing



Correction for slightly different imaging timing for multi-slice acquisition in a TR.

For example:
Acquire 5 slices in 1 TR
➔ Temporal offset between slices

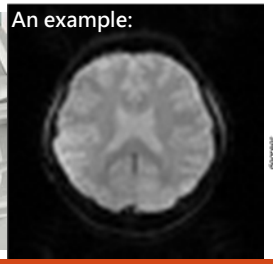


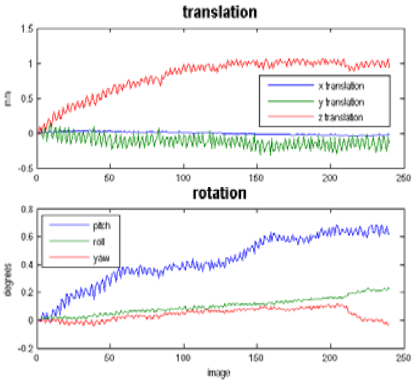
Sladky et al, NeuroImage 2011,58:588-594.

Realignment of head motion

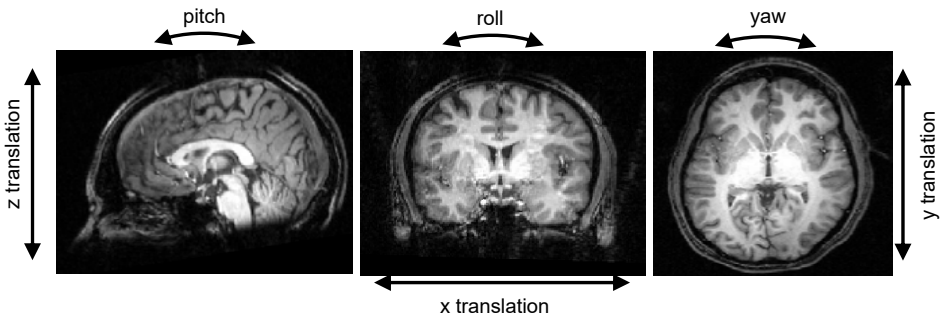
The signal variation from movement is larger than hemodynamic response.

6-parameter Rigid body registration
& transformation (align to the 1st volume)
➔ 6 co-variates for rs-fMRI analysis





3 translations and 3 rotations



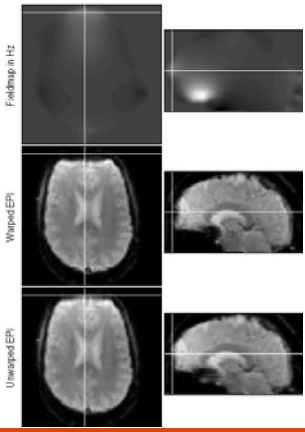
fMRI slides from http://culhamlab.ssc.uwo.ca/fmri4newbies/Tutorials.html

EPI undistortion/unwarp

Magnetic inhomogeneity can cause
- Signal loss
- Spatial distortion

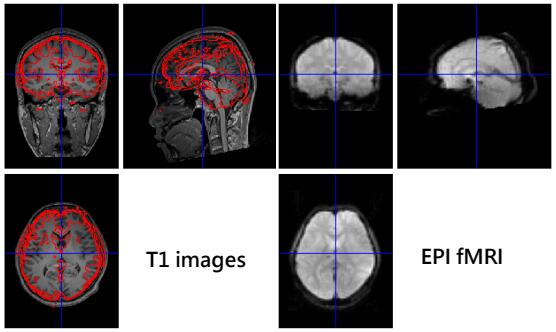
Magnetic field warps at tissue boundaries
- The frontal pole, orbito-frontal cortex
- Medial temporal lobe (hippocampus)

The benefit of undistortion/unwarp
- Make the shape of an individual's fMRI data more similar to their anatomical images.



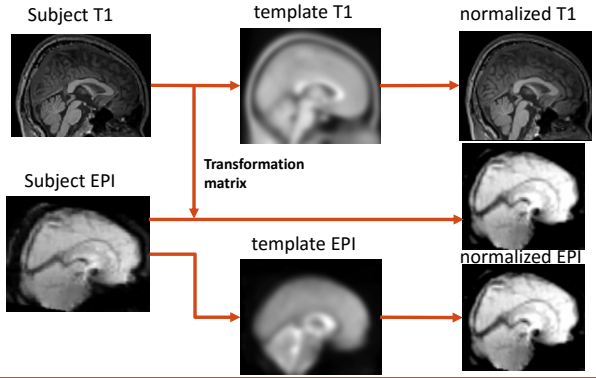
Co-registration

Align fMRI (EPI) data to structural (T1) images.
- Rigid body transformation using mutual information
- Manual adjustment



Normalization

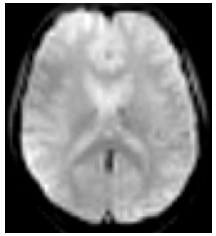
We can perform spatial normalization using either anatomical (T1) images or fMRI (EPI) data.



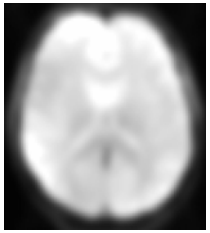
Gaussian Smoothing

- Each voxel becomes weighted average of surrounding voxels.
- Render the data more normally distributed.
- Compensate for inaccuracies in normalization between individuals.
- Increase signal-to-noise ratio

2 x 2 x 2 mm³



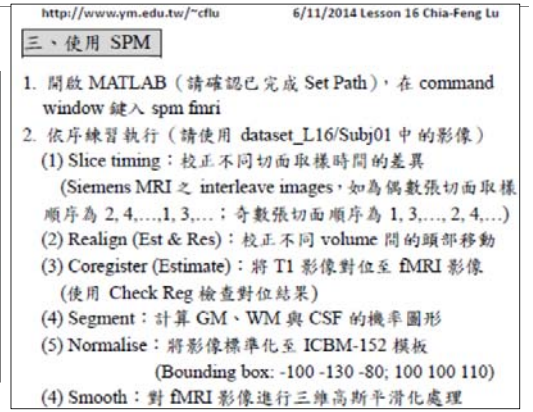
normalization



Normalization+smoothing

Preprocessing Step-by-step

fMRIprocess_CFLu.pdf



http://www.ym.edu.tw/~cflu 6/11/2014 Lesson 16 Chia-Feng Lu

三、使用 SPM

1. 開啟 MATLAB（請確認已完成 Set Path），在 command window 鍵入 spm fmri
2. 依序練習執行（請使用 dataset_L16/Subj01 中的影像）
   (1) Slice timing：校正不同切面取樣時間的差異
   (Siemens MRI 之 interleave images，如為偶數張切面取樣順序為 2, 4,...,1, 3,...；奇數張切面順序為 1, 3,..., 2, 4,...)
   (2) Realign (Est & Res)：校正不同 volume 間的頭部移動
   (3) Coregister (Estimate)：將 T1 影像對位至 fMRI 影像
   (使用 Check Reg 檢查對位結果)
   (4) Segment：計算 GM、WM 與 CSF 的機率圖形
   (5) Normalise：將影像標準化至 ICBM-152 模板
   (Bounding box: -100 -130 -80; 100 100 110)
   (4) Smooth：對 fMRI 影像進行三維高斯平滑化處理

http://www.ym.edu.tw/~cflu/MRI_PrinApp_Class16_CFLu.pdf

Batch Step-by-step

五、附錄：Batch 檔設定詳細說明

➢ 建立基本處理流程(dataset_L16\fMRIbatch_raw.mat)

1. 請先將下列順序的 module 加入至 batch 中
   - ✓ BasicIO -> Named Directory Selector
   - ✓ BasicIO -> Change Directory
   - ✓ BasicIO -> Make Directory
   - ✓ SPM -> Temporal -> Slice Timing
   - ✓ SPM -> Spatial -> Realign: Estimate & Reslice
   - ✓ SPM -> Spatial -> Coreg: Estimate
   - ✓ SPM -> Spatial -> Segmentation
   - ✓ SPM -> Spatial -> Normalise: Write
   - ✓ SPM -> Spatial -> Smooth

http://www.ym.edu.tw/~cflu 6/11/2014 Lesson 16 Chia-Feng Lu

➢ 輸入基本參數(dataset_L16\fMRIbatch_process.mat)

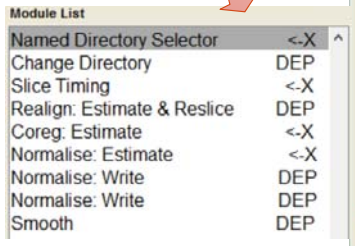
請按照以下步驟依序設定各 module 的參數

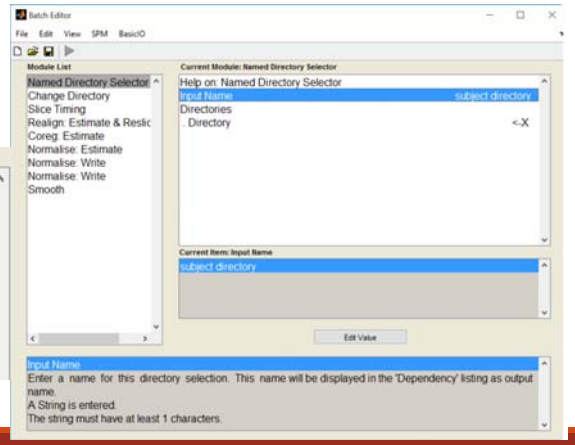
- ✓ **Named Directory Selector**：Input Name 填入 subject directory；在 Directories 中點兩下讓 Directory 出現一個<-X 的標記
- ✓ **Make Directory**：New Directory Name 輸入 stats，提供 SPM 統計分析擺放檔案的位置
- ✓ **Slice Timing**：Data 點兩下出現<-X；Number of Slices: 40；TR:2；TA 輸入 2-(2/40)；Slice order:[2:2:40,1:2:40]；Reference Slice:1
- ✓ **Realign**： Data 點兩下，讓 Session 出現<-X
- ✓ **Normalise**：Data 點兩下加入一個 Subject；更改 bounding box 為-100 -130 -80; 100 100 110
- ✓ **Sooth**：可調整 FWHM 參數

Batch of SPM fMRI preprocessing

>> spm fmri → Batch

fMRI_preprocess_v2.mat

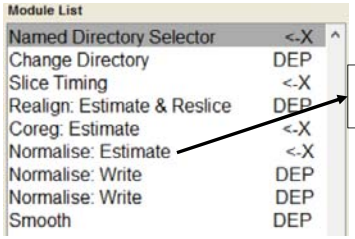




Batch of SPM fMRI preprocessing

>> spm fmri

Save as your own batch template

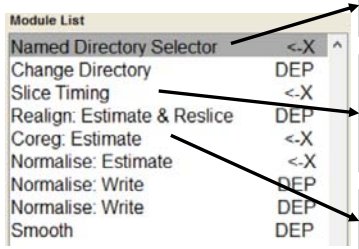


T1 template image
C:\Users\Alvin\Desktop\softwares\spm8\templates\T1.nii,1

Batch of SPM fMRI preprocessing

>> spm fmri

Save as subject's batch



Subject data folder
C:\Users\Alvin\Desktop\data\data\Subj01

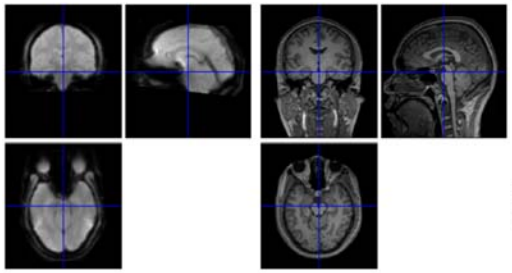
rs-fMRI data
C:\Users\Alvin\Desktop\data\data\Subj01\REST.img,1
....
C:\Users\Alvin\Desktop\data\data\Subj01\REST.img,240
240 volumes

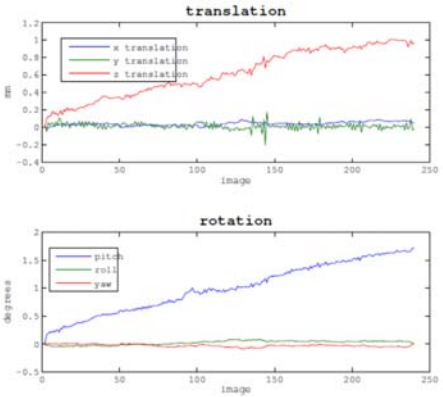
T1W data
C:\Users\Alvin\Desktop\data\data\Subj01\anat.img,1

Always Check Your Data!

SPM processing logfile (spm_2016May28.ps)

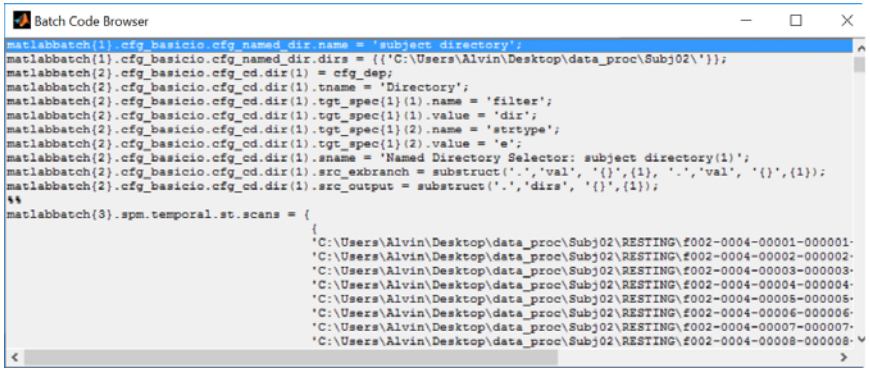
https://online2pdf.com/convert-ps-to-pdf





Modification of Batch File

Batch Editor → View → Show .m Code



Independent Component Analysis

A cocktail-party problem

$$x_1(t) = 0.7s_1(t) + 0.2s_2(t) + 0.1s_3(t)$$
$$x_2(t) = 0.3s_1(t) + 0.4s_2(t) + 0.3s_3(t)$$
$$x_3(t) = 0.1s_1(t) + 0.2s_2(t) + 0.7s_3(t)$$

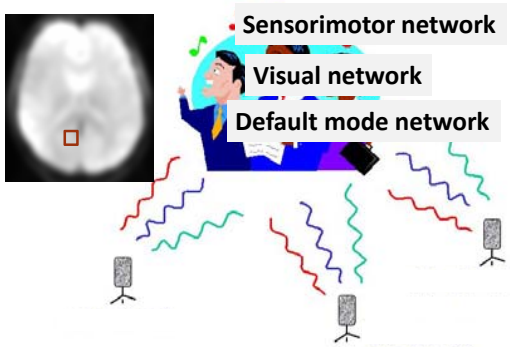
$$\begin{bmatrix} x_1(t) \\ x_2(t) \\ \vdots \\ x_m(t) \end{bmatrix} = \mathbf{A} \begin{bmatrix} s_1(t) \\ s_2(t) \\ \vdots \\ s_k(t) \end{bmatrix}$$

Number of microphones>=number of speakers

A is the mixing matrix

Independent Component Analysis

A cocktail-party problem



$$x_1(t) = 0.7s_1(t) + 0.2s_2(t) + 0.1s_3(t)$$
$$x_2(t) = 0.3s_1(t) + 0.4s_2(t) + 0.3s_3(t)$$
$$x_3(t) = 0.1s_1(t) + 0.2s_2(t) + 0.7s_3(t)$$

$$\begin{bmatrix} x_1(t) \\ x_2(t) \\ \vdots \\ x_m(t) \end{bmatrix} = \mathbf{A} \begin{bmatrix} s_1(t) \\ s_2(t) \\ \vdots \\ s_k(t) \end{bmatrix}$$

Number of microphones>=number of speakers

A is the mixing matrix

Independent conponents

A. parts of visual cortex

B. default mode network

C & D. left and right memory function

E. visual cortex

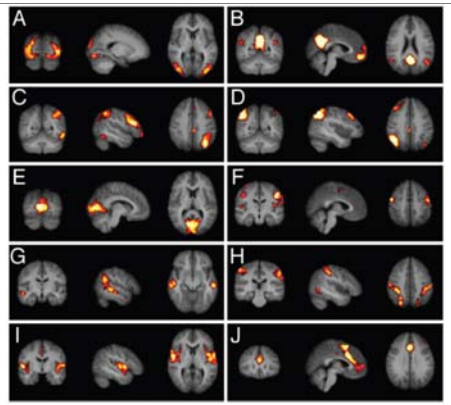
F. sensorimotor cortex

G. occipitotemporal pathway (ventral stream)

H. superior parietal cortex

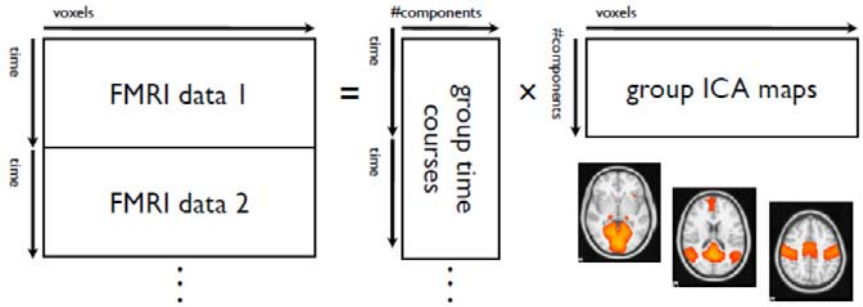
I. auditory cortex

J. executive control & working memmory



Consistent resting-state networks across healthy subjects. PNAS 2006, 103 37): 13848-13853.

Group ICA/ Concat-ICA



Group comparison of resting-state FMRI data using multi-subject ICA and dual regression

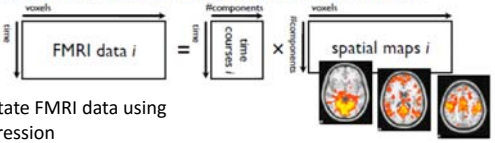
Dual Regression

② *Dual Regression:* This is used to identify, within each of the *N* individual subjects' FMRI data, spatial maps and associated timecourses corresponding to the multi-subject ICA components. For each individual dataset separately:

(A) use the group-level spatial maps as a set of spatial regressors in a GLM, to find temporal dynamics associated with each group-level map

(B) normalization of these timecourses to unit variance (optional, depending or what question the experimenter wants to ask later)

(C) use these timecourses as a set of temporal regressors in a GLM, to find subject specific maps (still associated with the group-level spatial maps:



Group comparison of resting-state FMRI data using multi-subject ICA and dual regression

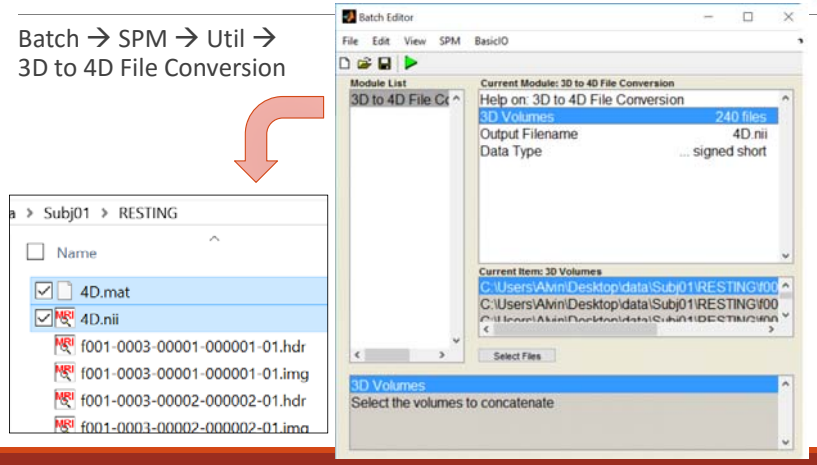
Q & A

THE END

alvin4016@ym.edu.tw

3D to 4D File Conversion

Batch → SPM → Util →
3D to 4D File Conversion



Create Your First Batch