

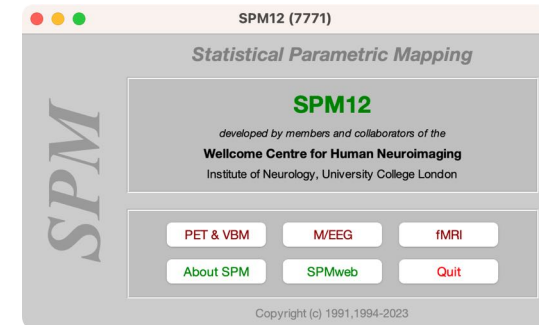
Statistical Parametric Mapping (SPM) for Voxel-Based Morphometry & PET analysis

Practices

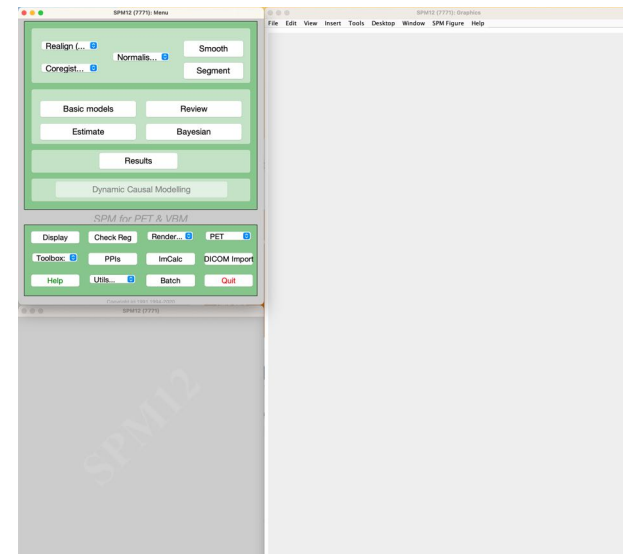
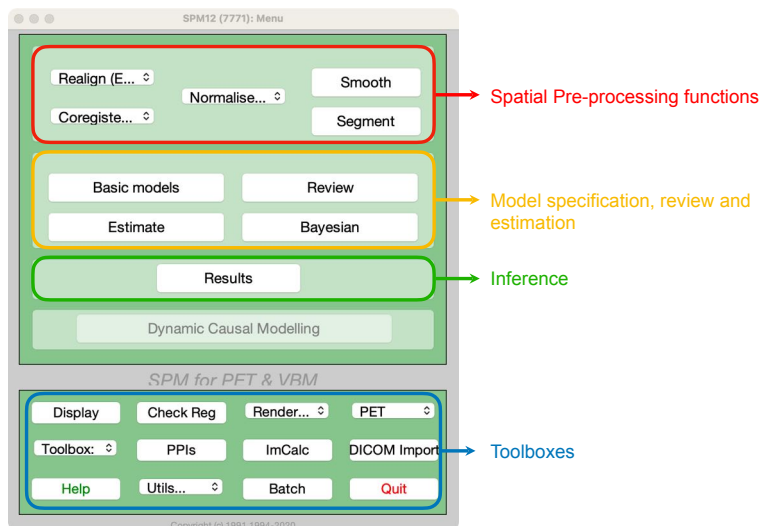
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Department of Psychiatry
CHA Bundang Medical Center
CHA University School of Medicine

Getting started



SPM12 Main window



Overview

Spatial preprocessing

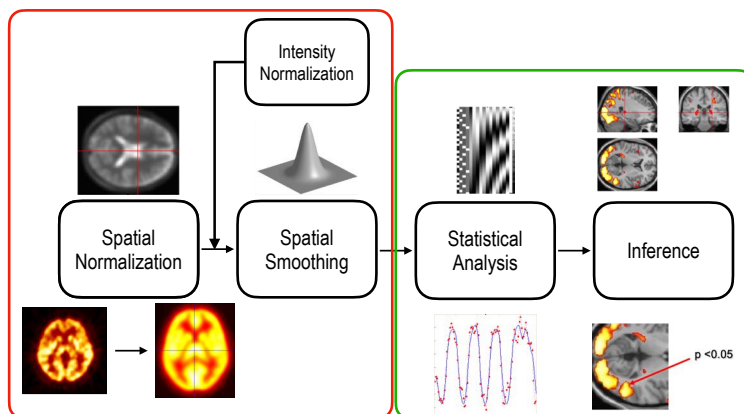
1. Coregister
2. Segmentation
3. Normalize
4. Count normalization
5. Smoothing

Statistical analysis & Inference

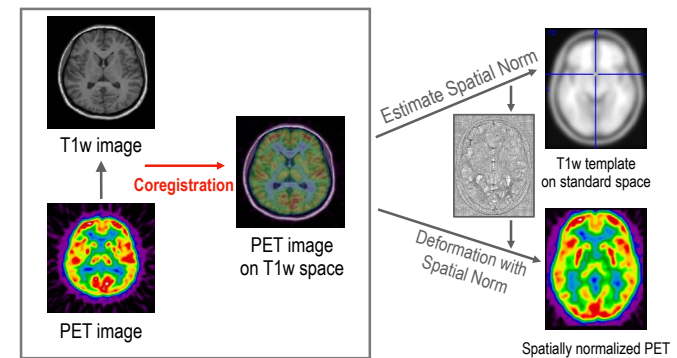
6. Basic model
7. Parameter estimation
8. Inference

Part I: Spatial Preprocessing

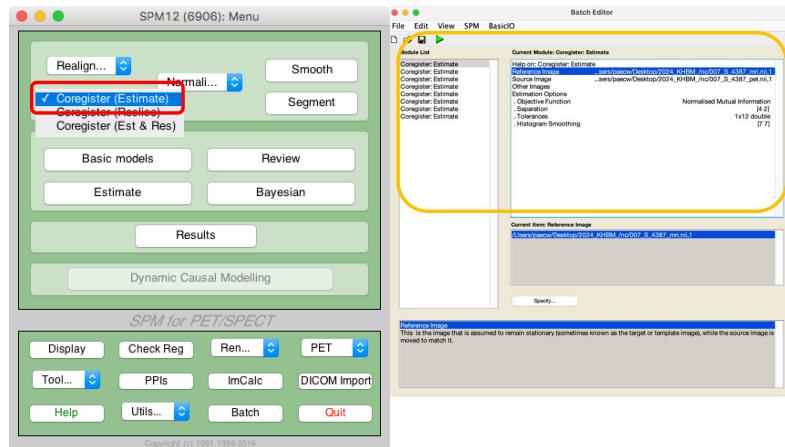
Statistical Parametric Mapping of PET



Pipeline of spatial normalization

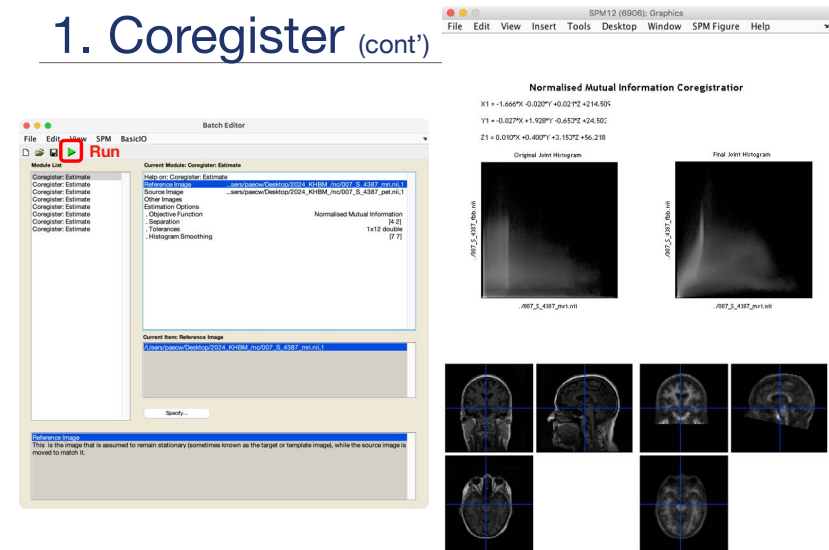


1. Coregister

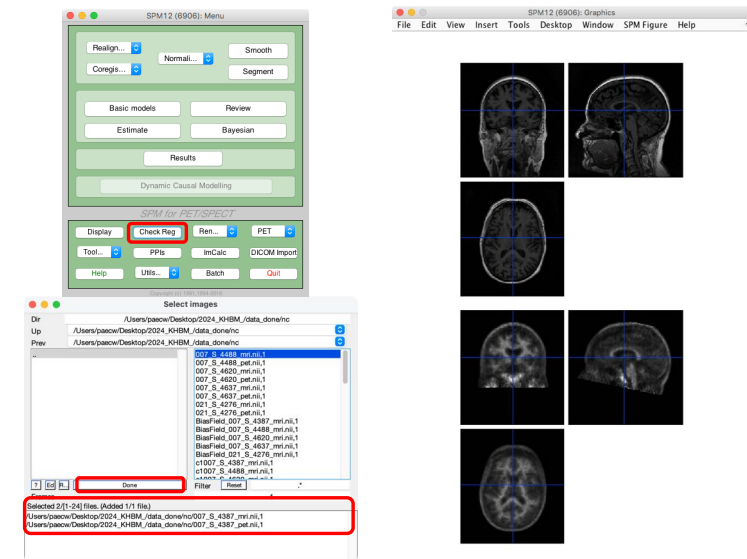


1. Coregister - Estimate 을 선택하고
2. subject마다 module을 만들어 T1w를 reference에, PET을 source 에 입력.
3. 하나의 모듈마다 하나의 subject 내용이 들어가야 하며, 동일한 subject의 두 영상을 선택했는지 확인해야 함.

1. Coregister (cont')

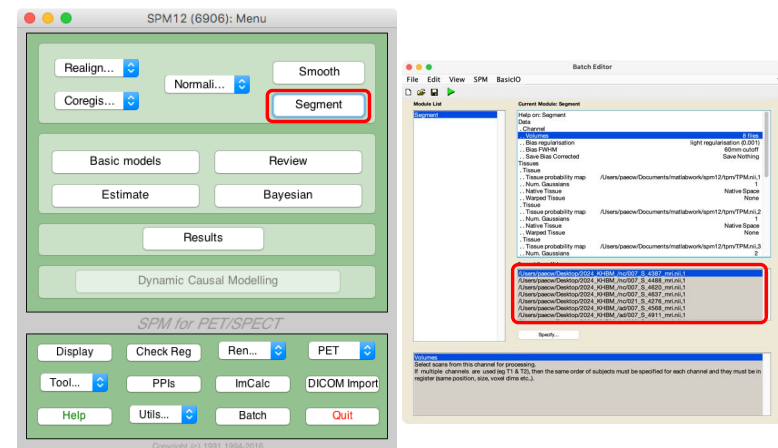


녹색 화살표를 눌러서 Run을 수행하면 영상 간 coregister가 수행되고, 결과는 PET의 영상 파일 내부에 변환된 정보값만 저장됨.



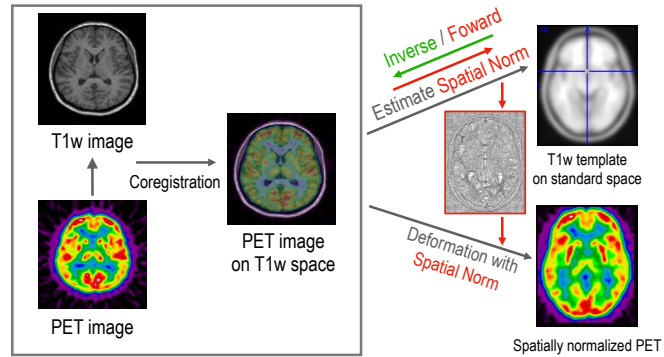
Toolbox의 'Check Reg' 기능으로 각 subject 마다 coregister가 잘 이루어졌는지 확인 가능

2. Segment



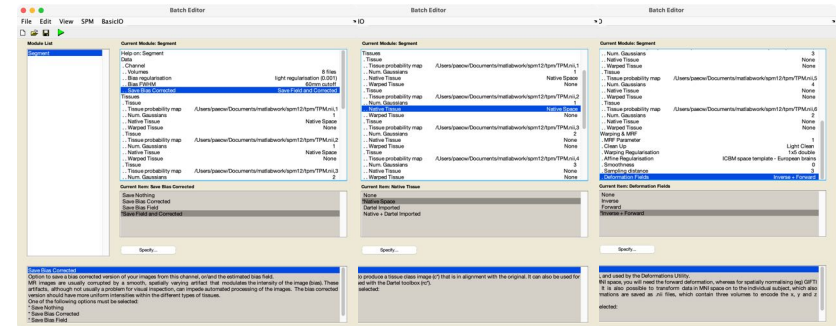
1. Segment 선택
2. Data 란에서 New:Channel을 선택하여 Volume 란에 모든 subject의 T1 image 입력

Pipeline of spatial normalization



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2. Segment (cont')



Segment 과정에서 조절해야 할 옵션:

1. Save Bias Corrected \Rightarrow Save Field and Corrected

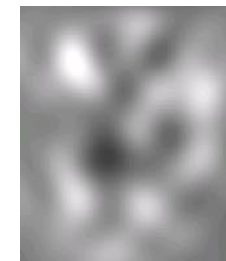
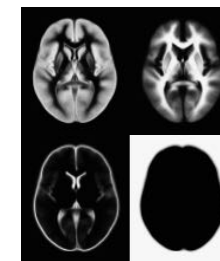
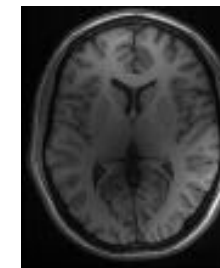
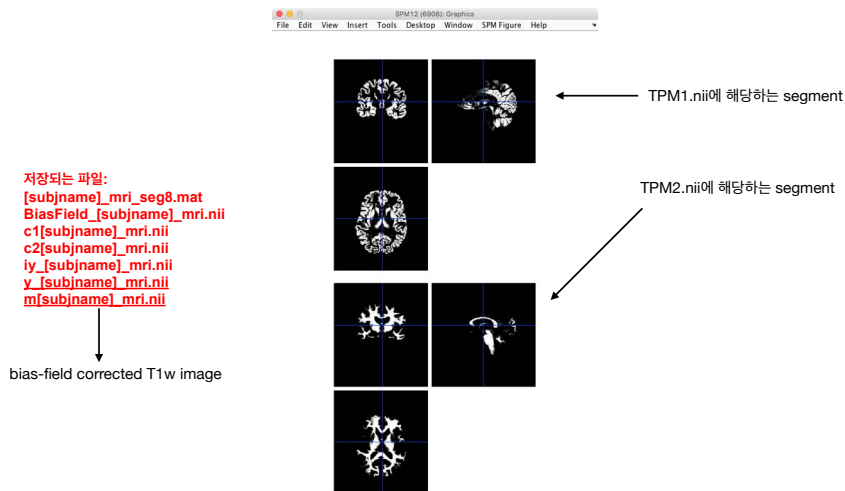
2. TPM options \Rightarrow TPM1, TPM2 는 Native Space, TPM3-6은 None으로 수정

- 참고: TPM1: Gray matter; TPM2: White Matter; TPM3: CSF; TPM4: dura; TPM5: non-brain

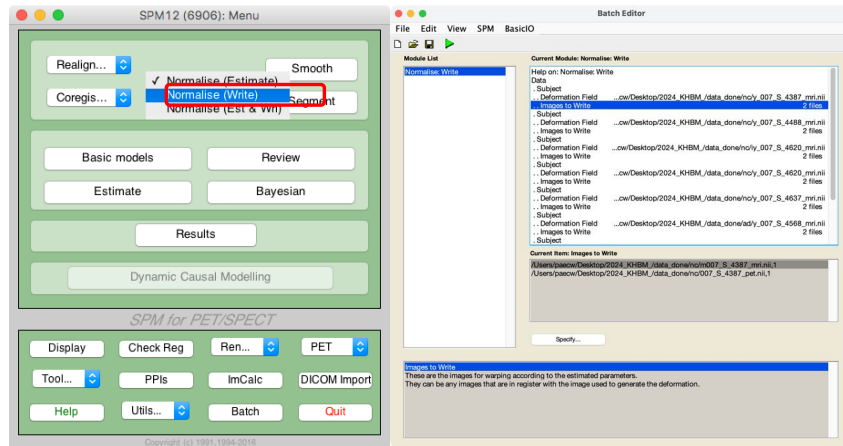
3. Deformation Fields \Rightarrow Inverse + **Forward**

2. Segment (cont')

수정한 설정과 함께 배치를 실행시키면 segmentation 결과와 함께 파일들이 저장됨.



3. Normalize



1. Normalize (Write) 선택
2. Data 란에서 subject 수만큼 추가 후
Deformation Field ⇨ segmentation 과정에서 나왔던 'y_[subname]_mri.nii' 선택
Images to Write ⇨ 같은 subject의 bias-field corrected T1w와 pet 데이터 선택 (2개 이미지 입력)

3. Normalize (cont')

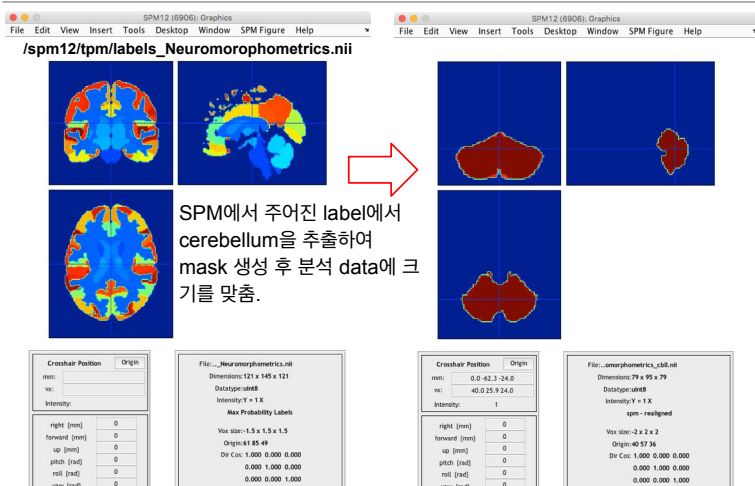
Output:

wm[subjname]_mri.nii
w[subjname]_pet.nii

spatial normalize가 완료된 파일

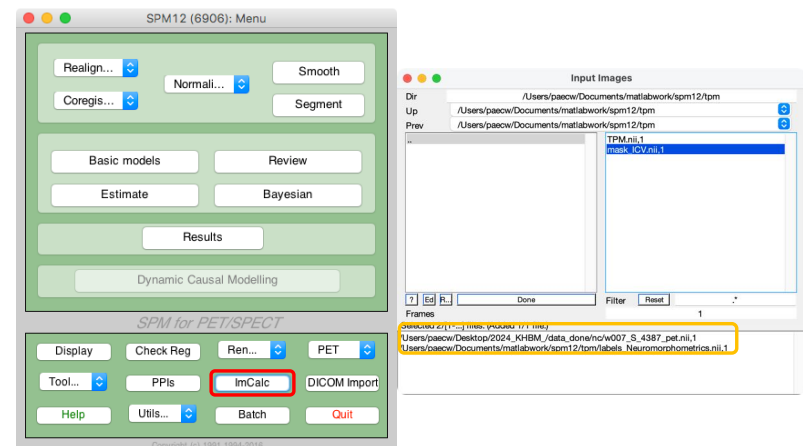


4. Count normalization



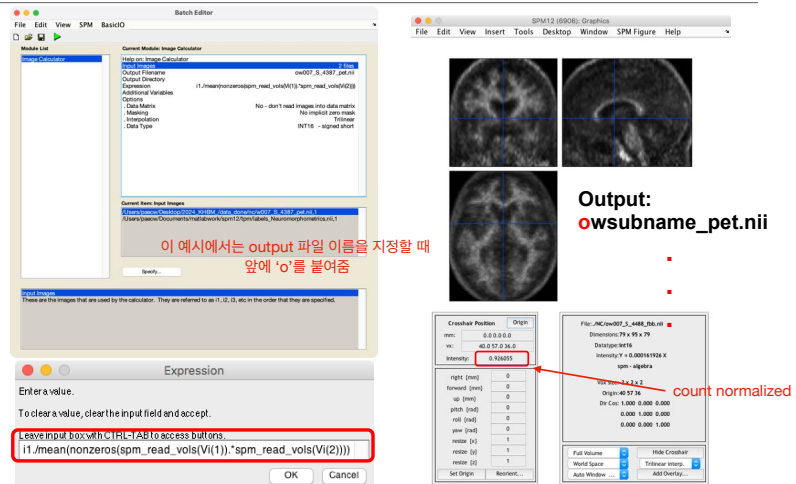
Cerebellum에는 아밀로이드 플라크가 없기 때문에 reference region이 될 수 있다.
V.Camus et al. Eur J Nucl Med Mol Imaging(2012)

4. Count normalization (cont')



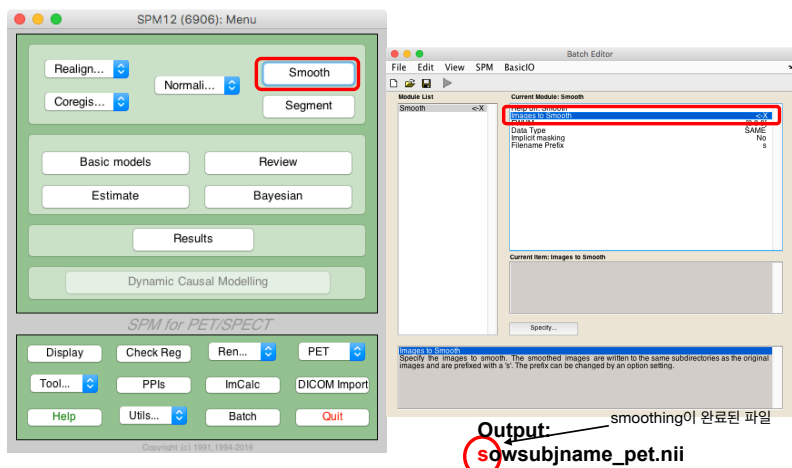
ImCalc에서 normalize된 pet 영상과 Cerebellum mask를 선택 (순서 중요)

4. Count normalization (cont')



1. Output file name, output directory를 지정해준 후
2. Expression에서 영상을 계산할 수식을 입력해주고 배치 수행: 개인별로 수행해야 함
⇒ `i1./mean(nonzeros(spm_read_vols(Vi(1)).*spm_read_vols(Vi(2))))`

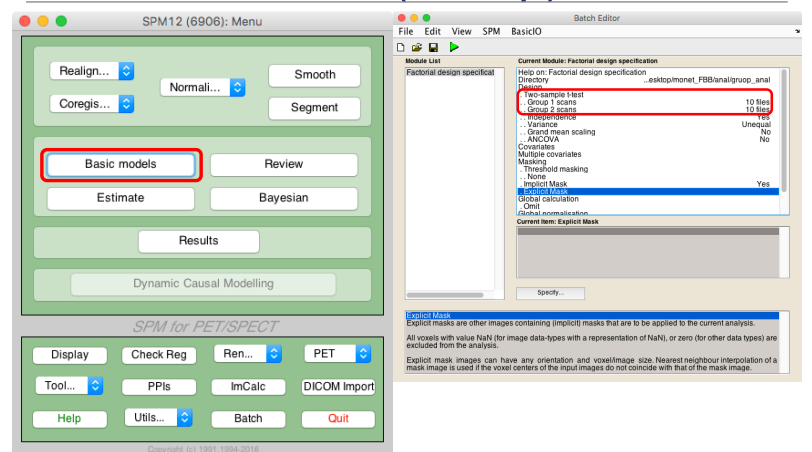
5. Smoothing



1. Smooth 선택
2. Data 란에 앞단계에서 나온 count normalized 영상들을 입력하고 배치 실행

Part II: Statistical Analysis & Inference

6. Basic model (Group)



1. Basic models 선택
2. Directory에 결과와 저장될 directory 지정
3. Design \Rightarrow Two sample t-test; Group1/2 scan에 이전 과정까지 전처리된 각 그룹 데이터 입력 ('sow-')
4. Explicit Mask 설정

6. Basic model (Individual)

Non-Brain tissue의 강한 신호 강도(red region)는 분석의 오류를 초래하기 때문에 마스크해줌.

(위치: spm디렉토리/tpm/mask_ICV.nii)

Output: .../output directory/
SPM.mat

Explicit 마스크 지정 후 배치를 수행하면 분석을 수행하기 위한 기본 모델이 SPM.mat 에 저장된다.

Output: .../output directory/
SPM.mat

Basic model (Group)과 동일한 절차이나, Group 2 scan에 개인 PET file을 입력하면 된다.

7. Estimate

Output:/output directory/
SPM.mat
RPV.nii
ResMS.nii
Beta002.nii
Mask.nii

Basic model에서 저장한 SPM.mat을 입력하고 배치 실행.
(그룹, 개인 분석 과정 동일)

Contrast

① $c = [1 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0]$

② $c = [0 \ 1 \ -1 \ 0 \ 0 \ \dots \ 0 \ 0 \ 0]$

- A contrast selects a specific effect of interest
 - A contrast c is a vector of length p
 - $c \times \beta$ is a linear combination of regression coefficients β
- Null hypothesis : $H_0: c^T \beta = 0$

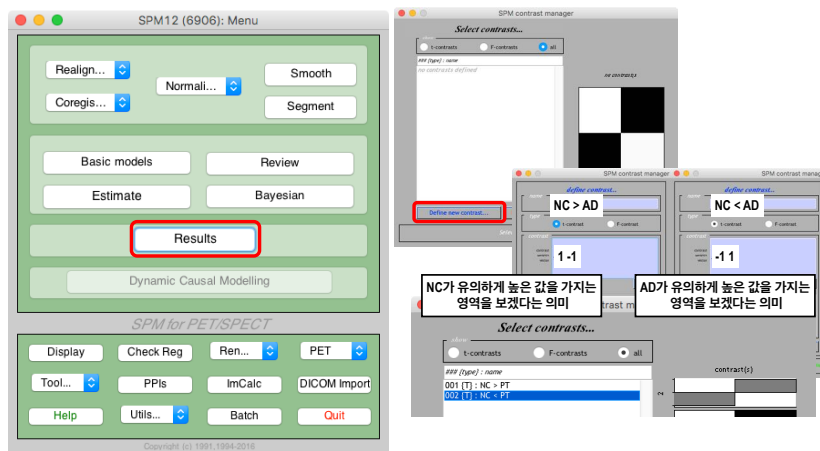
① $c = [1 \ 0 \ 0 \ 0 \ \dots]^T$

$$c^T \beta = 1 \times \beta_1 + 0 \times \beta_2 + 0 \times \beta_3 + 0 \times \beta_4 + \dots = \beta_1$$

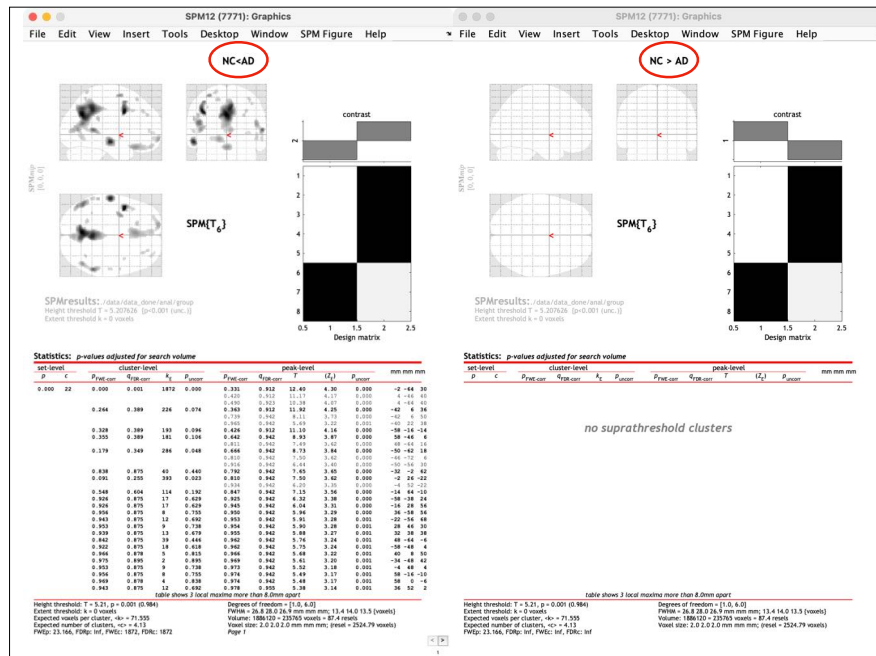
② $c = [0 \ 1 \ -1 \ 0 \ \dots]^T$

$$c^T \beta = 0 \times \beta_1 + 1 \times \beta_2 + -1 \times \beta_3 + 0 \times \beta_4 + \dots = \beta_2 - \beta_3$$

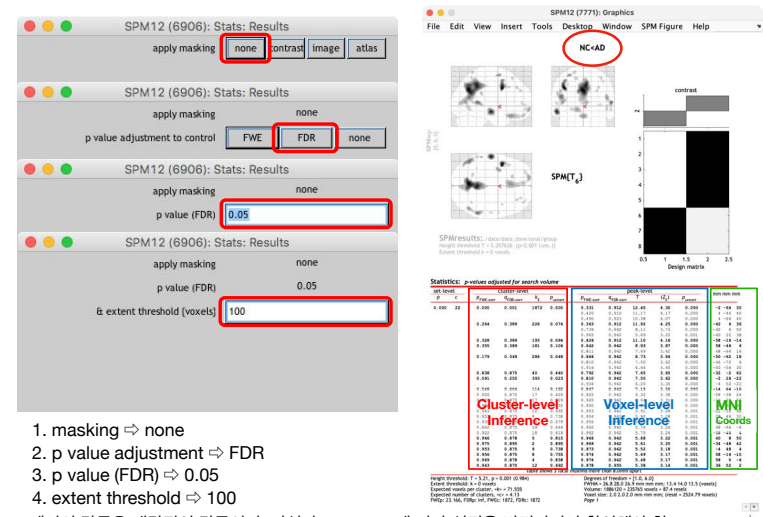
8. Results (Group)



1. Result 선택
2. Estimation이 끝난 SPM.mat 선택 후 contrast 정의 창으로 넘어감.
3. t-contrast 선택 ⇒ Define new contrast ⇒ contrast의 이름과 define을 입력

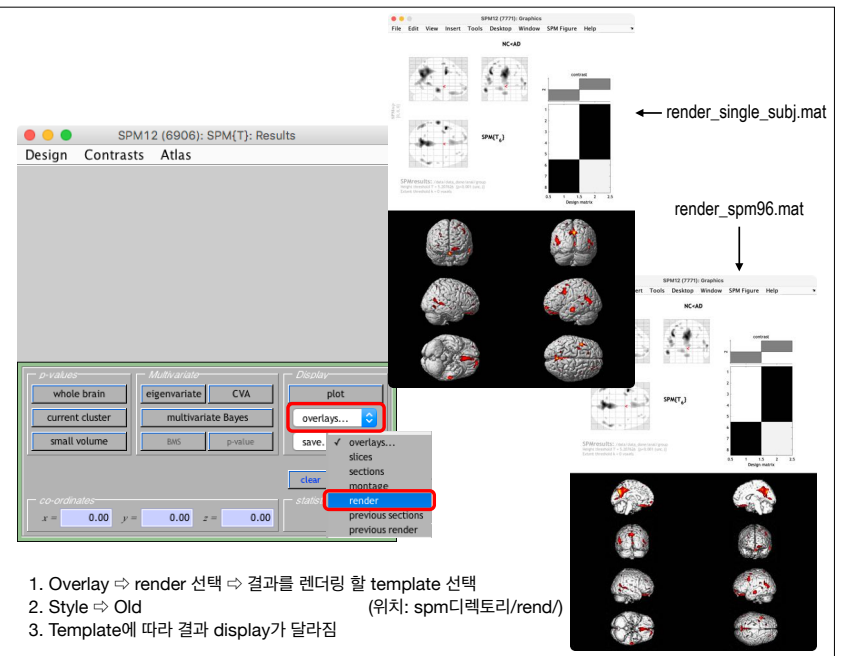


8. Results (Group) (cont')

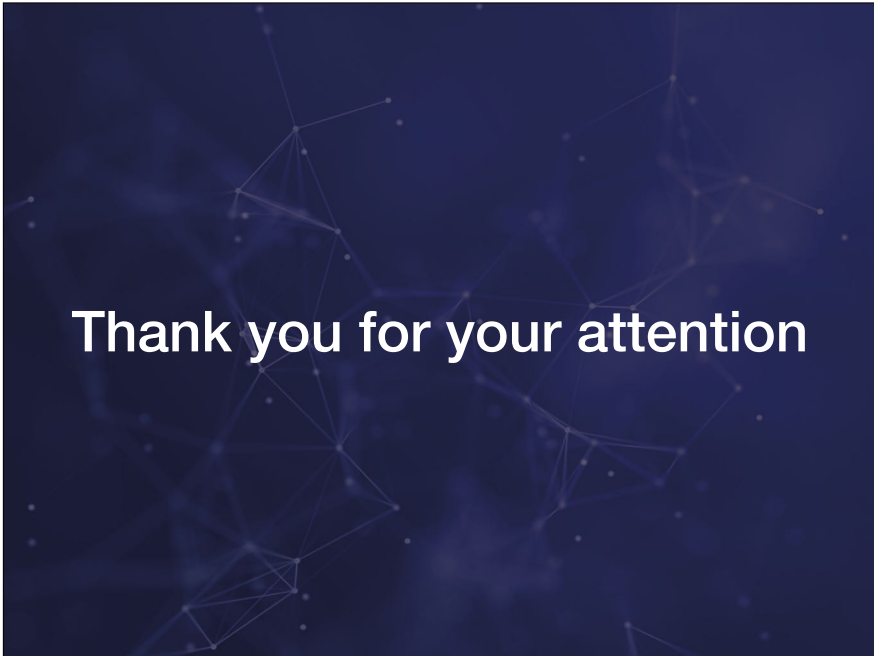
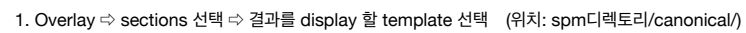


1. masking \Rightarrow none
2. p value adjustment \Rightarrow FDR
3. p value (FDR) \Rightarrow 0.05
4. extent threshold \Rightarrow 100

예시의 값들은 대략적인 값들이며, 가설과 inference에 따라 설정을 바꿔가면서 확인해야 함.



1. Overlay \Rightarrow render 선택 \Rightarrow 결과를 렌더링 할 template 선택
2. Style \Rightarrow Old (위치: spm디렉토리/render/)
3. Template에 따라 결과 display가 달라짐



Thank you for your attention