Connectivity-based Parcellation of Human Inferior Parietal Lobule using Diffusion MRI and Probabilistic Tractography

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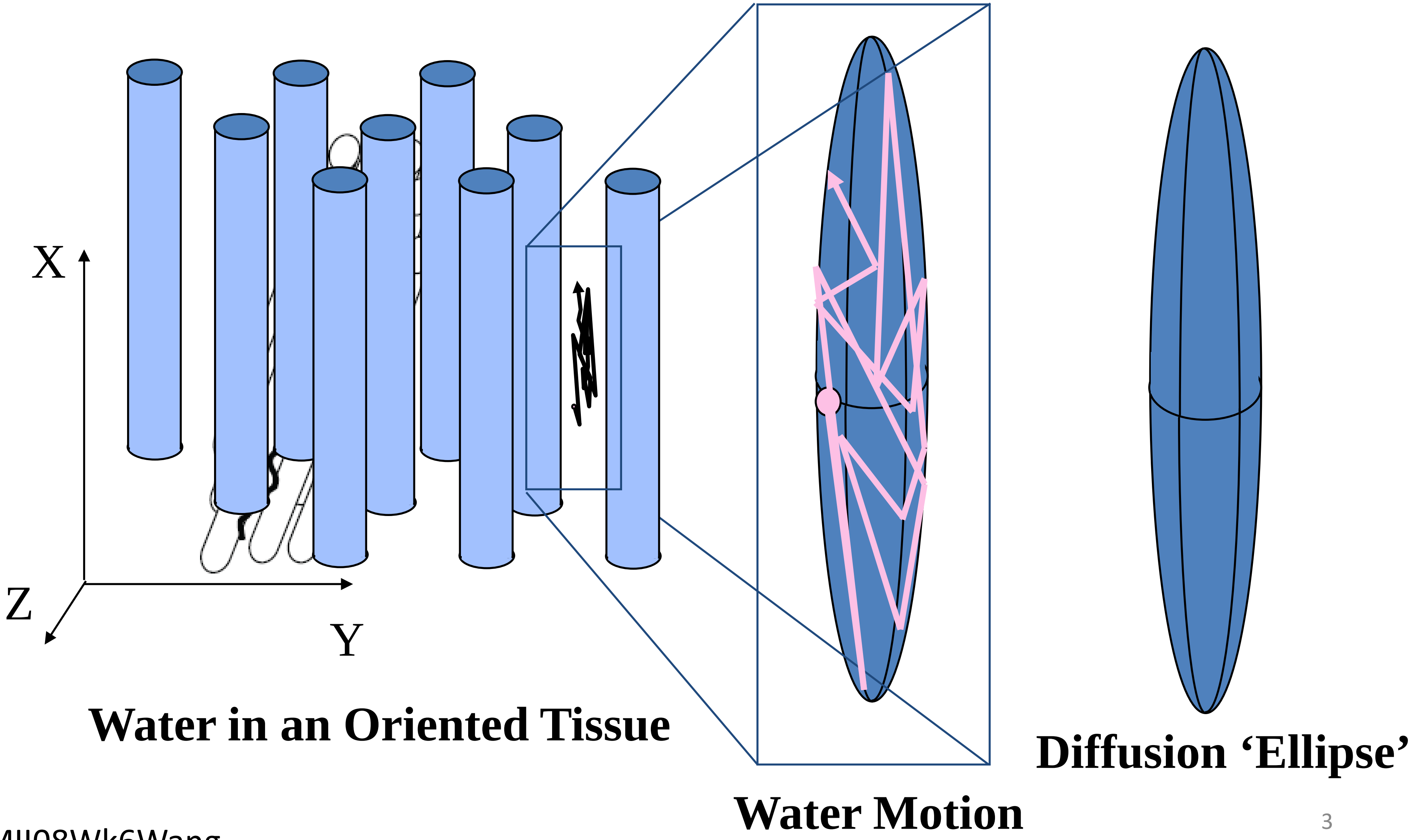
May 26, 2011

Outline

- Background
  - Diffusion MRI
  - Human inferior parietal lobule
- Materials & Methods
  - Data Collection
  - Connectivity Map Preparation via preprocessing
  - Unsupervised Classification Approaches (Spectral clustering)
- Results
  - Pseudo truth from Jülich Atlas
  - K means, Mixture Gaussian, and Spectral Clustering
  - Correspondence accuracy metric for parcellation evaluation

BACKGROUND

Diffusion in White Matter



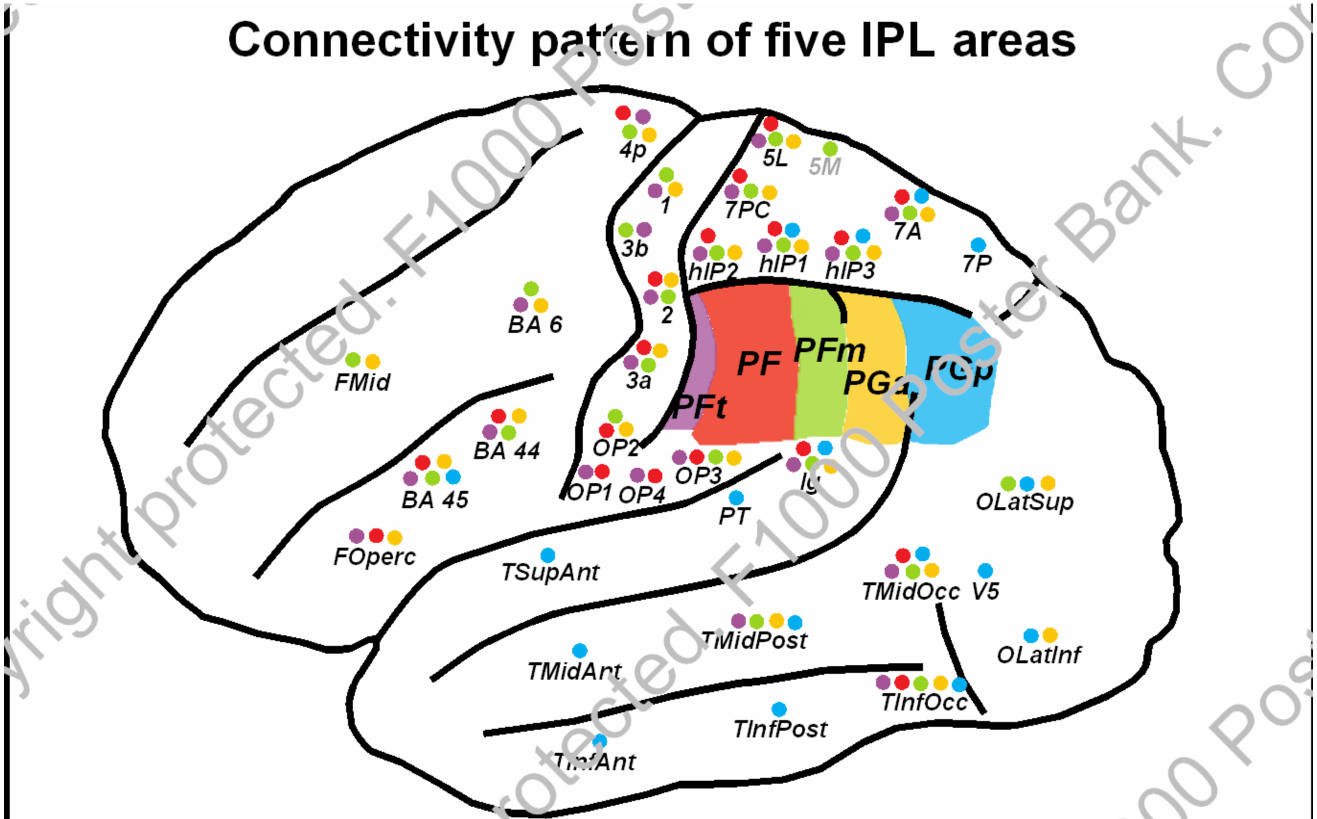
Inferior Parietal Lobule

- Brain region with marked functional heterogeneity involved in visuospatial attention, memory, and mathematical cognition

- Availability of ECoG electrodes to verify and make testable predications in our study

- Consisted of seven cytoarchitectonic regions (PGp, PGa, PF, PFcm, PFm, PFt, Pfop)

Prior Knowledge of IPL Connectivity



Significant results of the comparison of seed-target vs. "free" tracing for five IPL areas displayed on a schematic drawing of a hemisphere. Colored dots mark connections of the respectively color-coded IPL areas. Only target areas with at least one significant connection with an IPL area are displayed.

Rostral IPL areas: targets in the prefrontal, motor, somatosensory, and anterior superior parietal cortex

Caudal IPL areas: targets in the posterior superior parietal and temporal areas

Caspers, 2009

MATERIALS & METHODS

Data

- One subject
  - Diffusion weighted data (128x128x70)
    - B value – 1000
    - Acquired in 63 gradient directions
  - T1 coronal data (256x256x208)
    - Manually extracted brain data
- T1 MNI 152 1mm standard data (182x218x182)
  - Juelich atlas

Tools for Brain Analysis

- FreeSurfer: automated tools for reconstruction of the brain's cortical surface from structural MRI data, and overlay of functional MRI data onto the reconstructed surface.

- FSL: a comprehensive library of analysis tools for FMRI, MRI and DTI brain imaging data. FSL runs on Apples, Linux, and Windows. Most of the tools can be run both from the command line and as GUIs.

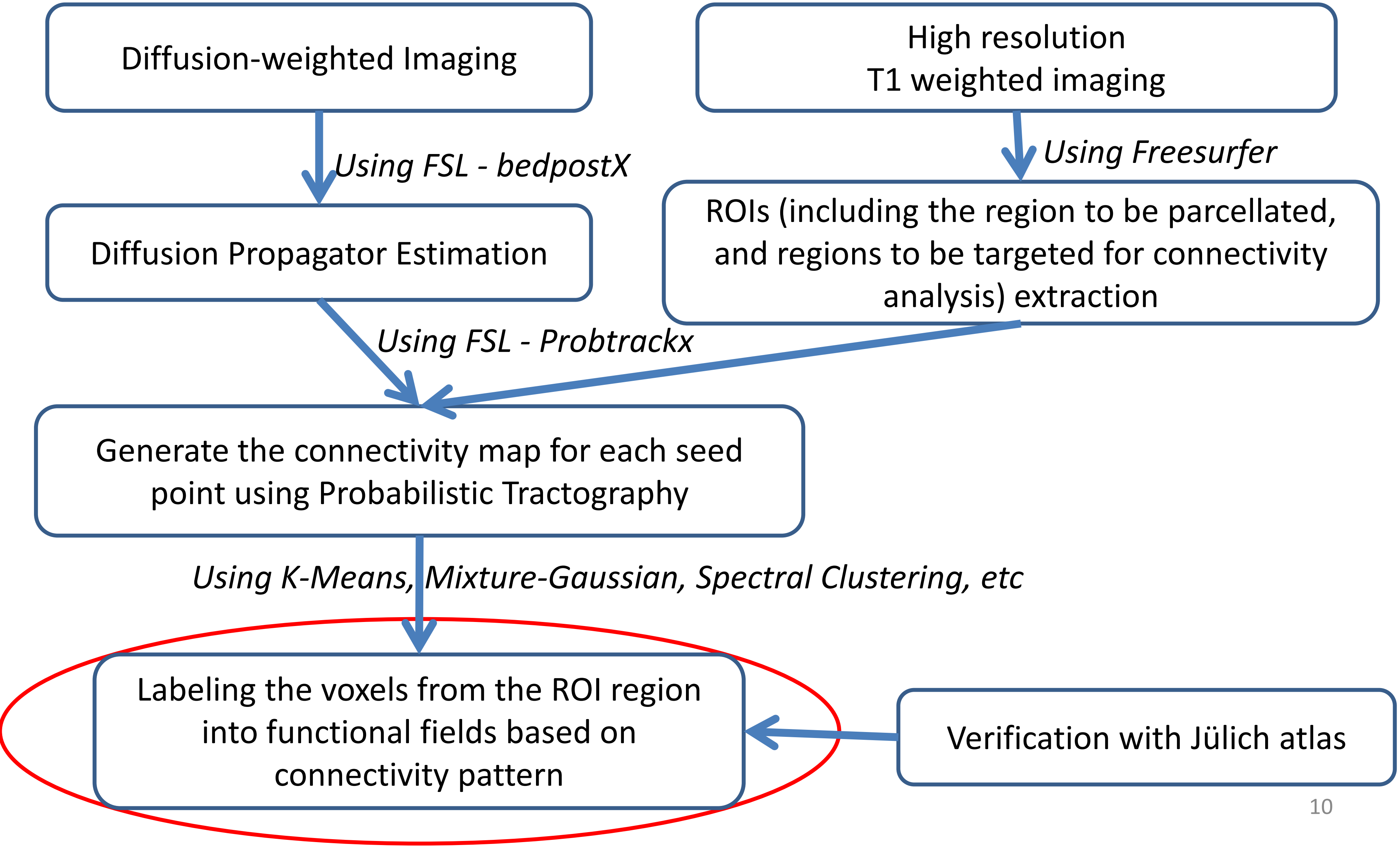
- SPM: a statistical package for processing brain data including fMRI, SPECT, PET, EEG, MEG.

Juelich Atlas

Juelich histological (cyto- and myelo-architectonic) atlas
A probabilistic atlas created by averaging multi-subject post-mortem cyto- and myelo-architectonic segmentations. The atlas contains 52 grey matter structures and 10 white matter structures. This is an update to the data used in Eickhoff's Anatomy Toolbox v1.5.

The atlas is based on the miscroscopic and quantitative histological examination of ten human post-mortem brains. The histological volumes of these brains were 3D reconstructed and spatially normalized into the space of the MNI single subject template to create a probabilistic map of each area. For the FSL version of this atlas, these probabilistic maps were then linearly transformed into MNI152 space.

Flowchart


Diffusion-weighted Imaging
High resolution
T1 weighted imaging
Using FSL - bedpostX
Using Freesurfer
Diffusion Propagator Estimation
ROIs (including the region to be parcellated, and regions to be targeted for connectivity analysis) extraction
Using FSL - Probtrackx
Generate the connectivity map for each seed point using Probabilistic Tractography
Using K-Means, Mixture-Gaussian, Spectral Clustering, etc
Labeling the voxels from the ROI region into functional fields based on connectivity pattern
Verification with Jülich atlas

Estimation of Distribution of Diffusion using FSL BEDPOSTX

- Bayesian Estimation of Diffusion Parameters Obtained using Sampling Techniques (BEDPOSTX) to build up distribution of diffusion parameters at each voxel
  - Partial model allowing for fiber direction mixed with an isotropic ally diffusion model
  - A parameterized model of the transfer function between a distribution of fiber orientations in a voxel and the measured diffusion weighted signal
  - Use of Markov Chain Monte Carlo (MCMC) sampling to estimate the posterior distribution on parameters of interest

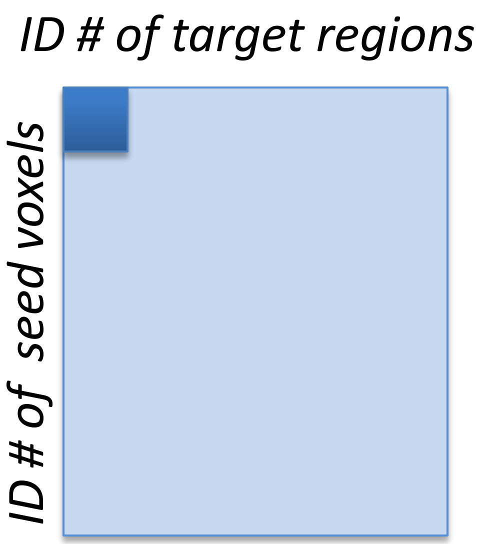
Behrens 2003

WGMI Partition using Freesurfer

- White gray matter interface (WGMI) Partition
  - Gray matter does not have enough connectivity information for parcellation
  - Atlas based cortical registration (a2009 atlas)
  - Seed regions: inferior parietal lobule (IPC) including angus and super marginal
  - Target regions: all cortical regions except IPC

Connectivity Matrix Calculation using Probabilistic Tractography (FSL PROBTRACKX)

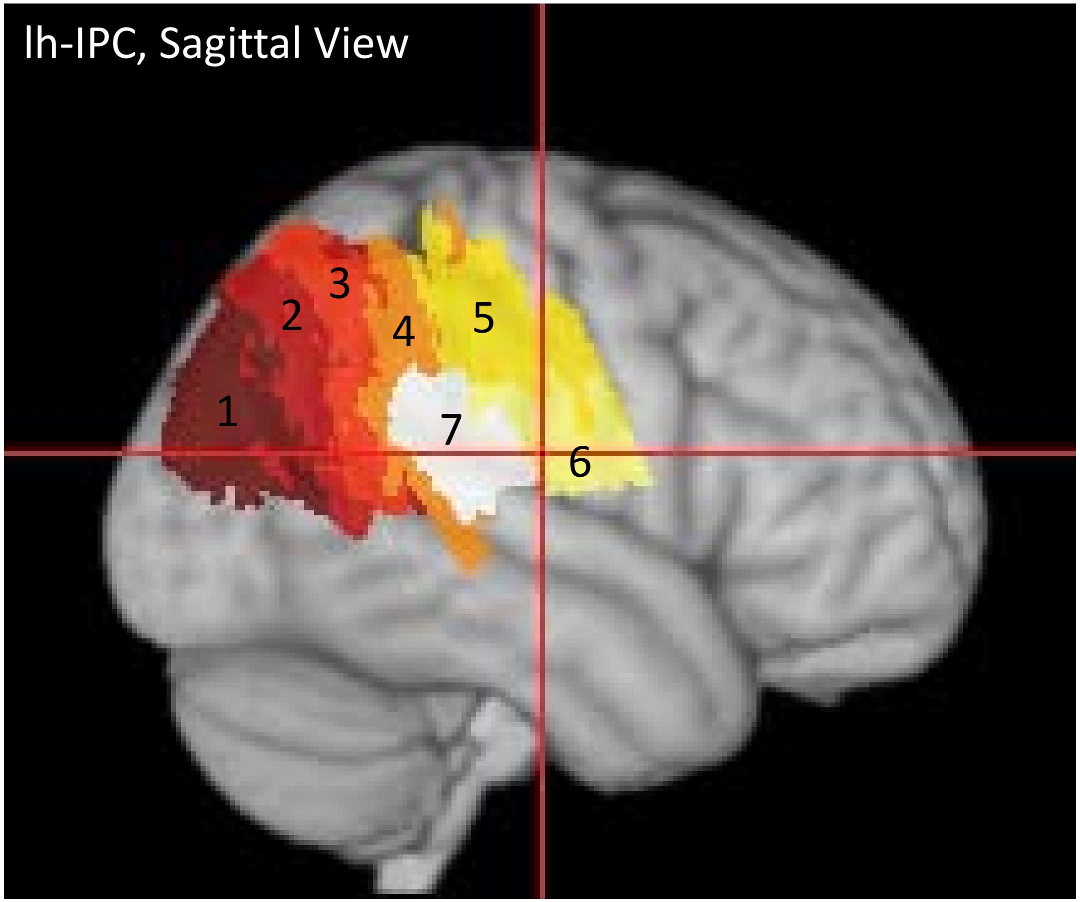
- Each value in the connectivity matrix indicates the probability that the seed particle can reach the target region through probabilistic tractography

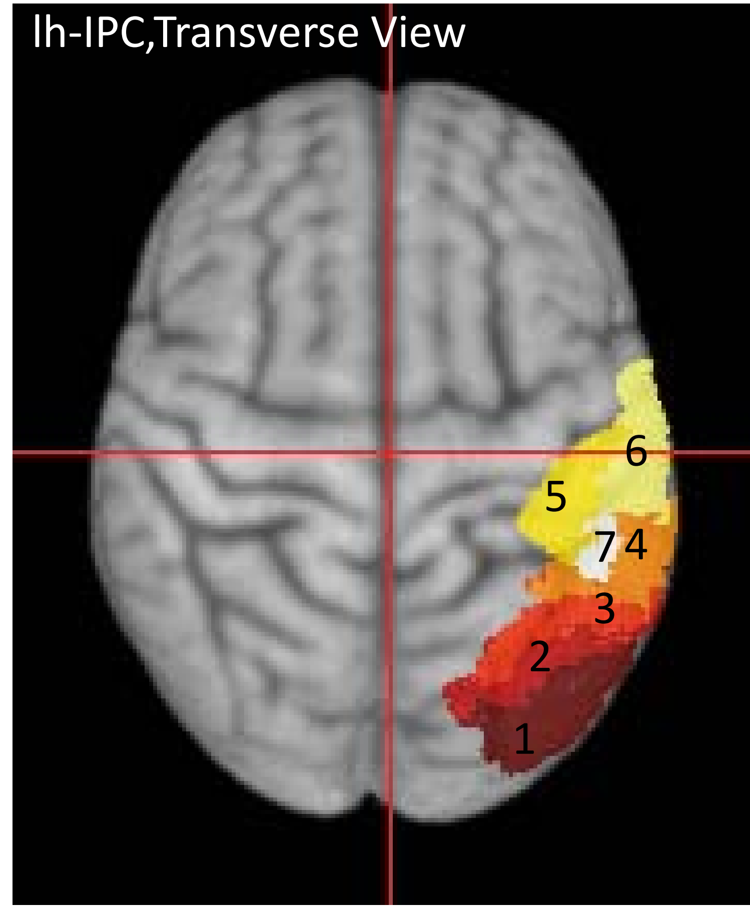


Connectivity matrix

connectivity probability =
(number of particles that reached the target region) /
(total number of particles issued from the seed voxel)

Juelich Atlas for Verification





Post-process group averaged probability map
to obtain the function field labels with highest probability

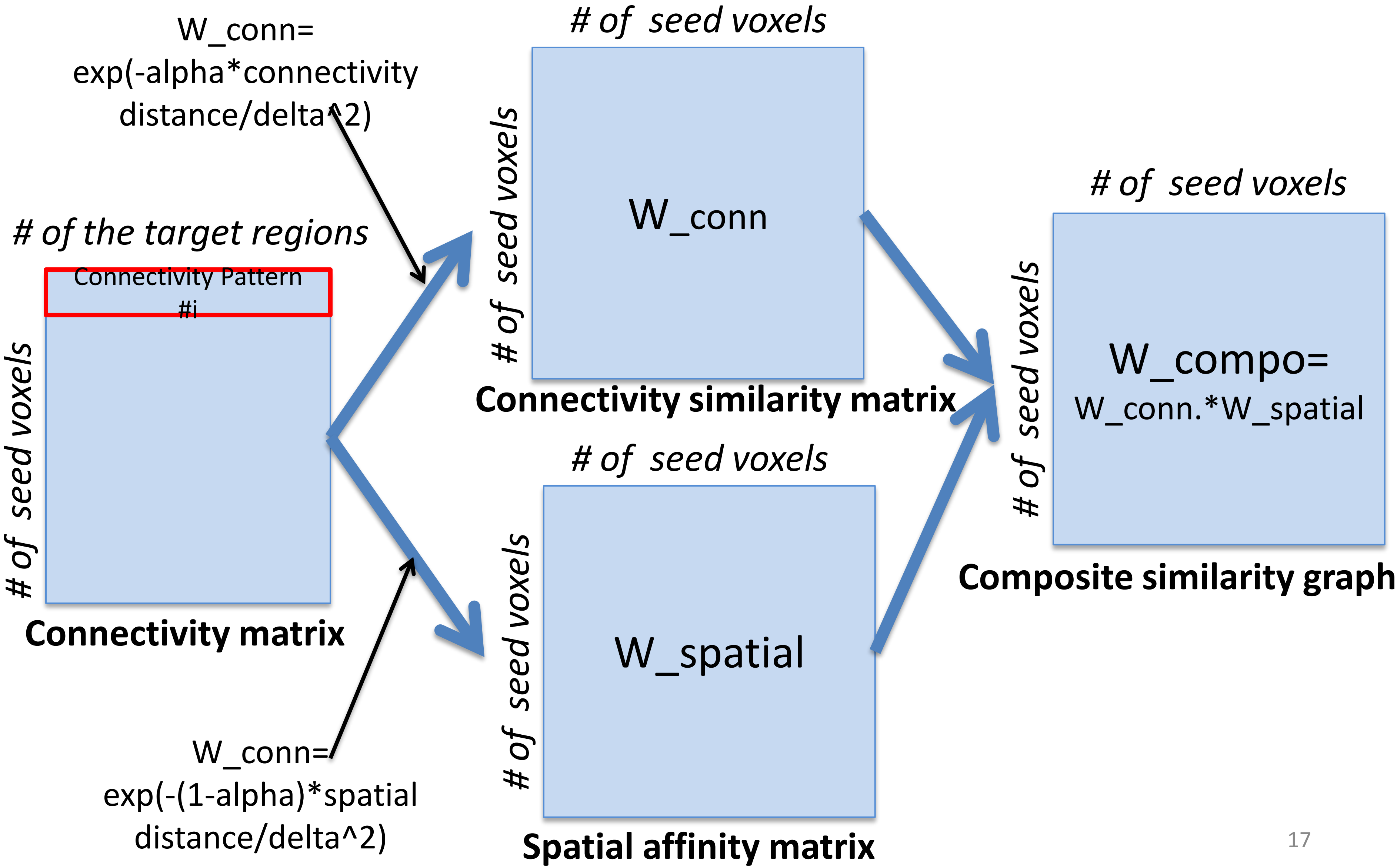
Labeling Approaches

- K–Means Clustering
- Mixture of Gaussians (EM Clustering)
- Spectral Clustering (Graph – cut)

Spectral Clustering

- Spectral Clustering
  - Build the similarity graph through pair-voxel correlation of connectivity similarity and spatial affinity
  - Solve the normalized graph-cut problem through Eigen decomposition of similarity matrix

Build the Similarity Graph

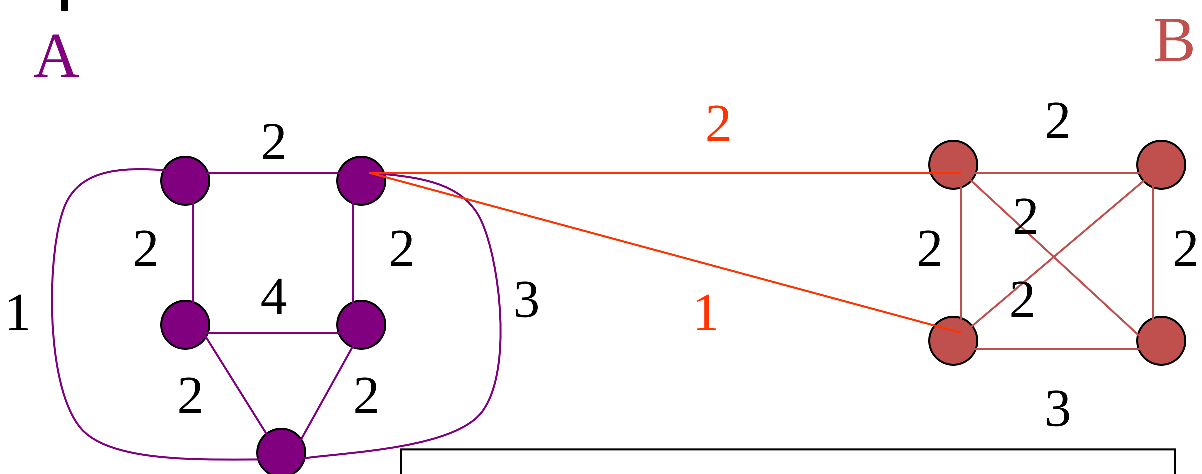


Normalized cut of the Similarity Graph

- Normalized cut

$$\text{Ncut}(A,B) = \frac{\text{cut}(A, B)}{\text{asso}(A,V)} + \frac{\text{cut}(A,B)}{\text{asso}(B,V)}$$

- Example



$$\text{Ncut}(A,B) = \frac{3}{21} + \frac{3}{16}$$

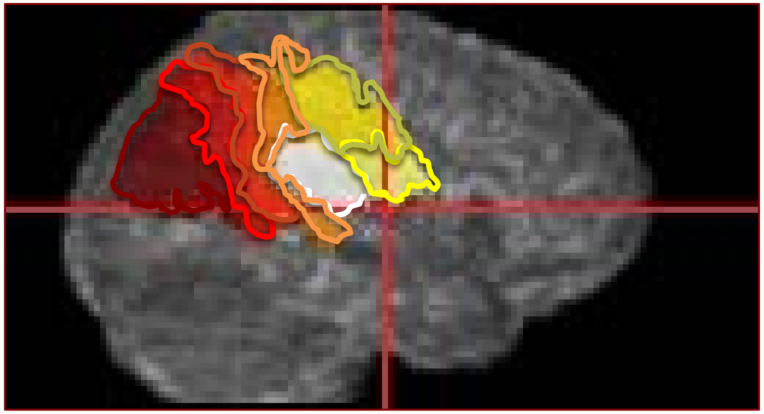
Shi & Malik, 2000

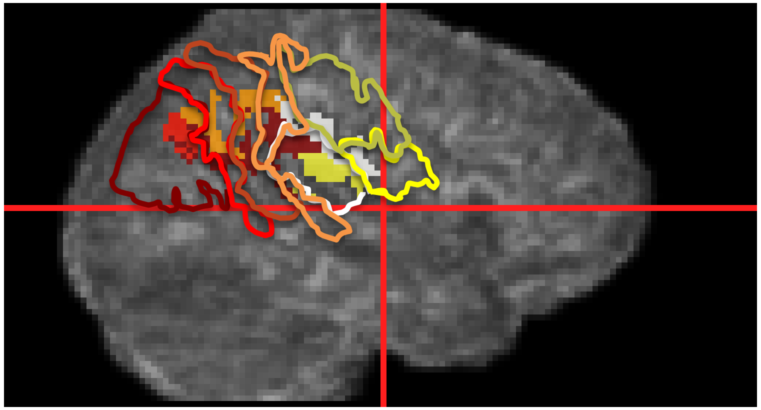
RESULTS

Data Summary

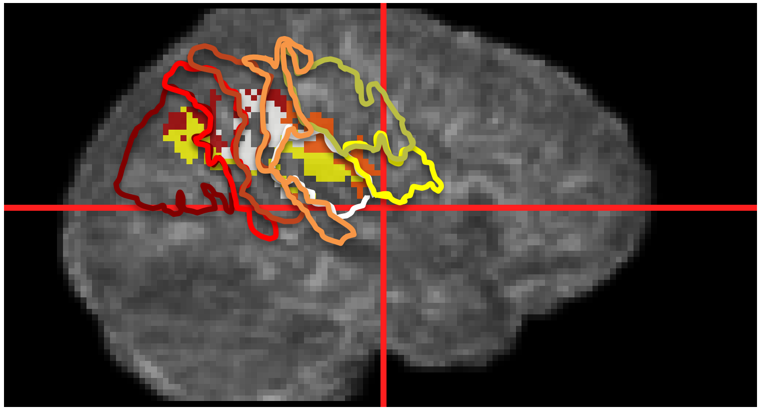
- Left Hemisphere IPL Parcellation (LH-IPL)
  - 667 voxels selected as seed for probabilistic tractography
  - 148 targets are selected for probabilistic tractography, 3 targets are discarded due to lack of enough connectivity
- Right hemisphere IPL Parcellation (RH-IPL)
  - 617 voxels selected as seed for probabilistic tractography
  - 148 targets are selected for probabilistic tractography, 2 targets are discarded due to lack of enough connectivity

Lh-IPL: 3D Sagittal View

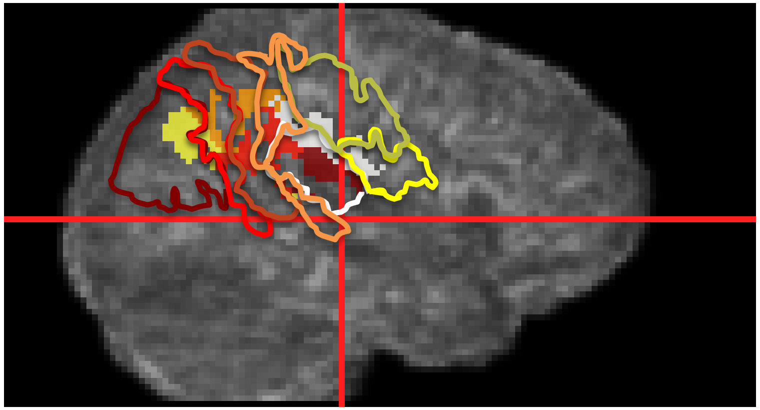




Kmeans (N=5)

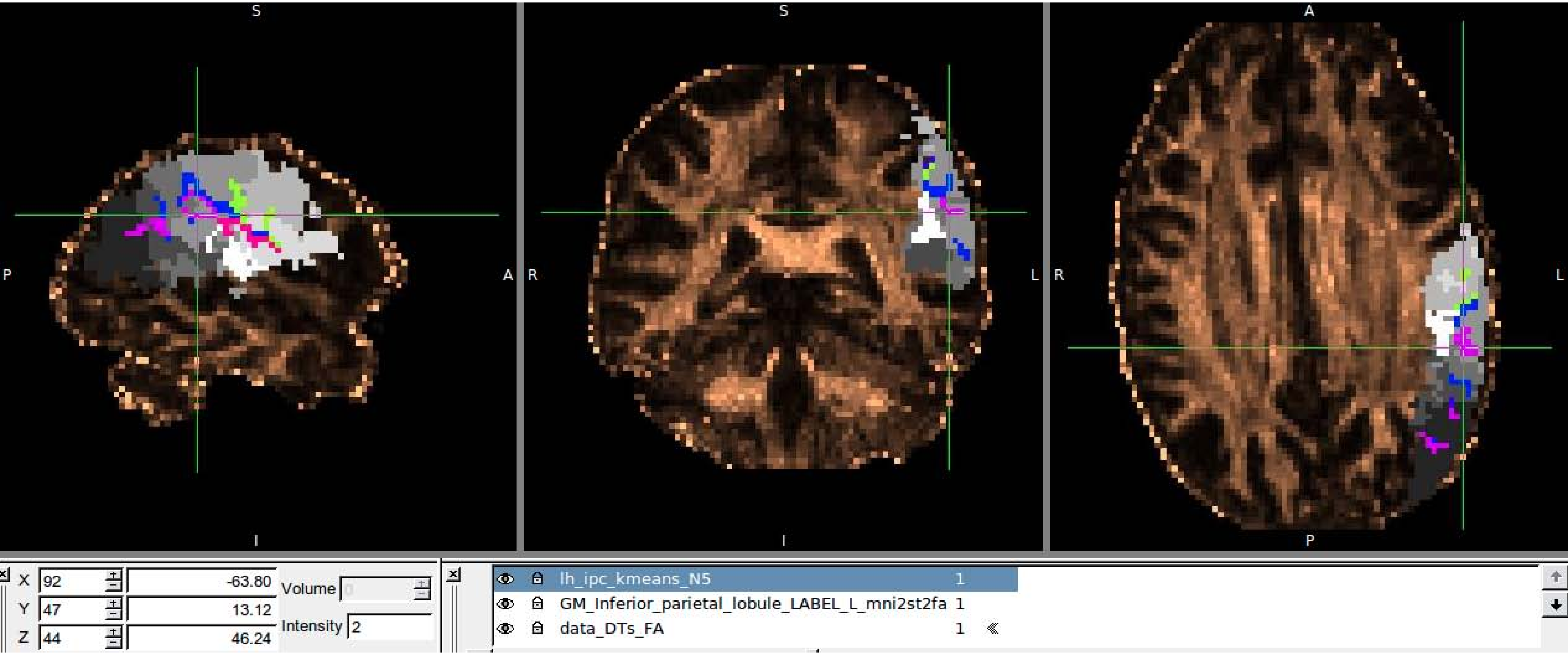


EM (N=5)



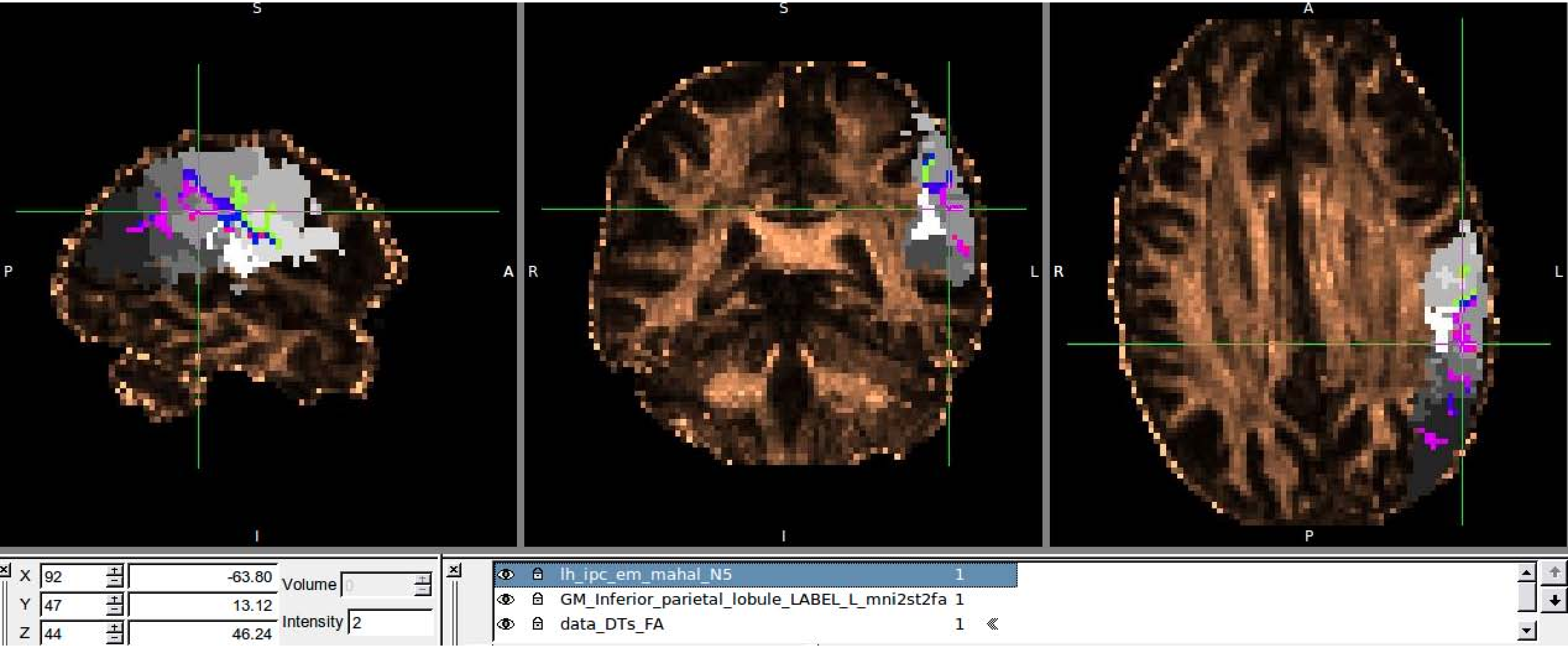
Spectral clustering (N=5)

Lh-IPL – 2D Views (Kmeans, N=5)



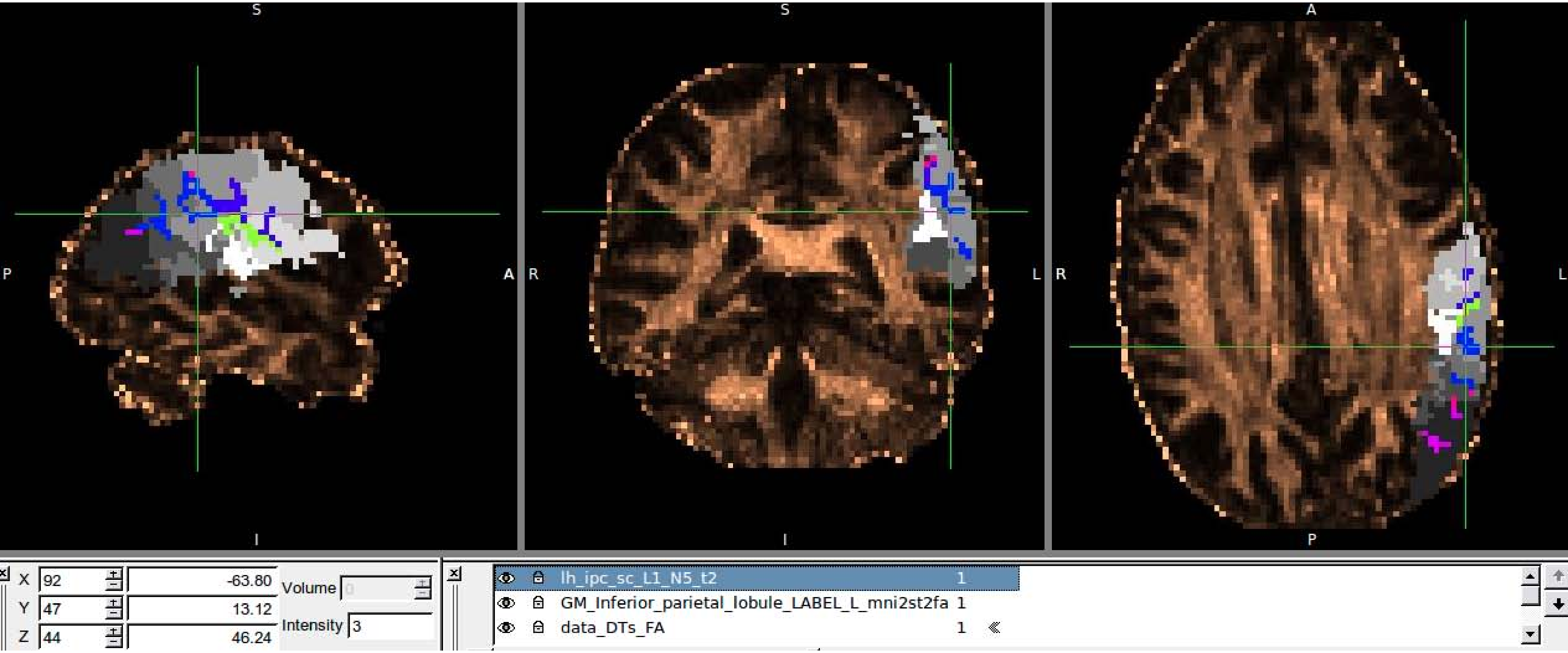
Grey clusters are the atlas, while the colored ones are clustered by kmeans

Lh-IPL – 2D Views (EM, N=5)



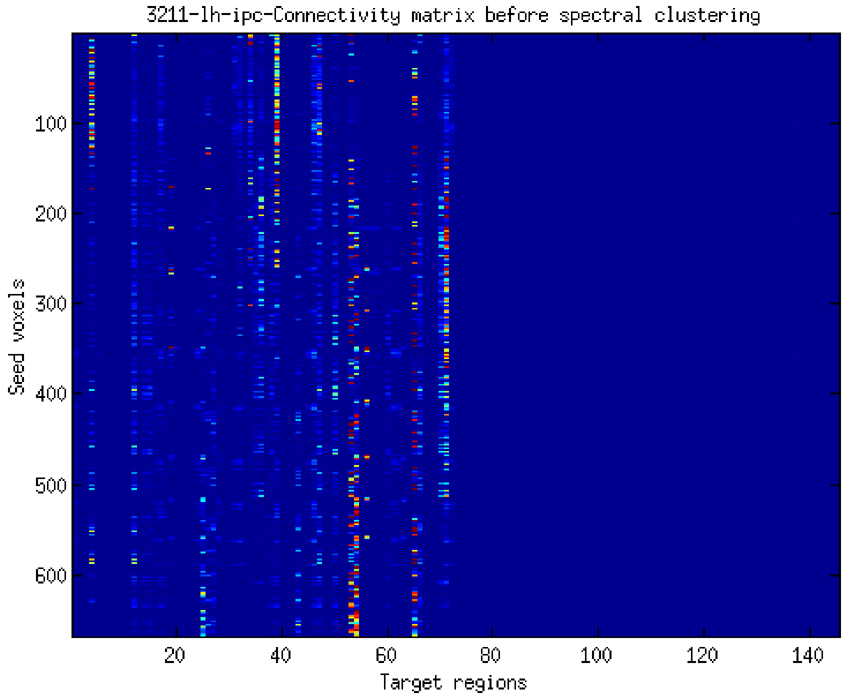
Grey clusters are the atlas, while the colored ones are clustered by EM

Lh-IPL – 2D Views (SC, N=5)

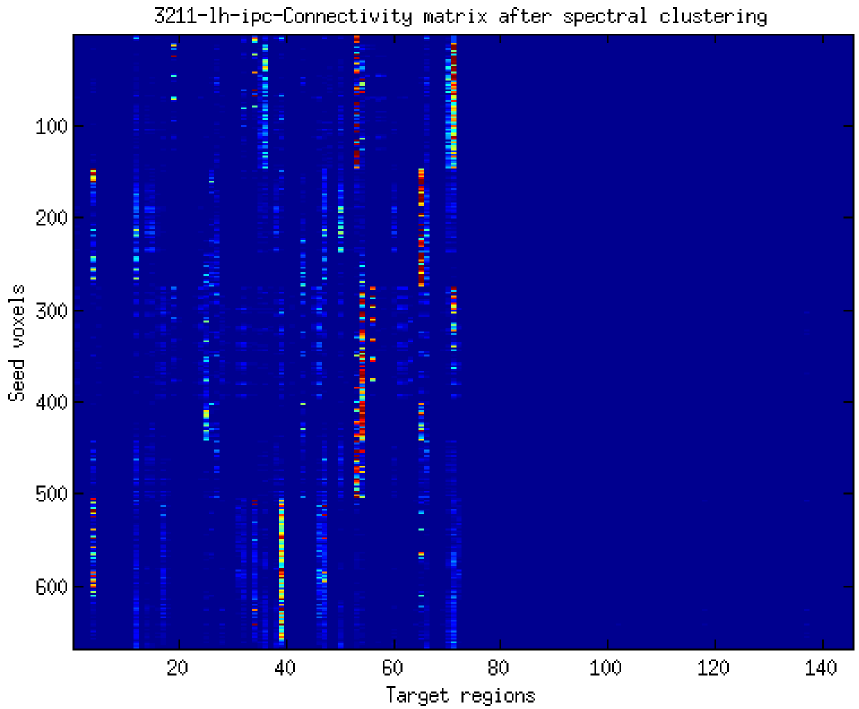


Grey clusters are the atlas, while the colored ones are clustered by Spectral Clustering

Normalized Connectivity Matrix

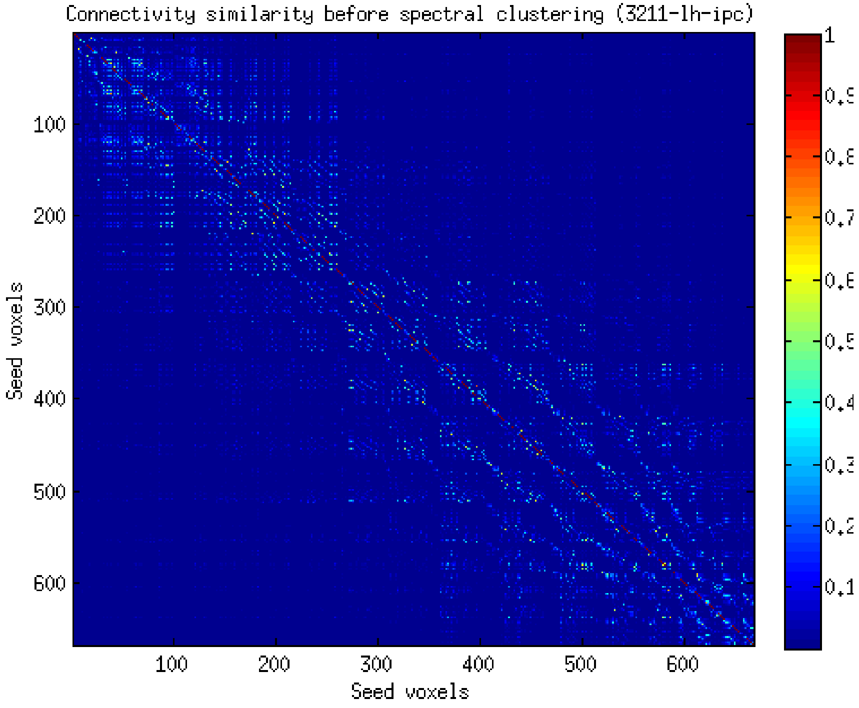


Before spectral clustering

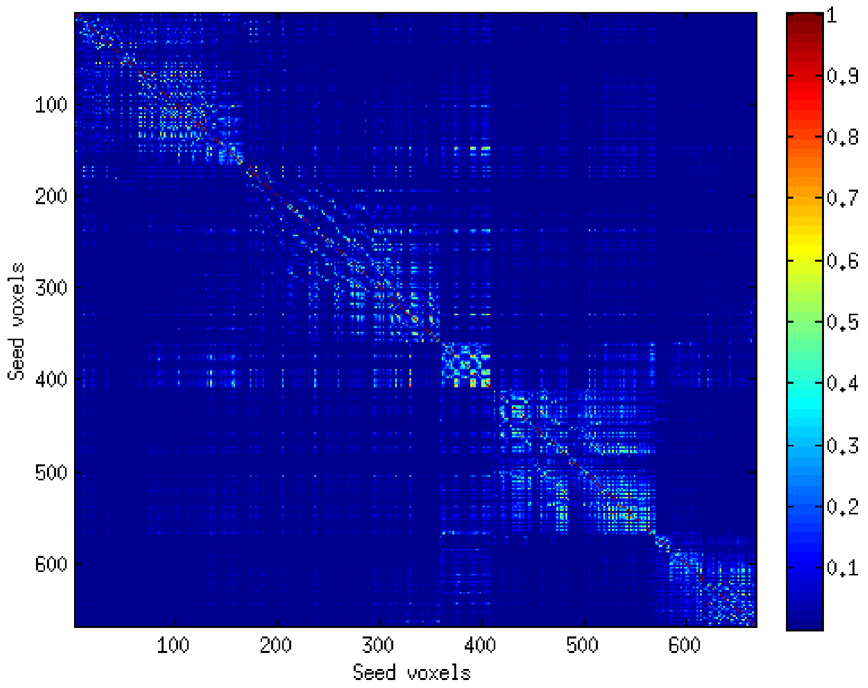


After spectral clustering

Connectivity Similarity Matrix of Spectral Clustering

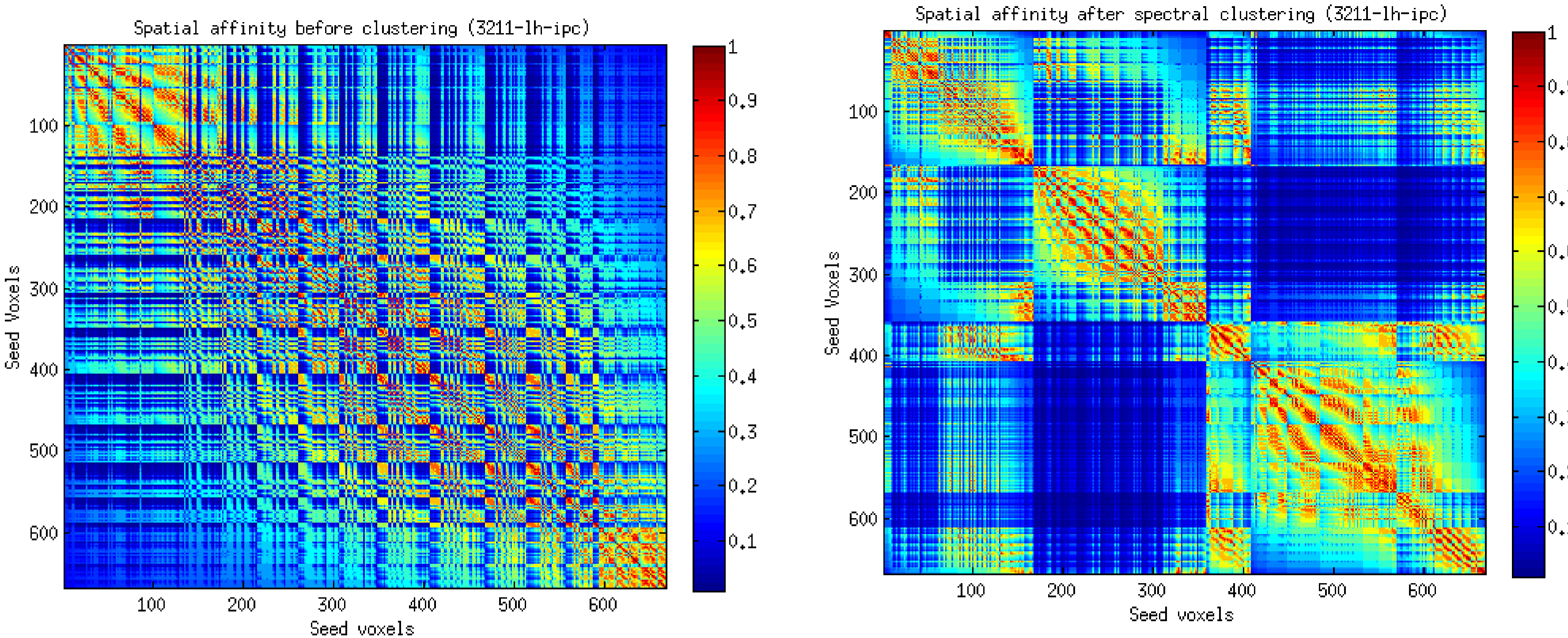


Before spectral clustering



After spectral clustering

Affinity Matrix of Spectral Clustering



Before spectral clustering

After spectral clustering

Interpretation of the Clusters (LH-IPL)

	PGp	PGa	PFm	PF	PFt	PFop	PFcm	Total	Top 3 connected targets
Cluster#1	88 (96.7%)	2	0	1	0	0	0	91	wm_lh_S_temporal_sup wm_lh_S_oc_sup_and_transversal wm_lh_S_intrapariet_and_P_trans
Cluster #2	0	0	4	69 (53.1%)	26	29	0	135	wm_lh_S_postcentral wm_lh_G_and_S_subcentral wm_lh_G_front_inf-Opercular
Cluster #3	48 (40.1%)	25	31	14	0	0	0	119	wm_lh_S_intrapariet_and_P_trans wm_lh_S_interm_prim-Jensen wm_lh_G_parietal_sup
Cluster #4	0	0	0	33	0	66 (46.5%)	43	163	wm_lh_Lat_Fis-post wm_lh_G_and_S_subcentral wm_lh_S_circular_insula_sup
Cluster #5	4	34	53	67 (42.1%)	0	0	1	159	wm_lh_S_interm_prim-Jensen wm_lh_S_temporal_sup wm_lh_G_temporal_middle

Additional Study

Bilge Soran
Quals Project
November 2011

Outline of Work

- Tried several variants of normalized graph cuts
- Used both connectivity and spatial distance information
- Tried several different connectivity similarity functions
- Tried several different spatial distance functions
- Developed a spatial affinity function
- Tried out a feature selection approach
- Developed a new metric for evaluation

Similarity matrix computation

- Build a normalized connectivity matrix using probabilistic tractography. The values are normalized by dividing by the largest value of the matrix.

- Build a symmetric spatial distance matrix

Connectivity Similarity Function

$$W_{conn}^{i,j} = exp(-\alpha * f_{conn}(p_i, p_j)/\sigma_{conn}^2)$$

(where σ is a weighting factor and set to 2.)

Distance Functions:

- Euclidean
- Standardized Euclidean
- Mahalanobis
- City Block
- Minkowski
- Cheybchev
- Jaccard
- Cosine
- Correlation
- Hamming

Spatial Affinity Functions

$$W^{i,j}_{spatial} = exp(-(1-\alpha) * dist(i,j)/\sigma^2_{spatial})$$

$$W^{i,j}_{spatial} = 2 * (1-\alpha) * (dist(i,j) < median(dist))$$

(where σ is a weighting factor and set to 0.5.)

$$dist(i,j) = max(\left|i_x - j_x\right|, \left|i_y - j_y\right|, \left|i_z - j_z\right|)$$

$$dist(i,j) = \sqrt{(i_x - j_x)^2 + (i_y - j_y)^2 + (i_z - j_z)^2}$$

$$dist(i,j) = dist(i,j) = (i_x - j_x) + (i_y - j_y) + (i_z - j_z)$$

Similarity matrix computation

- Compute the composite similarity matrix with one of the equations below:

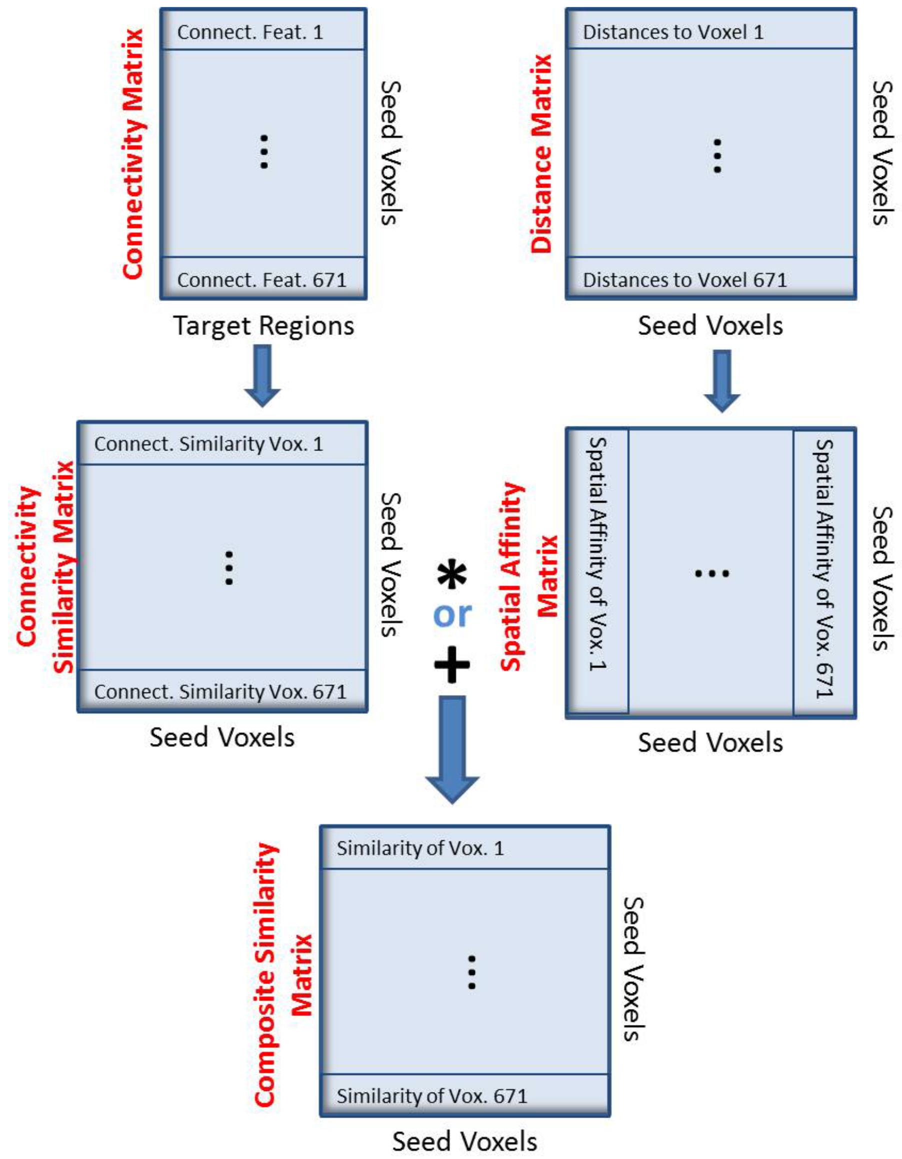
$$W_{similarity}^{i,j} = W_{conn}^{i,j} * W_{spatial}^{i,j}$$

$$W_{similarity}^{i,j} = W_{conn}^{i,j} + W_{spatial}^{i,j}$$

Graph-Cuts Variants

1. Standard Normalized Graph Cuts
2. Normalized Graph Cuts with Feature Selection
3. Normalized Graph Cuts with K-means

Similarity matrix computation



Feature Selection by Target Elimination

- Not all voxels have connections to all target regions.
- The variance of a target region is computed by using the connectivity values in its column of the connectivity matrix with the standard formula:

$$\frac{1}{n}\sum_{i=1}^{n}(x_i - \mu)^2$$

- After computing the variance for each target region, a threshold is applied to select targets with high variances since they are expected to carry discriminative information.

Evaluation

- An example table used in evaluation:

	Atlas Cluster 1	Atlas Cluster 2	Atlas Cluster 3	Atlas Cluster 4	Atlas Cluster 5	Atlas Cluster 6	Atlas Cluster 7
NCut Cluster 1	0	0	0	91	15	3	0
NCut Cluster 2	0	0	0	24	0	79	8
NCut Cluster 3	0	53	67	9	0	0	0
NCut Cluster 4	6	78	14	4	0	0	2
NCut Cluster 5	91	31	0	0	0	0	0

Evaluation Metric

$$A = (\sum_i max(row_i))/(\sum_{ij} cell_{ij})$$

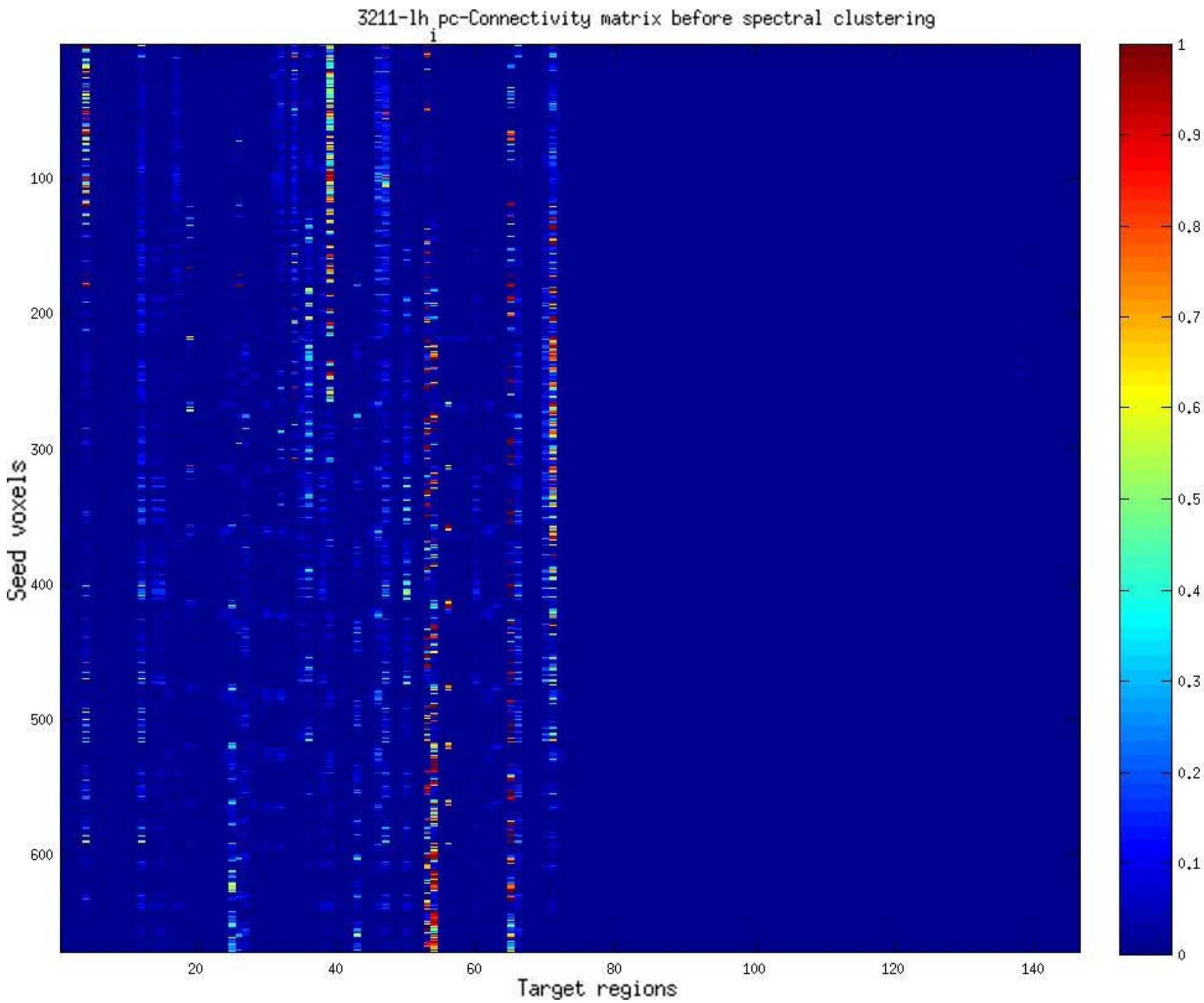
$$B = (\sum_j max(column_i))/(\sum_{ij} cell_{ij})$$

$$If (A - B) < 0.2 \qquad R = (A + B)/2$$

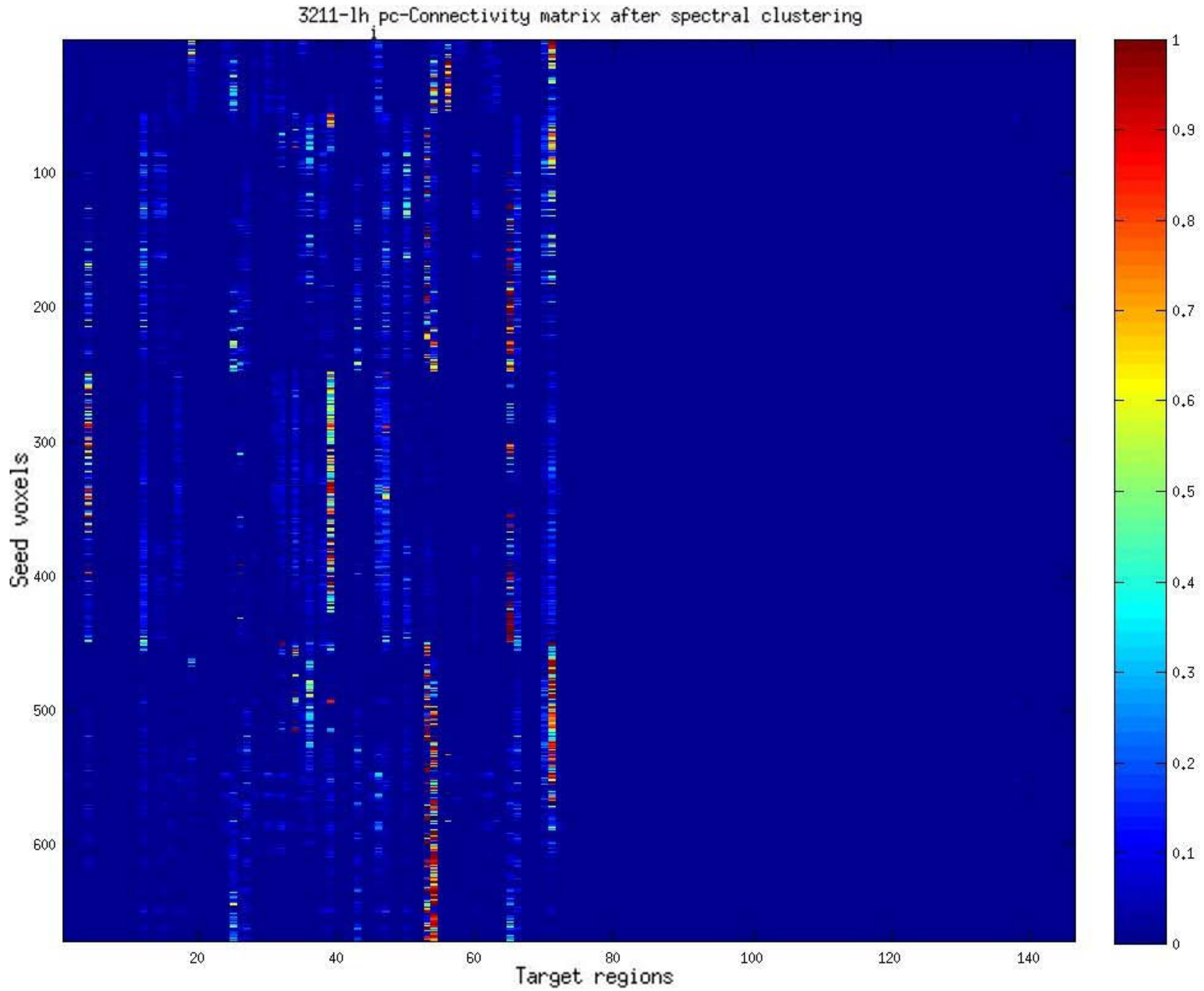
$$Else\ the\ resulting\ parcellation\ is\ wrong.$$

RESULTS

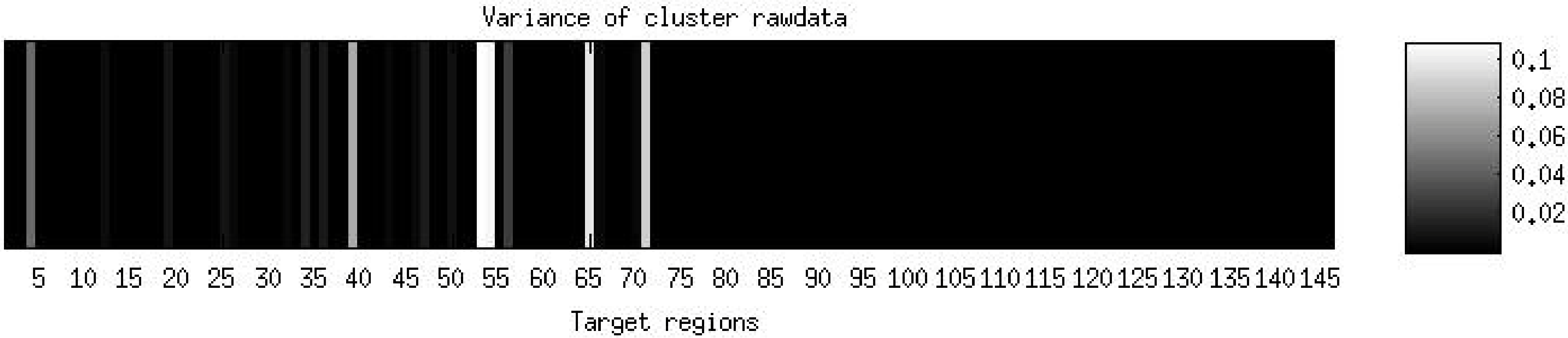
Parcellation of Subject 3211: Connectivity Matrix Before Parcellation



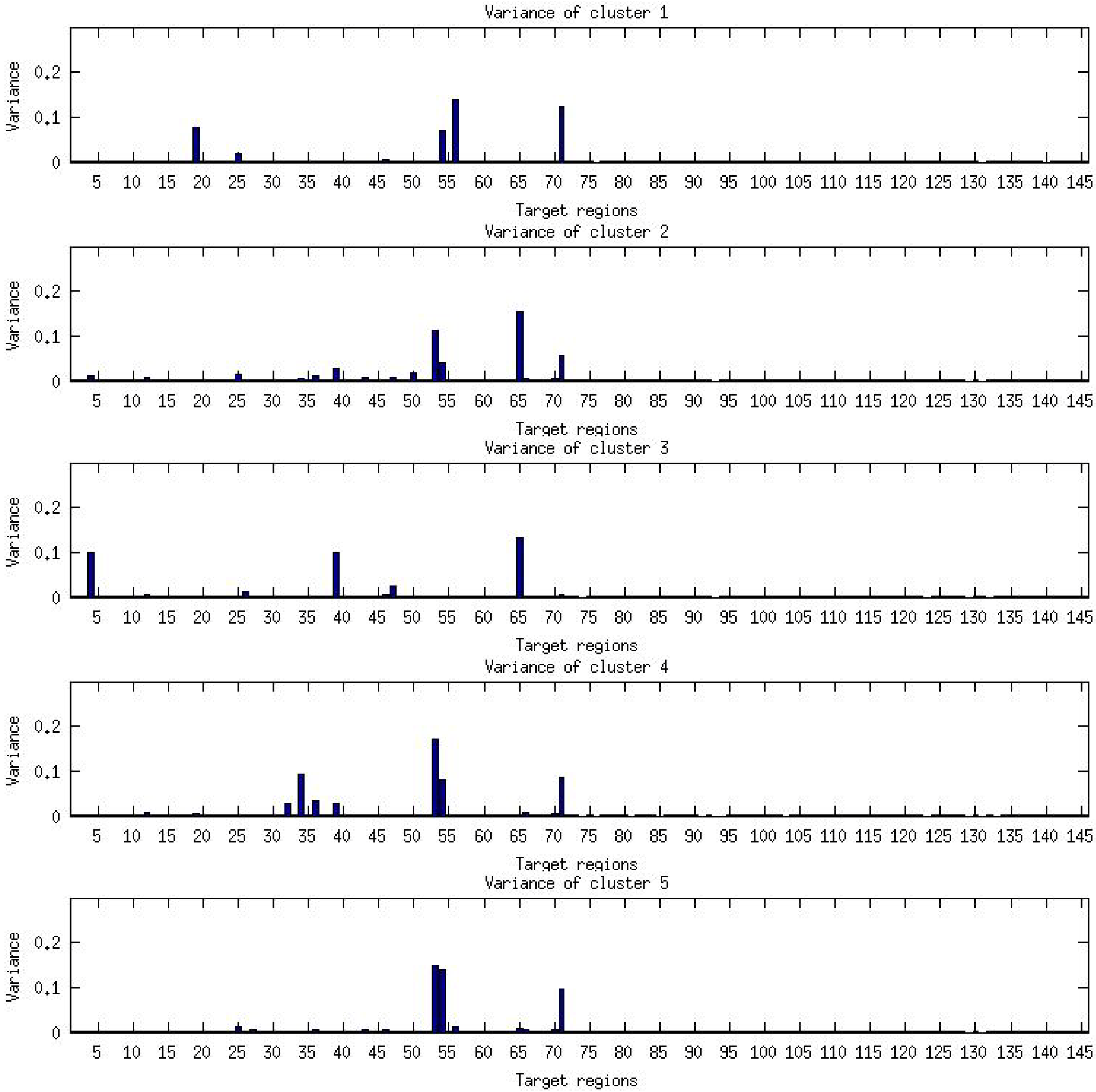
Parcellation of Subject 3211: Connectivity Matrix After Parcellation



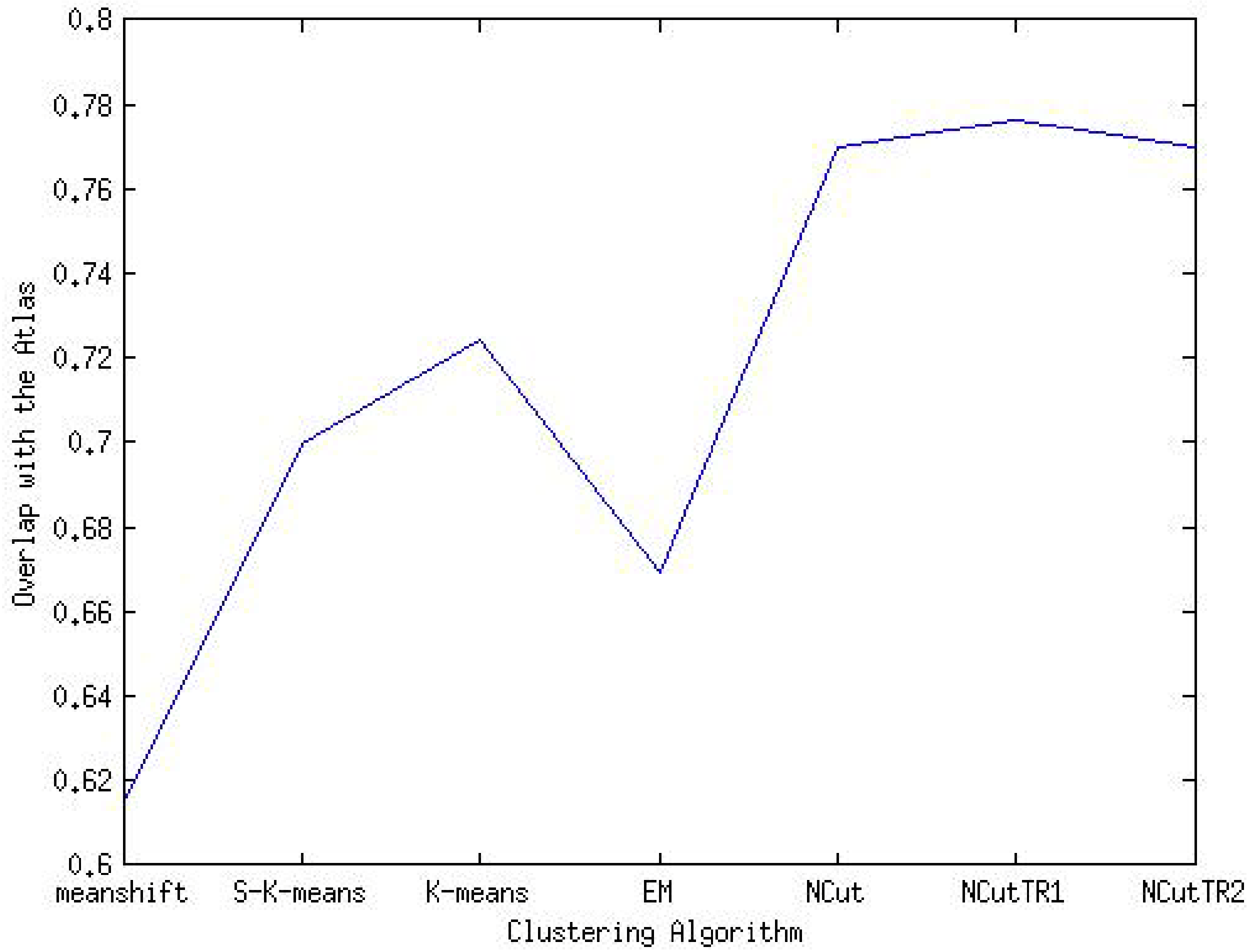
Parcellation of Subject 3211: Connectivity Variances Before Parcellation



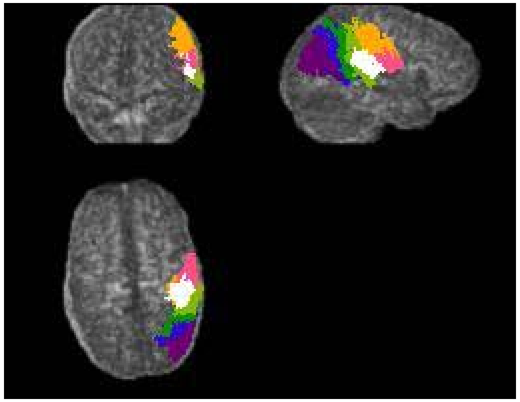
Parcellation of Subject 3211: Variance of Each Cluster After Parcellation



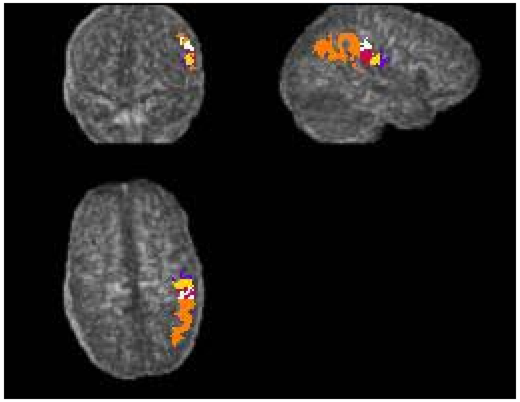
Parcellation of Subject 3211: Performances of Different Clustering Methods



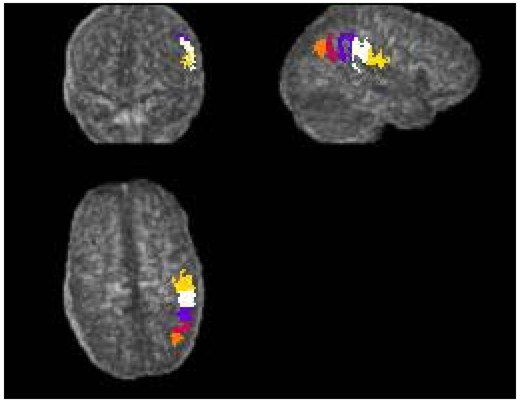
Parcellation of Subject 3211: Performances of Different Clustering Methods



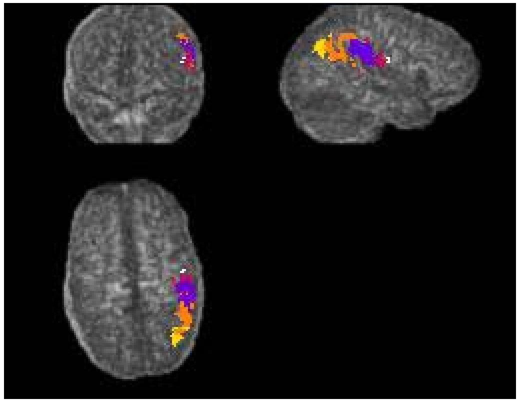
Atlas



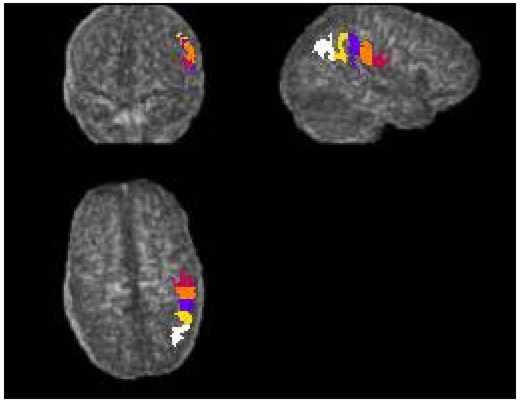
EM



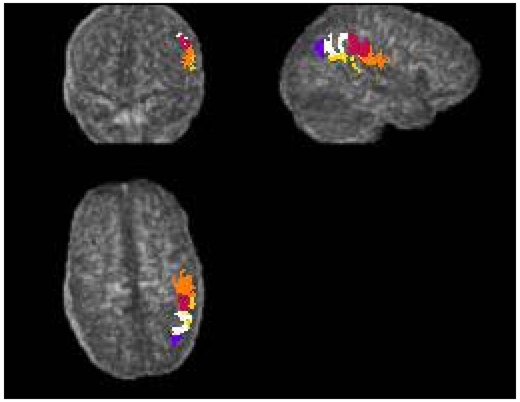
K-means



Mean-Shift



Sparse K-means



Normalized Graph Cuts

Work in Progress

Parcellation of 19 Subjects: Based on the selected parameters from the parcellation of Subject 3211

LEFT HEMISPHERE Normalized Cuts with Target Elimination Alpha =0.5 Similarity Matrix construction = SUM Distance Function = Jaccard	
SUBJECT	BEST RESULT
3211	0.650273
3402	0.603636
3407	0.520629
3414	0.697107
3422	0.607826
3424	0.621622
3425	0.537037
3484	0.635490
3485	0.638649
3486	0.607445
3487	0.604724
3488	0.686678
3492	0.615960
3496	0.621302
3497	0.567294
3498	0.588542
3503	0.648148
3504	0.685022
3505	0.644431

Parcellation of 19 Subjects: Based on the selected parameters from the parcellation of Subject 3211

RIGHT HEMISPHERE Normalized Cuts with Target Elimination Alpha =0.5 Similarity Matrix construction = SUM Distance Function =" Jaccard"	
SUBJECT	BEST RESULT
3211	0.619906
3402	0.671701
3407	0.597689
3414	0.620827
3422	0.638840
3424	0.564067
3425	0.673877
3484	0.575038
3485	0.566434
3486	0.551825
3487	0.633803
3488	0.561350
3492	0.671875
3496	0.669528
3497	0.608730
3498	0.660506
3503	0.575816
3504	0.645977
3505	0.617366

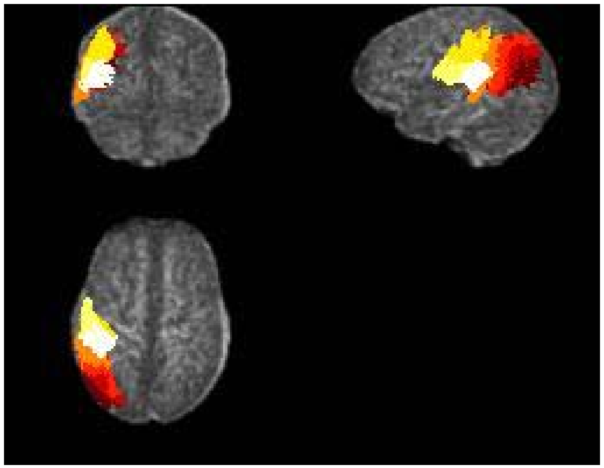
Parcellation of 19 Subjects: Best Parameters (Left Hemisphere)

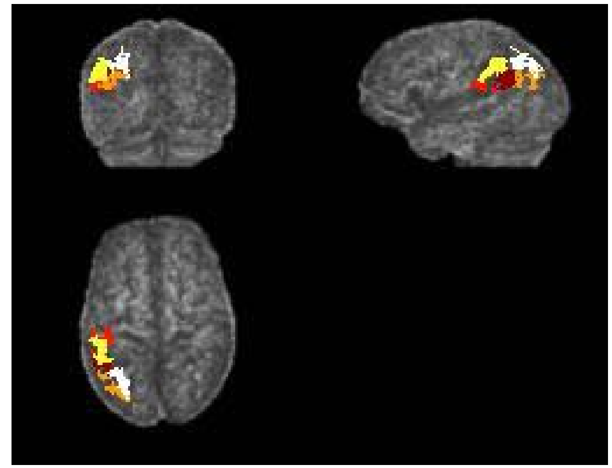
Method	# of Cluster	α	Distance Function	Spatial Coherence	Similarity Matrix
Normalized Graph Cuts	5	0.9	Hamming	Threshold	Multiply
Normalized Graph Cuts with target elimination	5	0.8	City block	Weight	Sum

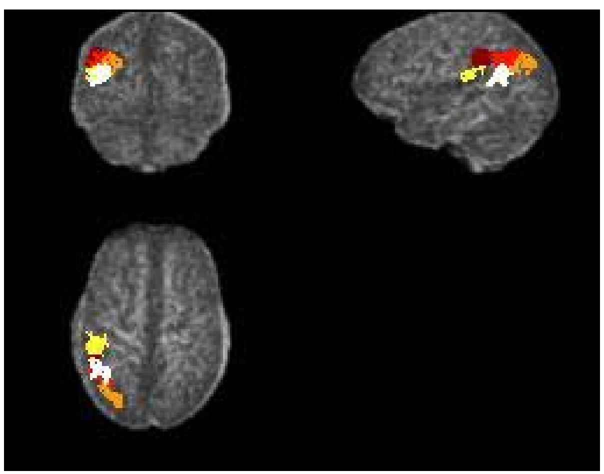
Parcellation of 19 Subjects: Parcellation Evaluation based on the training parameters (Left Hemisphere)

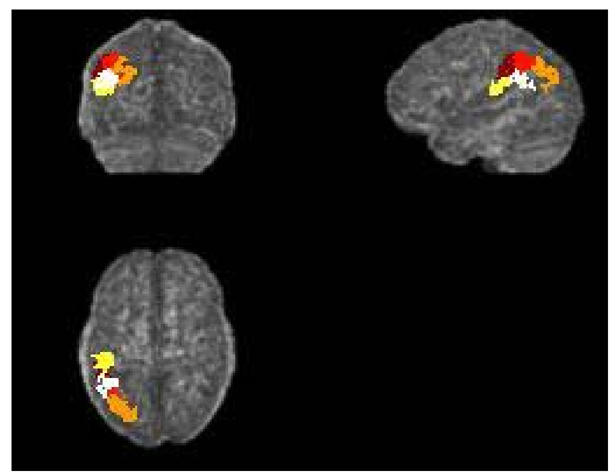
Subject	Normalized Graph Cuts	Normalized Graph Cuts With Target Elimination
3211	0.589481	0.661202
3402	0.660000	0.629091
3407	0.586444	0.605108
3414	0.706148	0.696203
3422	0.660870	0.726087
3424	0.689189	0.664619
3425	0.659612	0.567019
3484	0.597028	0.648601
3485	0.638649	0.630747
3486	0.586294	0.621827
3487	0.568504	0.609449
3488	0.696546	0.696546
3492	0.608479	0.569825
3496	0.640039	0.666667
3497	0.594067	0.569465
3498	0.618750	0.632292
3503	0.652778	0.577160
3504	0.615639	0.621145
3505	0.643819	0.605263
AVERAGE	0.632228	0.631490

Parcellation with Target Elimination Results: Subjects 3414, 3422, 3488 (Left Hemisphere)


Atlas in 3422’s FA space


3414


3422


3488

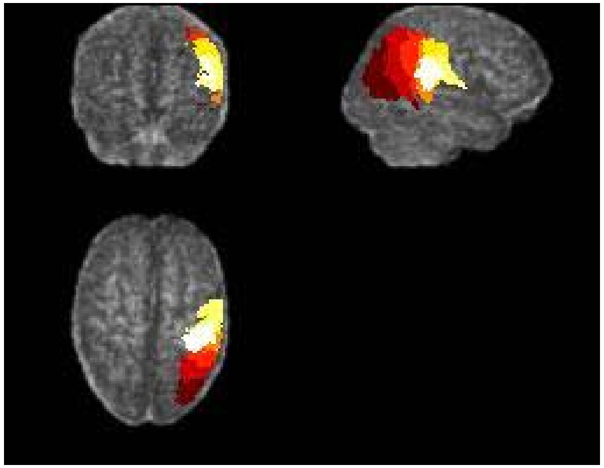
Parcellation of 19 Subjects: Best Parameters (Right Hemisphere)

Method	# of Cluster	α	Distance Function	Spatial Coherence	Similarity Matrix
Normalized Graph Cuts	5	0.6	Jaccard	Weight	Sum
Normalized Graph Cuts with target elimination	5	0.6	Jaccard	Weight	Sum

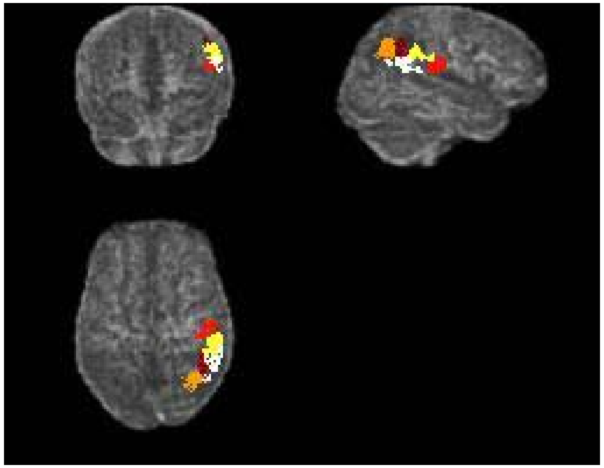
Parcellation of 19 Subjects: Parcellation Evaluation based on the training parameters (Right Hemisphere)

Subject	Normalized Graph Cuts	Normalized Graph Cuts With Target Elimination
3211	0.625392	0.626959
3402	0.753577	0.751987
3407	0.718487	0.710084
3414	0.569952	0.570747
3422	0.652021	0.655536
3424	0.637883	0.646240
3425	0.640599	0.640599
3484	0.593415	0.601072
3485	0.627622	0.628497
3486	0.683212	0.682482
3487	0.590669	0.590669
3488	0.611452	0.615542
3492	0.747917	0.746875
3496	0.657725	0.653433
3497	0.666667	0.666667
3498	0.657588	0.701362
3503	0.600768	0.599808
3504	0.611494	0.611494
3505	0.670802	0.669847
AVERAGE	0.648276	0.651047

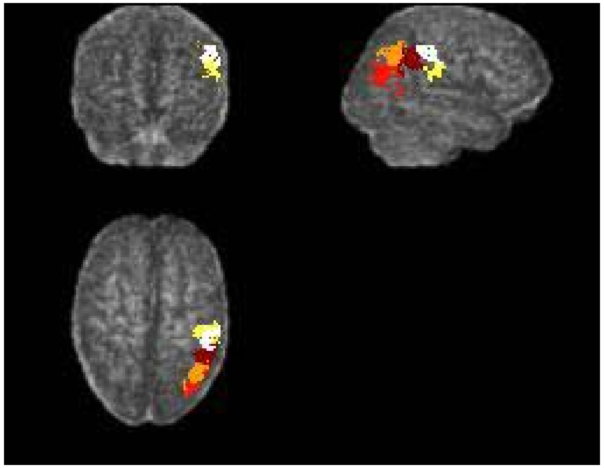
Parcellation with Target Elimination Results: Subjects 3402, 3407, 3492 (Right Hemisphere)



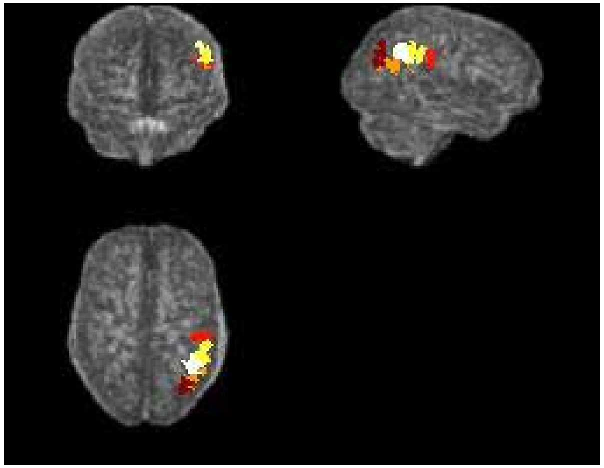
Atlas in 3402's FA space



3407



3402



3492

Comparison of Normalized Graph Cuts

- Standard NGC with feature selection produced best results in most of the tests.
- Standard NGC without feature selection produced results very close to those with feature selection.
- NGC with k-means produced incorrect parcellations according to the metric.

Conclusion

- Different clustering methods were applied to an anatomical connectivity map, which is obtained by DTI-based tractography of the IPL of a living subject to parcellate it into component regions with different connectivity patterns.

- Among the different methods investigated, normalized graph cuts showed the best performance.

Conclusion

- The main difficulty of the evaluation was having no ground truth data by which to measure the quality of our parcellation.

- How many different regions exist in the IPL of a human being is still an unknown. Therefore in this work, different numbers of clusters were tried and the evaluation metric was designed to measure the quality of the overlap with different numbers of clusters.