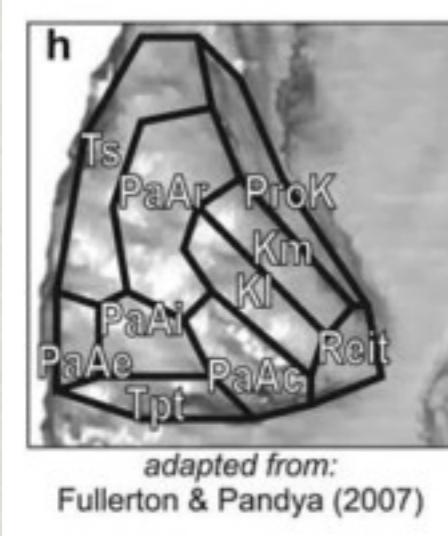
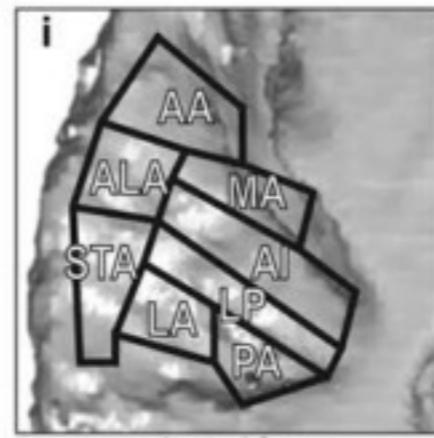


# NO SOUND CONSENSUS

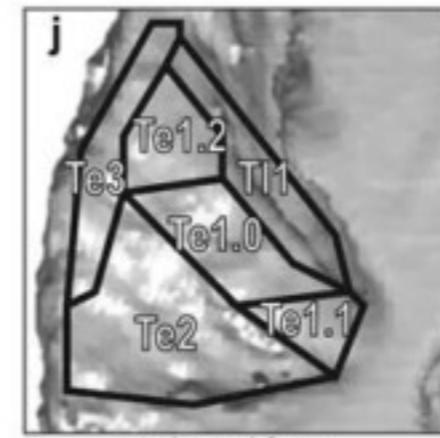
- No consensus on how to parcellate auditory cortex beyond A1



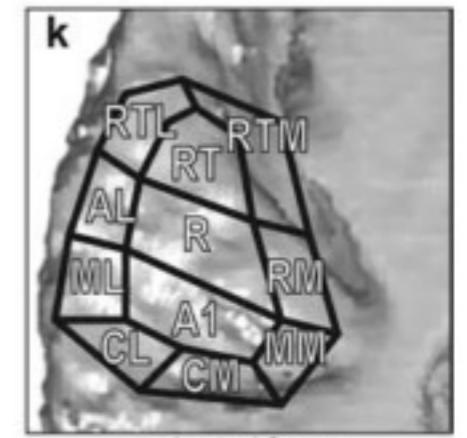
adapted from:  
Fullerton & Pandya (2007)



adapted from:  
Wallace et al. (2002)



adapted from:  
Morosan et al. (2001)



adapted from:  
Kaas & Hackett (2000)

LANGERS ET AL, 2011

- Why is this different from vision?
  - (1) Fewer researchers?
  - (2) Smaller regions/greater individual variability?
  - (3) Intrinsically less modular, perhaps due to the statistics of sensory signals



No sound consensus

# Aims

1. Quantify modularity in auditory and visual cortex
2. If appropriate, produce the best possible parcellation of auditory cortex and characterize the resulting modules

## Our approach

- Build team to fuse multiple data sources (*Human Connectome Project, Allen Brain Atlas, fc1000, Neurosynth*)
- Cluster on Amazon EC2 used to perform all analyses
- Integration of tools from multiple software packages (*FSL, SPM, Freesurfer, NiPy, NiBabel*) and programming languages (*Bash, Python, C, Matlab, Javascript, JQuery, d3*)

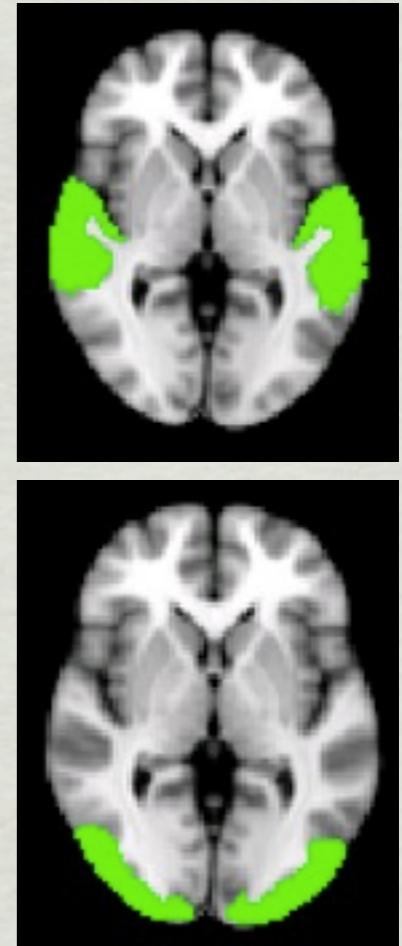


No sound consensus

# Methods

- Seed ROIs in auditory and visual cortex from Neurosynth
- 120 target ROIs spanning brain (from Craddock et al, 2011)
- Diffusion tractography and resting state to calculate connectivity of each seed voxel to each target ROI
- Cluster seed voxels by their signature of connectivity and calculate a modularity score, Q

*Awesome datasets from HCP Q1: dMRI has 90 directions of 3 b-values, 168x144x111 voxels; rsfMRI 4800 scans of 104x90x72 voxels*

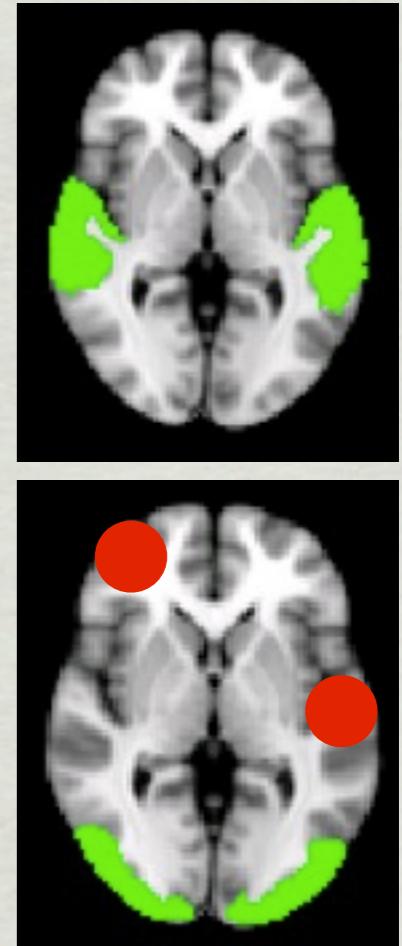


No sound consensus

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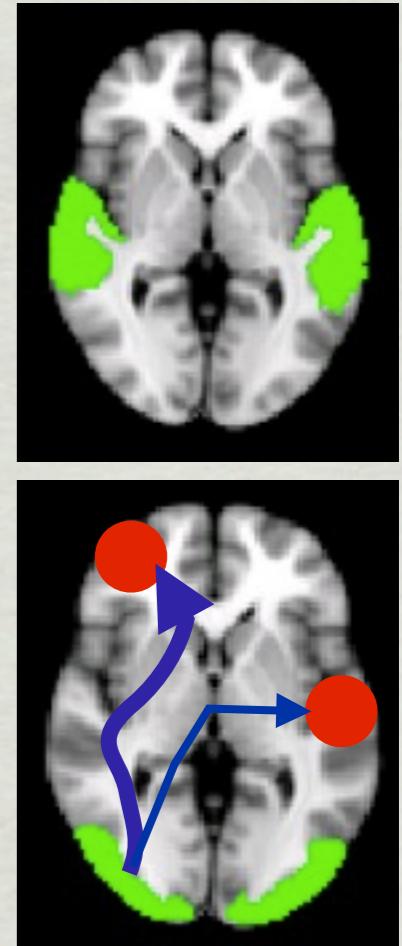


No sound consensus

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No sound consensus

# Analysis

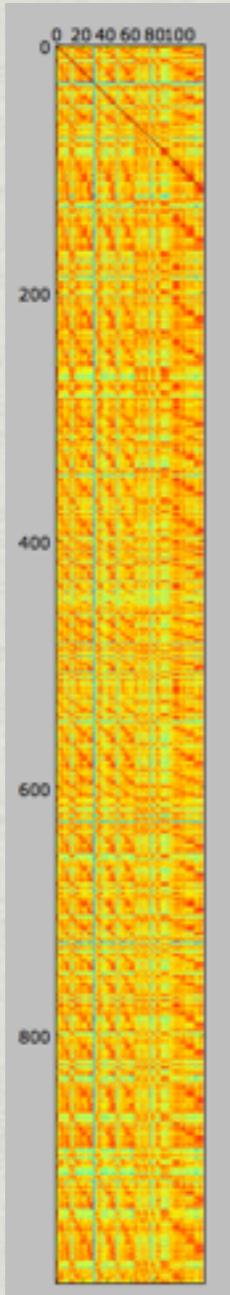
- Diffusion tractography
  - Warp seeds to individual space
  - bedpostx (~6 days per subject on Sandy Bridge E core)
  - probtrackx (~14 days per subject)
  - Warp results to MNI-152 and then Conte 69 surface space
- Resting state
  - Temporal bandpass filtering
  - Data scrubbing by modeling out movement (Volterra kernel expansion method), white and CSF signal



No sound consensus

# Form graph, calculate modularity

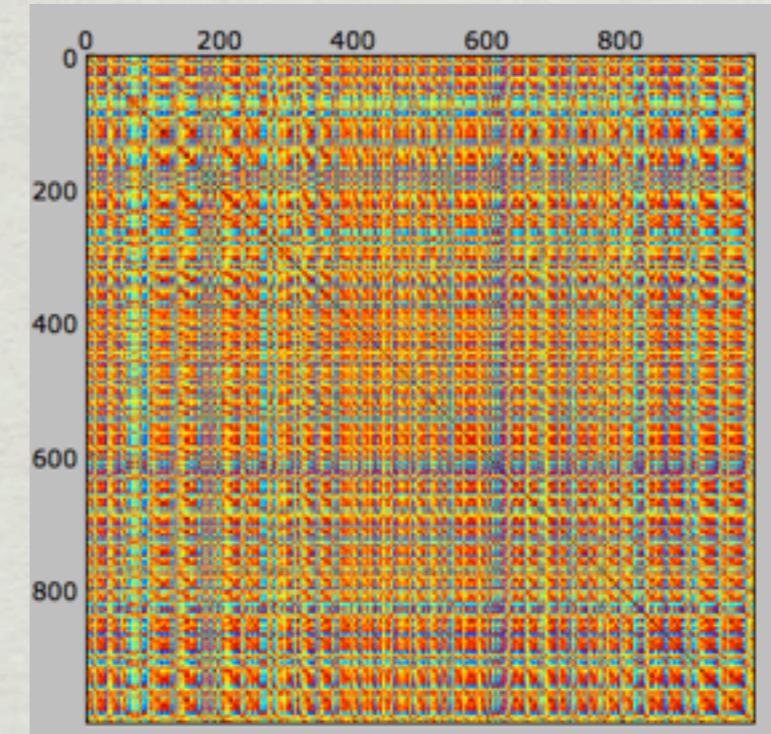
TARGETS



Pairwise Pearson product-moment coefficient



SEEDS



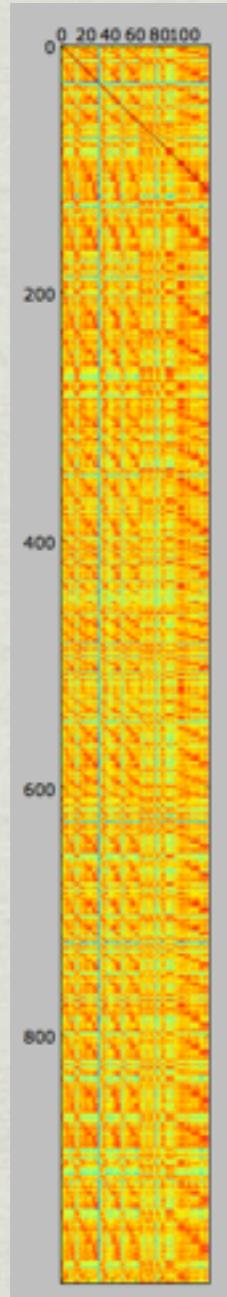
Tells us the *local story*.  
“Is this voxel ‘similar to’ that voxel?”



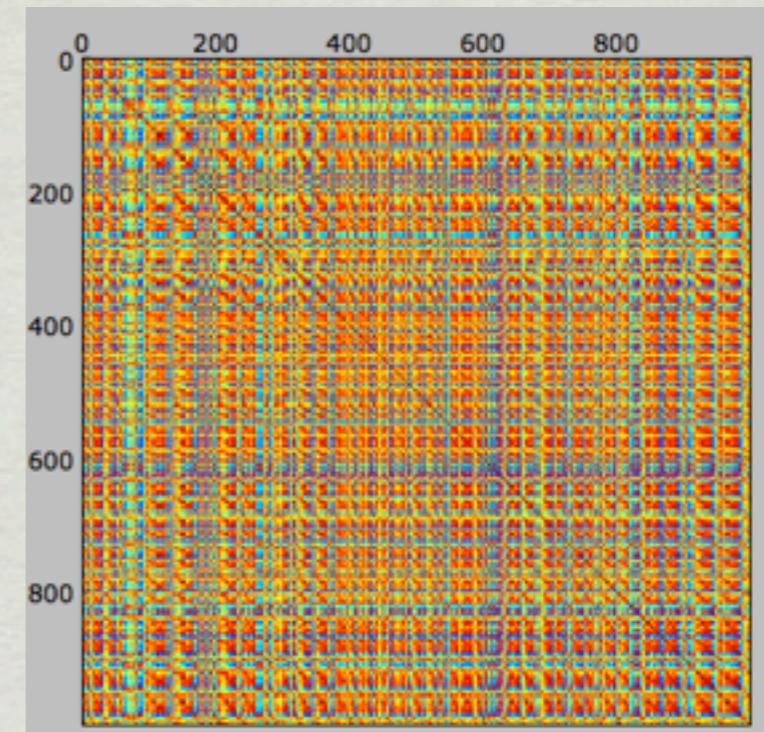
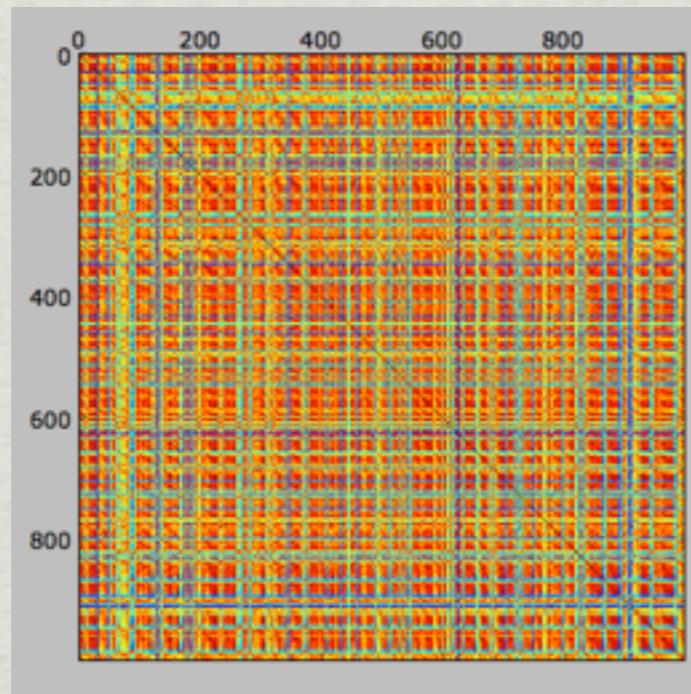
No sound consensus

# Form graph, calculate modularity

TARGETS



SEEDS



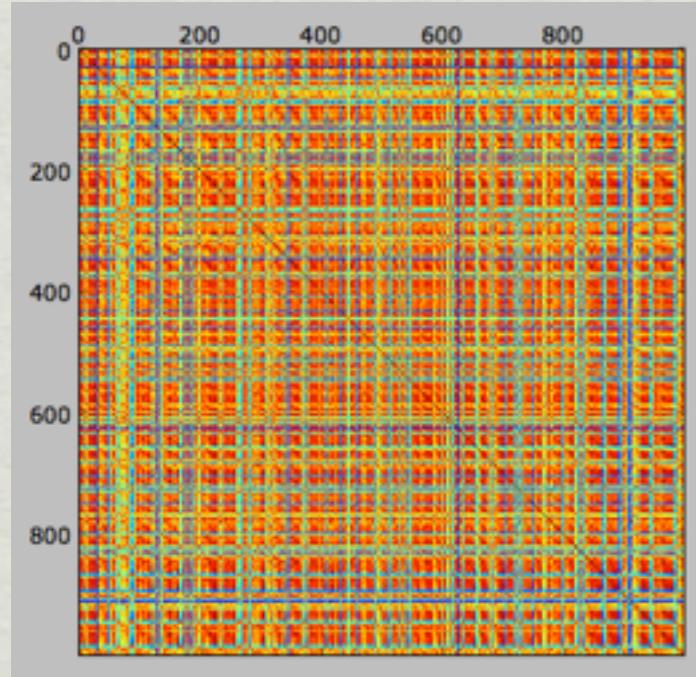
$$\text{eta}^2 = 1 - \frac{\sum_{i=1}^n [(a_i - m_i)^2 + (b_i - m_i)^2]}{\sum_{i=1}^n [(a_i - \bar{M})^2 + (b_i - \bar{M})^2]}$$

mean  
value      grand mean

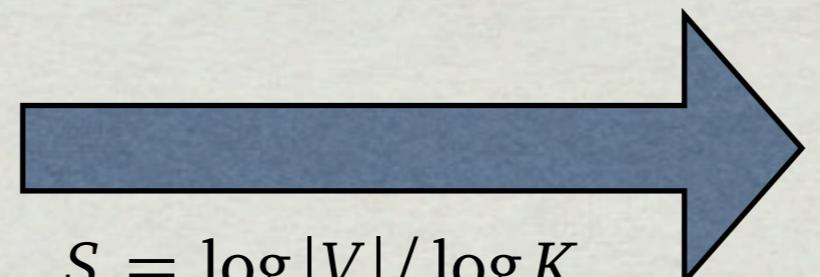
This tells the *global story*. “How much does the global connectivity pattern of *this* look like the global connectivity pattern of *that*? ”

No sound consensus

# Form graph, calculate modularity

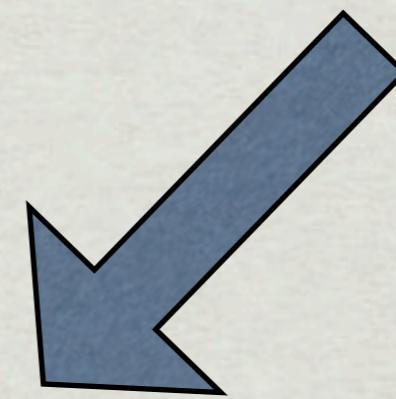
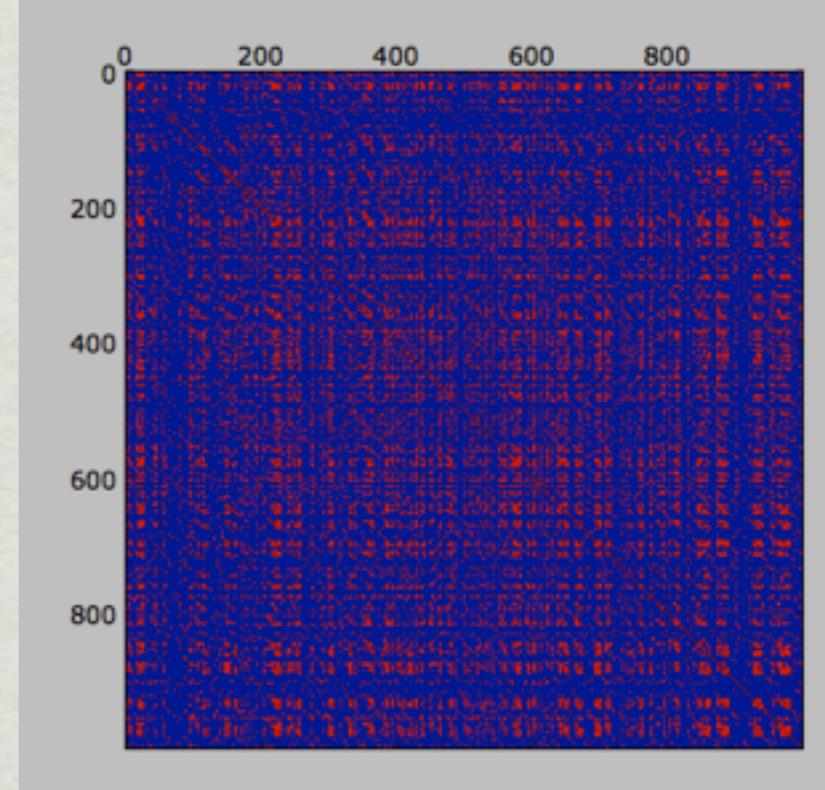


Threshold, S=2.0



$$S = \log |V| / \log K$$

# vertices      avg degree



Reinterpret as adjacency  
matrix for a graph



No sound consensus

# You need a cluster to cluster

- File server & development
  - cc2.8xlarge (32 cores, 61 GB RAM, 10Gb connect, 88 ECUs)
  - Ubuntu 12.04, NFS, 6 x 1TB EBS drives stitched together using LVM
  - Condor to manage queue. Matlab components compiled.
- Compute nodes
  - Either cc2.8xlarge or cr1.8xlarge (244 GB RAM)
  - Custom memory monitor to EC2 console.

| LINUX        | X86_64 | Claimed | Busy    | 1.000     | 1872    | 0+00:04:36 |          |
|--------------|--------|---------|---------|-----------|---------|------------|----------|
| LINUX        | X86_64 | Claimed | Busy    | 1.000     | 1872    | 0+00:03:40 |          |
| LINUX        | X86_64 | Claimed | Busy    | 1.000     | 1872    | 0+00:27:13 |          |
|              | Total  | Owner   | Claimed | Unclaimed | Matched | Preempting | Backfill |
| X86_64/LINUX | 294    | 0       | 285     | 9         | 0       | 0          | 0        |
| Total        | 294    | 0       | 285     | 9         | 0       | 0          | 0        |



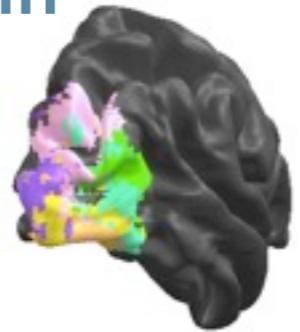
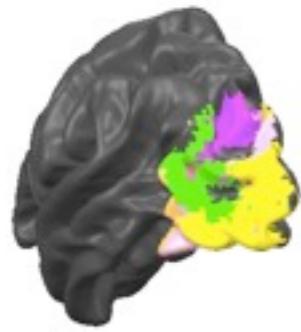
# Louvain modularity

- Tractography
  - Visual ( $Q=0.76$ ) higher ( $p<0.02$ ) than auditory cortex ( $Q=0.69$ ), but modular in both regions
- rs-fMRI
  - Visual ( $Q=0.66$ ) and auditory cortex ( $Q=0.66$ ) similar
- **First conclusion**
  - Auditory cortex is modular, although not quite to the same degree as visual cortex

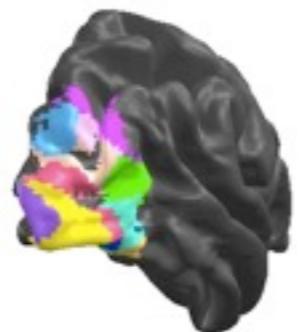
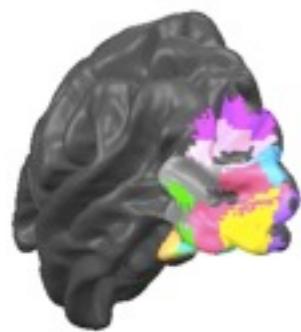


No sound consensus

## TRACTOGRAPHY



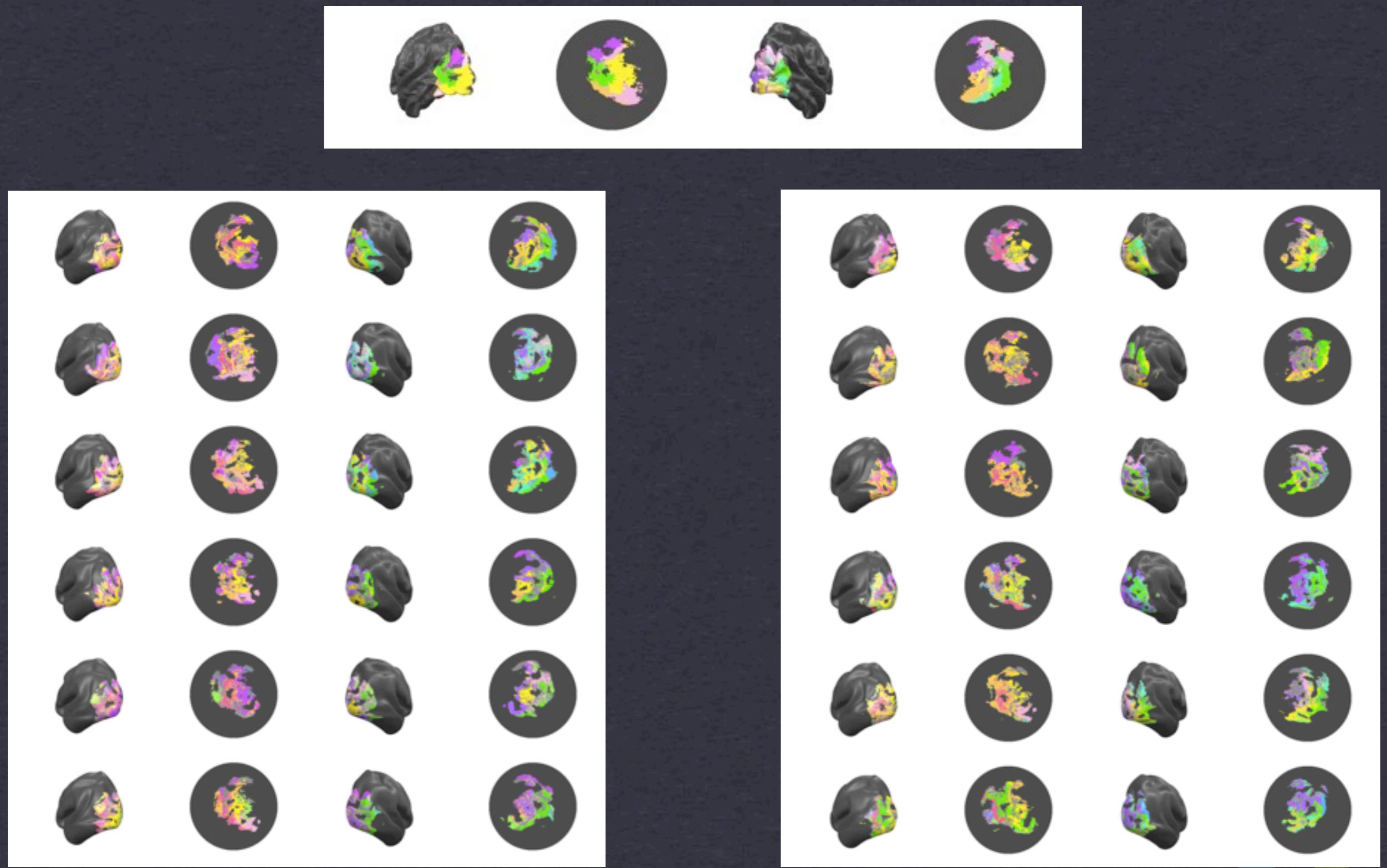
## RESTING



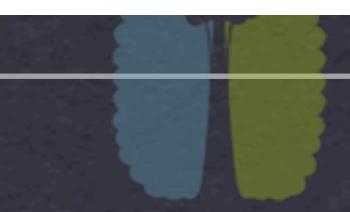
## GROUP DATA - VISUAL



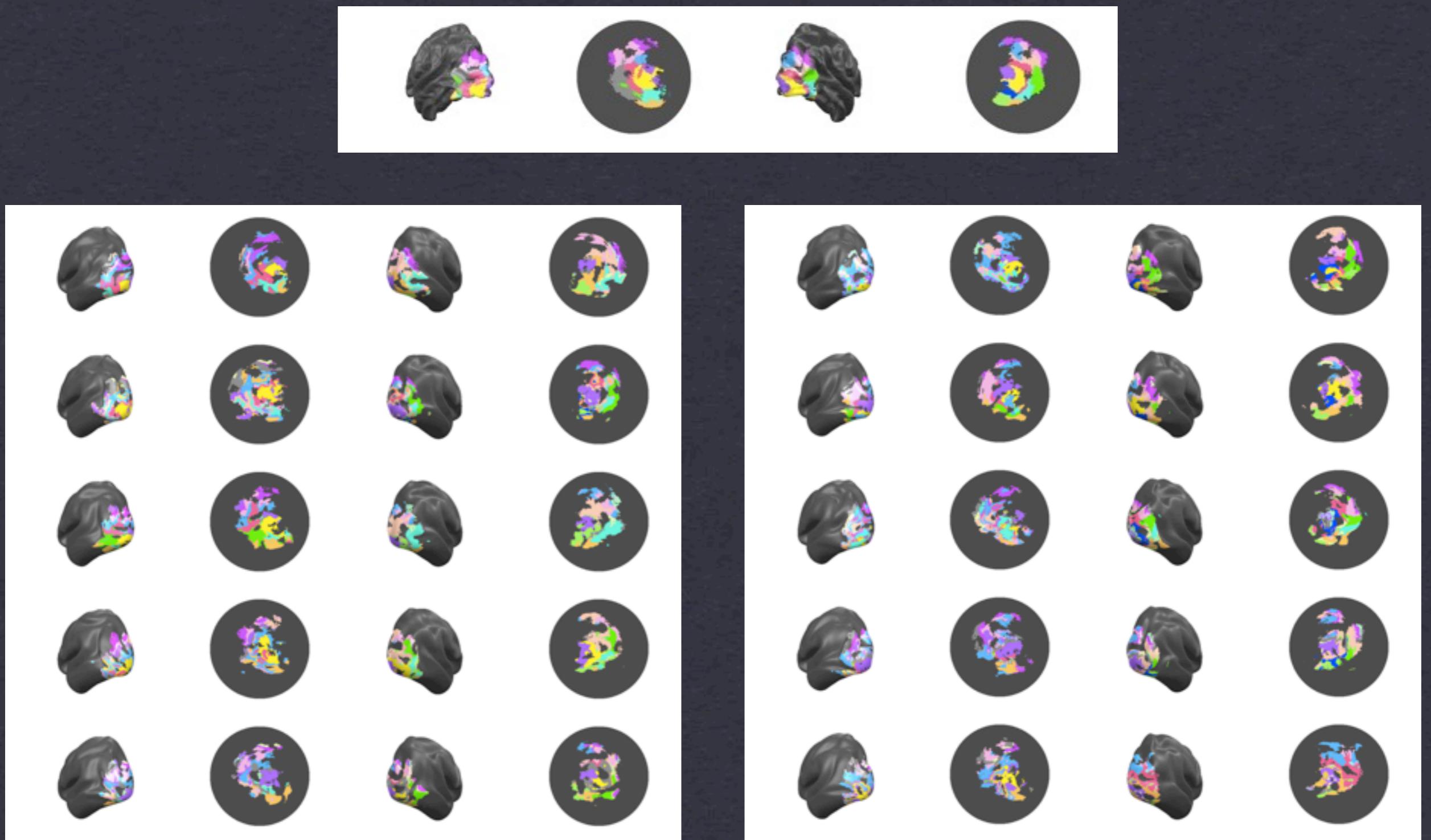
No sound consensus



## VISUAL - TRACTOGRAPHY - INDIVIDUALS



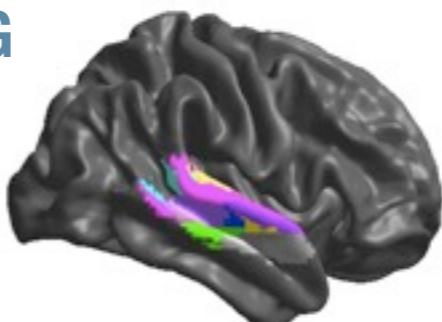
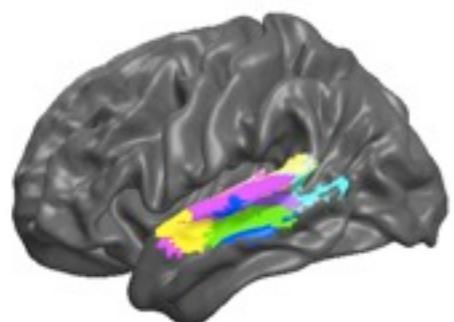
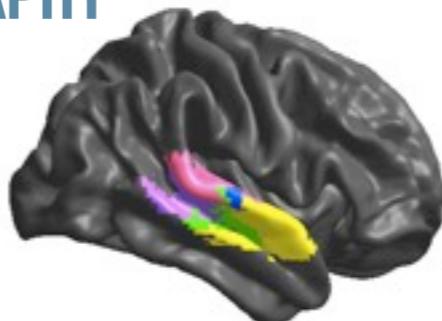
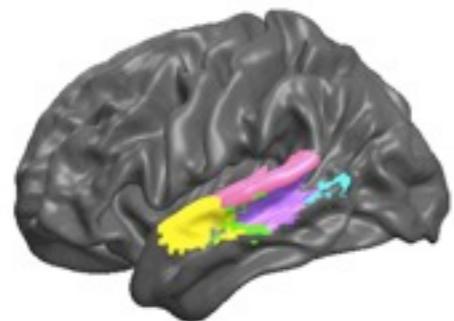
No sound consensus



## VISUAL - RESTING - INDIVIDUALS



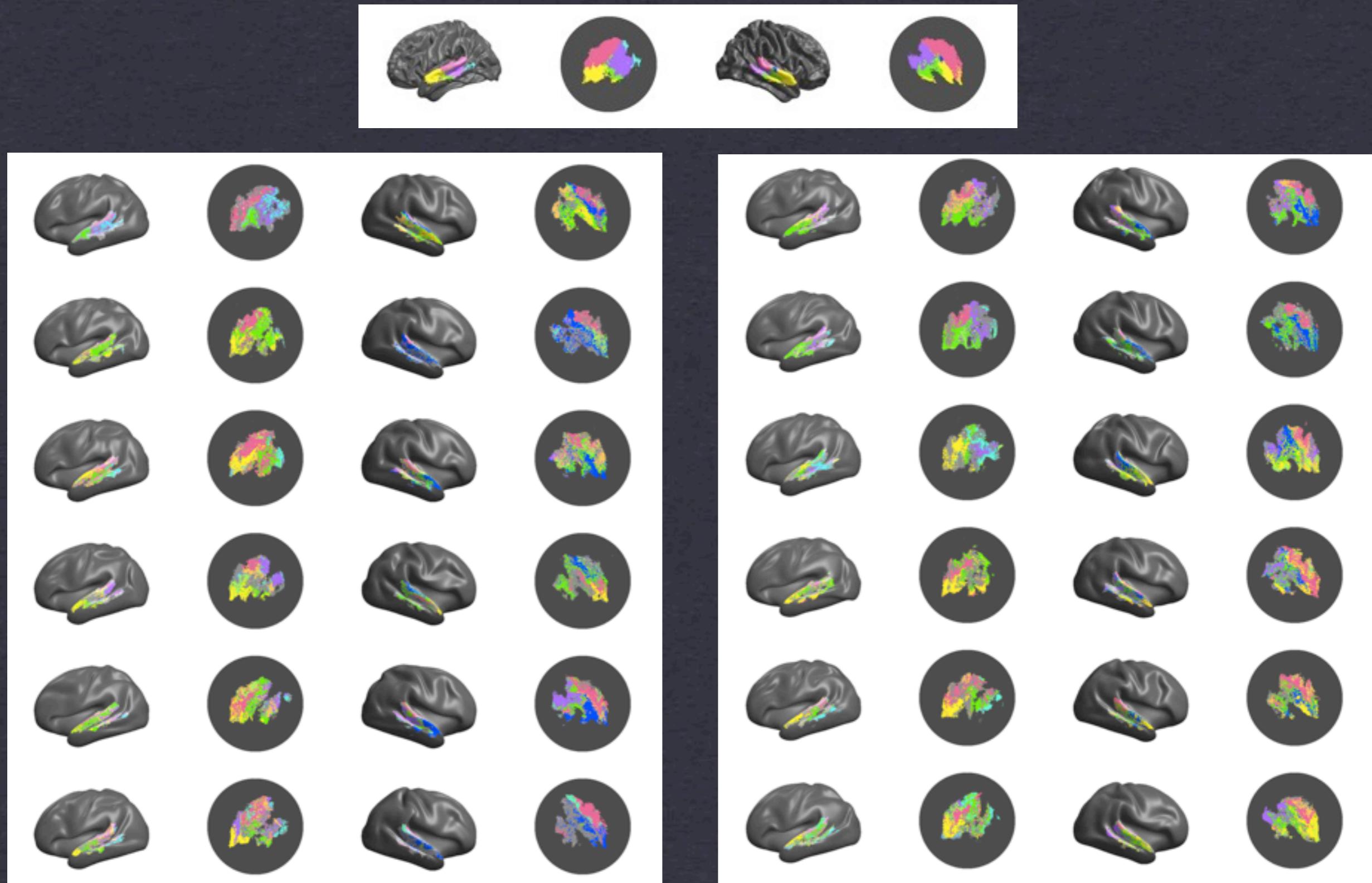
No sound consensus



## AUDITORY - GROUP

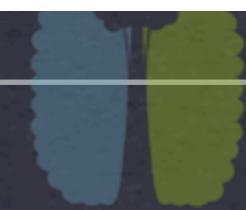


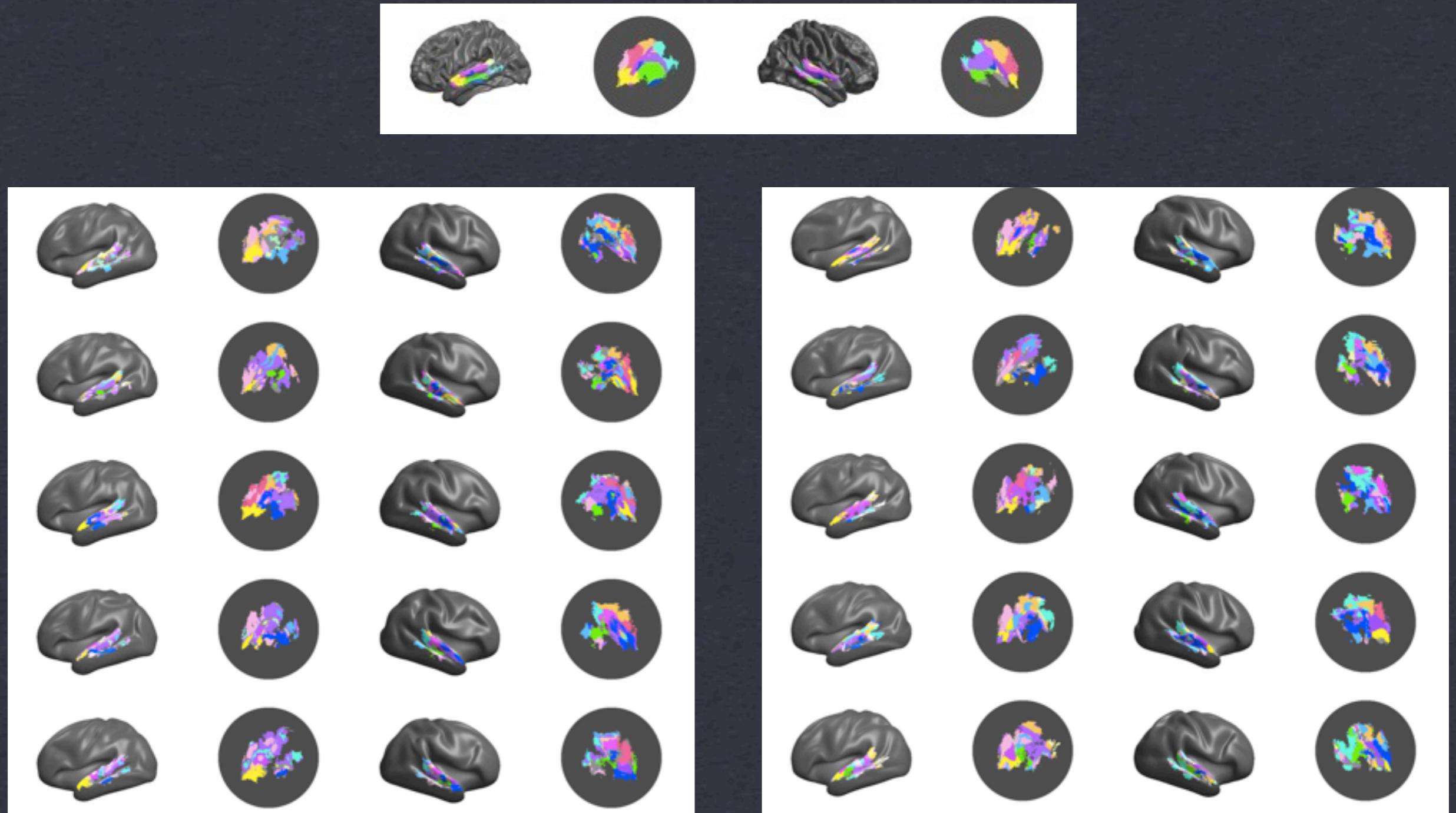
No sound consensus



## AUDITORY - TRACTOGRAPHY - INDIVIDUALS

No sound consensus





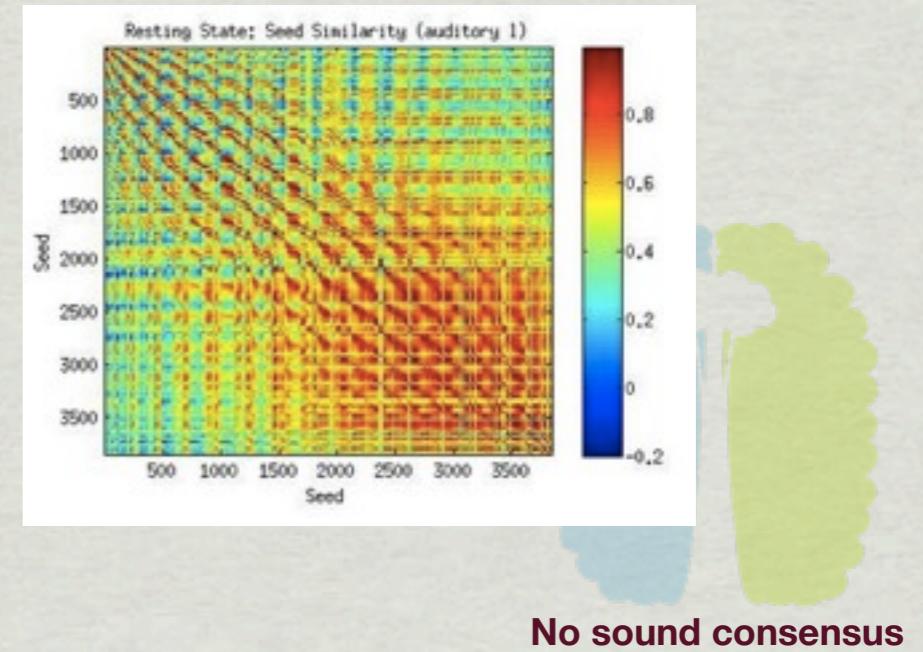
# AUDITORY - RESTING - INDIVIDUALS

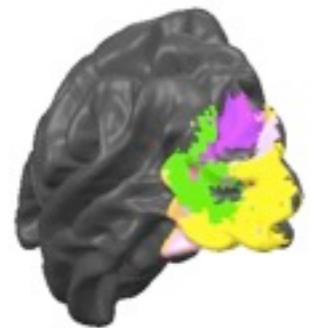


No sound consensus

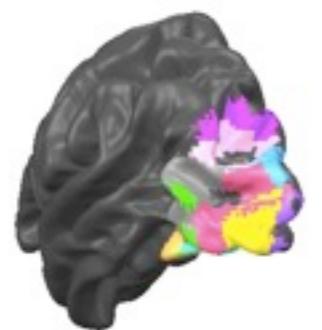
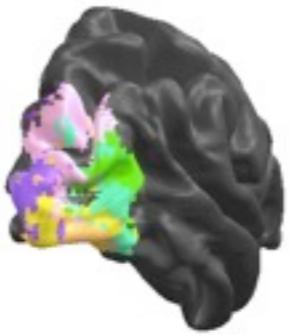
# Comparison of tractography & resting

- Seed-target connectivity patterns (2nd order RSA)
  - Auditory ( $r=0.03, 0.15$  for L, R, each  $p<0.0001$ )
  - Visual ( $r=0.11, 0.01$  for L, R each  $p<0.0001$ )
- Seed-seed similarity (3rd order RSA)
  - Auditory ( $r=0.29, 0.35$  for L, R, each  $p<0.0001$ )
  - Visual ( $r=0.26, 0.30$  for L,R each  $p<0.0001$ )

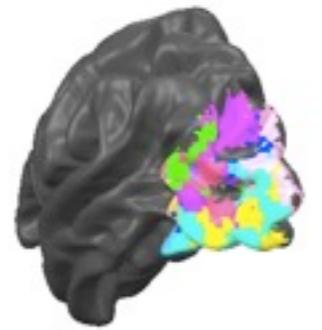
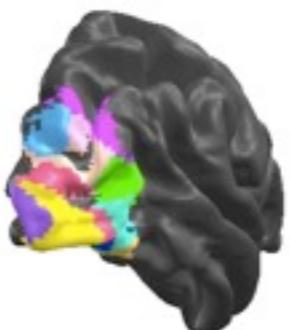




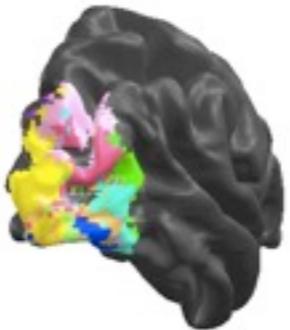
DIFF



RESTING



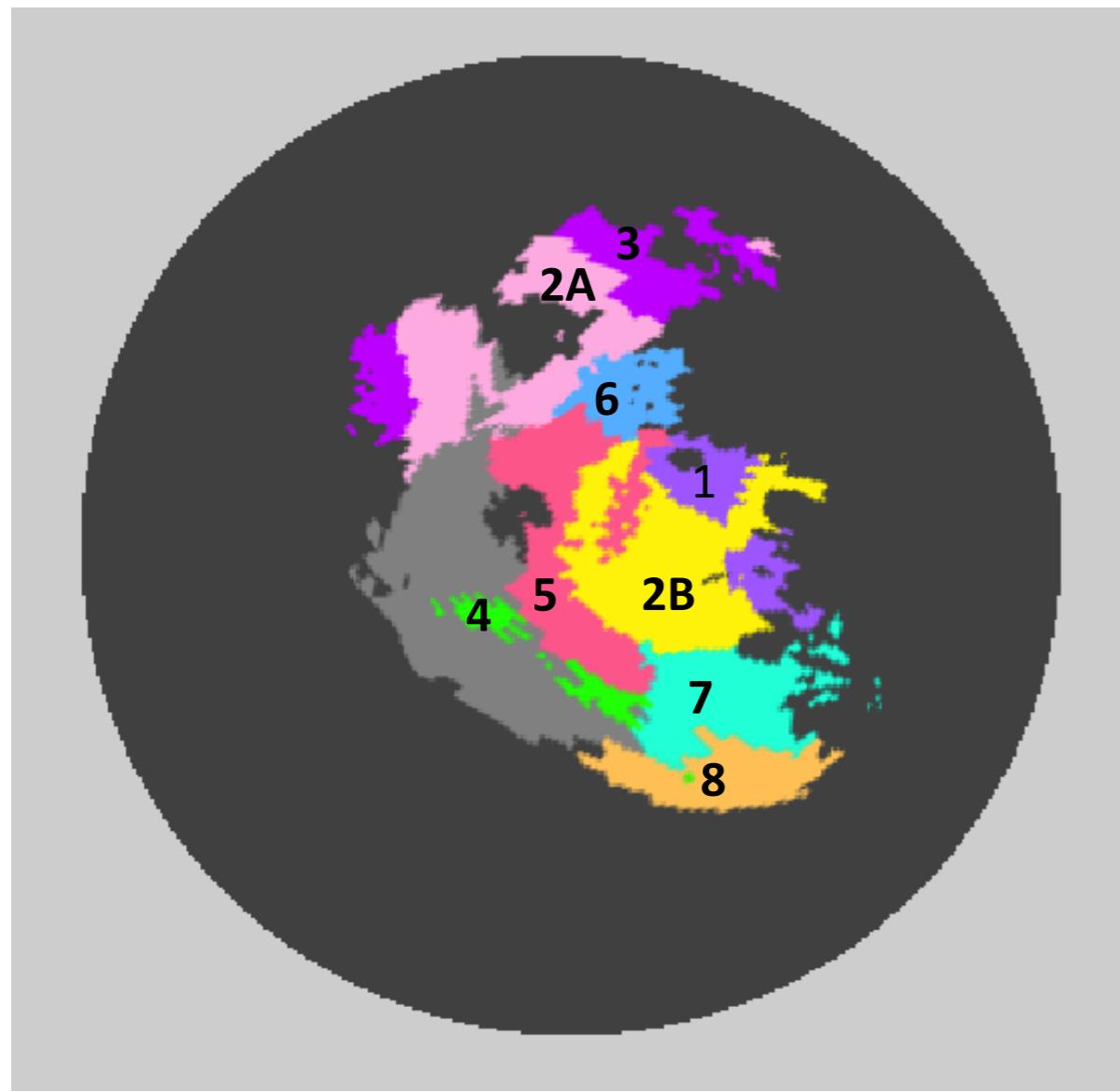
GRAND



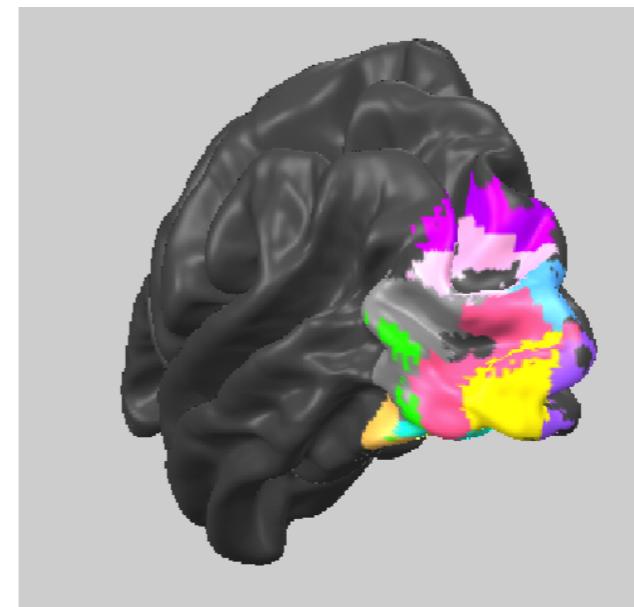
## GRAND PARCELLATION - VISUAL



No sound consensus



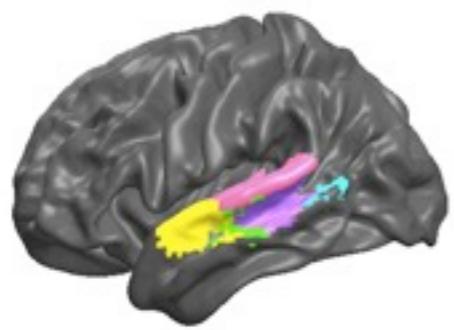
**Resting\_L\_Visual**



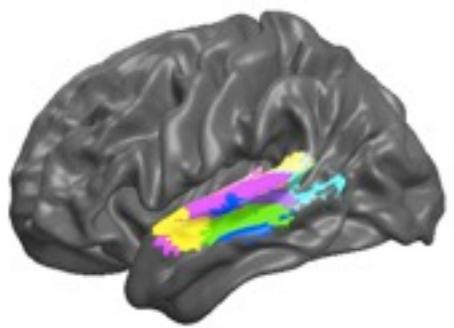
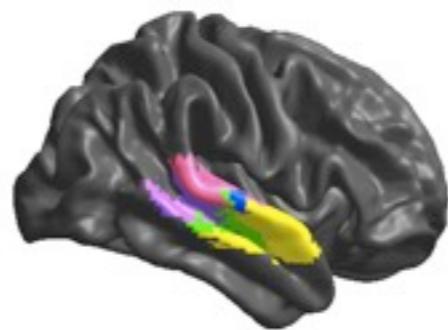
| Module # | Surface                              |
|----------|--------------------------------------|
| 1        | V1/V2                                |
| 2A       | V3b (more lateral)<br>V4/LO superior |
| 2B       | V2/V3                                |
| 3        | V4/LO superior                       |
| 4        | V5/MT                                |
| 5        | V3/V4                                |
| 6        | V3a                                  |
| 7        | V4/LO inferior                       |
| 8        | LO inferior/Fusiform gyrus           |



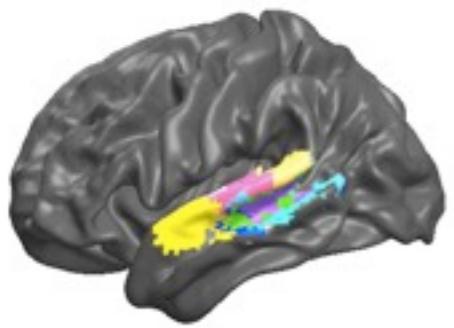
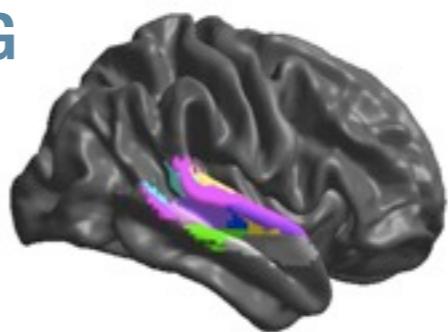
No sound consensus



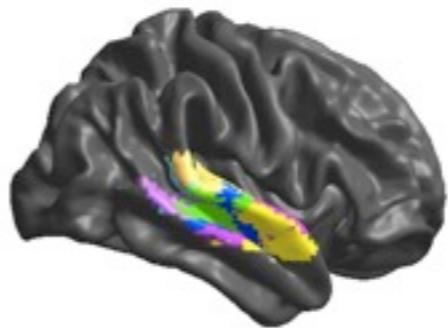
DIFF



RESTING



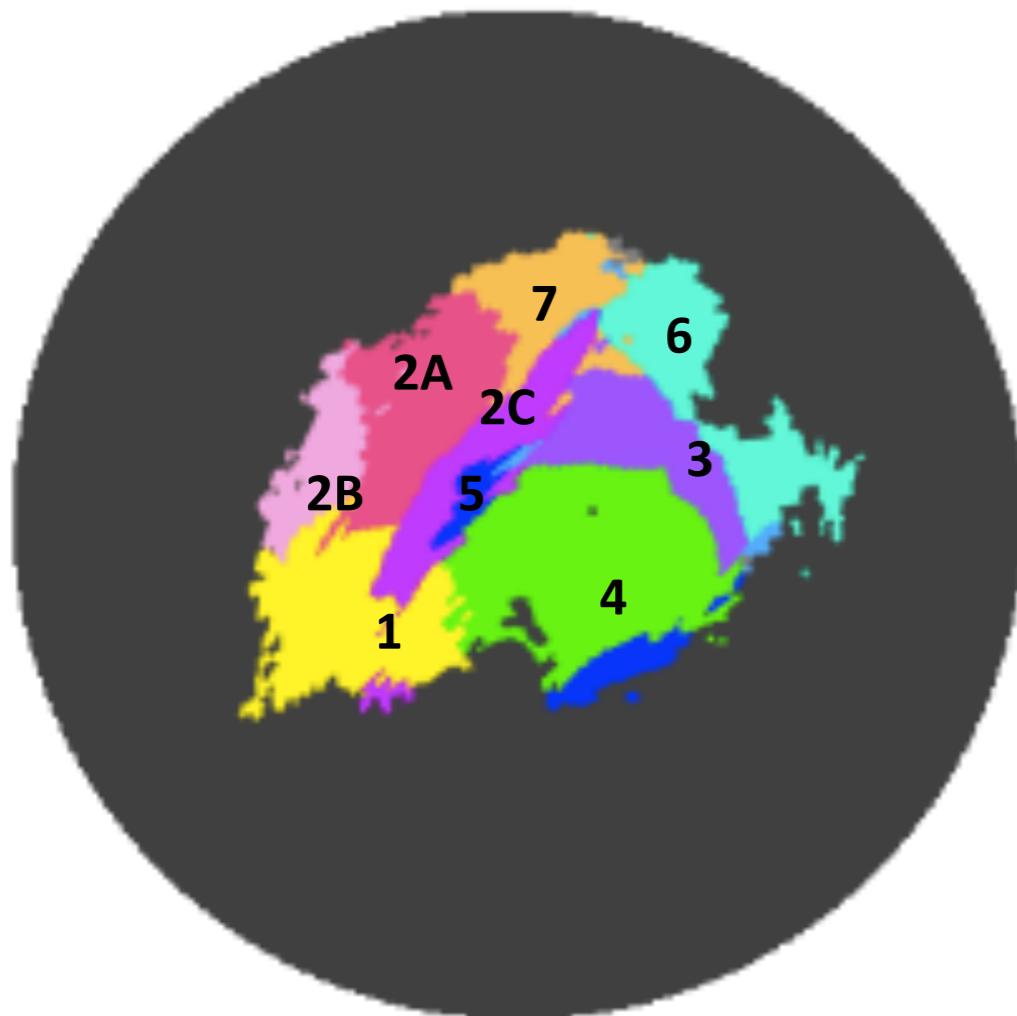
GRAND



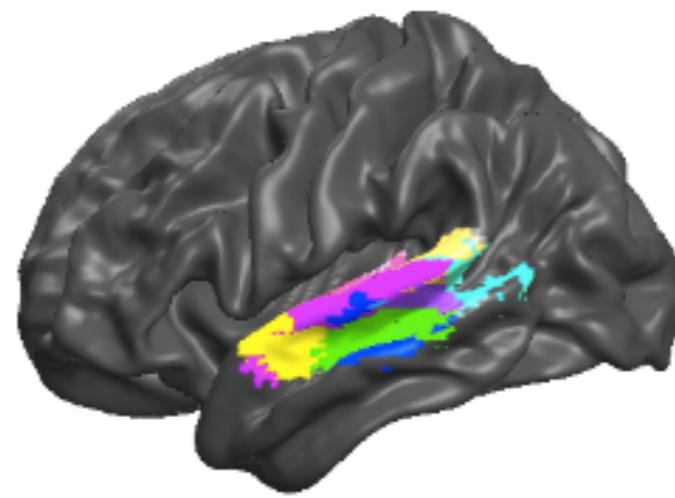
## GRAND PARCELLATION - AUDITORY



No sound consensus



**Resting\_L\_Auditory**



| Module # | Surface   |
|----------|---|
| 1        | Temporal pole<br>Anterior STG (lower bank) and MTG  |
| 2        | 2A: planum polare/STG (upper bank)/<br>Heschl's gyrus<br>2B: planum polare<br>2C: Heschl's gyrus<br><i>Juelich atlas: A1 TE 1.0/1.1/1.2</i> |
| 3        | MTG posterior(BA 21)/STG (lower<br>bank)  |
| 4        | MTG anterior (BA 21)/STG (lower bank)   |
| 5        | MTG upper bank<br><i>Juelich atlas: A1 TE 1.0</i>   |
| 6        | MTG posterior(upper bank)/STG<br>posterior part (lower bank)  |
| 7        | STG posterior (upper bank)  |



No sound consensus

# Gene expression from Allen Brain Atlas

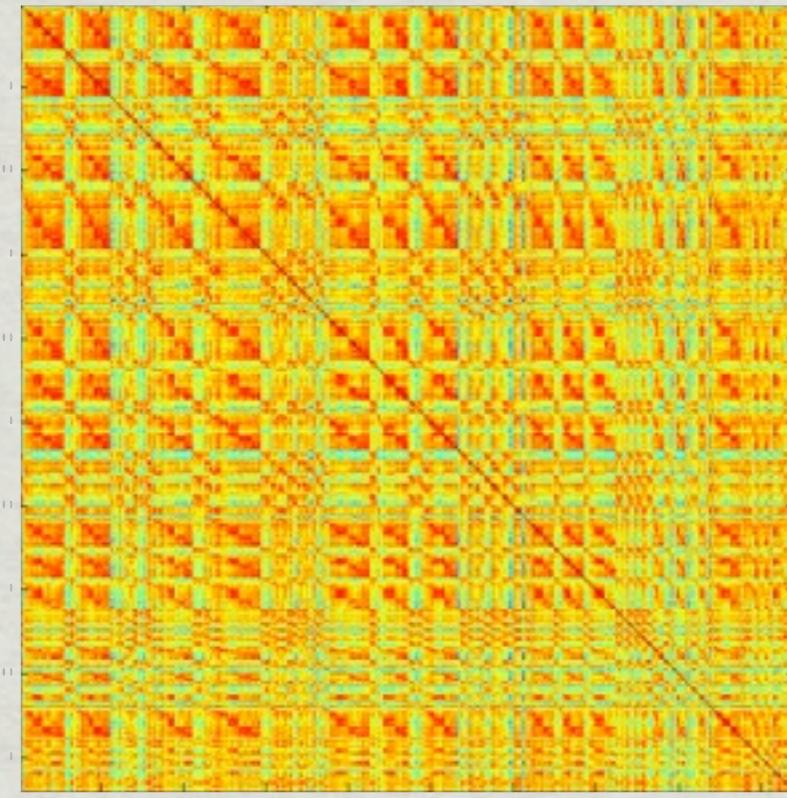
- Merge six subjects, select cortex, sort by lobe (frontal, parietal, temporal, occipital, limbic, insula, cortical nuclei)
- ~58000 genes per structure probe
- Cortical distribution of points, denser sampling on left:
  - 542 frontal
  - 290 parietal
  - 470 temporal
  - 212 occipital
  - 389 limbic
  - 44 insula
  - 342 cortical nuclei



No sound consensus

# Unexpected structure in similarity matrix

SEED



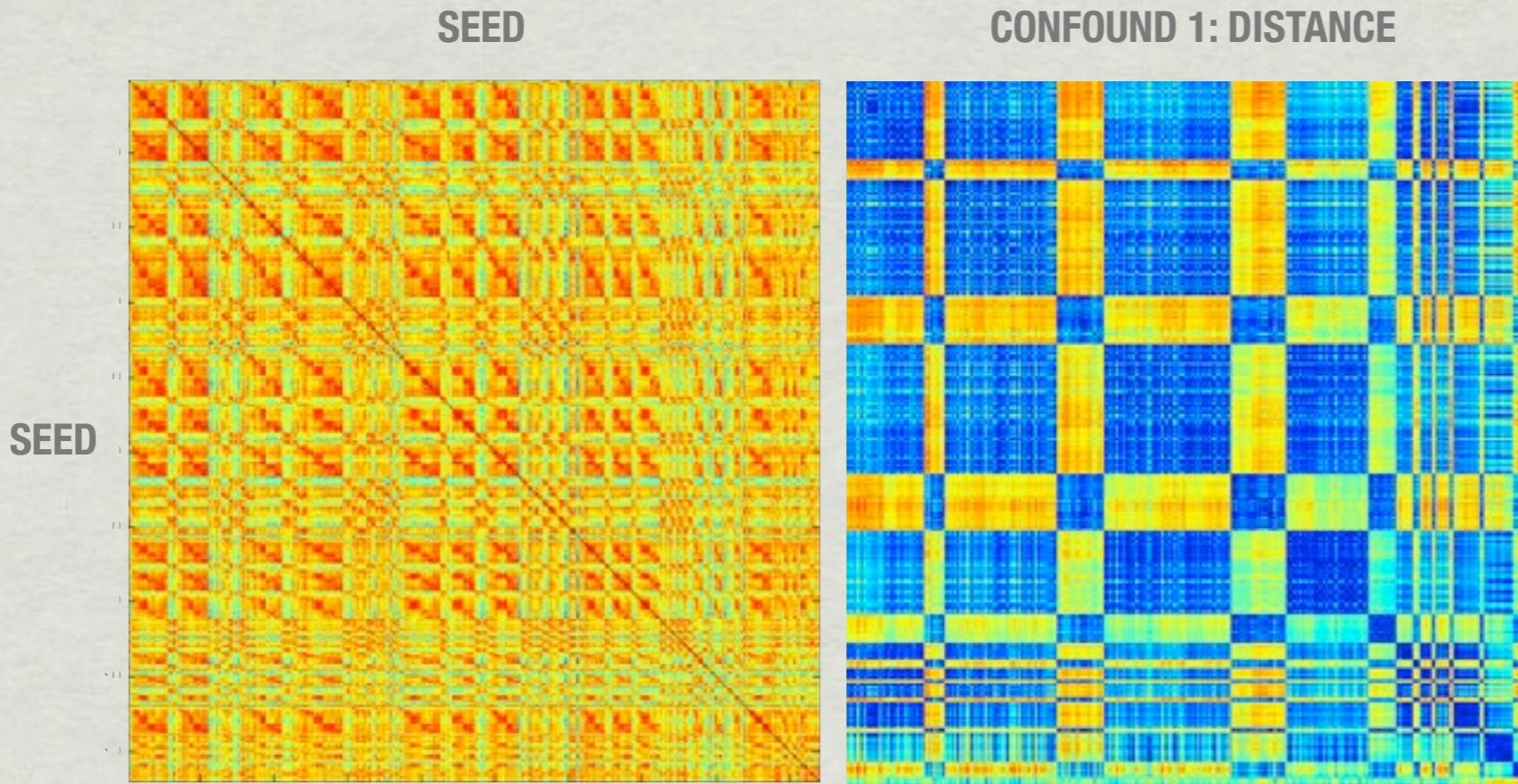
SEED

TEMPORAL LOBE



No sound consensus

# Unexpected structure in similarity matrix

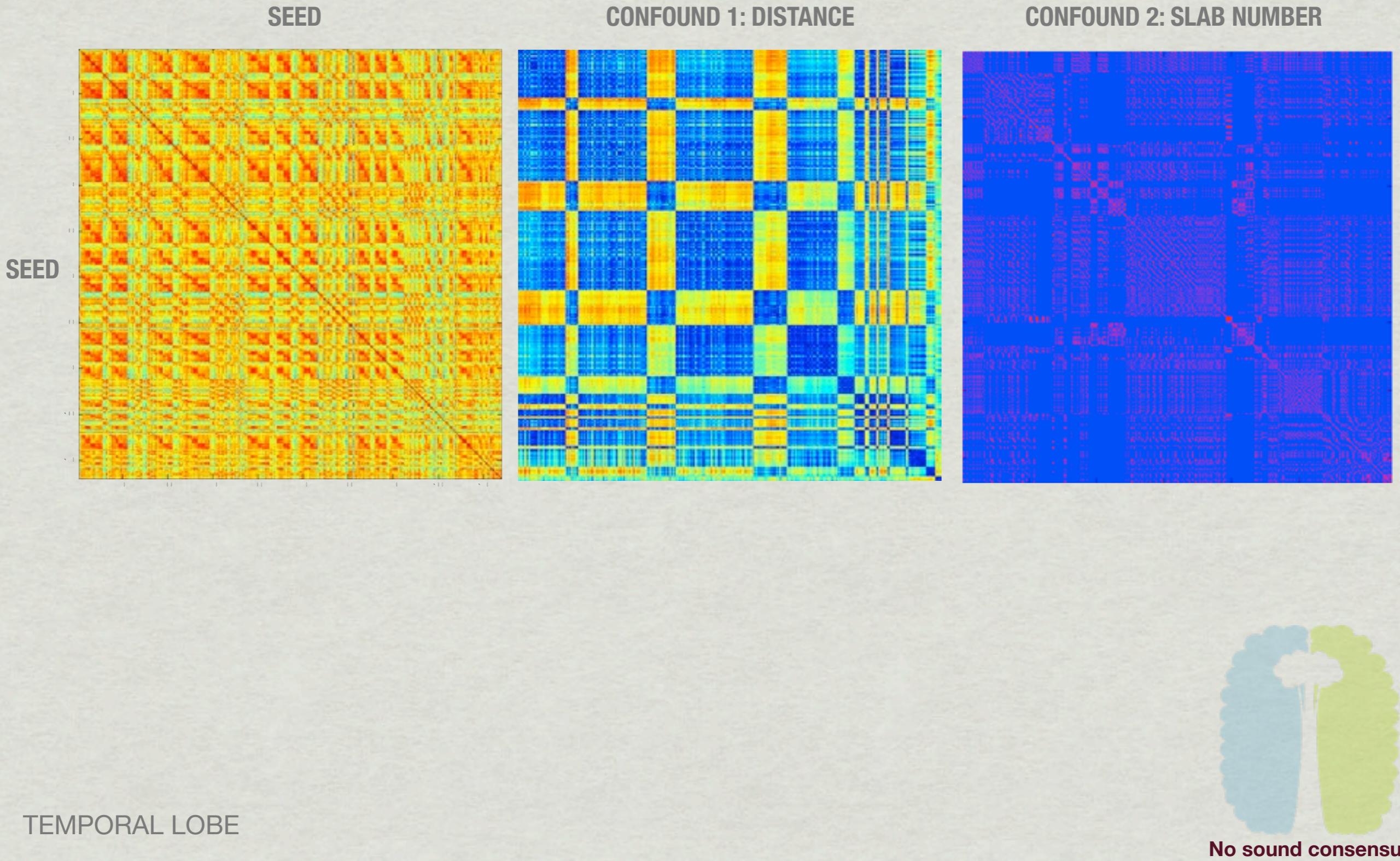


TEMPORAL LOBE

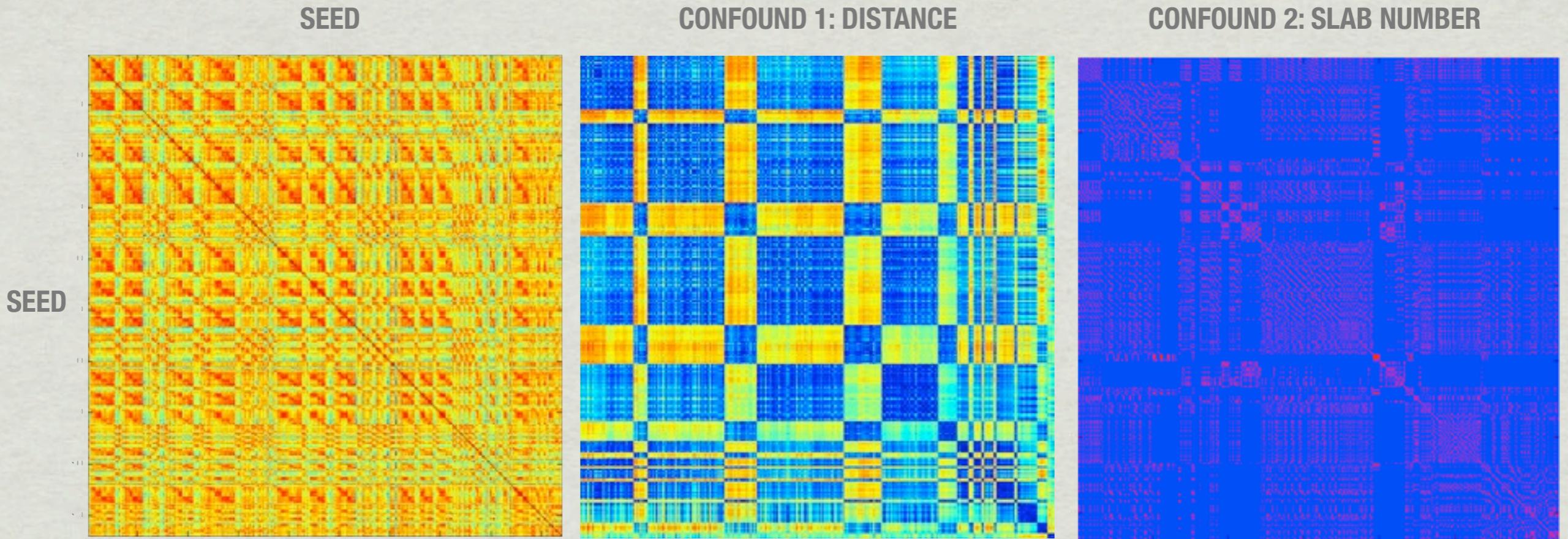


No sound consensus

# Unexpected structure in similarity matrix



# Unexpected structure in similarity matrix

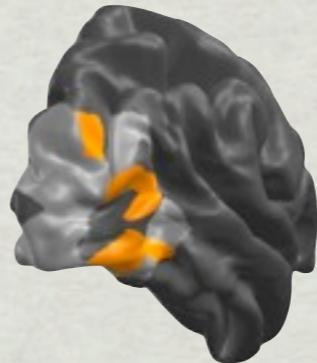
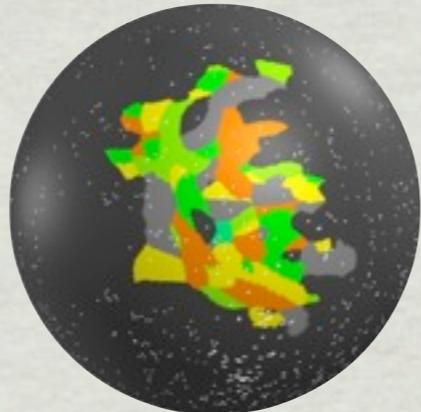
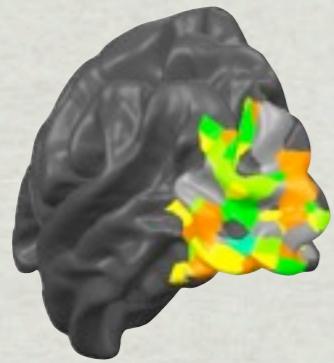
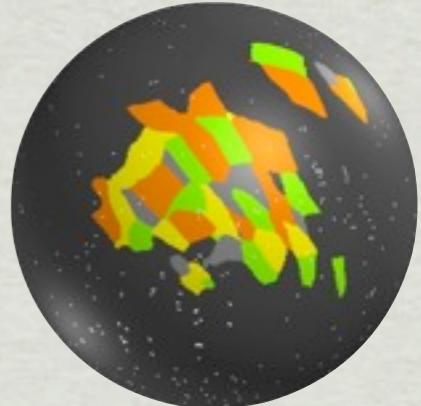
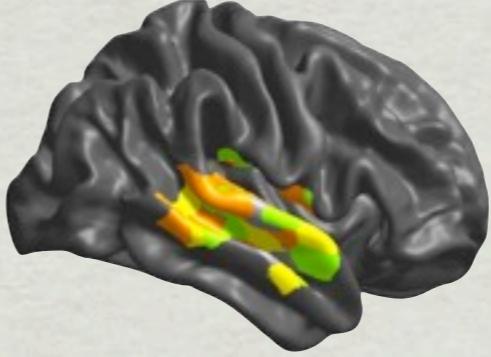
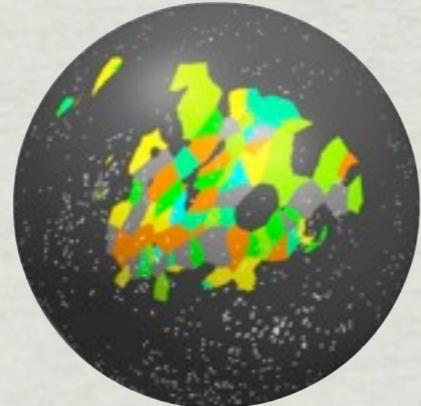
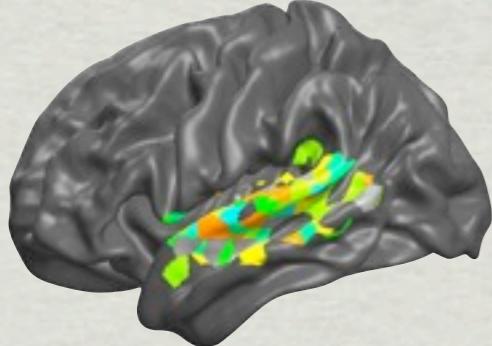


- Regress out confounds
- Cluster

TEMPORAL LOBE

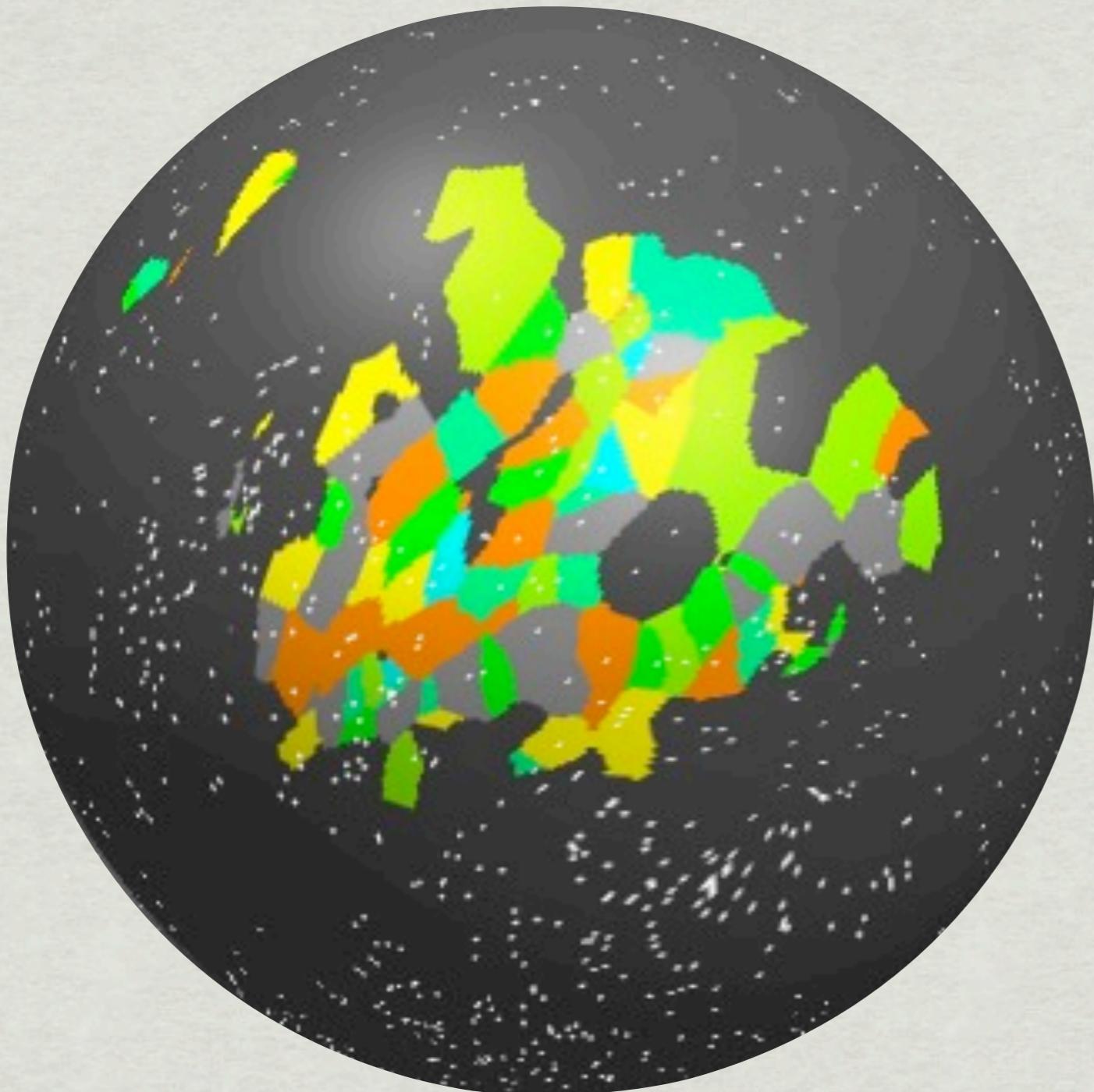


# Clustering by gene-ex



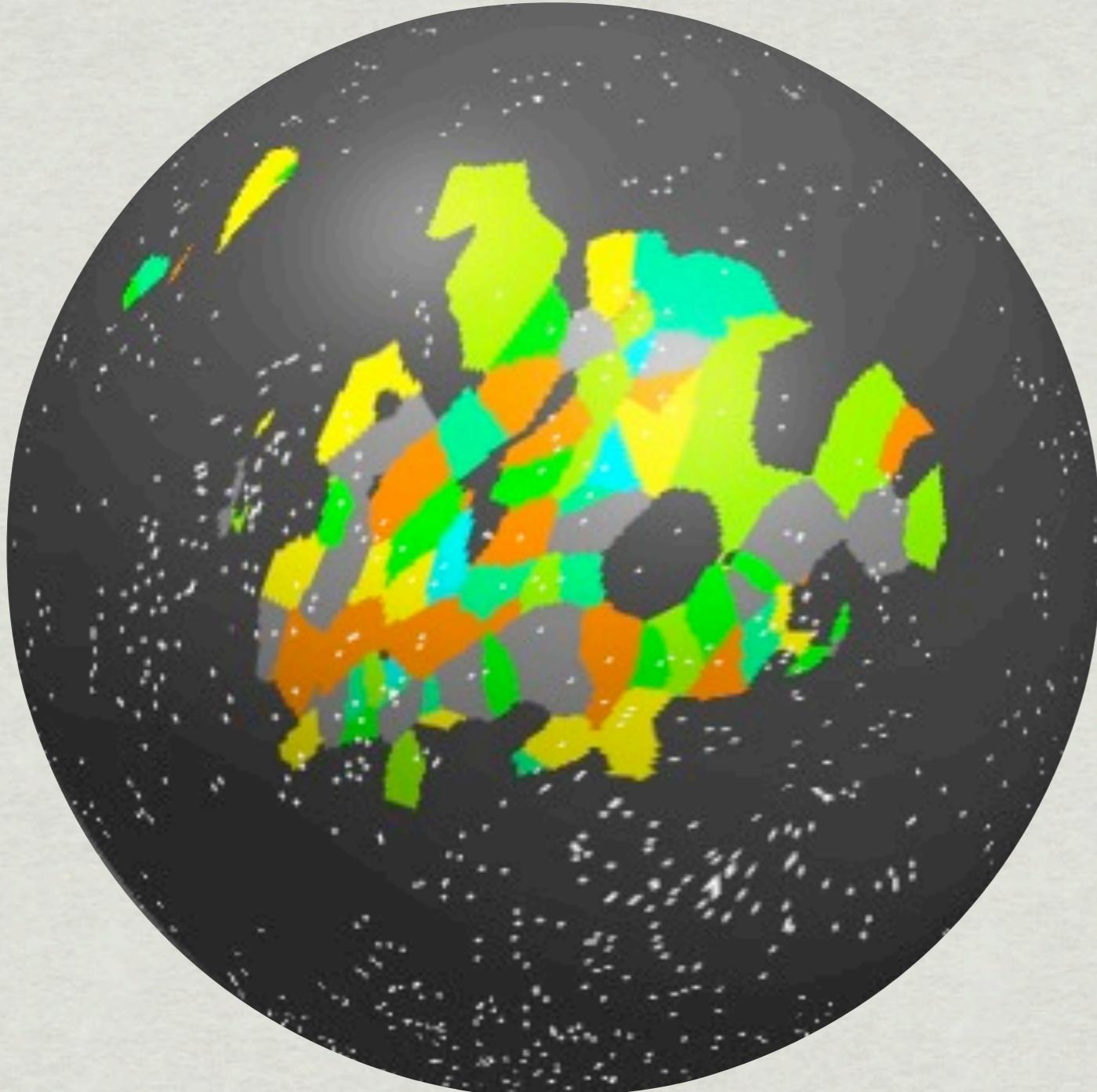
No sound consensus

# Clustering by gene-ex



No sound consensus

# Clustering by gene-ex



- Clustering not improved by: PCA dimension reduction; filtering by gene variability; change of clustering method (k-means with 5 modules)



No sound consensus

# Is gene expression more similar within modules?

- Calculate within & across module similarity scores
- Use permutation testing
- Gene-ex more similar within visual modules than across
  - Visual L:  $r=0.07$ ,  $p<0.00001$
  - Visual R:  $r=0.16$ ,  $p<0.00001$
- In auditory cortex, N.S. in right and low negative  $r=-0.04$  in left

**WWW.CUSACKLAB.ORG/NSC**



No sound consensus

# Conclusions

- Tractography and resting data showed good modularity for both visual and auditory cortices
- However, stronger modularity in gene expression found in visual cortex
- Broadly consistent parcellations found across hemispheres and modalities

## Future work

- Evaluate effect of retinotopic/tonotopic representation
- Mash with task-based fMRI
- Compare gene-ex in HG & neighboring regions
- Expand to developmental datasets



No sound consensus



**Western**  
The Brain and  
Mind Institute

**CUSACKLAB.ORG**

**Rhodri Cusack**

**Charlotte Herzmann**

**Annika Linke**

**Conor Wild**

**Leire Zubiaurre-Elorza**

**DALEYLAB.ORG**

**Mark Daley**



**Washington**  
University in St.Louis

**JONATHANPEELLE.NET**

**Jonathan Peelle**

**Once the digital dust had settled...**

- Hours of Skype & Hangout, \*many\* late nights
- Produced 4.5 TB of output, followed 3.2 billion diffusion streamlines, 1 trillion voxel steps
- 250 days of Sandy Bridge E core. Cluster of three machine configurations, up to 295 simultaneous cores, 1.7 TB RAM, 10 Gb interconnect
- We were nearly called: *Mödüüläär Füsön; (mod n); if ( size(data) > size(storage) ), problems += 1; ctrl+alt+deskFlip; The Connectome Canaries (we died in the DTI mine, so you don't have to!)*



**[www.cusacklab.org/nsc](http://www.cusacklab.org/nsc)**

**No sound consensus**