218: Functional Boundaries within the Cortical Speech Motor Control Network

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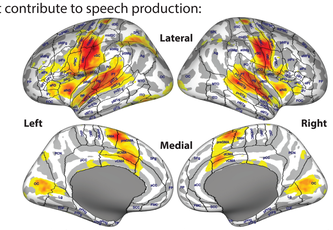
Motivation

- Neuroimaging has revealed a reliable core network of cortical regions that contribute to speech production:



- However, relatively little progress has been made toward identifying functional "units" within this network, perhaps due, in part, to relatively small sample sizes/power

Goals:

I. Improve our understanding of the functional organization of the speech motor network to speech by identifying ***functionally homogenous*** regions within it

II. Improve the sensitivity of fMRI data analysis by ***identifying reliable boundaries*** around functionally homogenous region

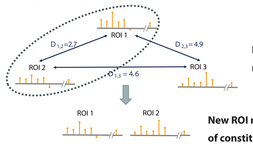
Approach

1. Pool over a large sample of speech fMRI data

- **163 subjects** (136 unique) and **39 speech conditions** for a total of **581 individual *Speech – Baseline*** contrast volumes
- Mono- and bi-syllabic words and pseudowords that ranged from single vowels and consonant-vowel pairs to short sentences.
- *Speech-Baseline* contrast estimated in individual volumes then mapped to FreeSurfer (Dale, 1999; Fischl, 1999) fsaverage cortical surface template = ***Contrast Map***

2. Hierarchical clustering

- Perform **between-subjects hierarchical clustering** on pooled contrast maps to sequentially group neighboring cortical vertices based on the similarity of their BOLD response patterns (cf. Seghier & Price, 2009)
- Start with response at each vertex (130k+) across all *Speech - Baseline* contrast maps.
- At each step, find Eulcidean distance (*D*) between response patterns of every pair of neighboring ROIs, merge most similar pair



Example of 3 neighboring ROIs

New ROI response is mean of constituent ROI response

- Repeat until left with a single ROI

At each step, *minimize within-cluster variance* = *maximize functional homogeneity*

3. Determine boundary reliability

- Use bootstrap resampling to build a population-level boundary distribution to identify significant boundary locations across speakers and conditions

References

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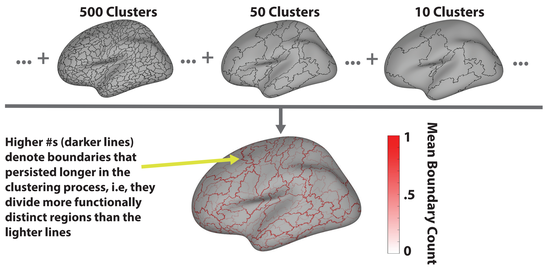
Acknowledgments

This research was supported by NIDCD R01 grants DC007683 and DC002852 (PI: FG) and NIMH P50 DC013027 (PI: H Tager-Flusberg, PI) .

Boundary reliability

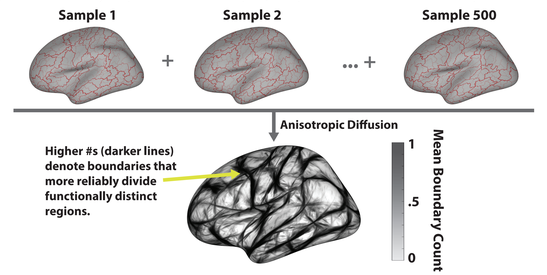
1. Sample-level boundary distribution

- Generate 500 random samples of dataset: select from pool of contrast maps 581 times with replacement
- For each random sample we apply clustering then aggregate the boundary map across the last 500 "trim levels" (i.e, # of ROIs)



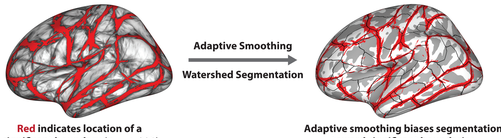
2. Population-level boundary distribution

Aggregate the boundary maps from all 500 samples; sharpen boundaries with anisotropic diffusion



3. Boundary statistics and completion

- Compare population boundary distribution to a null distribution generated from random data
- Apply adaptive smoothing and watershed segmentation to form fully-bounded regions

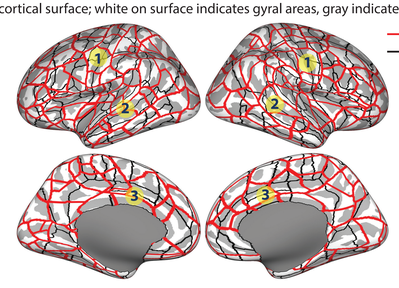


Red indicates location of a significant boundary ($p_{FDR} < .001$)

Adaptive smoothing biases segmentation toward significant boundaries

fROI boundaries: relation to cortical anatomy

Functional (red) and structural (black; Tourville & Guenther, 2012) boundaries shown on inflated cortical surface; white on surface indicates gyral areas, gray indicatea sulcal areas



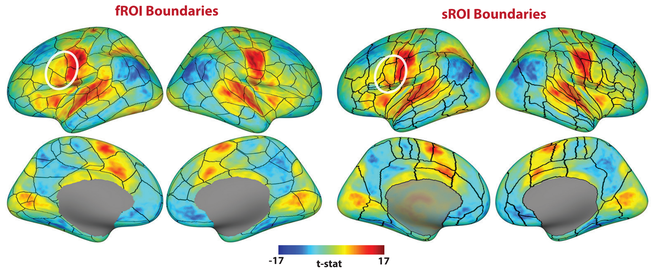
functional ROI boundaries

structural ROI boundaries

- fROI boundaries are shifted from sulci toward gyral crown, e.g., sensorimotor (1), superior temporal (2), and cingulate (3) areas
- medial-lateral segmentation of sensorimotor cortex (1) is apparent
- anterior-posterior segmentation of superior temporal cortex (2) is apparent

fROI boundaries: relation to BOLD response

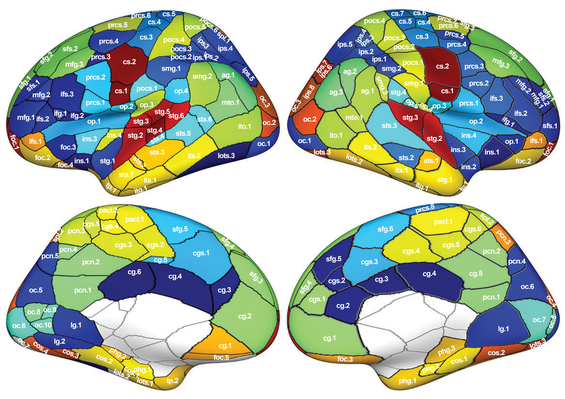
fROI (left) and sROI (right) boundaries overlaid on the group ***Speech - Baseline*** contrast map



- Activation level and direction are generally consistent within fROIs, i.e., see large changes across but not within boundaries (notable exceptions: dorsal insula/operculum, dorsal motor cortex).
- Response uniformity is greater in fROIs than sROIs in left lateral premotor and adjacent inferior frontal cortex (white circle)

fROI response similarity: identifying subnetworks

- Used hierarchical clustering to construct a dendrogram representation (bottom) of fROI response similarity. Clustering was based on the Euclidean distance between the mean BOLD response pattern (averaged across all vertices) across all *Speech-Baseline* contrast maps.
- Colors were assigned to each region according to its position in the dendrogram to visualize response similarity: **fROIs with similar colors exibit similar response patterns**
- Labels based on local anatomy were assigned to each fROI (117 in left hemisphere, 109 in right) to aid localization.

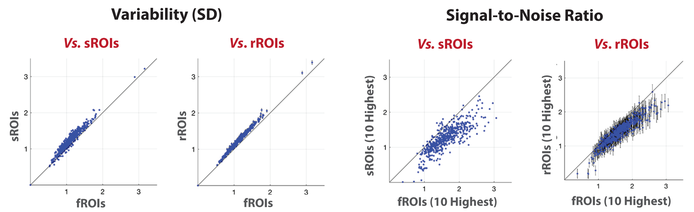


Notable clusters of similarly responding fROIs:

- a "core" cluster of lateral sensorimotor and medial auditory fROIs (see burgunday-filled areas above and region labels highlighted in red in dendrogram below for complete list)
  - this core disrupts the typical uniform "sensory-motor" resting state network
- around this core region, the medial prefrontal, lateral premotor, insula, anterior and posterior opercula, lateral somatosensory, and posterior higher order auditory cortex (see light blue-filled areas above and region labels highlighted in blue below
- areas typically associated with the "default mode" resting state network are clustered together and shown in green

fROI-based analysis sensitivity: validation

Compared variability (left) and signal-to-noise ratio (SNR; right) of fROI mean response to: (i) sROIs (left subplots) and ROIs resulting from a random parcellation of the cortex into the same # of parcels (rROIS; right subplots) for each of the 581 *Speech - Baseline* contrast maps



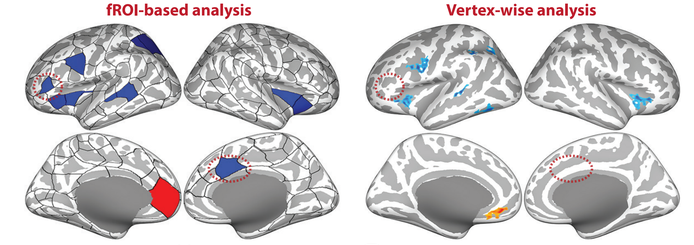
rROI plots: error bars show 95% confidence intervals across 500 random samples

Result: ***Higher homogeneity and SNR*** in fROIs in *nearly all* individual contrasts

fROI-based analysis sensitivity: application

Compared fROI-based and vertex-wise assessment of speech BOLD contrast in an independent fMRI sample from adults who stutter (AWS)

Task: produce meaningless *Novel* and *Learned* syllables that contain illegal consonant clusters (e.g., GVAFZ, TPIPF)



Result: fROI-based analysis of the *Learned - Novel* contrast detected all clusters identified by vertex-wise analysis and ***revealed additional areas of activation*** (compare areas indicated by red dashed oval)

Summary

- Between-subjects clustering of the pooled data revealed reliable fROI boundaries across a large sample of subjects and speech conditions
- Boundaries align with some putative functional-anatomical divisions but suggest that sulcal fundi do not form functional divisions in some key speech regions including sensorimotor cortex
- Reduced variability within fROIs = increased sensitivity and improved analysis of speech fMRI data
- Clustering the mean fROI response revealed core and secondary auditory-motor networks of similarly responding fROIs in addition to "default mode" and other resting state networks

Future Directions

- Assess brain-behavior correlations to begin to map fROIs to speech processes
- Expand to include subcortical and cerebellar regions
- Shift focus from fROI parcellation to boundary distribution map: integrate fROI and sROI boundar-