

Structural predictors of receptive language selectivity in temporal cortex



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Summary

The brain bases of language are often examined in the context of macroanatomical gray matter regions or large white matter pathways selected *a priori*. Here, we instead used a data-driven, individualized approach to understand the structural features associated with fMRI-localized core receptive language areas. We used logistic regression modelling to reveal the collections of features that predict nodes of the Receptive Language Network in left and right temporal cortex in individual brains. The accuracy of these models indicates that the location of language-selective areas in individual brains is associated with a unique structural profile. This adds to existing evidence of “cortical areas” for higher-level language [1-4]. Key structural features included curvature, thalamic connectivity, and connectivity within temporal cortex. LH aSTG stood out for the variety in its connectivity targets, suggesting a more integrative, higher-level role relative to posterior and RH temporal areas. Understanding the nuanced structural organization of language areas may clarify language disorders, development, and evolution.

Methods

MRI data:

- N = 25, mean age = 23.3, typical language & hearing
- Anatomical, diffusion-weighted, and functional volumes
- fMRI Receptive Language Localizer contrast (listening to intact speech > acoustically degraded, unintelligible speech) [5]

fROI delineation:

- N > 800 Language Localizer probability map [6] → search-space parcels in which individuals are likely to have significant activation [7,8]
- Individualized fROIs: the elbow of the plot of localizer activation values (percentiles) vs. effect size values within the parcel was used as the fROI cutoff point (in terms of activation significance %ile)

Structural features: (all intra-hemispheric to parcel)

- curvature, cortical thickness (*FreeSurfer*)
- intra-cortical myelin content (T1w/T2w) [9]
- diffusion tensor metrics (FA, AD; *FSL DTIFIT*)
- macroanatomical atlas region (e.g., planum temporale)
- connectivity with atlas regions (*FSL ProtrackX*) – all tractography visualizations shown with pial surfaces are from representative individuals

The model: Logistic Regression with Hierarchical Group-LASSO Regularization [10]

- *glinternet* in R: (i) performs feature selection, (ii) handles correlated predictors, (iii) includes first-order interaction terms
- objective function: $\min_{\mu, \theta} \text{Logistic Loss} + \lambda(\text{Hierarchical LASSO Penalty}(\theta))$

Leave-one-subject-out nested CV:

- inner loop: find λ that maximizes AUC for left-out subject (train set: n - 2 subjects, test set: 1 subject)
- outer loop: fit optimal model (from inner loop) and get predictions for left-out subject (train set: n - 1, test set: subject not included in inner loop)

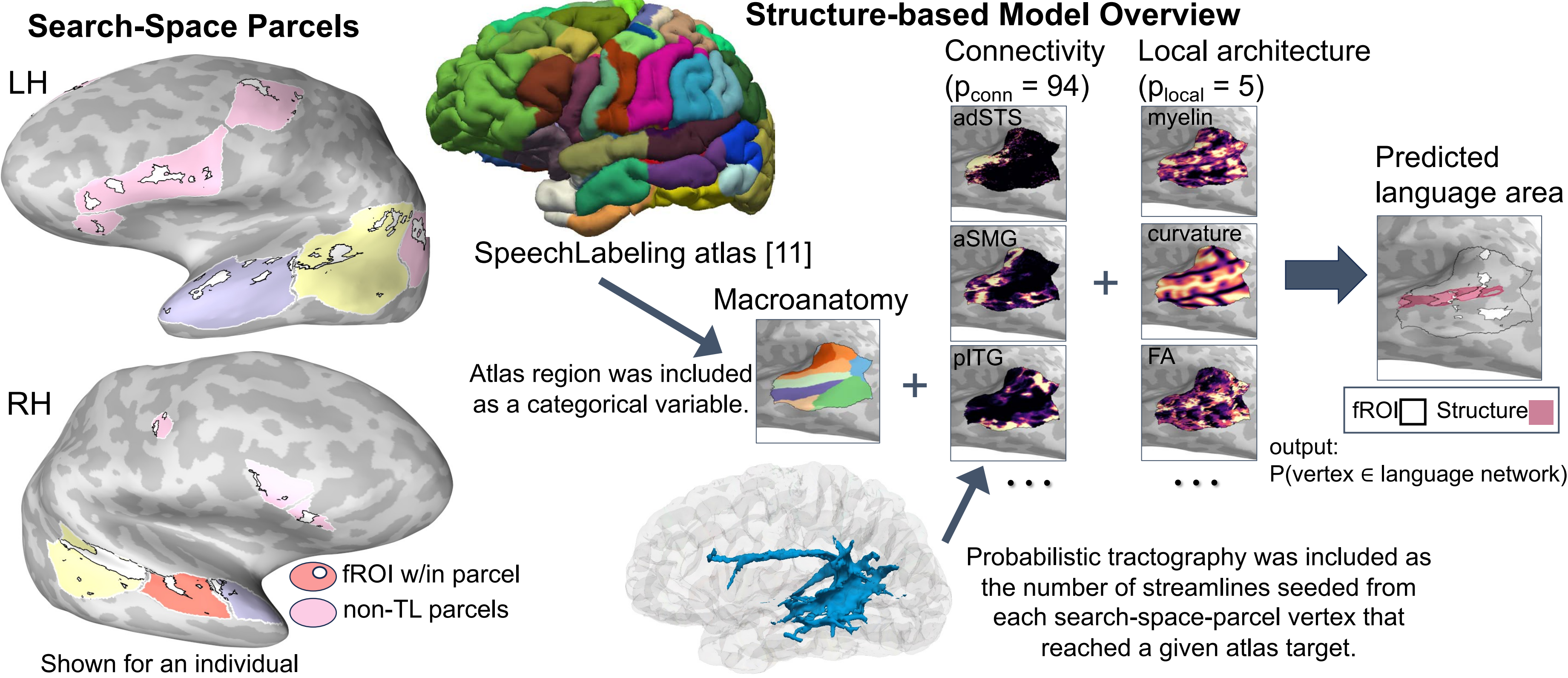
Baseline models:

- *Group*: one-sample mean (mixed-effects, one-subject-left-out, n = 24) – How well is the location of each subject’s fROI predicted by the group average fMRI z-statistic map?
- *Prob. Map*: n > 800 language localizer probability map

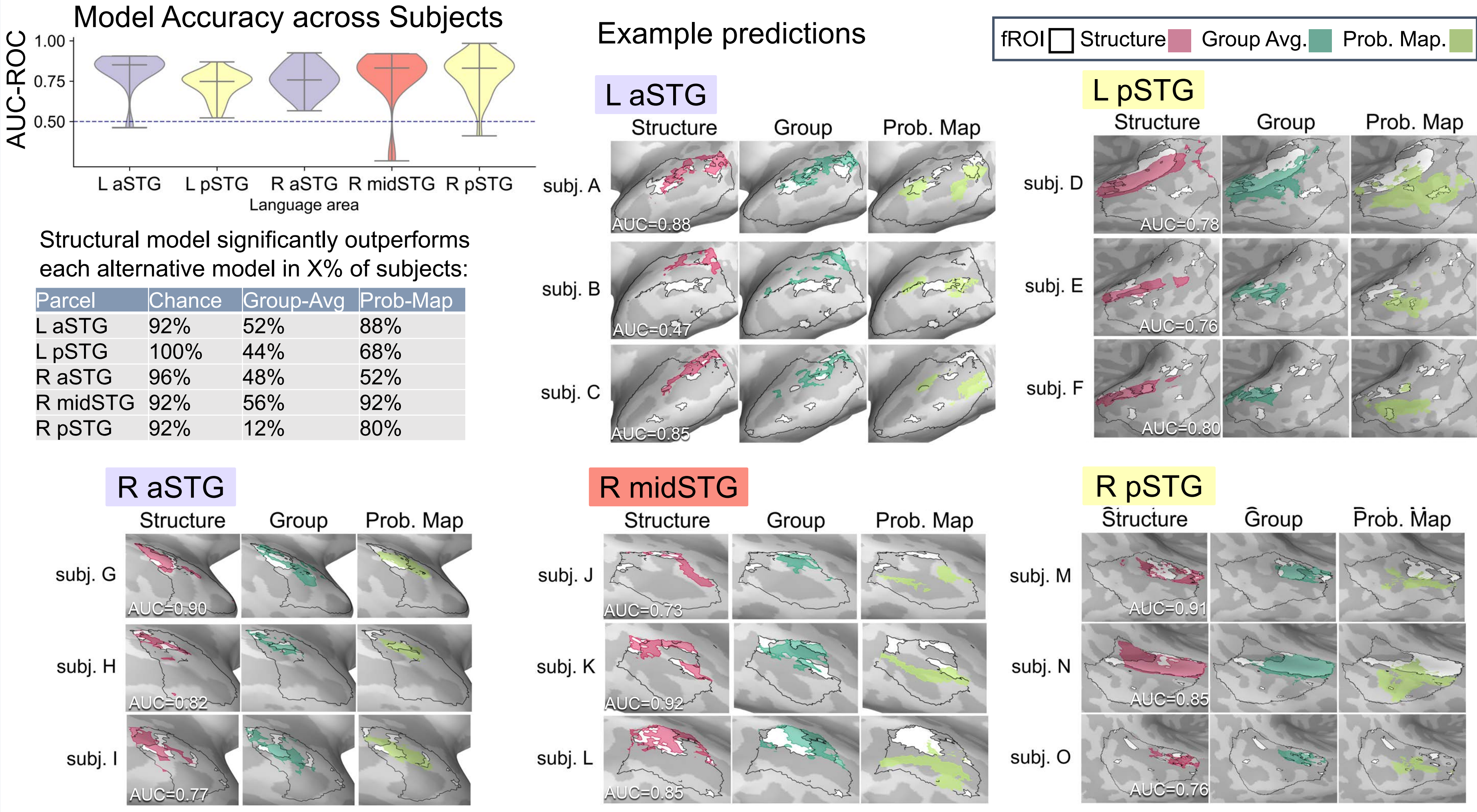
Within-subject tests – prediction accuracy:

- Mann Whitney U-test: structure-based model vs. random guessing (AUC-ROC = 0.50)
- DeLong’s test: structure model vs. baseline models
- Benjamini-Hochberg multiple comparisons correction

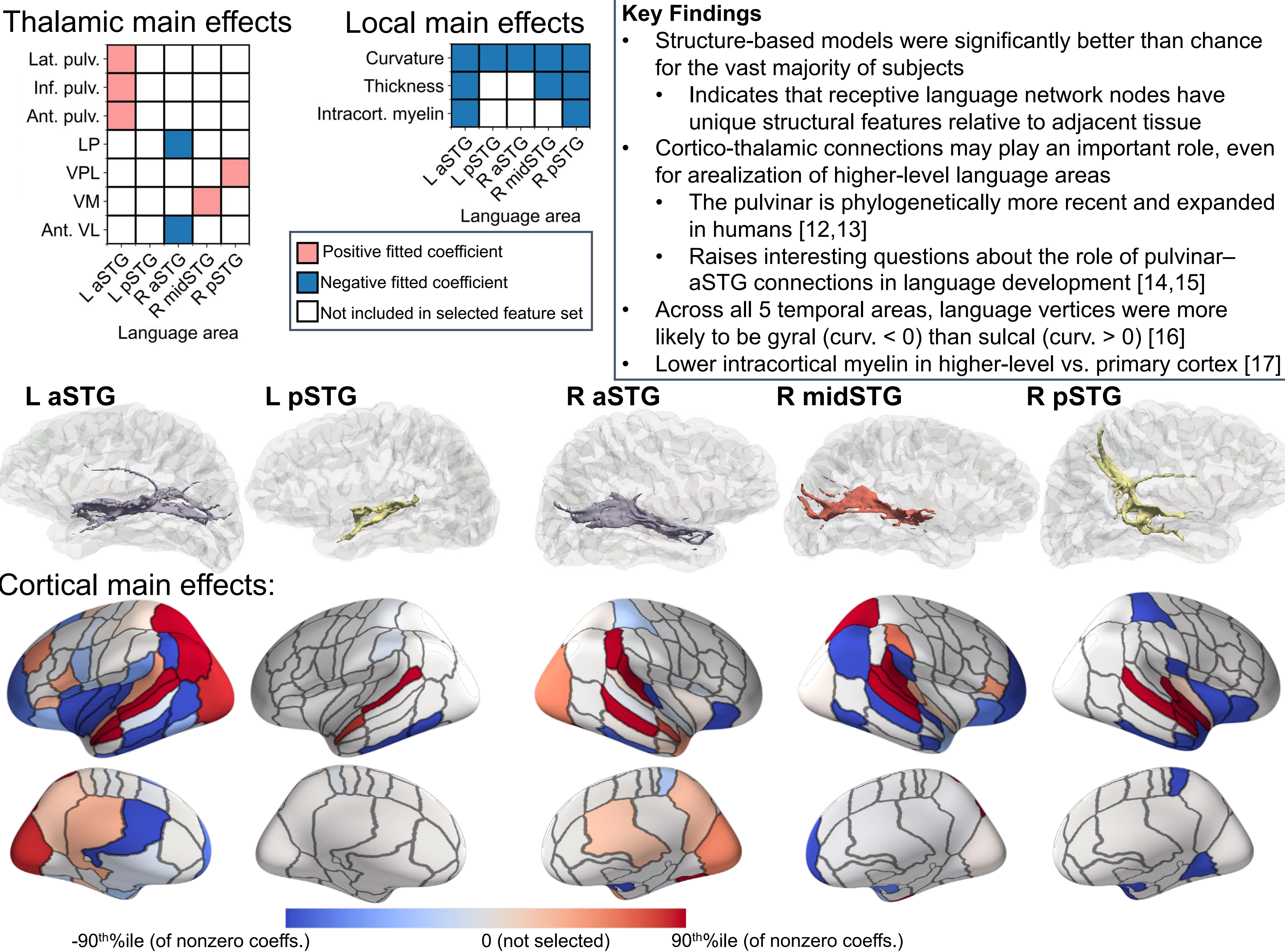
Structure → Function



Language fROI Prediction Accuracy



Structural Predictors



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