Multimodal Neuroimaging for Cardiovascular Disease Risk Prediction

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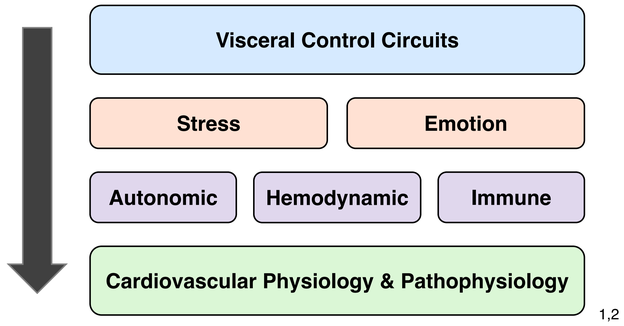
Visceral control circuits



[1,2]

- Neurocardiology[3,4] focuses on identifying brain-based markers of cardiovascular disease (CVD) risk that can improve upon conventional clinical markers[5].
- Hypothesis: a multimodal approach will generate a brain-based biomarker that reliably predicts a vascular marker of CVD risk, specifically carotid artery mean intima media thickness (IMT).

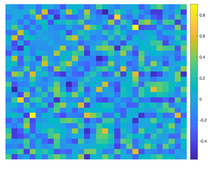
Methods

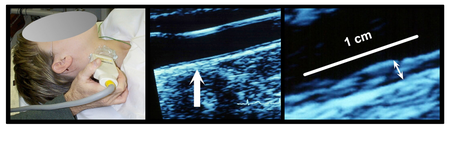
Participants:

- Neuroimaging and demographic data from n=324 participants (49% female, ages 30-51, mean 40) from the Pittsburgh Imaging Project were included in our analyses.

Data:

- 3 Tesla whole-body scanner, 12-channel phased-array head coil
- T1-weighted MPRAGE acquisition:
  - 7 minute 17 second scan
  - FOV = 256×208mm, matrix size = 256×208, TR = 2100ms, inversion time = 1100ms, TE = 3.31ms, FA = 8° (192 slices, 1mm thickness, no gap)
  - cortical surface area, cortical thickness and subcortical volume extracted using FreeSurfer v6
- Resting-state functional connectivity (FC) acquisition:
  - 5 minute scan, eyes open
  - FOV = 205×205mm, matrix size = 64×64, TR = 2000ms, TE = 28ms, and FA = 90° (39 slices interleaved inferior-to-superior for each of 150 volumes, 3mm thickness, no gap)
  - Pearson correlation to estimate edges for FC (image below left)





- IMT acquisition: Carotid artery mean IMT was measured bilaterally at distal common carotid artery, carotid artery bulb, and internal carotid artery then averaged (image above right)

Methods

Multimodal stacking:

- Five-fold cross-validation prediction stacking algorithm, see Figure 1:
  - Step 1: train individual support vector regression models on each of the input data sources: resting-state FC, cortical surface area, cortical thickness, subcortical volumes
  - Result: four predictions of IMT for each participant, one from each data source
  - Step 2: stack SVR predictions as input into random forest model to give one final prediction for each participant

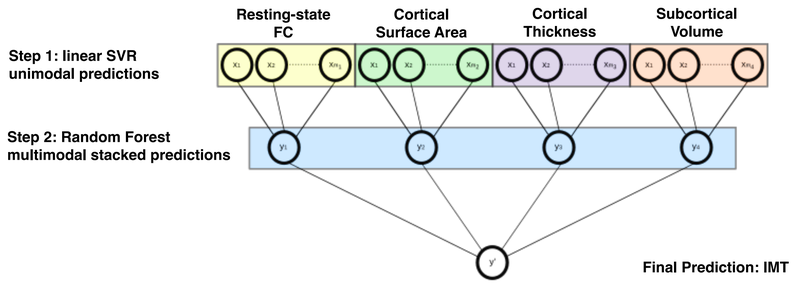


Figure 1: Prediction stacking model schematic, with linear SVR used in the unimodal predictions and random forest used in the multimodal prediction. FC = functional connectivity. SVR = support vector regression.

Results: model performance

Coefficient of determination for unimodal and multimodal model predictions

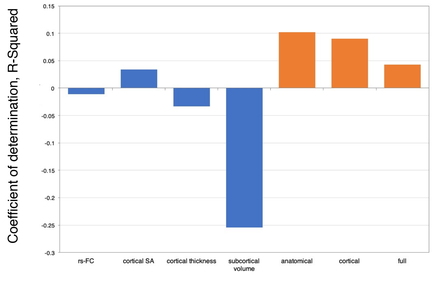


Figure 2: Coefficient of determination, r-squared, for single data sources from Step 1(blue) and best three candidate models from Step 2 (orange): anatomical (cortical surface area, cortical thickness), cortical (resting-state FC, cortical surface area, cortical thickness), full (resting-state FC, cortical surface area, cortical thickness, subcortical volume). rs-FC = resting-state functional connectivity, SA = surface area.

Correlation between observed IMT and predicted IMT

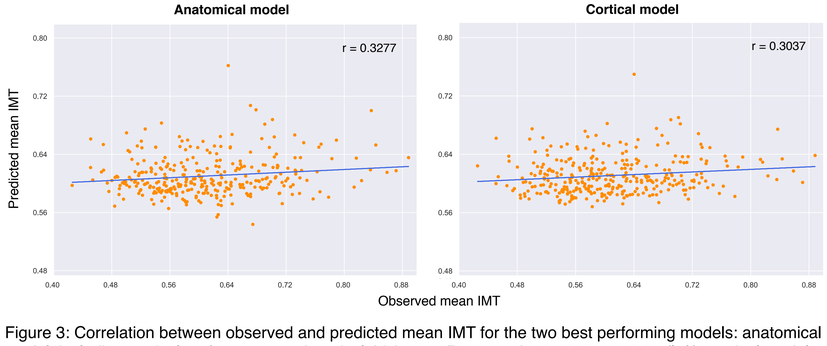


Figure 3: Correlation between observed and predicted mean IMT for the two best performing models: anatomical model, including cortical surface area and cortical thickness, R-squared = 0.1017, p < 0.01 (left), cortical model, including resting-state FC, cortical surface area and cortical thickness, R-squared = 0.08982, p < 0.01 (right).

Results: informative feature loadings

Projection of Support Vector Regression coefficients onto the brain

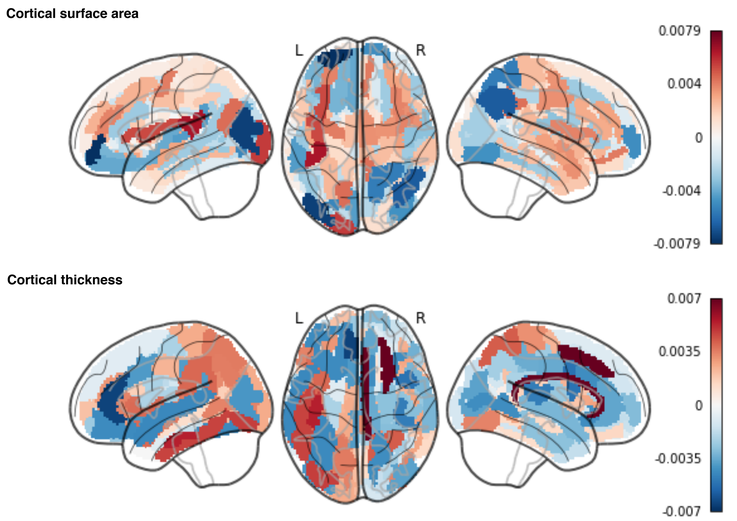


Figure 4: Single-source SVR coefficients back-projected onto the brain for the cortical SA (top) and cortical thickness (bottom) data sources. These are the anatomical data sources included in the best performing prediction model, the anatomical model.

Summary and future directions

Summary:

- Our anatomical and cortical models performed most strongly, accounting for 10.1% and 8.9% of the variance in mean IMT, respectively.
- This work builds on growing neuroimaging evidence by showing that functional and structural features of neural circuits may complement and add to the utility of conventional risk factors for predicting CVD.

Future Directions:

- We will perform interaction analyses using covariates such as gender and age to determine if these biomarkers behave differently in different demographic subsets.
- We will evaluate whether limiting resting-state FC features to those within the visceral control circuits that influence physiology will improve model performance.

References

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