Predictive Modeling of Anatomical Appearance from Genetic and Clinical Data

Adrian V. Dalca[1], Ramesh Sridharan[1], Mert Sabuncu[1,2], and Polina Golland[2]

[1]CSAIL, EECS, Massachusetts Institute of Technology [2]Martinos Center, Harvard Medical School

Question

Can we predict anatomical appearance from genetic and clinical factors?

We predict **entire follow-up MR images after observing a single scan** using **genetic** and **clinical** information

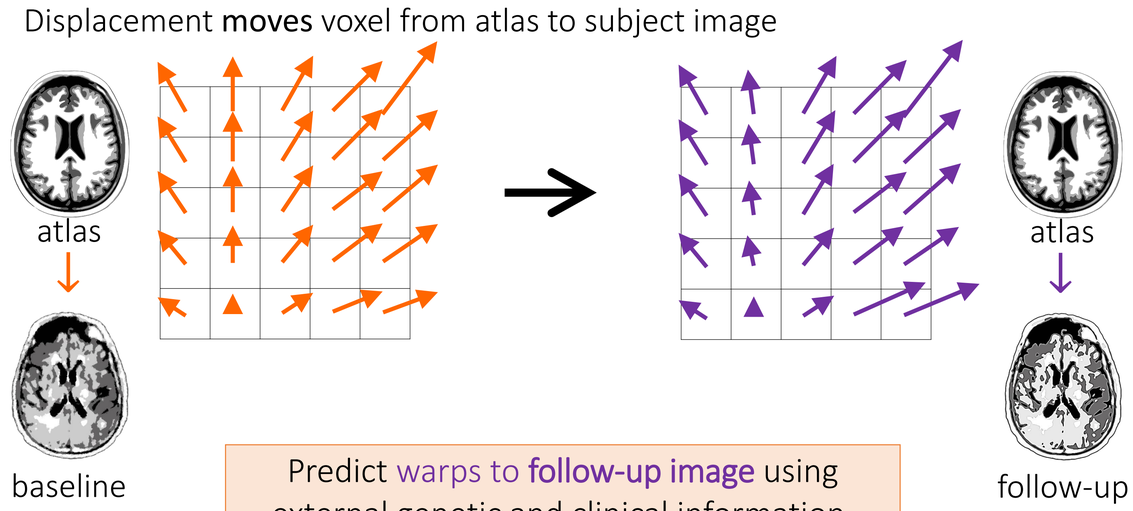
Scan at age 50 Scan at age 60

tablet space

Scan QR code or visit http://adalca.mit.edu/predict for video presentation

MRI Prediction via Anatomical Change

- Represent subject MRI **as a deformation** from an atlas
- Displacement **moves** voxel from atlas to subject image

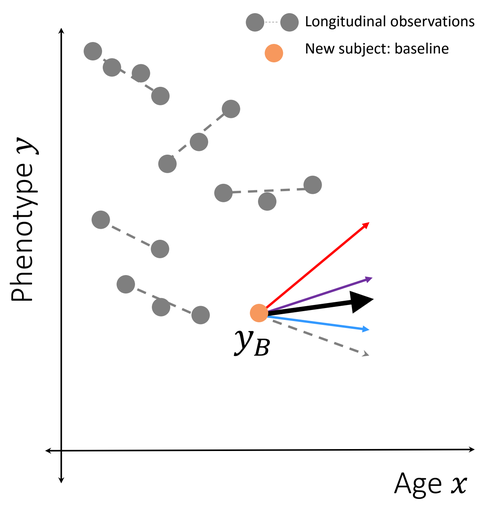


Predict warps to **follow-up image** using external genetic and clinical information.

- Voxel warps are dense and not truly independent
- Use PCA **components as phenotypes**

Prediction of a Scalar Phenotype

- Given scalar measurement for **longitudinal population** of subjects
- Observe **only the baseline** of a **new patient**
- **Goal**: predict new patient phenotype at a later time
- Model **change in phenotype** with respect to age as average population change modified by a **health profile**
- **Use kernel-based regression** to capture subject's similarity to population in terms of genetics, clinical and baseline phenotype



$$y_t = y_B + \Delta x\,(\bar{\beta} + h_G + h_C + h_y) + \epsilon$$

$$h_X(z_i) \sim \sum_j \underbrace{\alpha_j}_{\text{subject } j \text{ weight}} \underbrace{K(z_i, z_j)}_{\text{phenotype } z \text{ similarity}}$$

$$K_G(g_i, g_j) = \frac{1}{2S}\sum_s (2 - |g_i(s) - g_j(s)|)$$

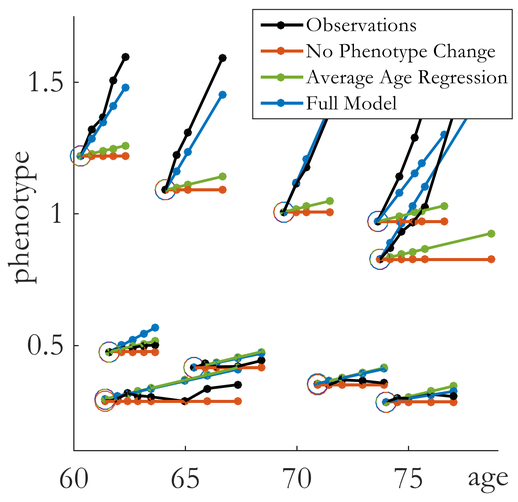
$$K_C(c_i, c_j) = exp\left\{-\frac{1}{\sigma_C^2}(c_i - c_j)^T \boldsymbol{W}(c_i - c_j)\right\}$$

$$K_y(y_i, y_j) = \exp\left\{-\frac{1}{\sigma_y^2}\|y_i - y_j\|_2^2\right\}$$

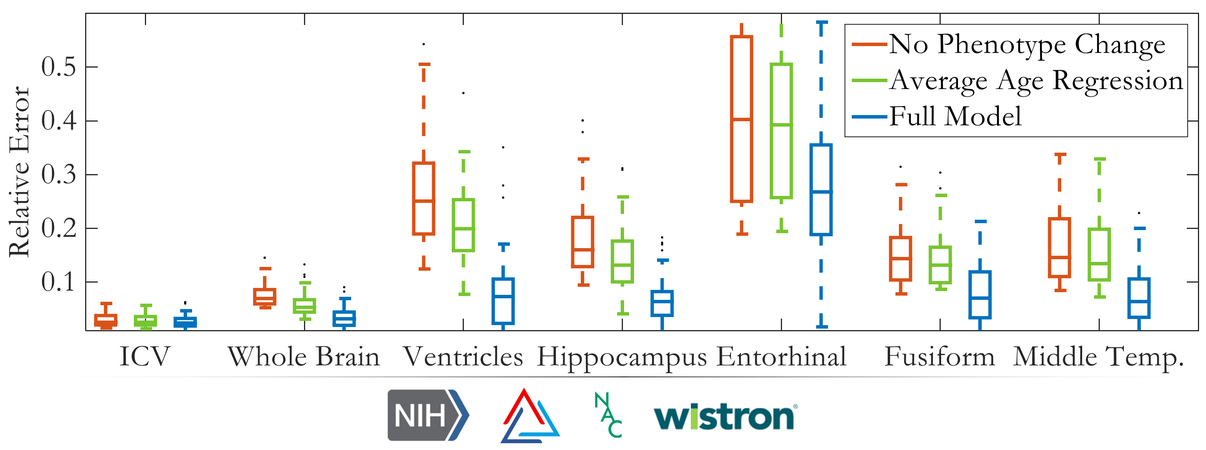
- Main model parameters: α_j and $\bar{\beta}$

Experiments (ADNI)

- 800 subjects, various scalar phenotypes
- Predict phenotype via no change, average age regression, full kernel regression model
- **Genetic** and **clinical** information **strongly improves** results

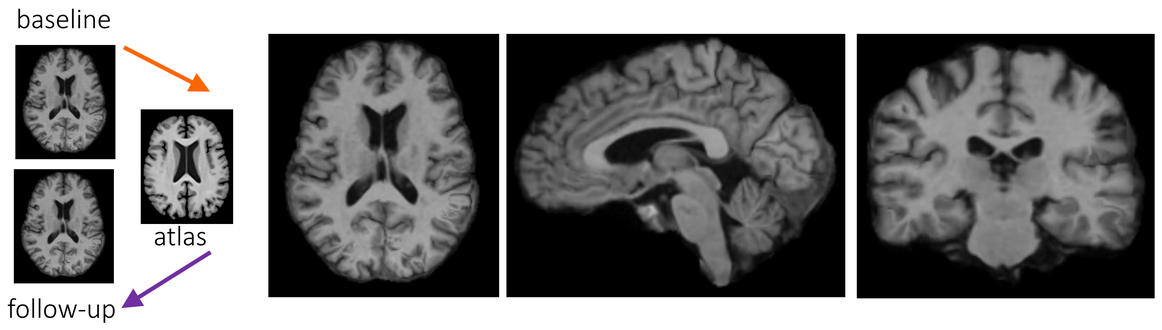


All subjects with significant phenotype change

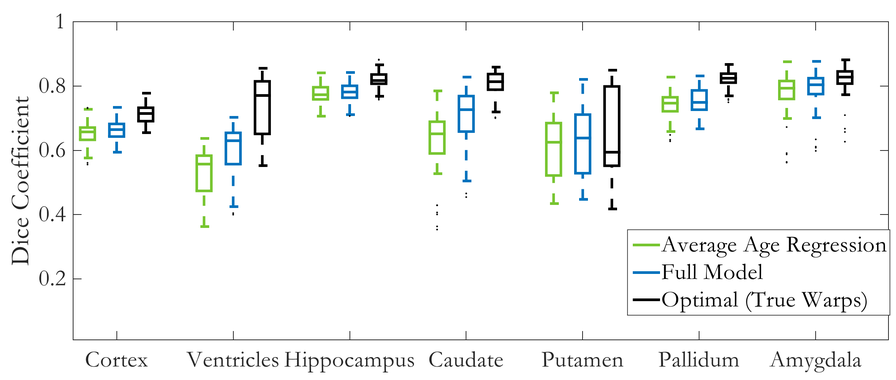


Experiments (ADNI)

- Predicted follow-ups look plausible
- Use volume overlap to quantify prediction
- Predict images via average age regression, and our full model
- **Control measure**: direct baseline to follow up registration



Anatomical predictions look plausible, and are improved by use of **genetic and clinical information**



Predict Healthy Anatomy

- Get baseline scan of Alzheimer's patient
- Train model on **healthy** subjects only
- Predict follow-up scans if ***patient had been healthy***
- Right: example **predicted healthy** image
- Overlay: differences from **real** follow-up
- Ventricles would expand significantly less if the patient had been healthy