

Gaussian Process Progression Modelling of structural MRI changes in Huntington's disease

Peter A. Wijeratne^{1,2}, Sara Garbarino³, Eileanoir B. Johnson², Sarah Gregory², Rachael I. Scahill², Sarah J. Tabrizi², Marco Lorenzi⁴, Daniel C. Alexander¹

ISMRM & SMRT Virtual Conference & Exhibition

Session Title: AI Applications in Neuroimaging: High Novelty & Impact
08-14 August 2020

¹Centre for Medical Image Computing, Department of Computer Science, University College London, United Kingdom

²Huntington's Disease Research Centre, Queen Square Institute of Neurology, University College London, United Kingdom

³Dipartimento di Matematica, Università di Genova, Italy

⁴Inria, Epione Research Project, Université Côte d'Azur, France



ONE COMMUNITY

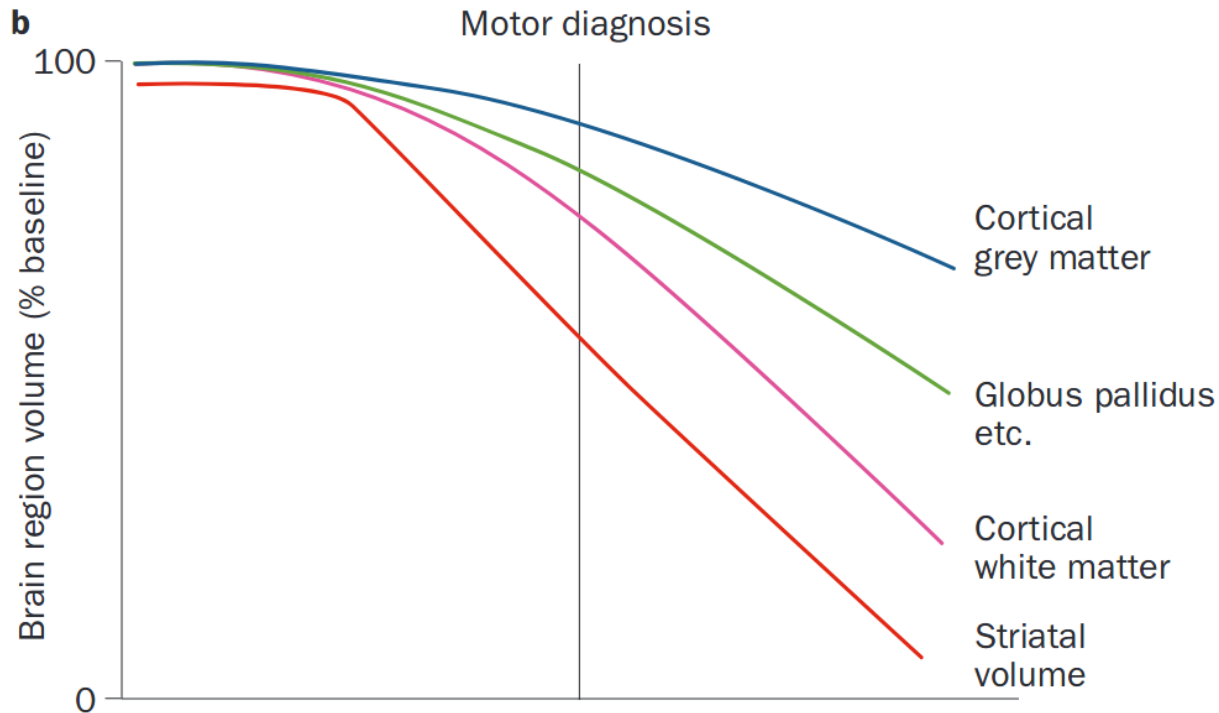
ISMRRM & SMRT
Virtual Conference & Exhibition
08-14 August 2020



Declaration of Financial Interests or Relationships

Speaker Name: Peter A. Wijeratne

I have no financial interests or relationships to disclose with regard to the subject matter of this presentation.



- Neurodegenerative disease that causes progressive deterioration and death ~ 55 years old
- Caused by an expansion in the number of cytosine-adenine-guanine (CAG) repeats in the huntingtin gene
- Characterised by a long (~10 years) pre-manifest period before clinical symptoms develop
- Clinical progression is mirrored by monotonic change in regional brain volumes

Objectives

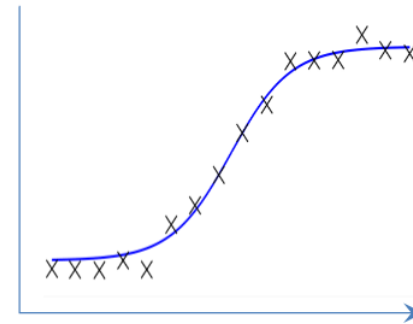
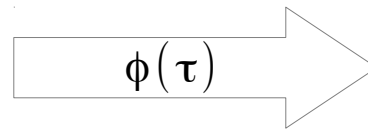
1. Infer biomarker dynamics from longitudinal individual-level data
2. Estimate where a patient is along the disease trajectory

• **Problem** – patients are observed at unknown disease time which doesn't necessarily correspond to observation time; this confounds time-series regression

• **Solution** – learn both temporal covariance (regression) and latent disease stage (time-shift) using a generative, time-reparameterised Gaussian Process Progression Model (GPPM)*



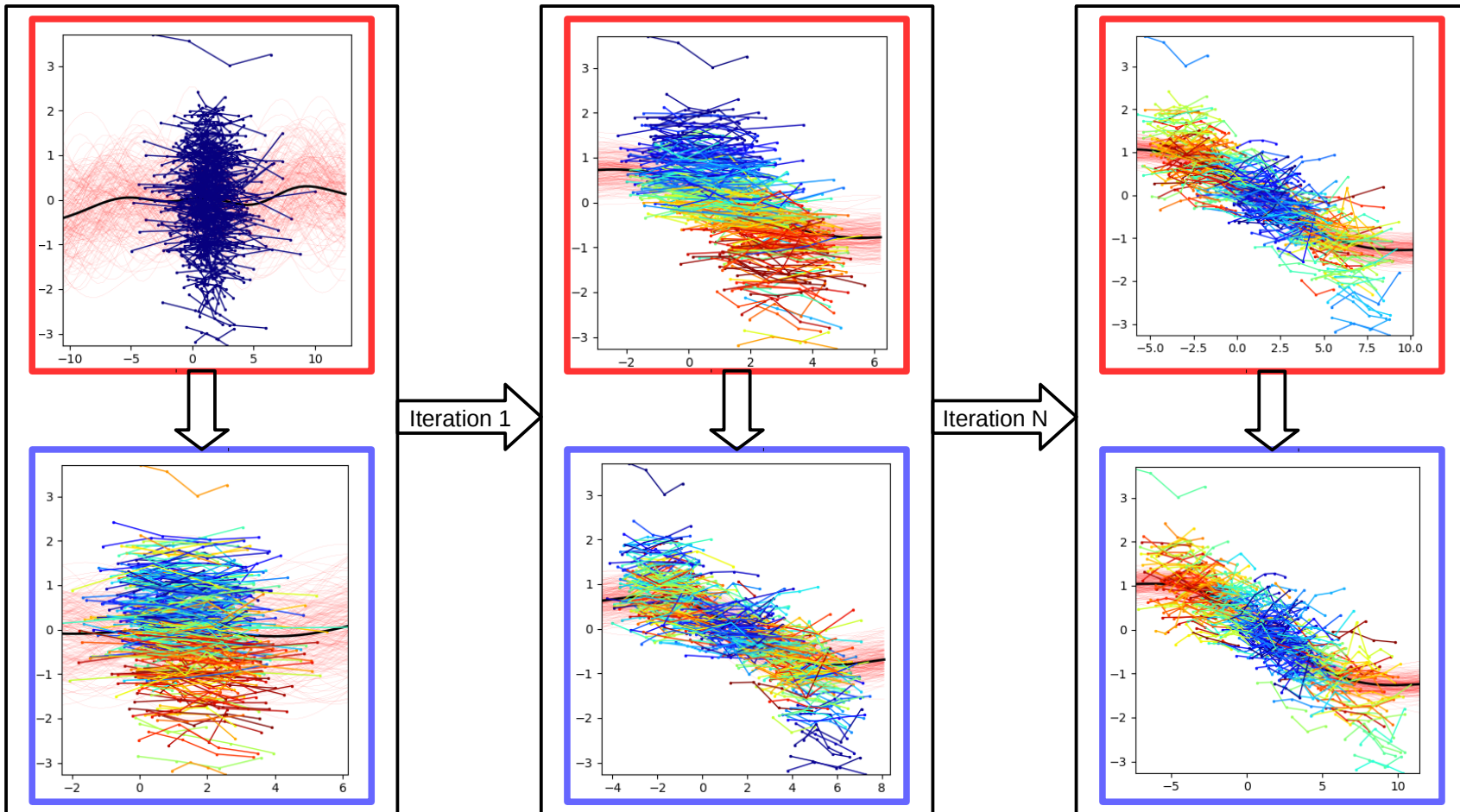
$$y^j(t) = f(t) + v^j(t) + \epsilon$$



$$y^j(\phi^j(\tau)) = f(\phi^j(\tau)) + v^j(\phi^j(\tau)) + \epsilon$$

Regression

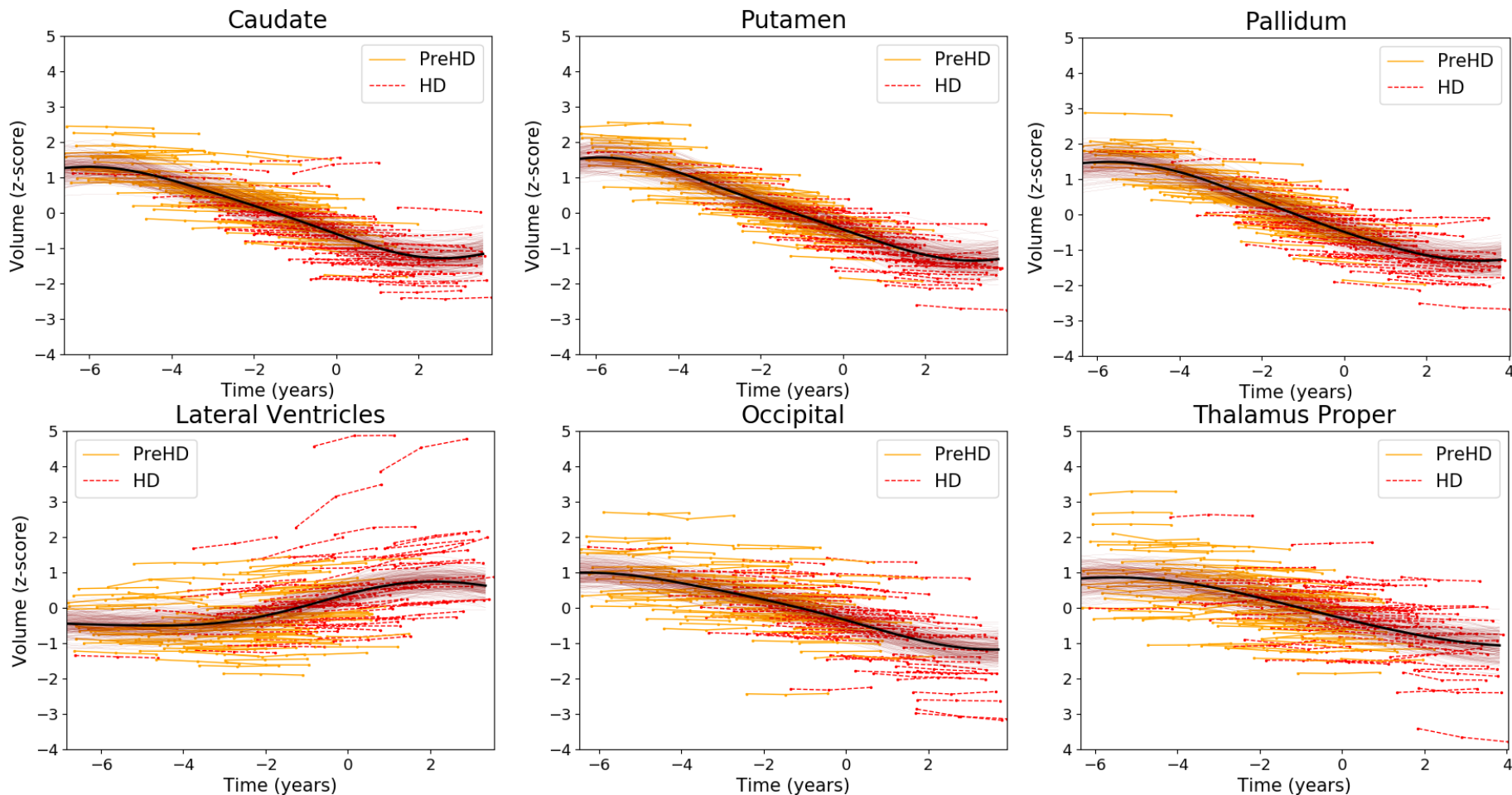
Time shift



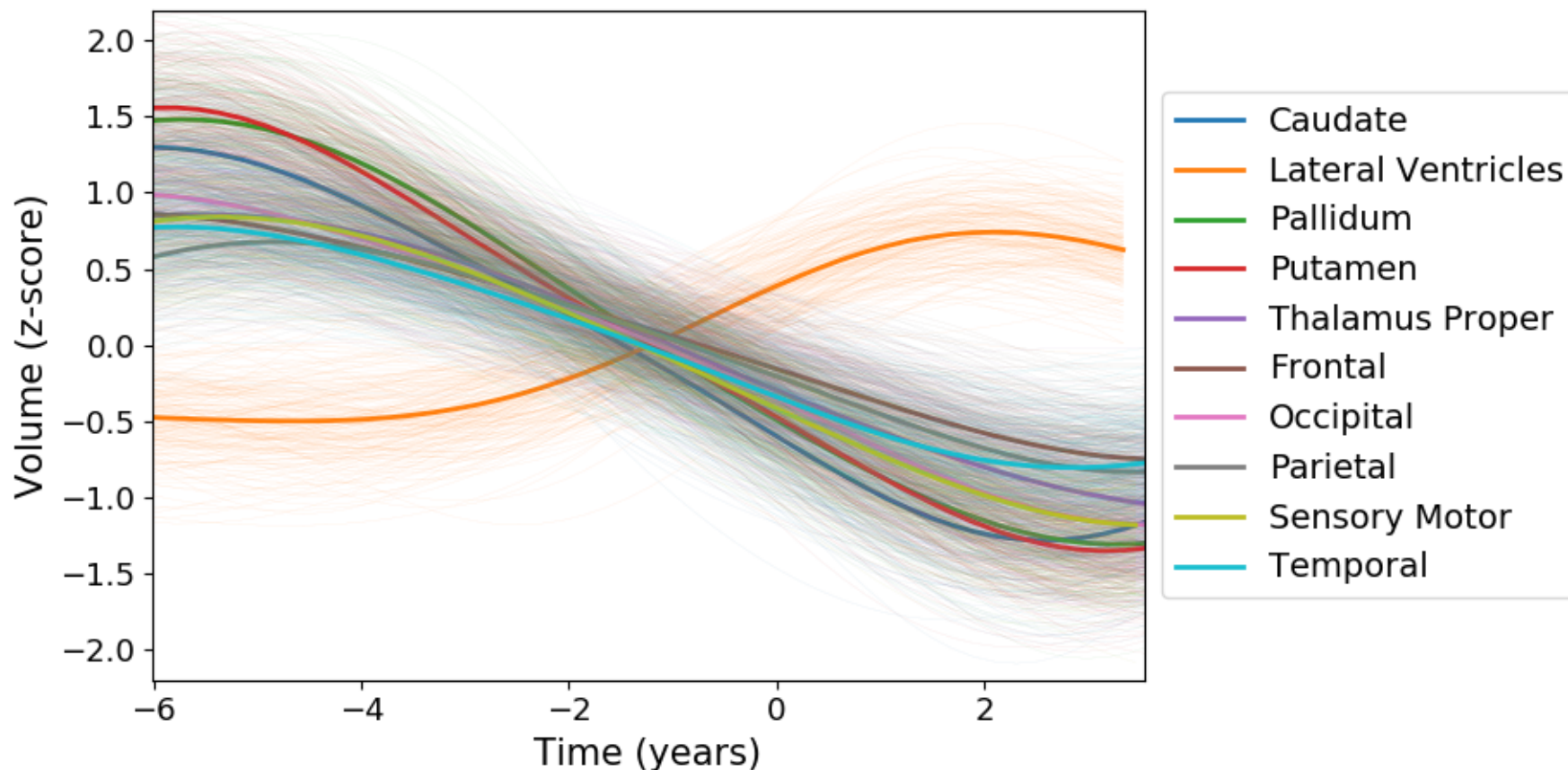
- We define a cost function: sum of model likelihood + regularisation term
- Monotonicity constraint* – enforced by constraining first derivative of fixed-effects
- Sequentially fit regression parameters and individual time shift

Demographic Characteristic	HC (TRACK-HD)	PreHD (TRACK-HD)	HD (TRACK-HD)	HC (PREDICT-HD)	PreHD (PREDICT-HD)
N	100	104	80	36	128
Sex (F:M)	58:42	55:49	43:37	25:11	82:46
Age (mean \pm std)	46.3 \pm 10.4	41.2 \pm 8.8	48.5 \pm 9.3	45.1 \pm 10.9	41.5 \pm 10.9
CAG (mean \pm std)	-	43 \pm 2.3	43.8 \pm 3	-	42.5 \pm 2.7

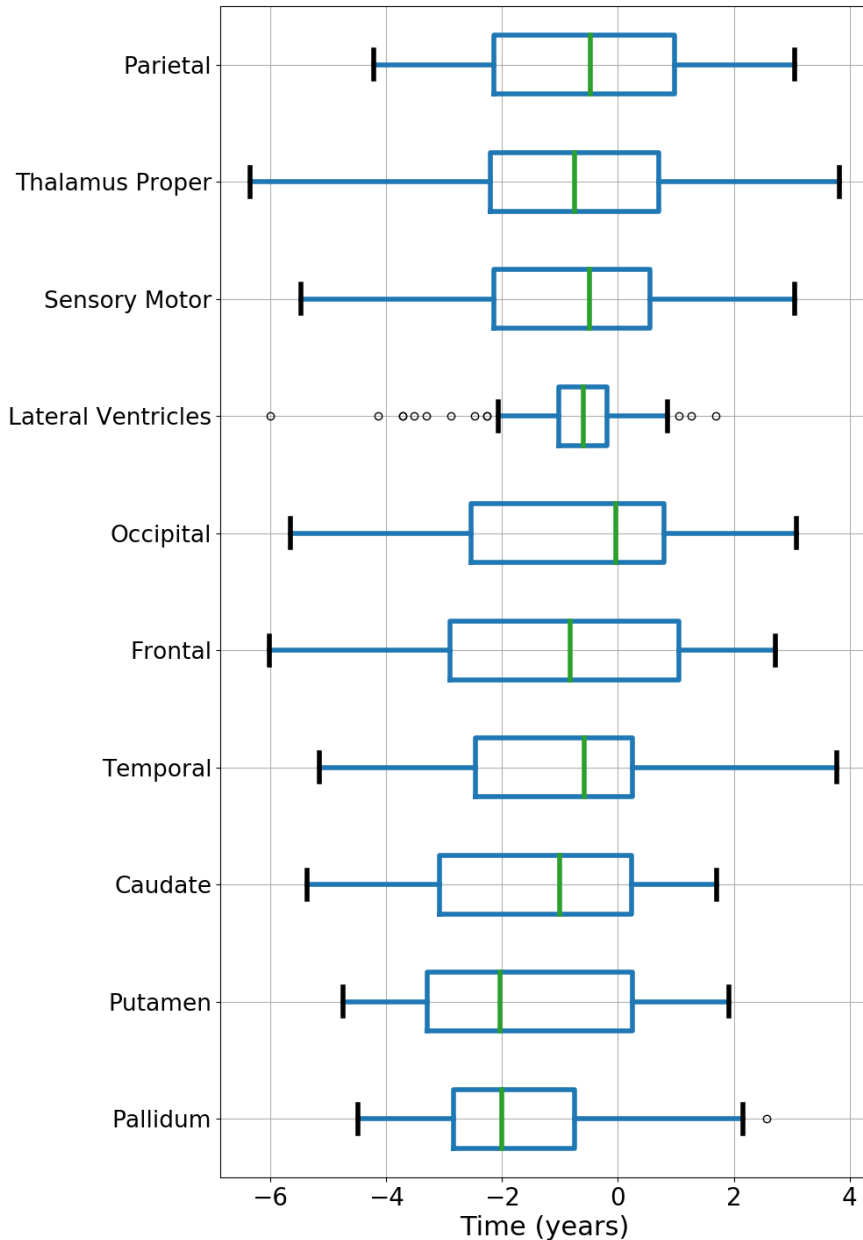
- TRACK-HD and PREDICT-HD are longitudinal multi-centre cohort studies of Huntington's disease
- T1-weighted 3T sMRI scans from 3 time-points were longitudinally registered using SPM12
- Regional volumes were segmented and parcellated using the GIF segmentation tool*
- Regional volumes were adjusted for covariates (age, sex, site, total intracranial volume)
- CAG data used for evaluation, not training



- Predicted volumetric changes in 6 key anatomical regions
- Mostly sigmoidal, but pronounced non-linearity in lateral ventricles
- Absolute magnitude ranging from 7-22% over ~11 years



- Predicted volumetric changes in 10 key sub-cortical and cortical regions
- Larger and mostly non-linear change in sub-cortex (except thalamus)
- Smaller and mostly linear change in cortex (except sensory motor)



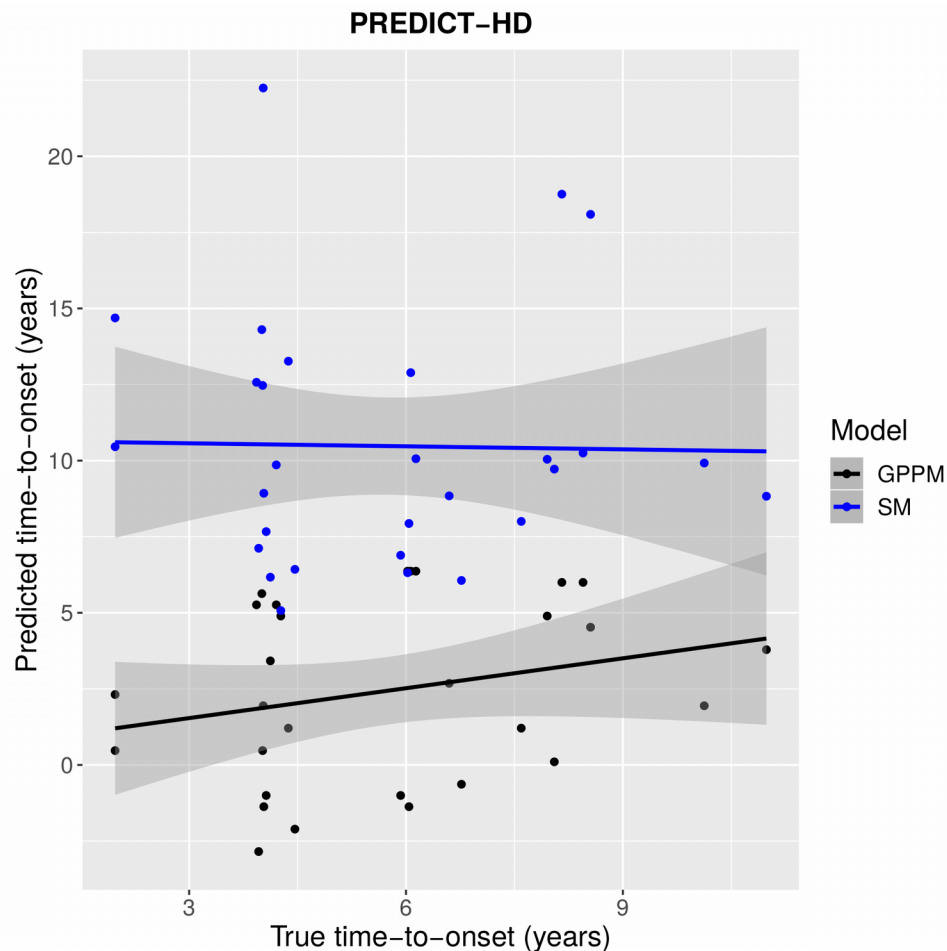
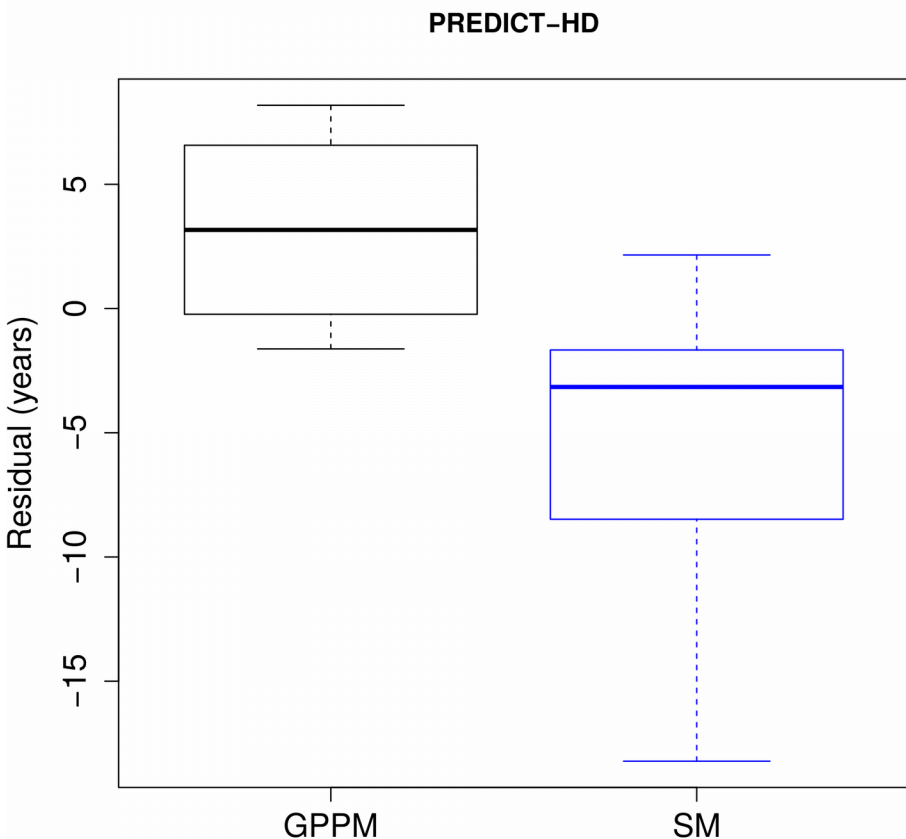
- Time at maximum gradient
→ time at transition from pre-manifest to manifest HD

- Estimate maximum change time from 1000 samples from posterior for each region

- Model predicts earliest changes in basal ganglia (pallidum, putamen, caudate)

- Also predicted by completely separate methodology using cross-sectional data*

- Followed by changes across the cortex over period of ~2 years

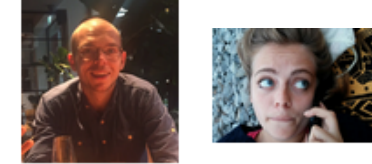


- Compare accuracy of predicted time-to-onset with benchmark survival model (SM) based on age and CAG*
- GPPM provides a smaller uncertainty and tracks disease progression better than the SM

- The Gaussian Process Progression Model (GPPM) can be used to infer longitudinal changes in regional imaging volumes
- Provides clinically meaningful information:
 - Biomarker temporal progression (group-level)
 - Staging (individual-level)
 - Biomarker temporal ordering
- GPPM predictions also outperforms the benchmark survival model in HD
 - **Disease progression modelling can improve sMRI as a biomarker**
- Can easily used to model to include any types of dynamic marker – different imaging modalities (e.g. DWI, PET), biofluids, clinical markers...
- Online GPPM interface available here: <https://epione-demo.inria.fr/>

Thanks for listening – get in touch!

pond



And all the participants of the Huntington's disease studies used here.

