

Mixed effect models for the spatio-temporal analysis of manifold valued data: application to Alzheimer's disease screening

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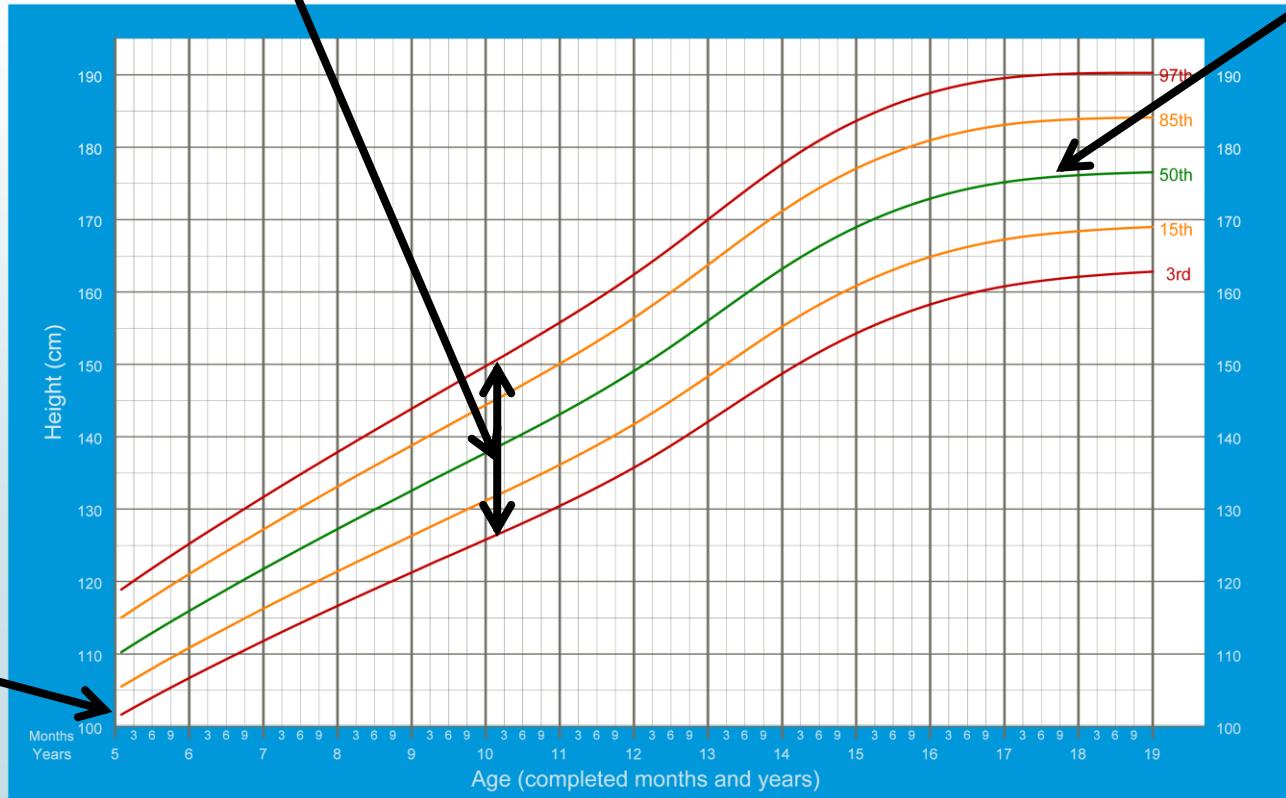


Have you ever seen these curves?

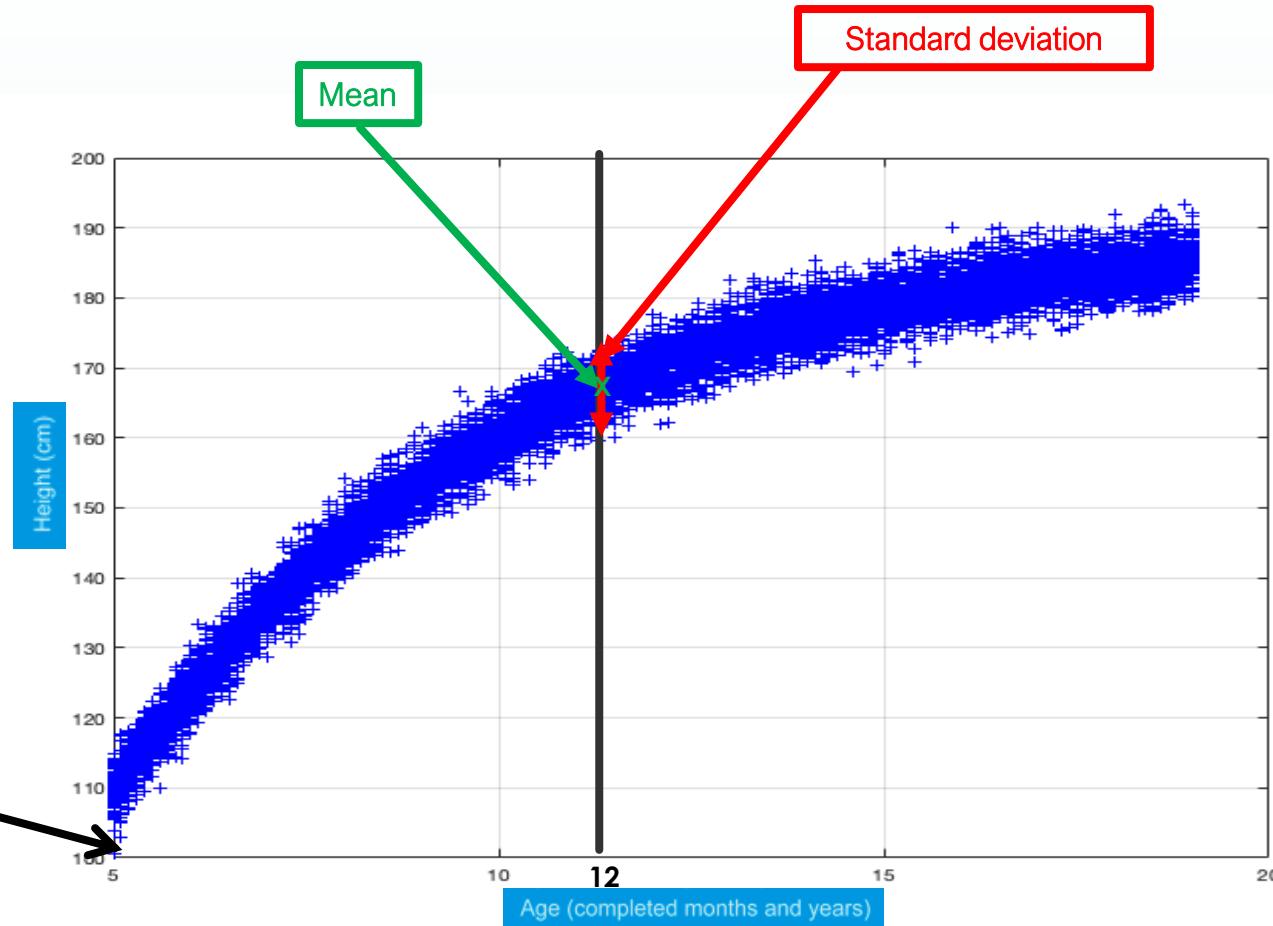
Mean growth evolution

Variability in height

Reference
timepoint



In real life:



And even more:

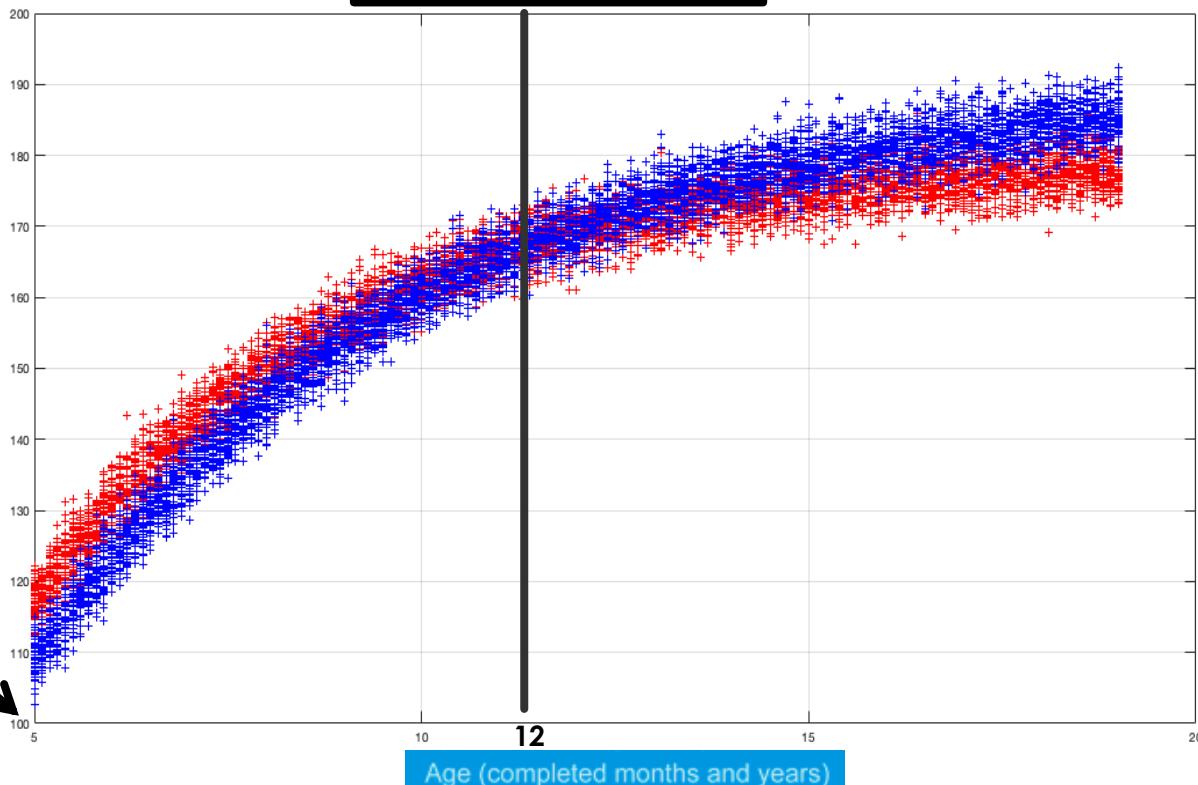
Mean

Standard deviation

Not that well defined

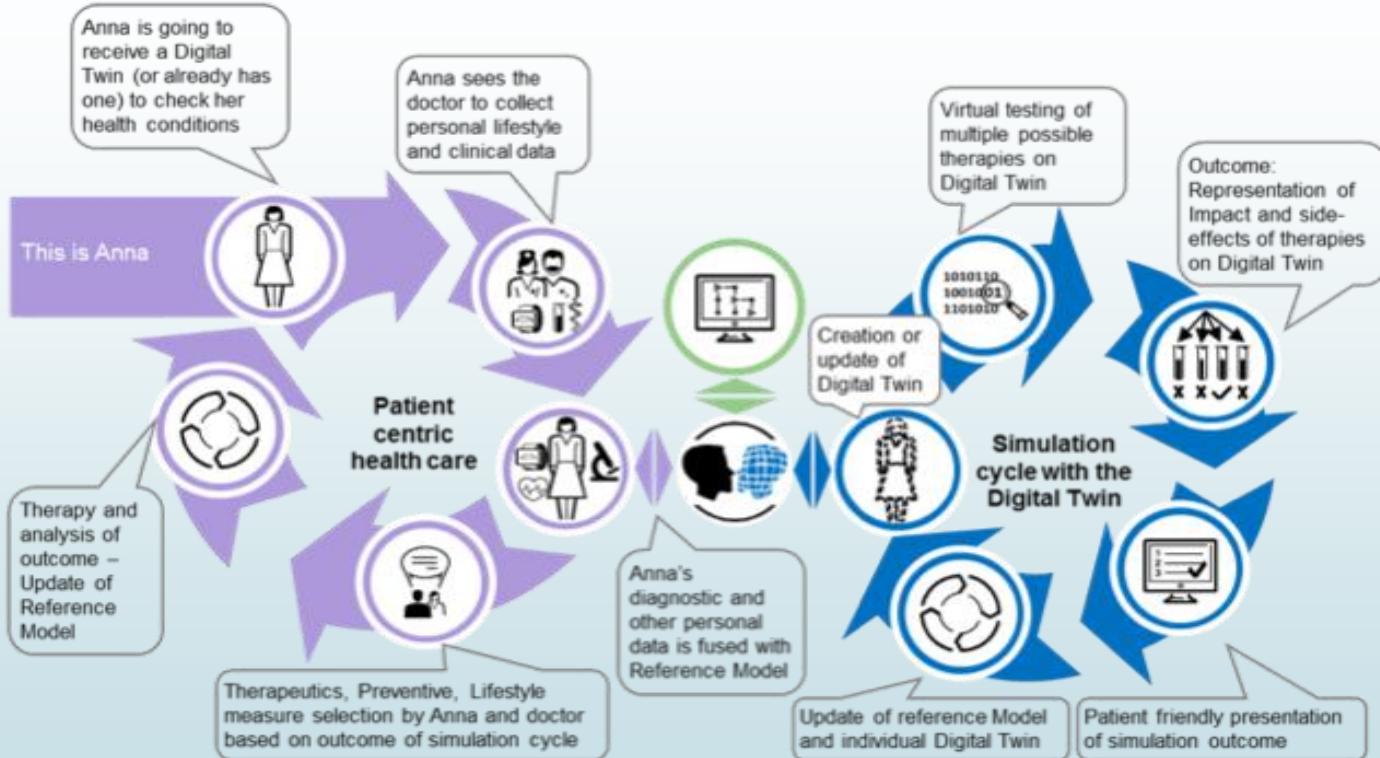
Height (cm)

Reference
timepoint



Le jumeau numérique

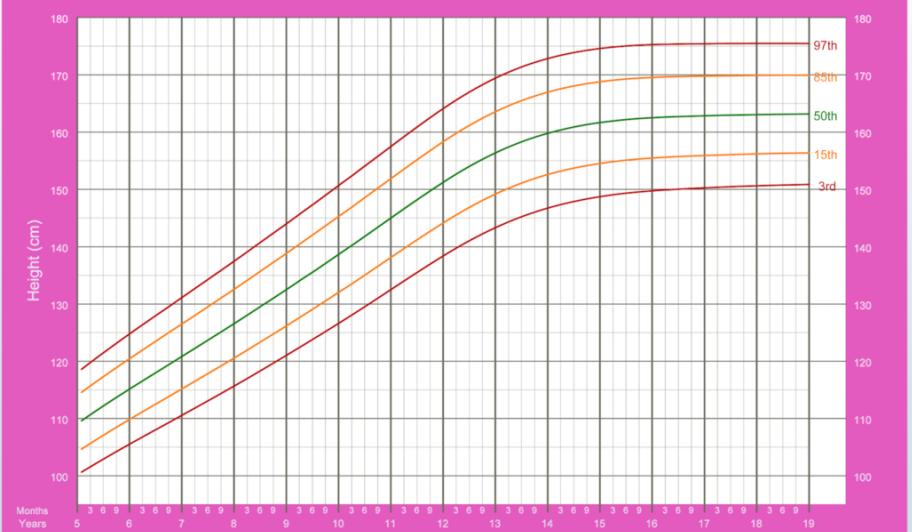
LE JUMEAU NUMÉRIQUE :



Existence of clusters:

Height-for-age GIRLS

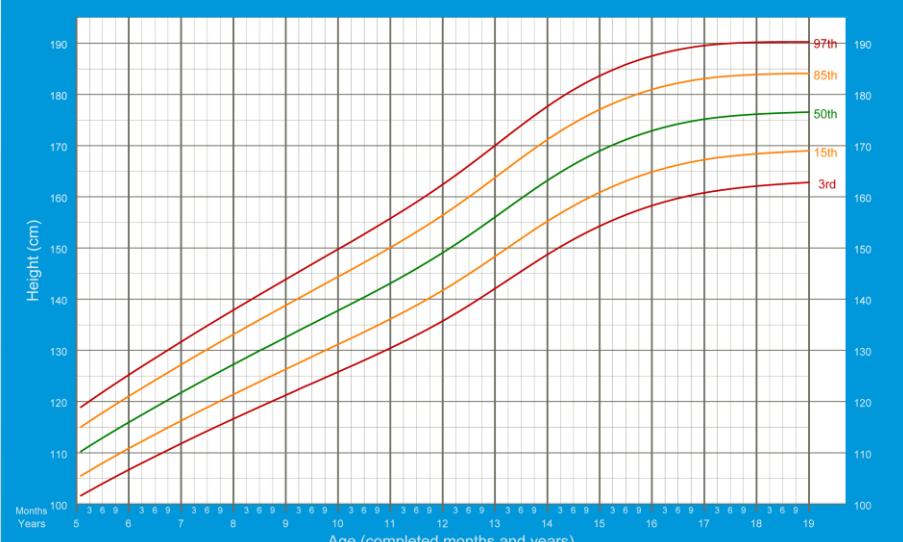
5 to 19 years (percentiles)



2007 WHO Reference

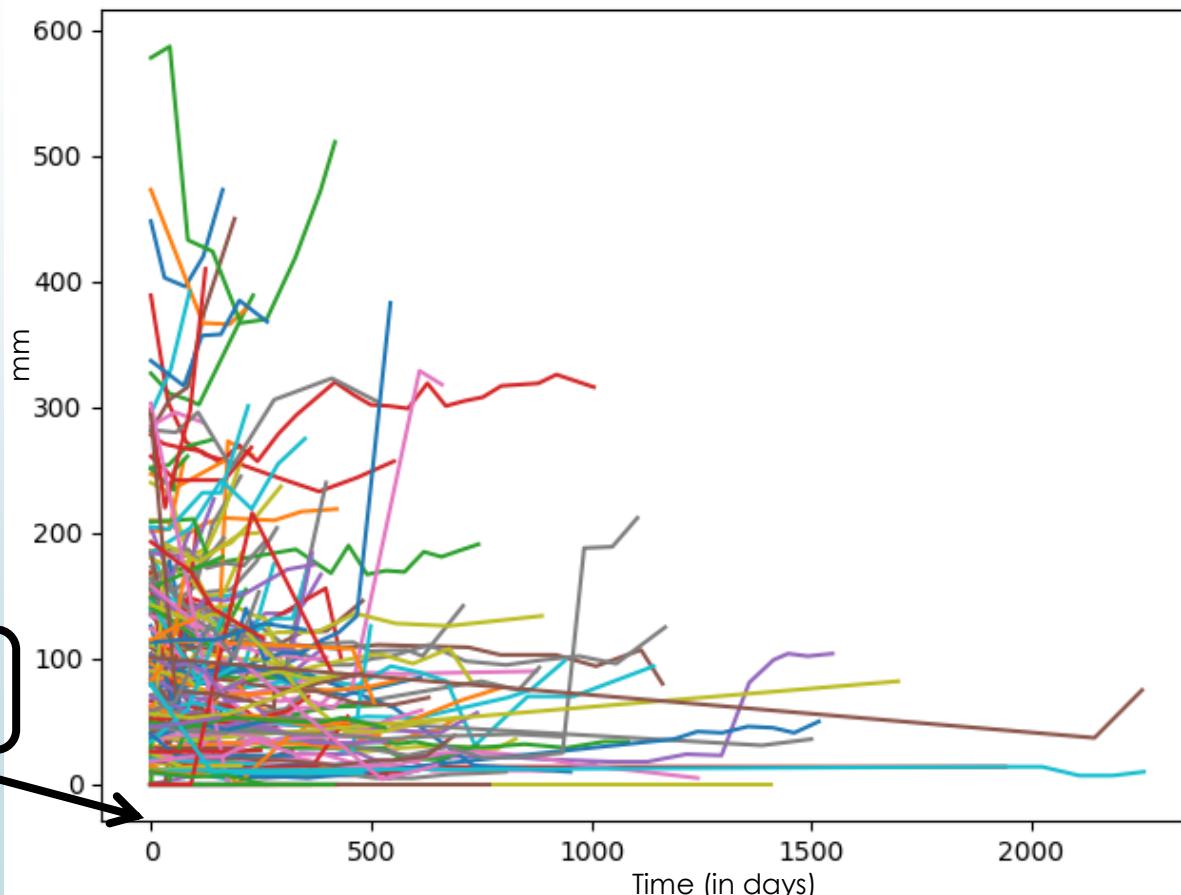
Height-for-age BOYS

5 to 19 years (percentiles)

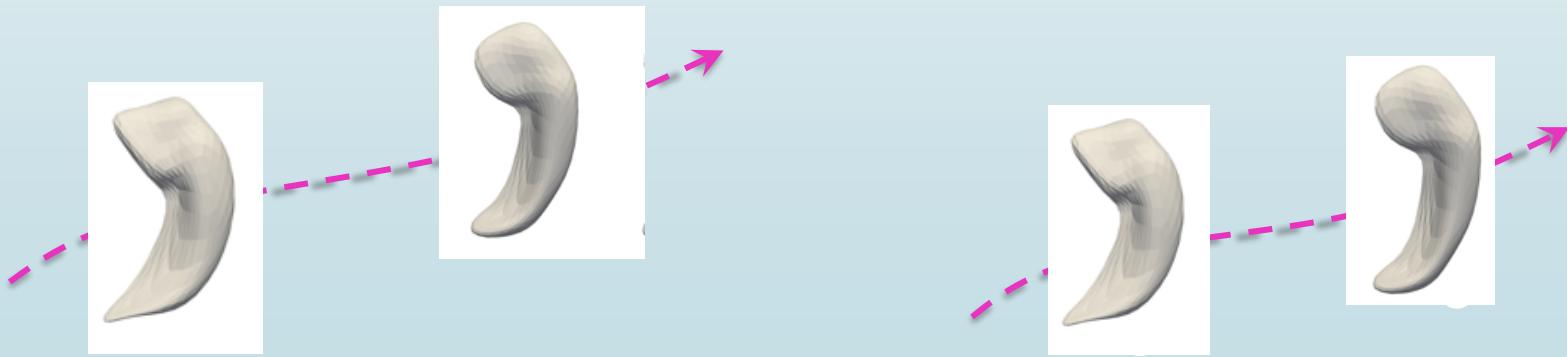
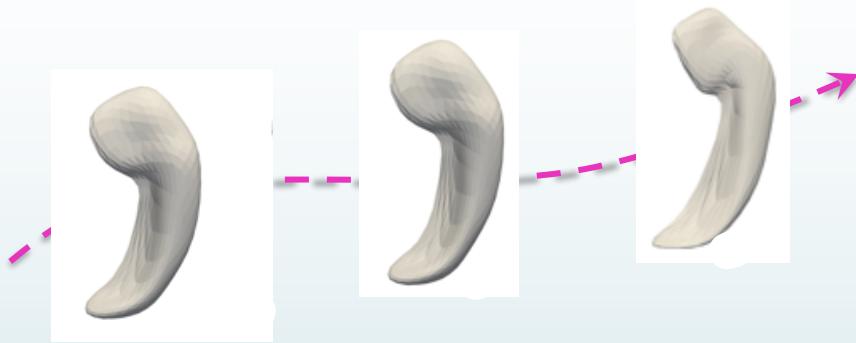


2007 WHO Reference

Now, imagine that the data look more like this:



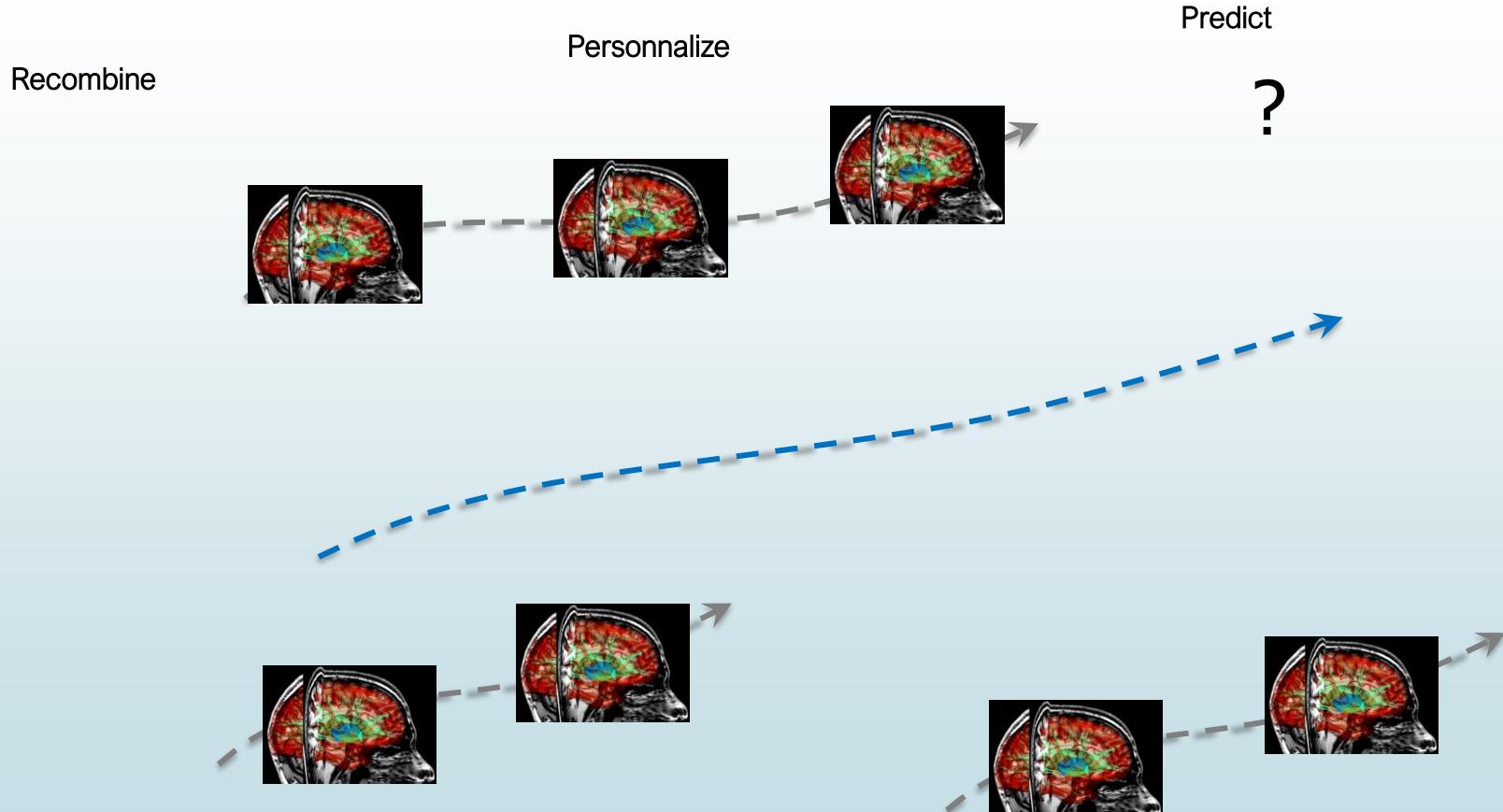
Or this:



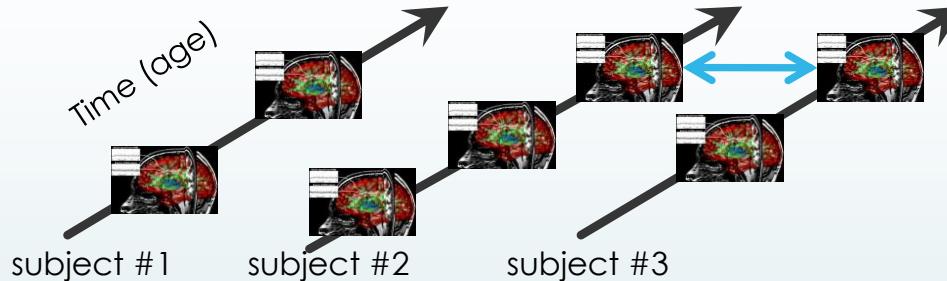
Or even this:



What is now an « average » evolution?



Longitudinal Data Analysis



How to learn representative trajectories of data changes from longitudinal data?

Temporal marker of progression
(e.g. time since drug injection, seeding, birth, etc..)

No temporal marker of progression
(e.g. in aging, neurodegenerative diseases, etc..)

Regression
(e.g. compare measurements at same time-point)

Learning **spatiotemporal distribution** of trajectories

- Find temporal correspondences
- Compare data at corresponding stages of progression

Linear mixed-effects models
[Laird et al., 2000; Agresti et al.,
Fitzmaurice et al.]

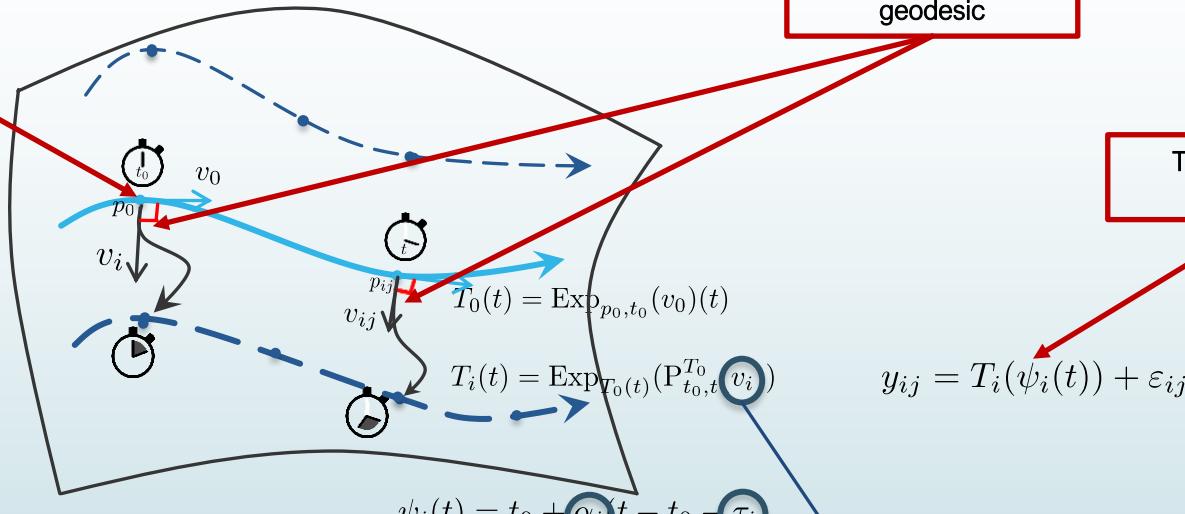
Needs to disentangle differences in:
manifold-valued data
(normalized data, positive matrices, shapes, etc.;)
Dynamics of measurement changes

Spatiotemporal mixed effect model

Orthogonality ensures unique space/time decomposition

Invariance w.r.t. reference point on geodesic

Time is random variable



Random effects:

Acceleration factor

$$\alpha_i \sim \log \mathcal{N}(0, \sigma_\alpha^2)$$

Fixed effects:

$$(p_0, t_0, v_0)$$

Time-shift

$$\tau_i \sim \mathcal{N}(0, \sigma_\tau^2)$$

Space-shift

$$v_i = (A_1 | \dots | A_K) s_i$$

$$A_k \perp v_0$$

Spatiotemporal Statistical Model

$$\left. \begin{array}{ll} y_{ij} = T_i(\psi_i(t)) + \varepsilon_{ij} & \text{Submanifold value observations} \\ T_i(t) = \text{Exp}_{T_0(t)}(\text{P}_{t_0,t}^{T_0}(v_i)) & \text{Parallel curve} \\ T_0(t) = \text{Exp}_{p_0,t_0}(v_0)(t) & \text{Representative trajectory} \\ \psi_i(t) = t_0 + \alpha_i(t - t_0 - \tau_i) & \text{Linear time reparametrization} \\ \alpha_i \sim \log \mathcal{N}(0, \sigma_\alpha^2) \\ \tau_i \sim \mathcal{N}(0, \sigma_\tau^2) \\ v_i = (A_1 | \dots | A_K) s_i \\ A_k \perp v_0 \end{array} \right\} \quad \begin{array}{l} \textbf{Hidden random variables:} \\ \text{Acceleration factor} \\ \text{Time shift} \\ \text{Space shift} \end{array}$$

$$\left. \begin{array}{l} (p_0, t_0, v_0) \\ (\sigma_\alpha^2, \sigma_\tau^2, A_1, \dots, A_K) \end{array} \right\} \quad \begin{array}{l} \textbf{Parameters:} \\ \text{Mean trajectory parametrization} \\ \text{and prior parameter} \end{array}$$

Parameter Estimation: EM algorithm

$$y = (y_1, \dots, y_N), \quad z = (z_1, \dots, z_N), \quad \theta = (\sigma_z^2, \sigma_\varepsilon^2, A_1, \dots, A_K, p_0, t_0, v_0)$$

- Maximum Likelihood: $\max_{\theta} p(y|\theta) = \int p(y, z|\theta) dz$
- EM: $\theta_{k+1} = \operatorname{argmax}_{\theta} \sum_{i=1}^N \int \log \left(\underbrace{p(y_i, z_i|\theta)}_{p(y_i|z_i, \theta)p(z_i|\theta)} \right) p(z_i|y_i, \theta_k) dz_i$
- Distribution from the curved exponential family

$$\log p(y_i, z_i|\theta) = \phi(\theta)^T \color{red} S(y_i, z_i) - \log(C(\theta))$$

$$\theta_{k+1} = \operatorname{argmax}_{\theta} \left\{ \phi(\theta)^T \sum_{i=1}^N \int S(y_i, z_i) p(z_i|y_i, \theta_k) dz_i - N \log(C(\theta)) \right\}$$

Parameter Estimation: stochastic algorithm

- SA-EM: replaces integration by **one simulation of the hidden variable**:

sample $z_{i,k+1}$ from $p(z_i|y_i, \theta_k)$,

and a **stochastic approximation** of the sufficient statistics

$$\bar{S}_{k+1} = (1 - \Delta_k) \bar{S}_k + \Delta_k \left(\frac{1}{N} \sum_{i=1}^N S(y_i, z_{i,k+1}) \right)$$

Maximization step (unchanged) $\theta_{k+1} = \operatorname{argmax}_{\theta} \{ \phi(\theta)^T \bar{S}_{k+1} - \log(C(\theta)) \}$

- MCMC-SAEM: replaces sampling by a **single Markov Chain** step

• For each subject, sample the random effect w.r.t a transition kernel of a geometrically ergodic Markov chain targeting the conditional distribution $q(z_i|y_i, \theta_k)$

Parameter Estimation: stochastic algorithm

To escape from local maxima
With tempered distributions

- SA-EM: replaces integration by one simulation of the hidden variable:

sample $z_{i,k+1}$ from $p(z_i|y_i, \theta_k)$,

and a stochastic approximation of the sufficient statistics

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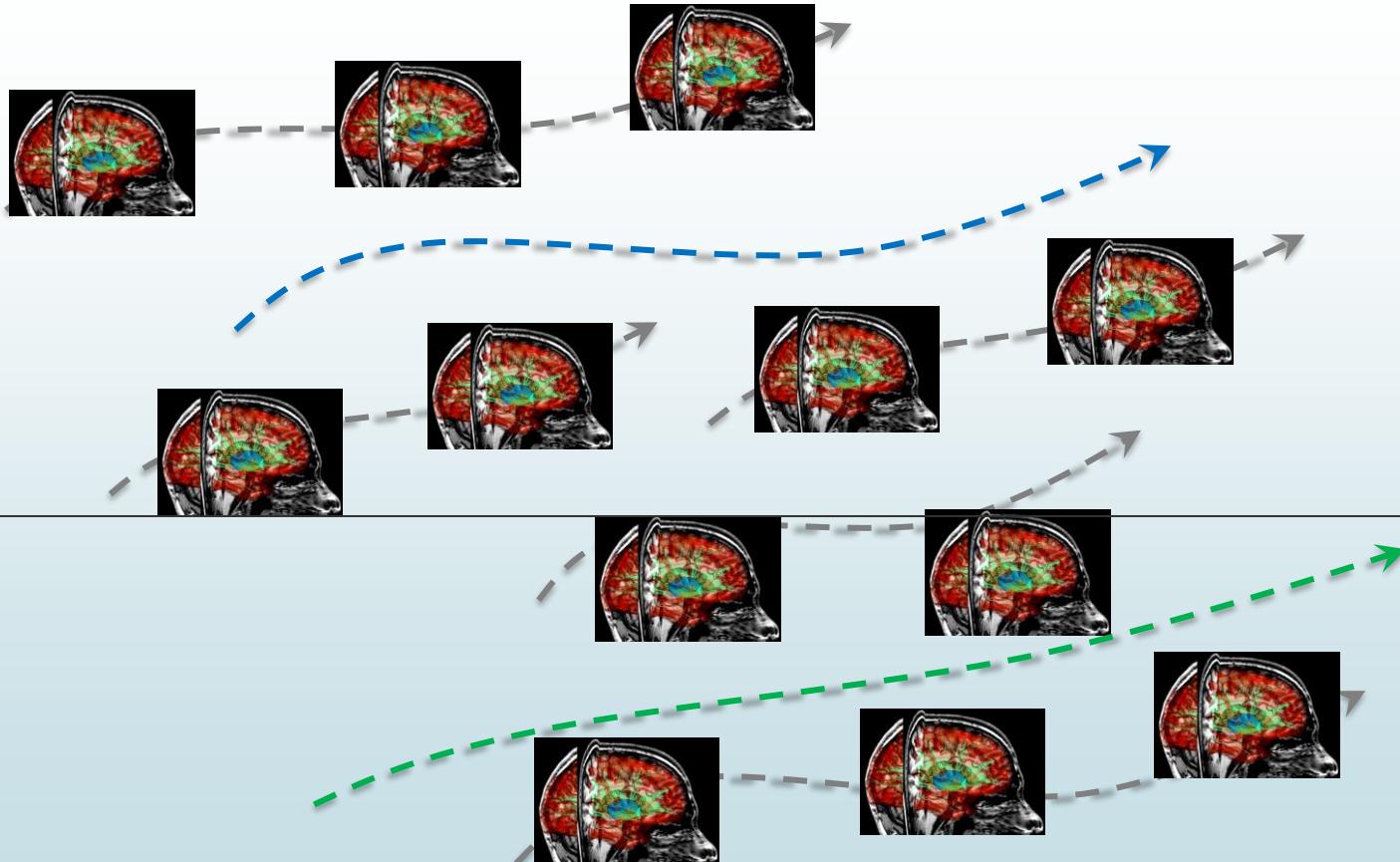
Maximization step (unchanged) $\theta_{k+1} = \operatorname{argmax}_{\theta} \{ \phi(\theta)^T \bar{S}_{k+1} - \log(C(\theta)) \}$

- MCMC-SAEM: replaces sampling by a single Markov Chain step

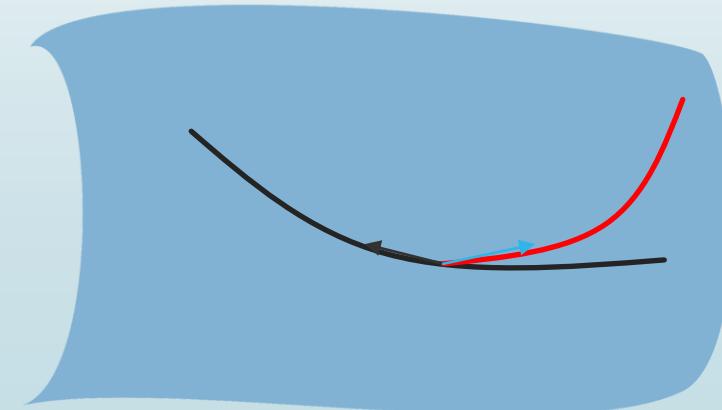
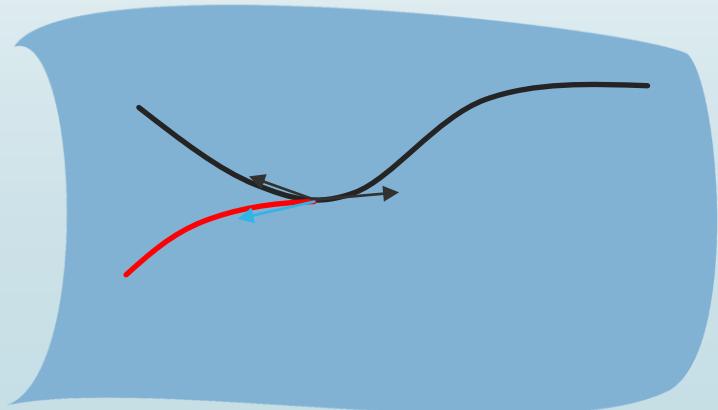
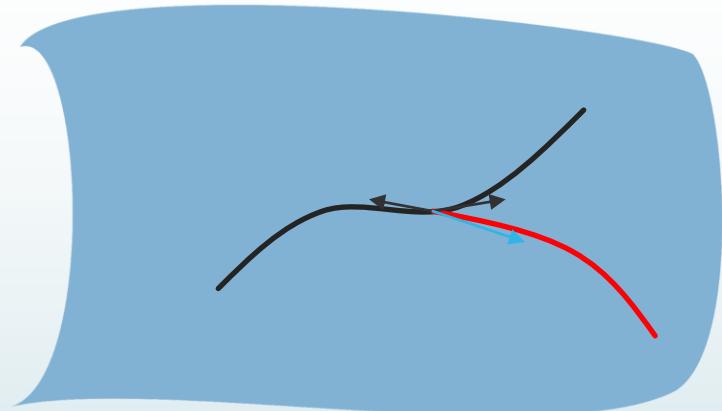
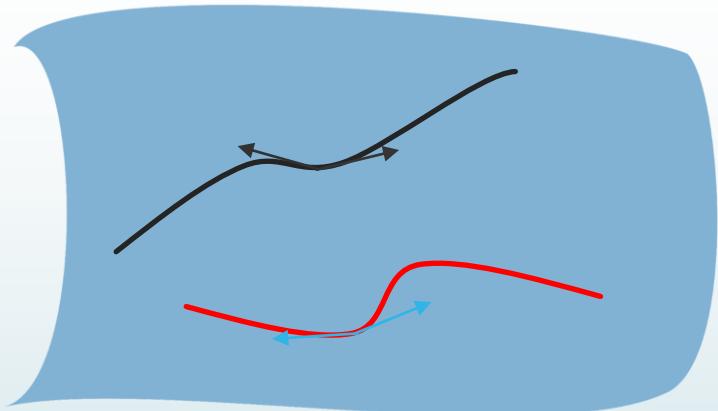
• For each subject, sample the random effect w.r.t a transition kernel of a geometrically ergodic Markov chain targeting the conditional distribution $\tilde{q}_k(z_i, \theta_k)$

• As long as \tilde{q}_k “converges towards” $q(z_i|y_i, \theta_k)$ as $k \rightarrow \infty$

When facing heterogeneous populations:



Including many possible variations in the population:





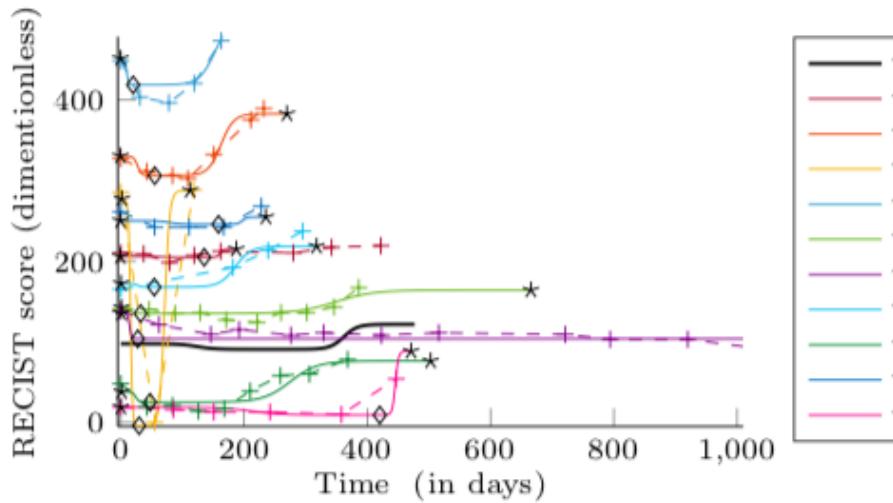
- Model implemented using deformetrica.
- Soon to be released as a part of this software.

<https://www.deformetrica.org/>

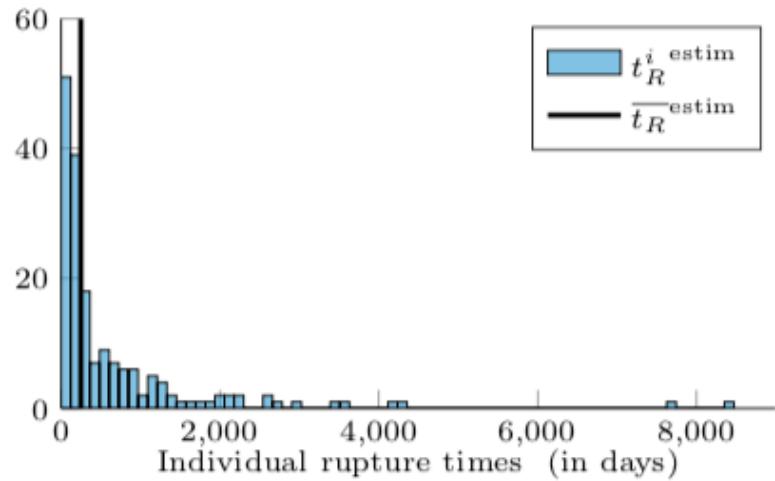


- <https://gitlab.com/icm-institute/aramislab/leaspy>

Model of Antiangiogenic response



(a) After 600 iterations.

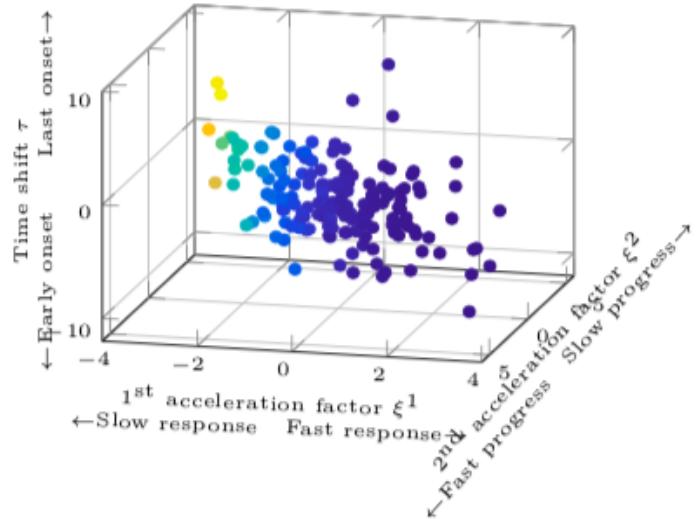


(b) Individual rupture times t_R^i (in days).

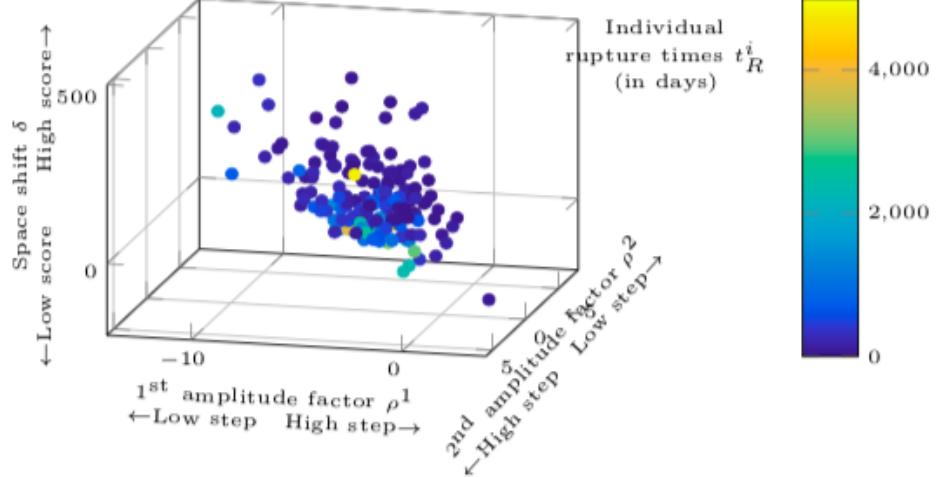
Fig. a. RECIST score for 10 patients among the 176.

Fig. b. Histogram of the estimated rupture times.

Model of Antiangiogenic response



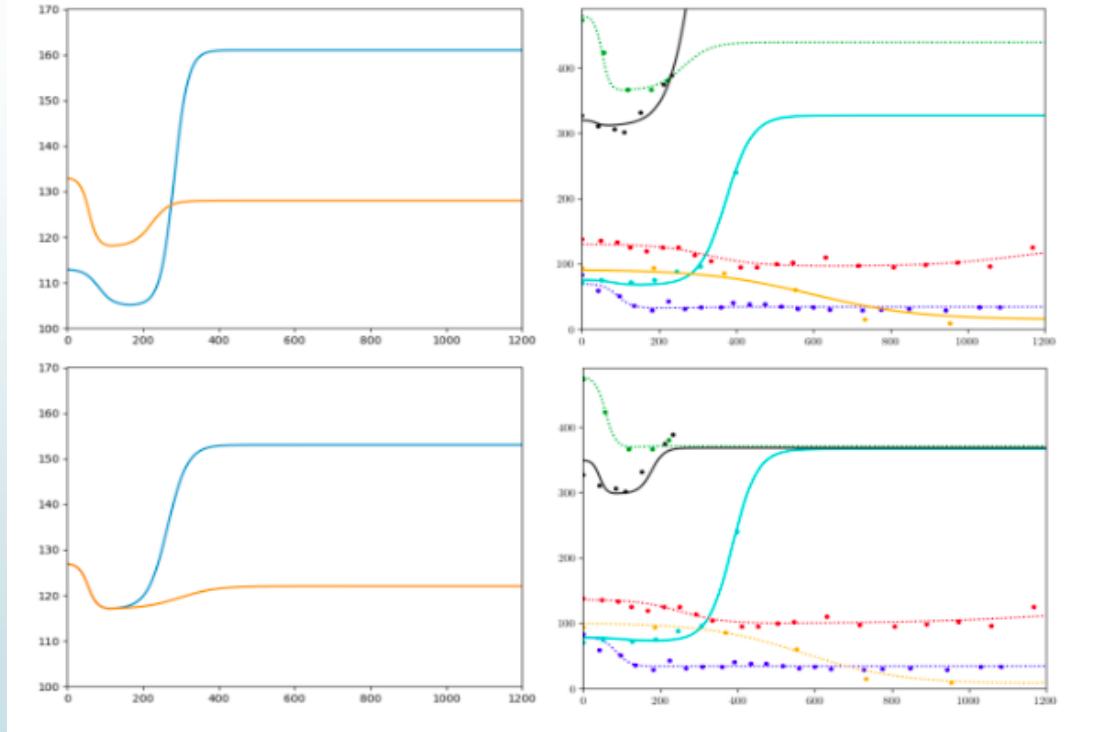
(a) The time warp.



(b) The space warp.

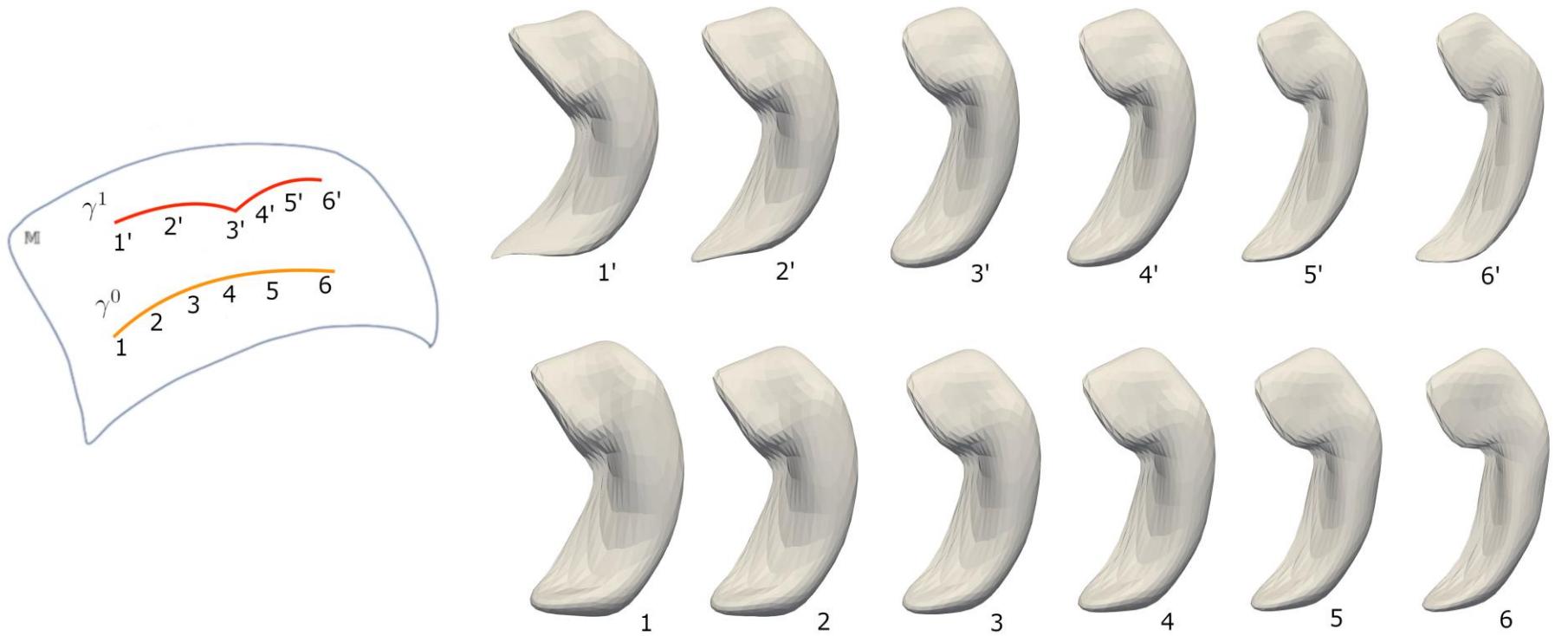
Fig. 5. Individual random effects. Fig. 5a: log-acceleration factors ξ_i^1 and ξ_i^2 against times shifts τ_i . Fig. 5b: log-amplitude factors ρ_i^1 and ρ_i^2 against space shifts δ_i . In both figure, the colour corresponds to the individual rupture time t_R^i . These estimates hold for the same run as Fig. 4.

Model of Antiangiogenic response considering the heterogeneity of the population

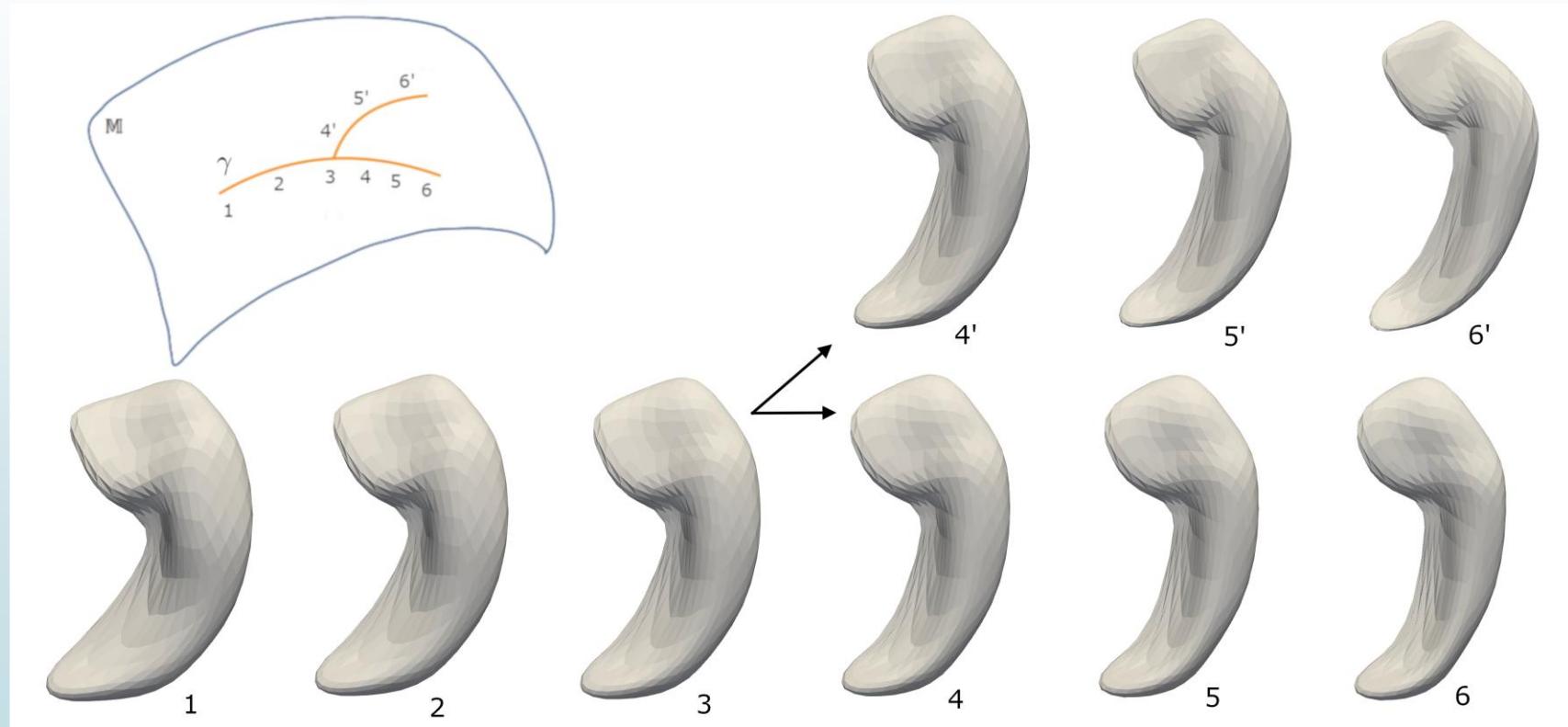


Top: two different clusters. Bottom: two clusters whose first dynamic is shared. Left: Estimated templates. Right: 6 subjects and their reconstructed trajectories. In dotted lines, subjects in the cluster of the orange template. In plain lines subjects in the cluster of the blue template

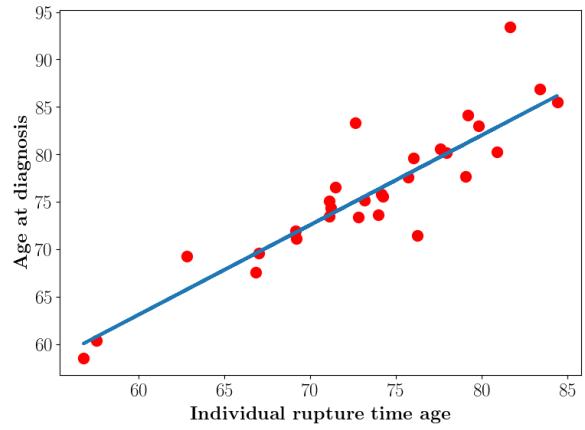
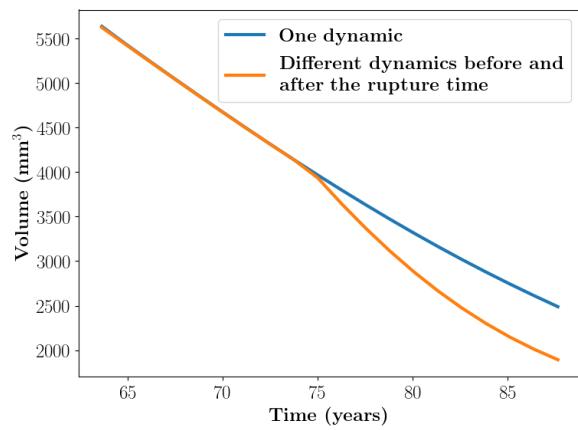
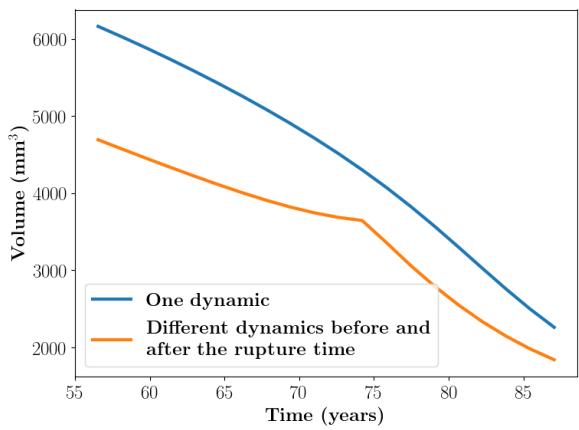
Model of Alzheimer's disease conversion in heterogeneity of the population



Model of Alzheimer's disease conversion in heterogeneity of the population



Comparisons of these models of Alzheimer's disease conversion



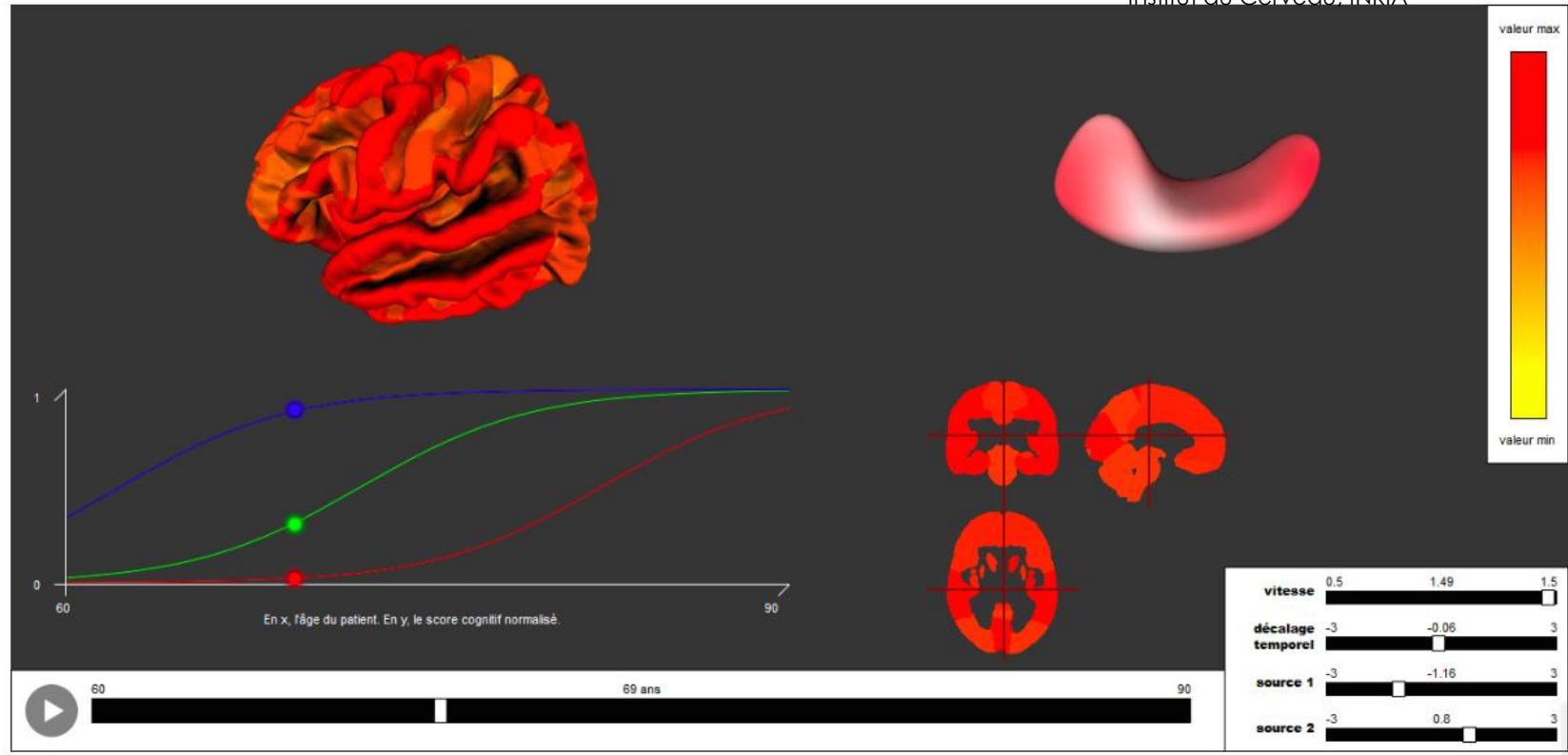
Un exemple concret :

La clinique du docteur memo : The experts of
brain aging



ÉVOLUTION DE LA MALADIE D'ALZHEIMER

Collaboration à l'équipe
Aramis, de Stanley
Durrleman,
Institut du Cerveau, INRIA



AUTOMATIC PROGNOSIS SYSTEM (PATENTED)

Parametres

alpha : 1.00

tau: 0.00

s1: 0.00

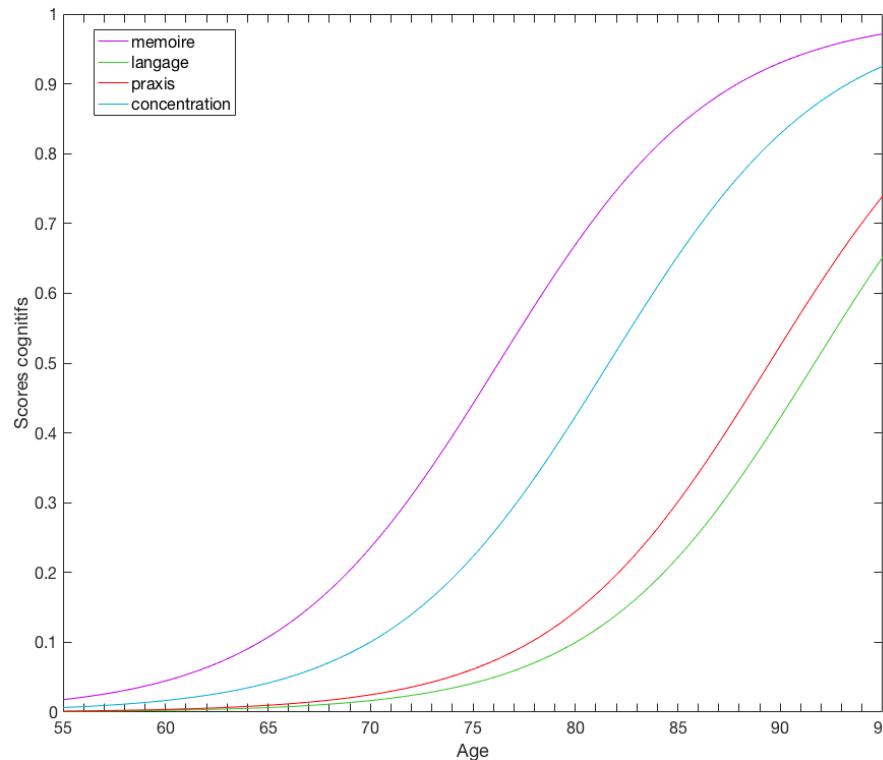
s2: 0.00

Sujet

Numero sujet

Nombre de visites

Reset



AUTOMATIC PROGNOSIS SYSTEM (PATENTED)

Parametres

alpha :0.93

tau:3.51

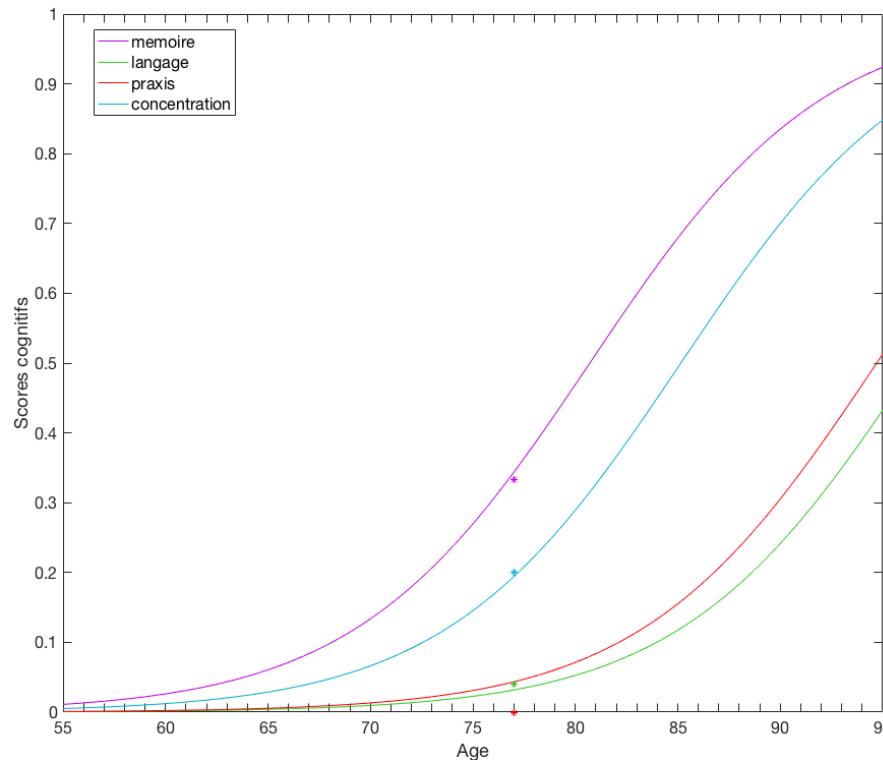
s1:-0.41

s2:0.49

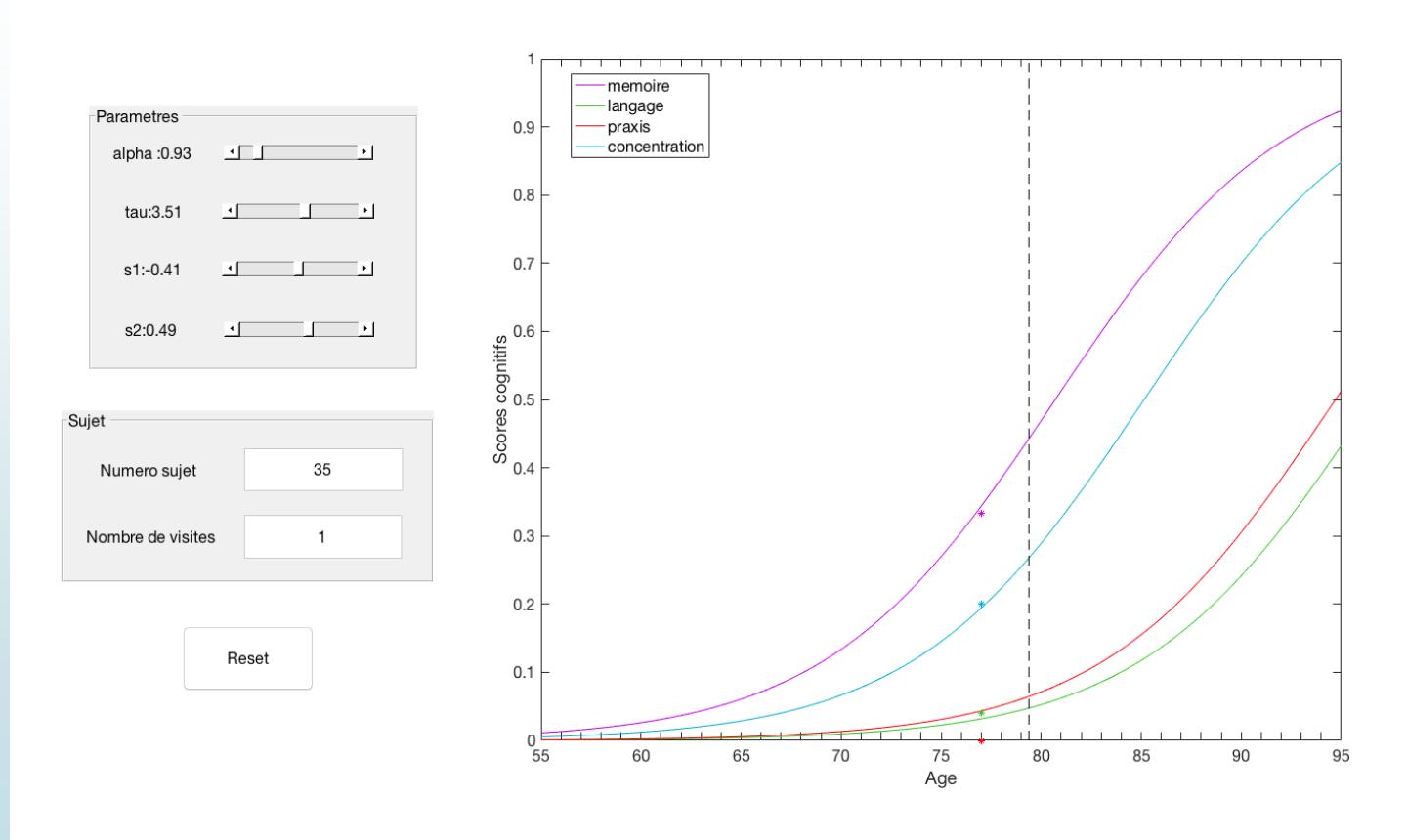
Sujet

Numero sujet

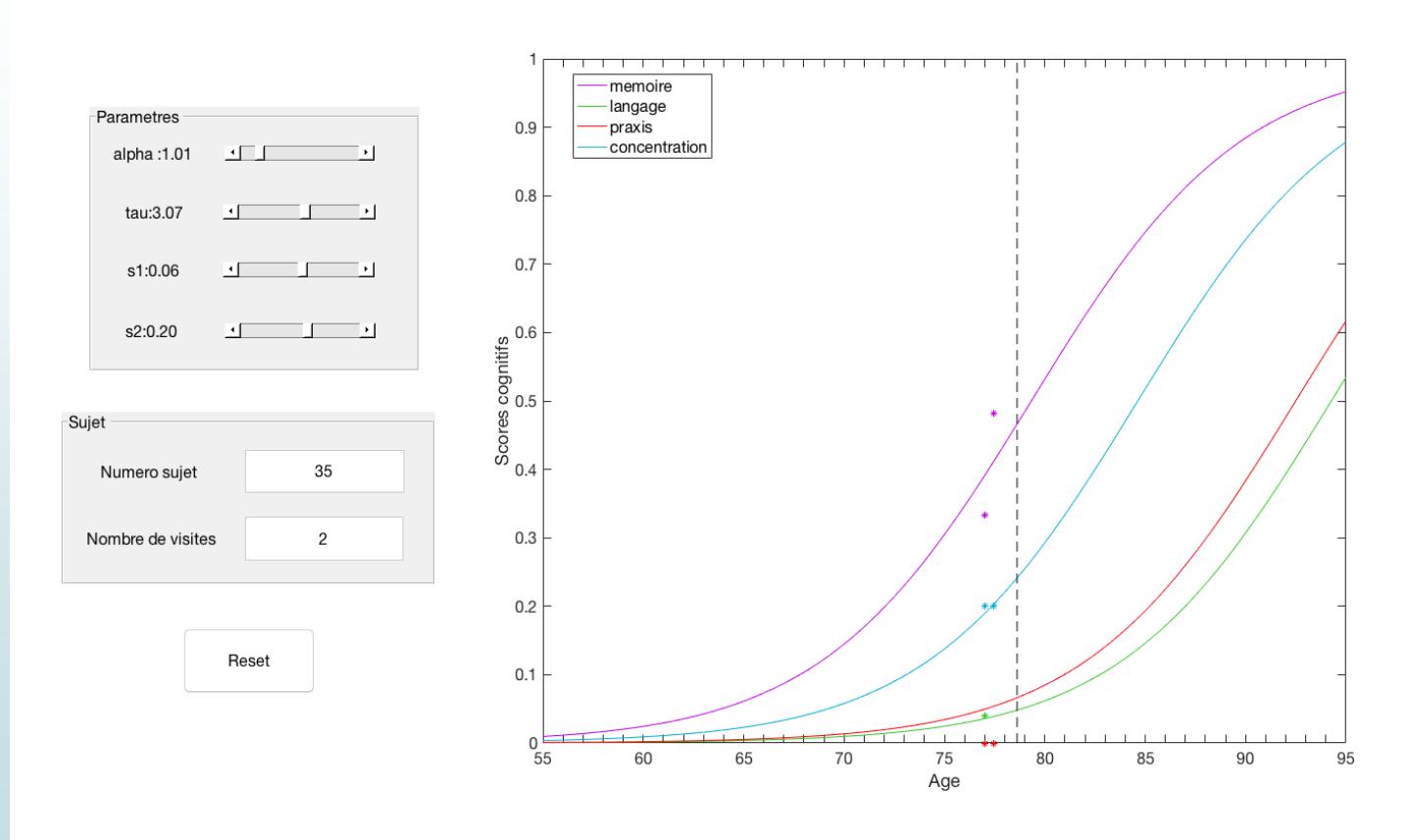
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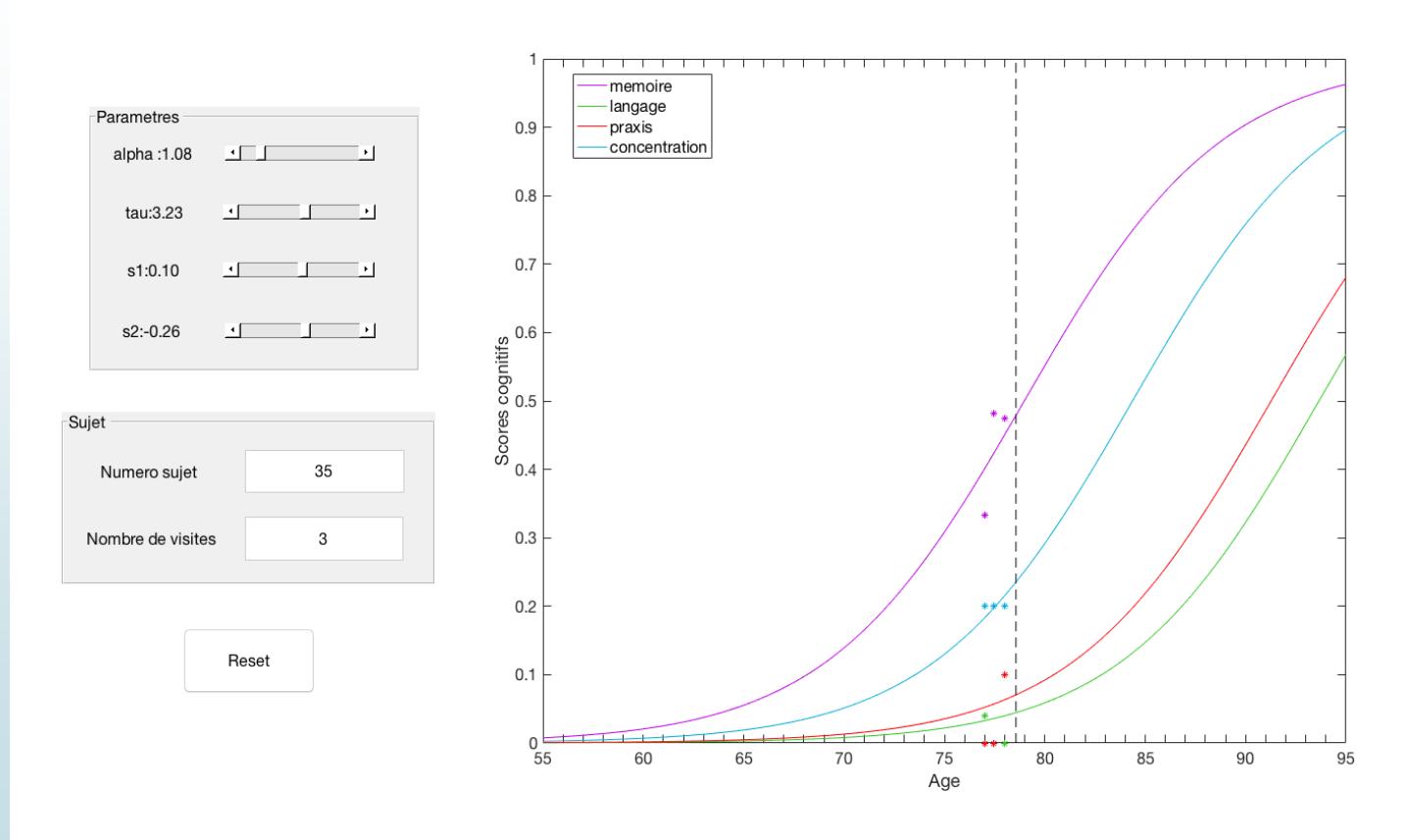
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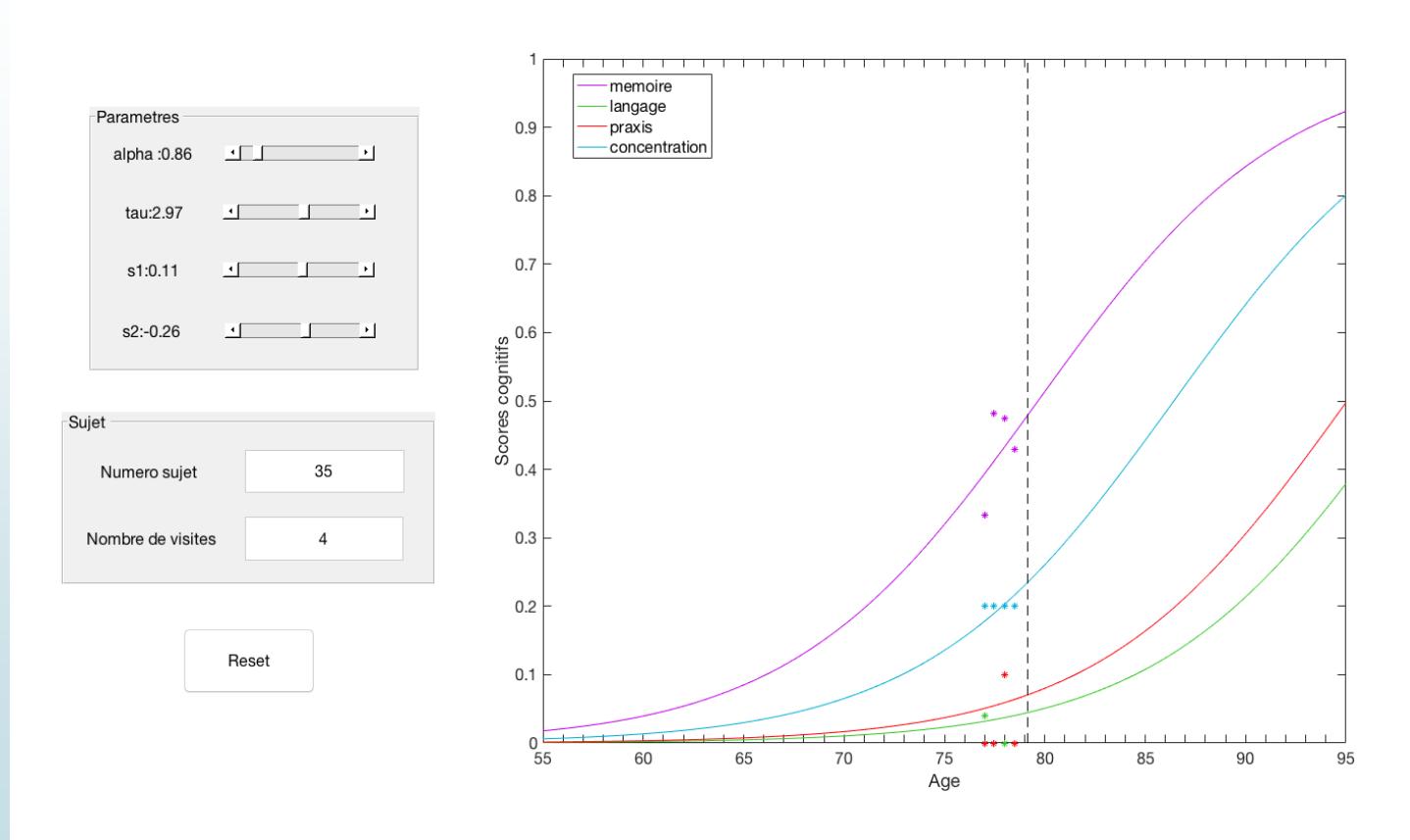
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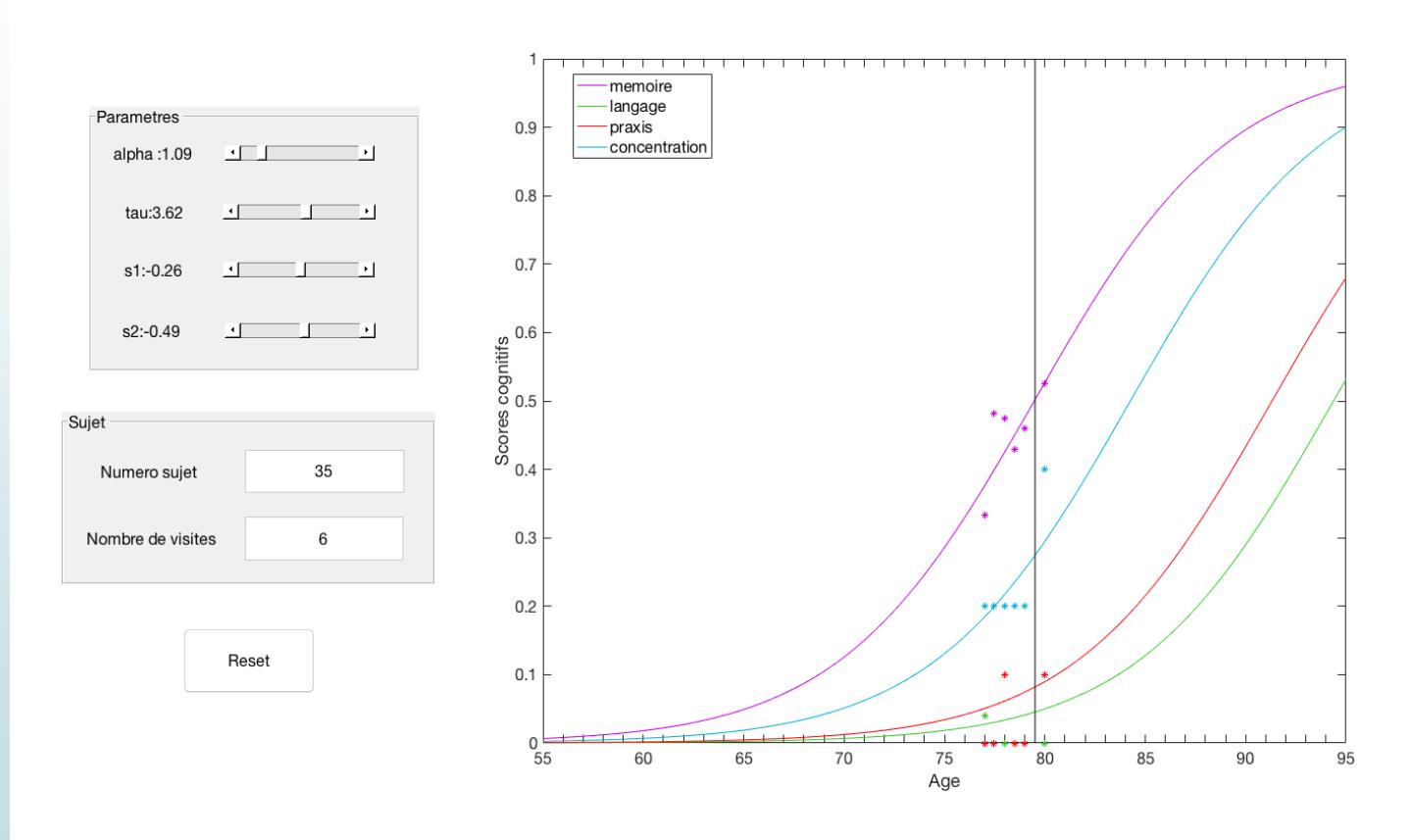
AUTOMATIC PROGNOSIS SYSTEM (PATENTED)



AUTOMATIC PROGNOSIS SYSTEM (PATENTED)



AUTOMATIC PROGNOSIS SYSTEM (PATENTED)



Thank you!

