



# Mixed effect model for the spatiotemporal analysis of longitudinal manifold value data

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# Computational Anatomy

- Represent and analyse **geometrical** elements upon which **deformations** can **act**
- Describe the observed objects as **geometrical variations** of one or several representative elements
- **Quantify** this variability inside a population

## Deformable template model from Grenander

- How does the deformation act?
- What is a representative element?
- How to quantify the geometrical variability ?

# Computational Anatomy

## Important issues in atlas estimation:

- Register any new data in the « coordinates » of the reference shape:
  - Transport the available information from the representative element
  - « Registration » penalised as a function of its « normality »
- Quantify anatomical structure variability in different sub-groups

## Targetted applications:

- Pathology effects
- Classification of new patients
- Early diagnostic

# Computational Anatomy

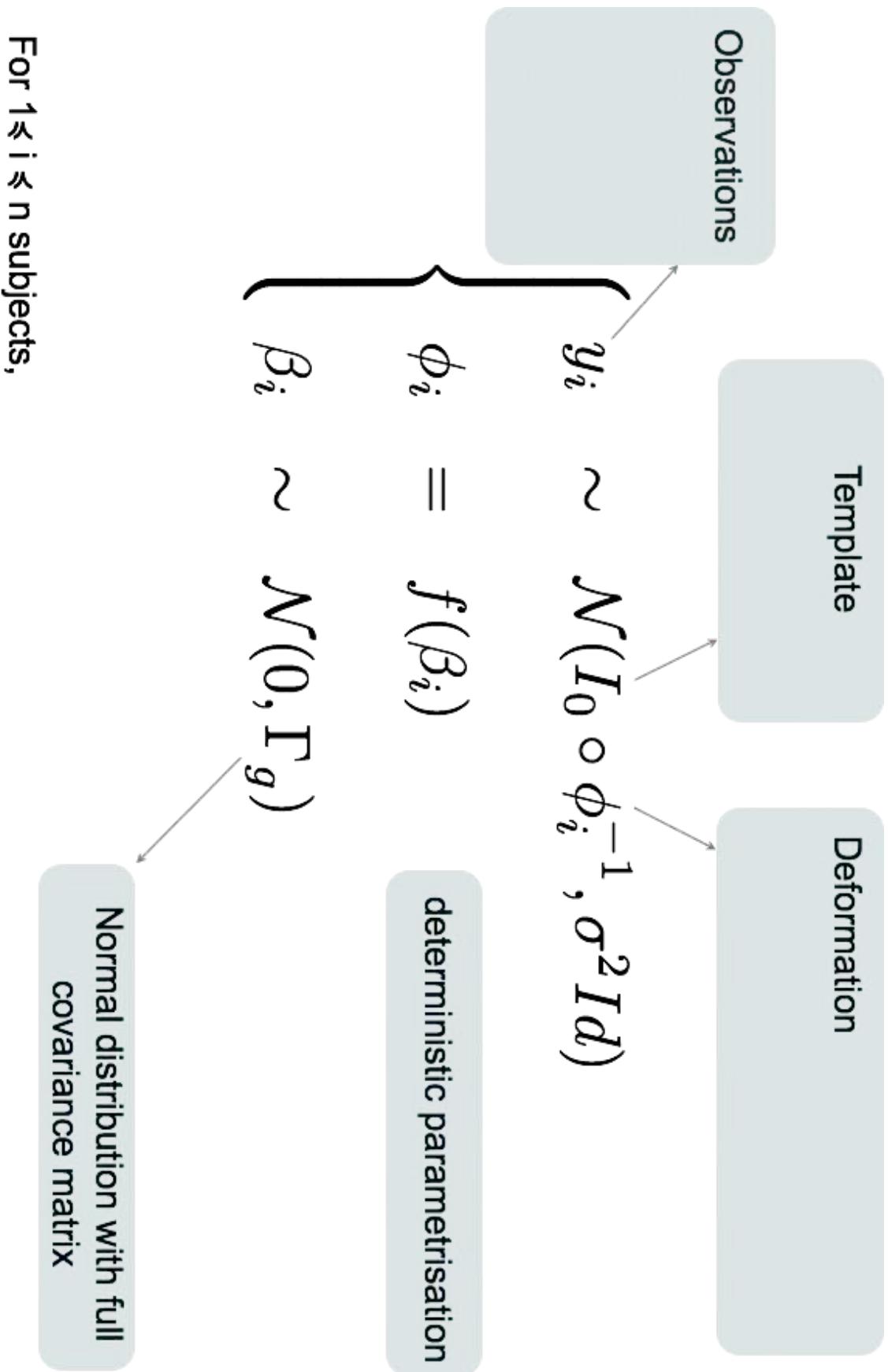
**One solution:**

- Quantify the distance between images using deformations
- Provide a **statistical model** to approximate the generation of the observed population from the atlas
- Propose a **statistical learning algorithm**
- Optimise the numerical estimation

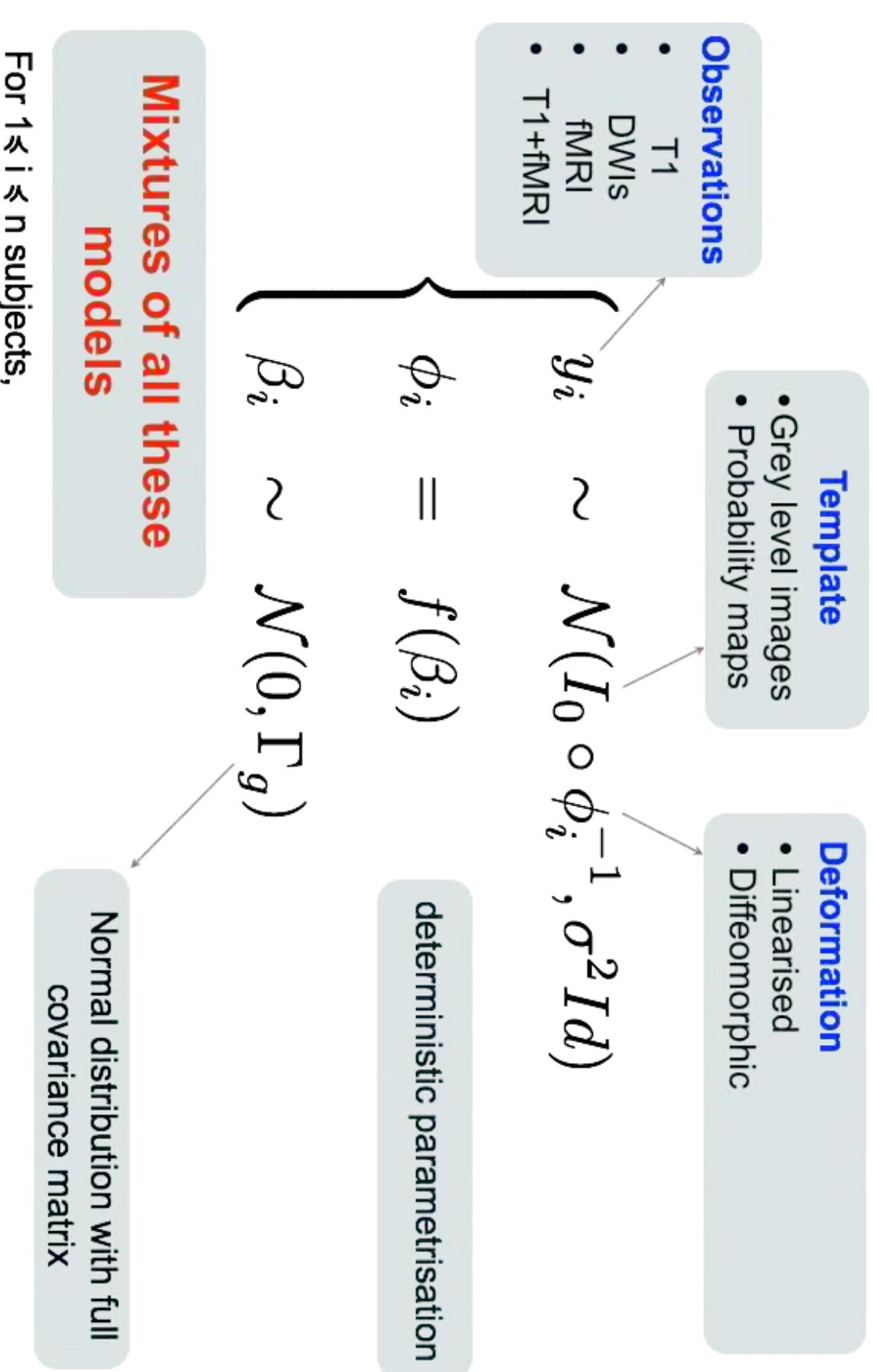
# Bayesian Mixed Effect model

- First model:
  - One observation per subject
  - Image or shape (viewed as currents)
  - Deformations either linearized or diffeomorphic
  - Homogeneous or heterogeneous populations (mixture models)

# Bayesian Mixed Effect model



# Bayesian Mixed Effect model



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- First model:

  - One observation per subject
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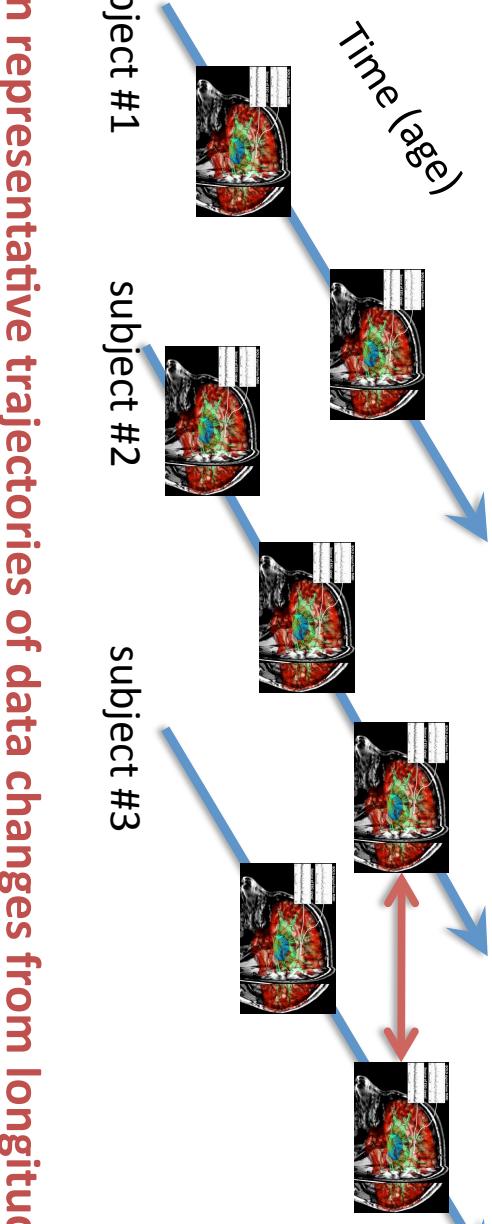
➤ **Limitations**

  - One observation per subject
  - Corresponding acquisition time

# Longitudinal Data Analysis

- Longitudinal model:
  - Several observation per subject
  - Image, shape, etc
  - Atlas = representative trajectory and population variability

# 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..)

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

Linear ~~vector space effects models~~ ~~models~~  
[Laird & Ware '82, Diggle et al.,  
Fitzmaurice et al.]

- Learning spatiotemporal distribution of trajectories**
- No temporal marker of progression**  
(e.g. in aging, neurodegenerative diseases, etc..)
- Find temporal correspondences
  - Compare data at corresponding stages of progression
  - Dynamics of progression/development changes

# Spatiotemporal Statistical Model

- Statistical model inclinding:
  - a **representative trajectory** of data changes
  - **spatiotemporal variations** in:
    - measurement values
    - pace of measurement changes



$$T_0(t) = \text{Exp}_{p_0, t_0}(v_0)(t)$$

$$T_i(t) = \text{Exp}_{T_0(t)}(P_{t_0, t}^{T_0} v_i)$$

$$y_{ij} = T_i(\psi_i(t)) + \varepsilon_{ij}$$

$$\psi_i(t) = t_0 + \alpha_i(t - t_0 - \tau_i)$$

• Orthogonality condition ensures **identifiability** (unique space/time decomposition)

• Time is not a covariate but a random variable

Acceleration factor      Time-shift      Space-shift

$$\begin{aligned} \text{Random effects: } \quad \alpha_i &\sim \log \mathcal{N}(0, \sigma_\alpha^2) & \tau_i &\sim \mathcal{N}(0, \sigma_\tau^2) & v_i &= (A_1 | \dots | A_K) s_i \\ &&&& A_k \perp v_0 & \end{aligned}$$

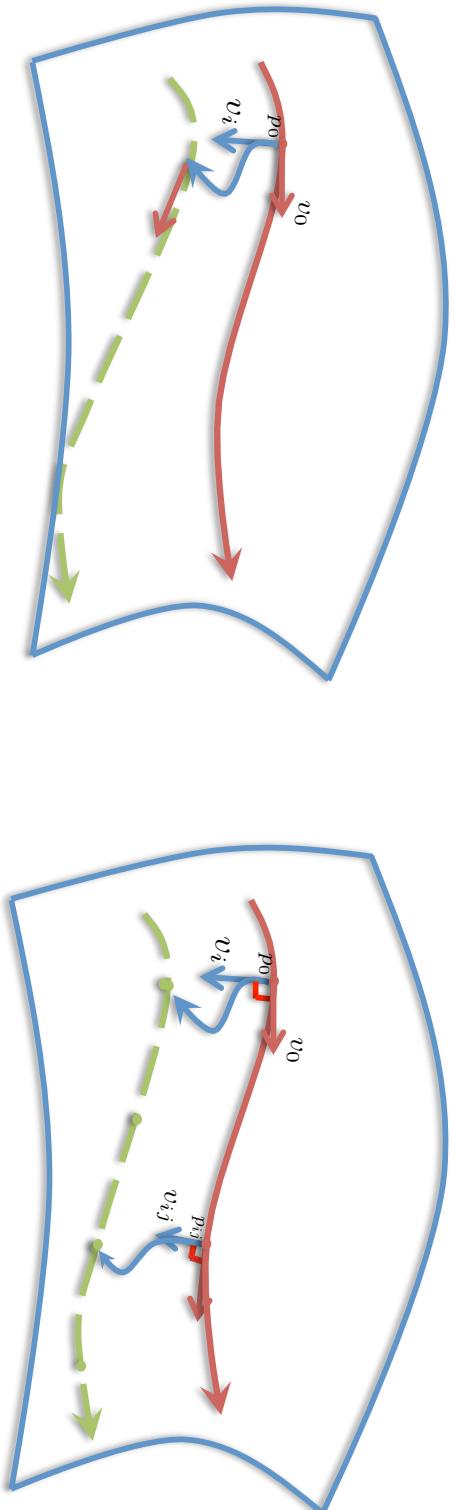
Fixed effects:  $(p_0, t_0, v_0)$  and  $(\sigma_\alpha^2, \sigma_\tau^2, A_1, \dots, A_K)$

# Spatiotemporal Statistical Model

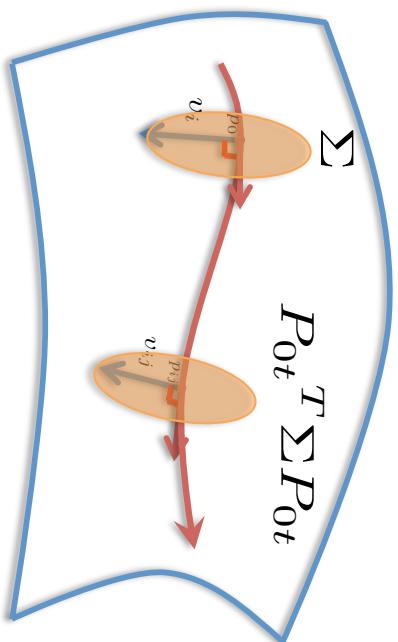
$$\left. \begin{array}{l}
 y_{ij} = T_i(\psi_i(t)) + \varepsilon_{ij} \\
 T_i(t) = \text{Exp}_{T_0(t)}(\mathbf{P}_{t_0,t}^{T_0}(v_i)) \\
 T_0(t) = \text{Exp}_{p_0,t_0}(v_0)(t) \\
 \psi_i(t) = t_0 + \alpha_i(t - t_0 - \tau_i) \\
 \alpha_i \sim \log \mathcal{N}(0, \sigma_\alpha^2) \\
 \tau_i \sim \mathcal{N}(0,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

# Spatiotemporal Statistical Model

Comparison with previous work:

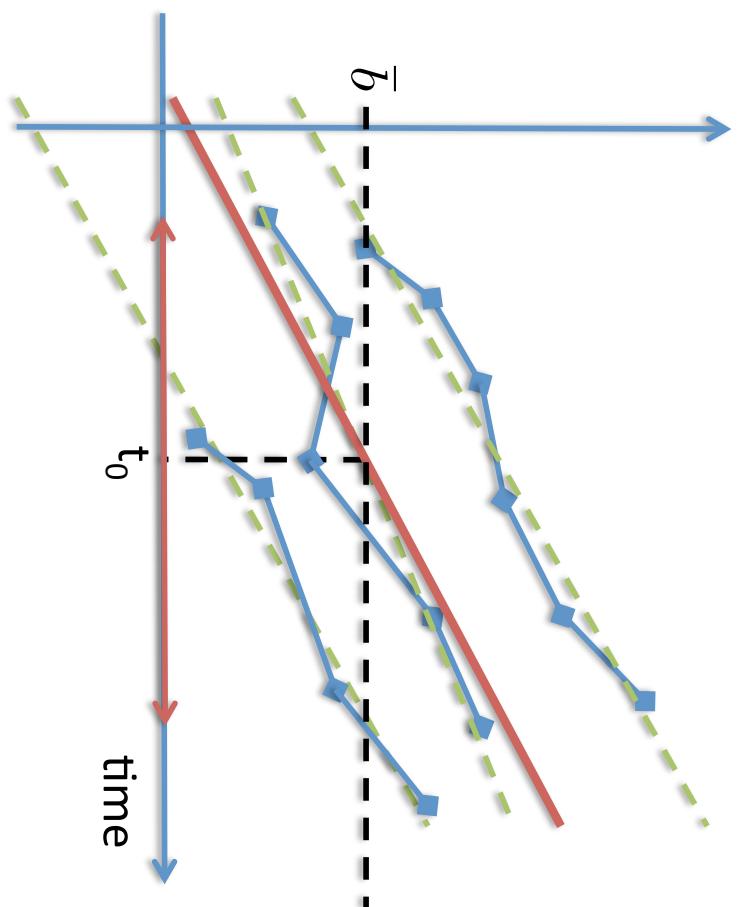


**Interest:** Parallel transport keep invariant the structure of the distribution, but updated it in time



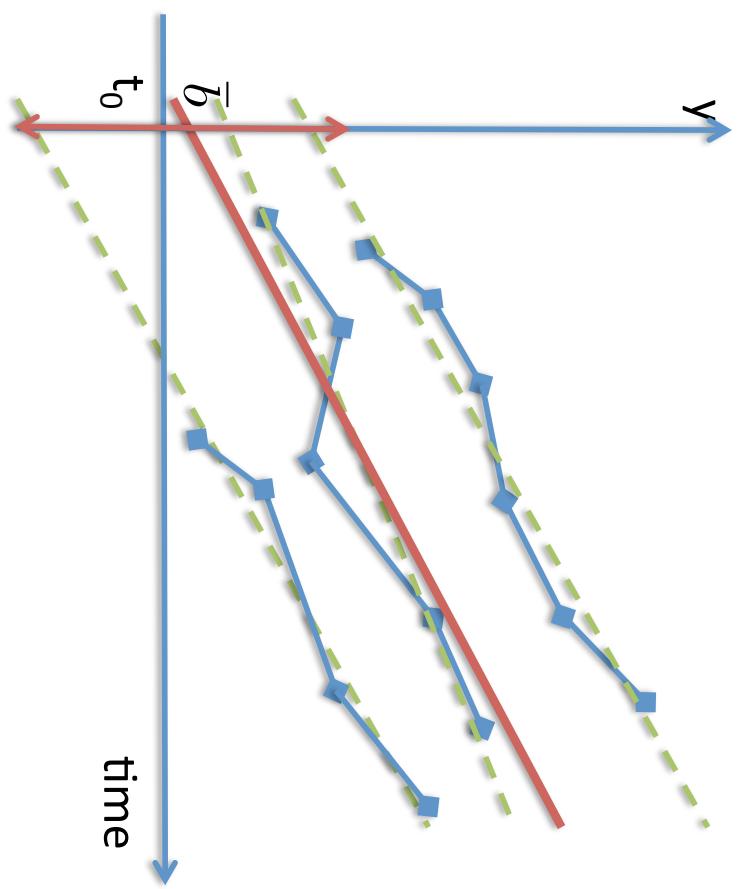
# Spatiotemporal Statistical Model

- The straight line model  $M = \mathbb{R}$



$$y_{ij} = (\bar{a} * a_i)(t_{i,j} - \underbrace{t_0 - \tau_i}_{\text{Time at which measurement of the } i^{\text{th}} \text{ subject reaches } \bar{b}}) + \bar{b} + \varepsilon_{i,j}$$

Time at which measurement of the  $i^{\text{th}}$  subject reaches  $\bar{b}$



$$y_{ij} = (\bar{a} * \underbrace{a_i}_{\text{Measurement of the } i^{\text{th}} \text{ subject at time } t_0})(t_{i,j} - t_0) + \underbrace{\bar{b} + b_i}_{\varepsilon_{i,j}} + \varepsilon_{i,j}$$

Measurement of the  $i^{\text{th}}$  subject at time  $t_0$

# Spatiotemporal Statistical Model

- The logistic curve model  $\mathbb{M} = ]0, 1[, g(p)(u, v) = \frac{uv}{p^2(1-p)^2}$

- Geodesic are **logistic curves**

$$\gamma_0(t) = 1 + \frac{(1-p_0)/p_0}{\exp\left(-\frac{v_0}{p_0(1-p_0)}(t-t_0)\right)}$$
$$y_{ij} = \gamma_0\left(t_0 + \alpha_i(t - t_0 - \tau_i)\right) + \varepsilon_{ij}$$

- It is *not* equivalent to a linear model on the logit of the observations (i.e. the Riemannian log at  $p_0 = 0.5$ ), since  $p_0$  is estimated
- If we fix  $p_0 = 0.5$  in our model  $\rightarrow$  end up with **our** previous linear case (different from Laird&Ware)

# Spatiotemporal Statistical Model

- The **propagation** model  $\mathbb{M} = ]0, 1[^N$ ,  $g(p)(u, v) = \sum_{k=1}^N \frac{u_k v_k}{p_k^2(1 - p_k)^2}$

- Geodesics are logistic curves in each coordinate

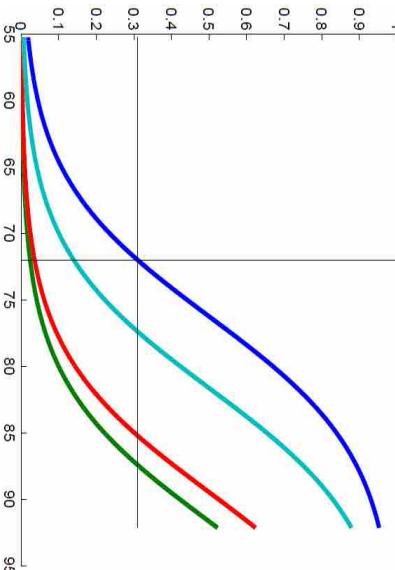
- Parametric family of geodesics seen as a model of propagation of an effect

$$\gamma_\delta(t) = \left( \gamma_0(t), \gamma_0(t - \delta_1), \dots, \gamma_0(t - \delta_{N-1}) \right)$$

- The parallel curve in the direction of the space-shift  $v_i$  writes

$$\left( \gamma_0 \left( t + \frac{v_{i,1}}{v_0} \right), \gamma_0 \left( t - \delta_1 + \frac{v_{i,2}}{v_0} \right), \dots, \gamma_0 \left( t - \delta_{N-1} + \frac{v_{i,N}}{v_0} \right) \right)$$

→ The parallel changes the *relative timing* of the effect onset across coordinates



# Parameter Estimation

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

- Maximum Likelihood:

$$\max_{\theta} p(y|\theta) = \int p(y, z|\theta) dz$$

$$\bullet \text{EM: } \theta_{k+1} = \arg\max_{\theta} \sum_{i=1}^N \int \log \left( \underbrace{p(y_i, z_i|\theta)}_{p(y_i|z_i, \theta)p(z_i|\theta)} \right) p(z_i|y_i, \theta_k) dz_i$$

- Distribution from the **curved exponential family**

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

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

# 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 coordinate  $p$  (Gibbs sampler) sample  $\tilde{z}_i^p \sim p(z_i^p | z_i^{q \neq p}, \theta)$
- Set  $z_{i,k+1}^p = \tilde{z}_i^p$  with probability  $1 \wedge \frac{p(y_i | \tilde{z}_i, \theta)}{p(y_i | z_i, \theta)}$
- $z_{i,k+1}^p = z_{i,k}^p$  otherwise

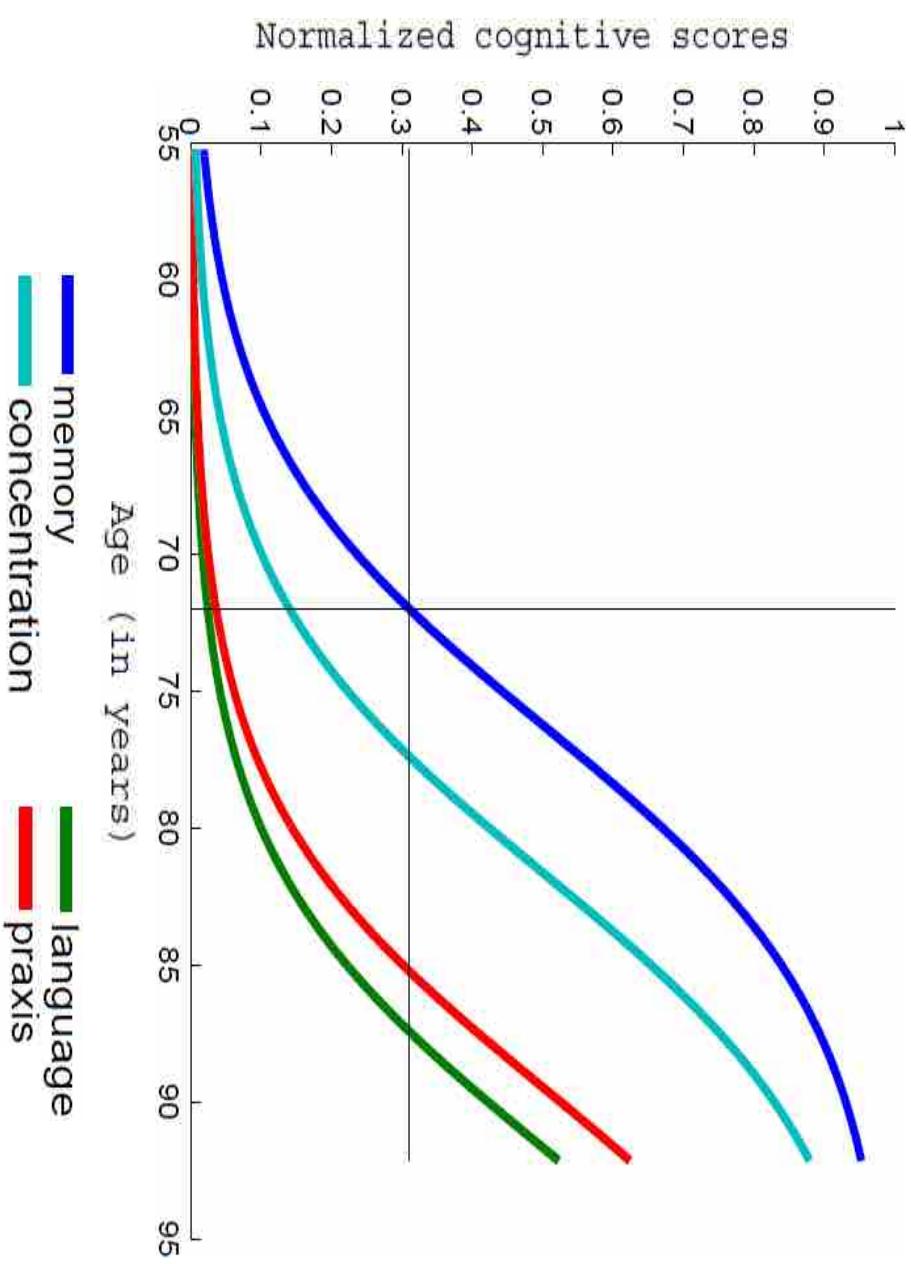
# Parameter Estimation: stochastic algorithm

- Theoretical properties of the sampler:
  - Under mild conditions:
    - Drift property
    - Small set
    - **Geometric ergodicity uniformly on any compact set** of the parameters
- Theoretical properties of the estimation algorithm:
  - a.s. convergence towards the MAP estimator
  - **Normal asymptotic behaviour:** speed  $1/\sqrt{\Delta_k}$
  - Normal asymptotic behaviour with optimal speed with averaging sequences  $1/\sqrt{k}$

# Model of Alzheimer's disease progression

## The average trajectory of data changes

- Neuropsychological tests ADAS-Gog from ADNI
- 248 subjects who converted from MCI to AD
- 6 time-points per subjects on average (min 3, max 11)
- Data points  $y_{ij} \in ]0, 1[^4$  with propagation logistic model



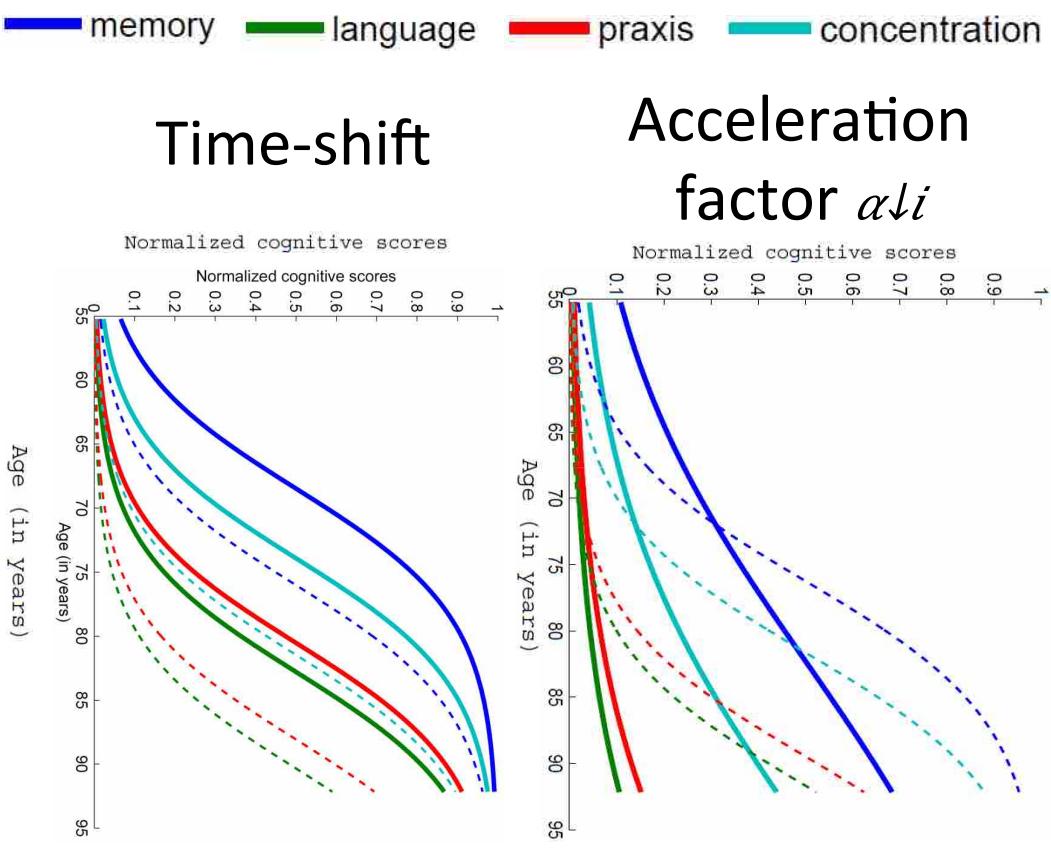
# Model of Alzheimer's disease progression

$-1\sigma$

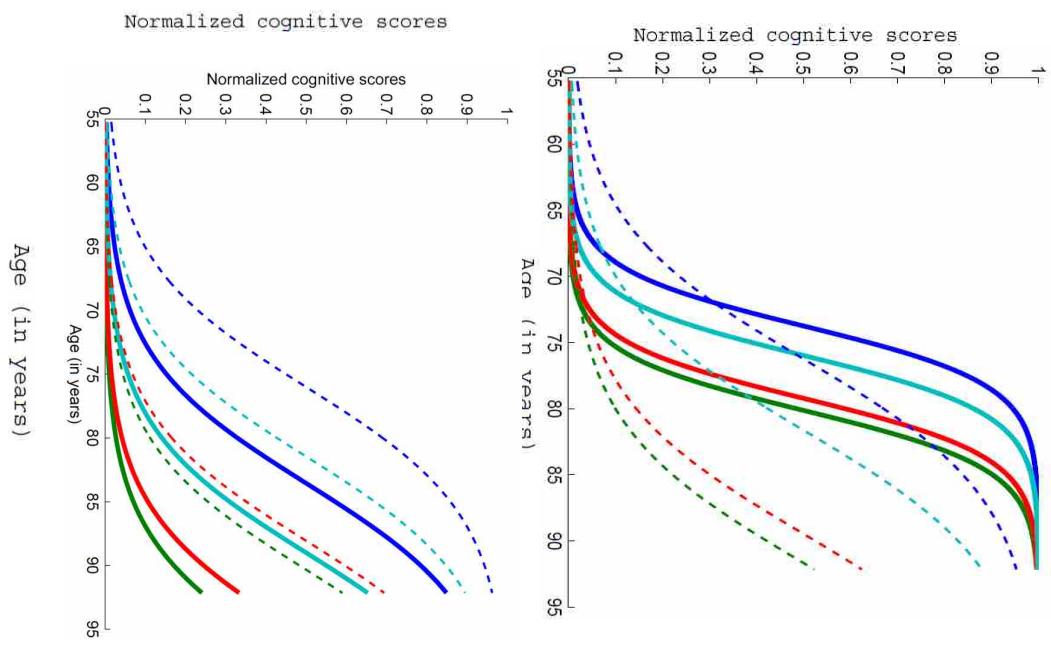
$+1\sigma$

## Acceleration factor $\alpha \downarrow i$

Distinguish fast vs. slow progressors



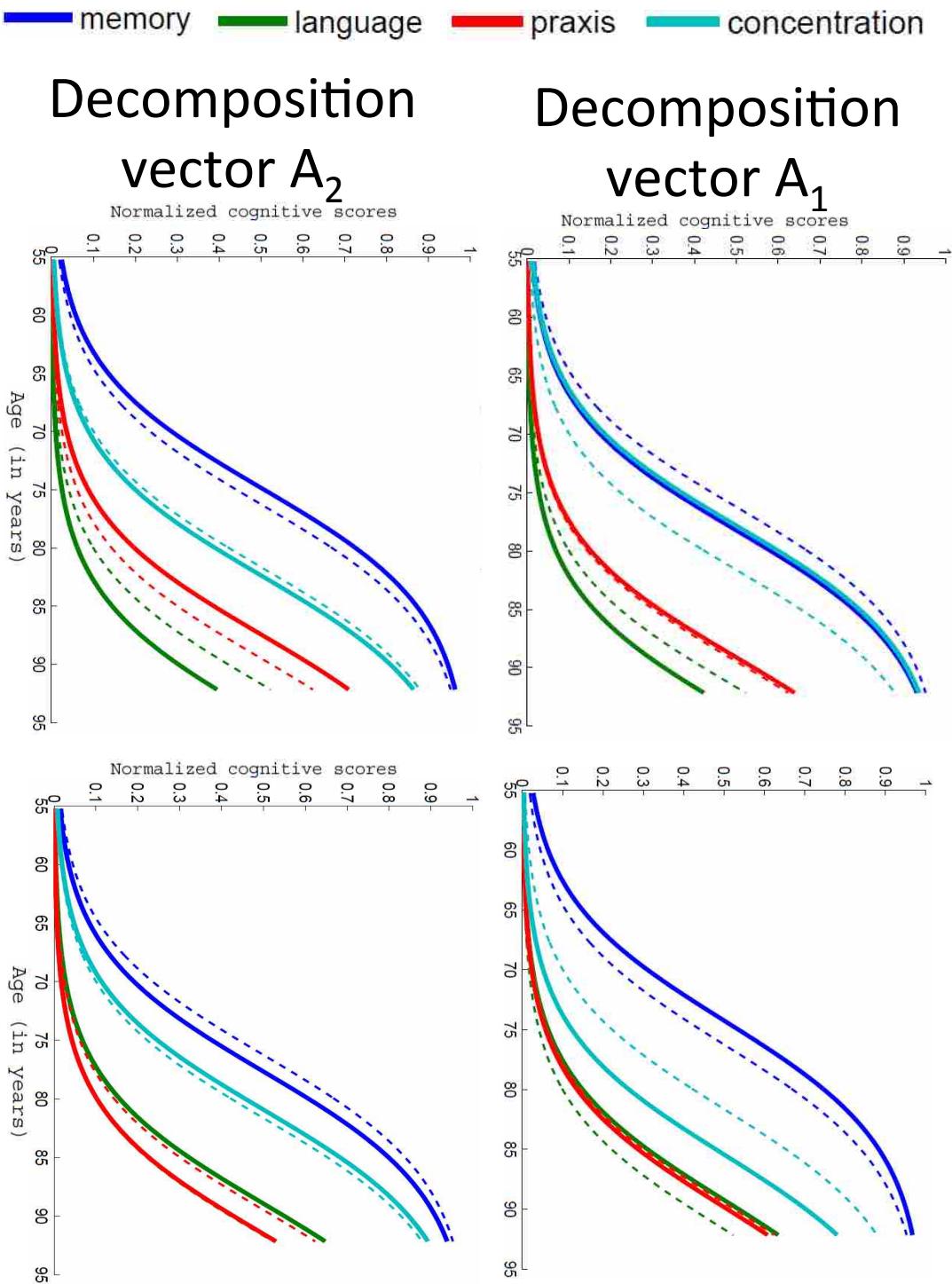
Distinguish early vs. late onset individuals



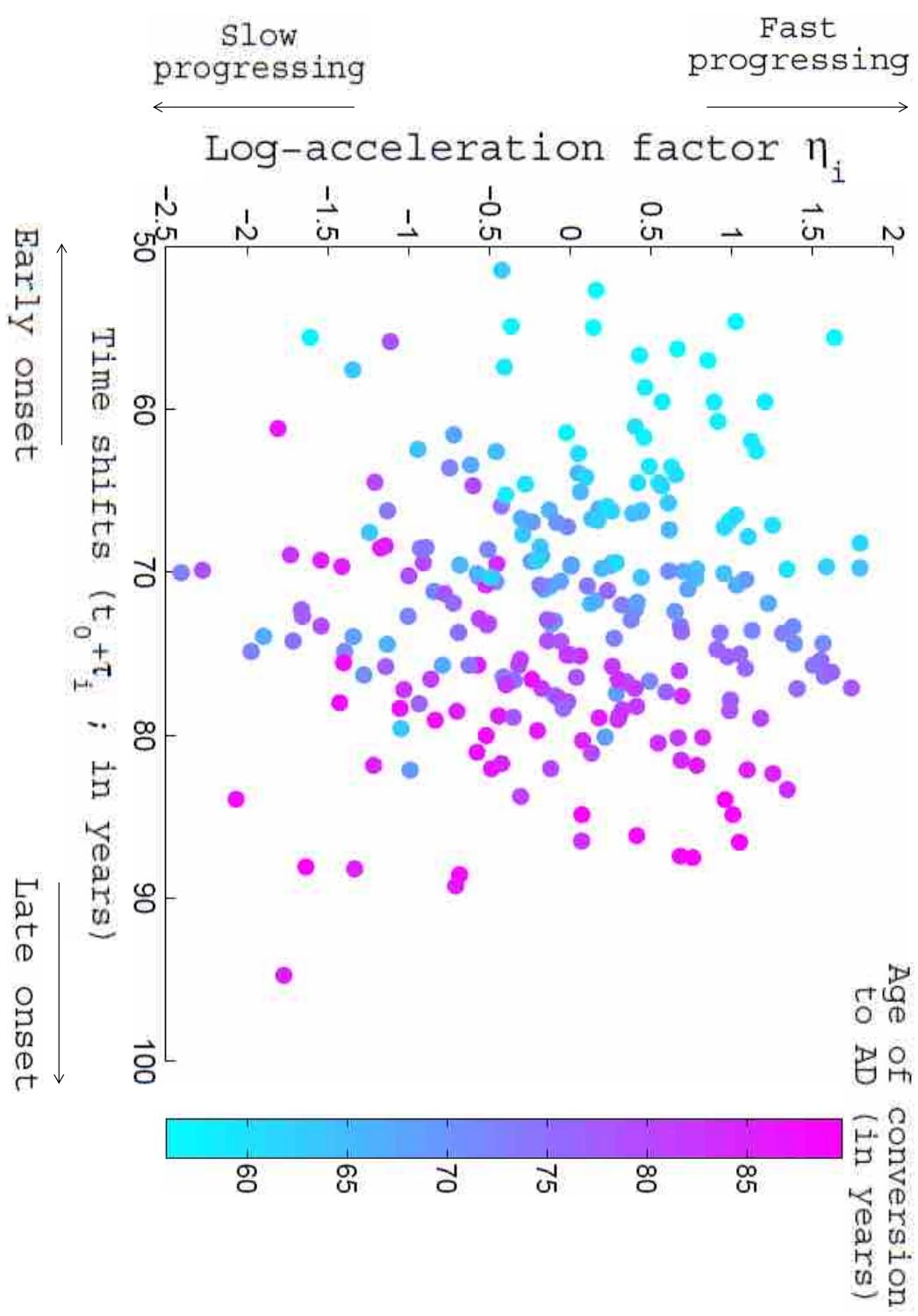
# Model of Alzheimer's disease progression

$-1\sigma$   
 $+1\sigma$

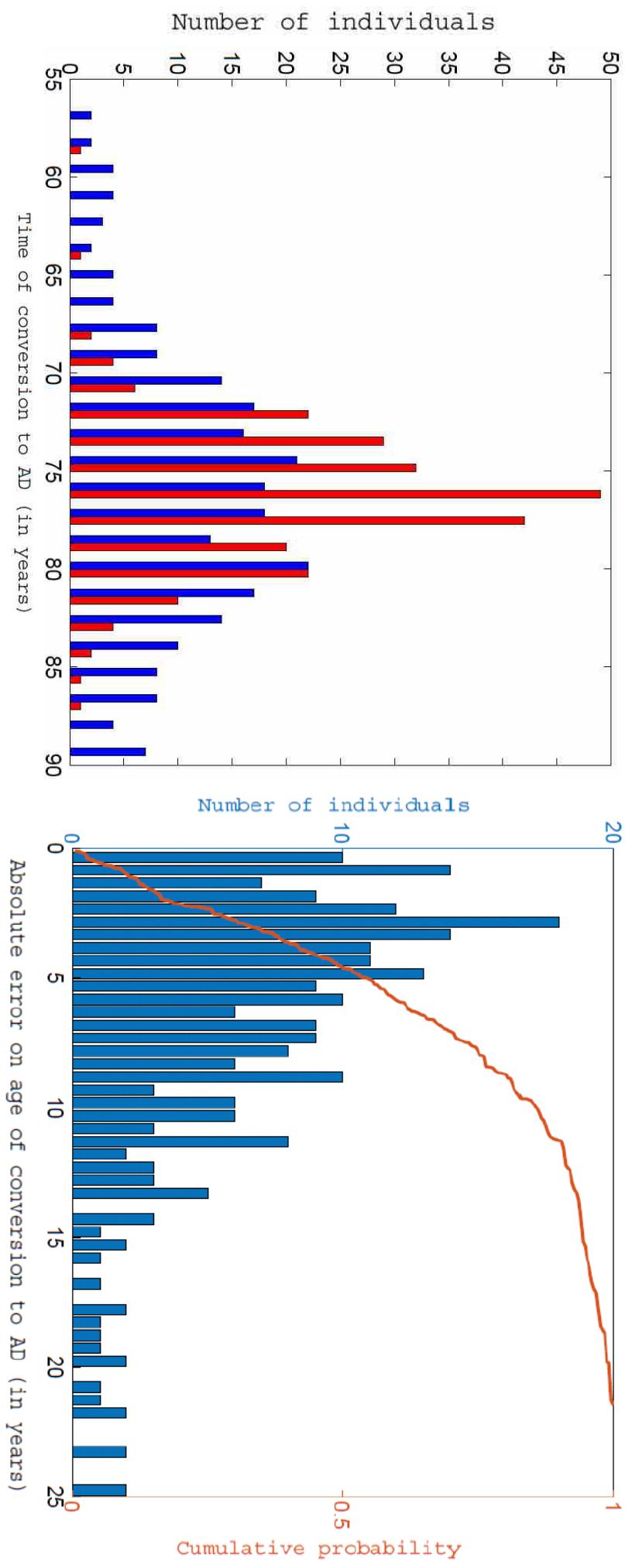
Variability in the **relative timing**  
and **ordering** of the events



# Model of Alzheimer's disease progression



# Model of Alzheimer's disease progression

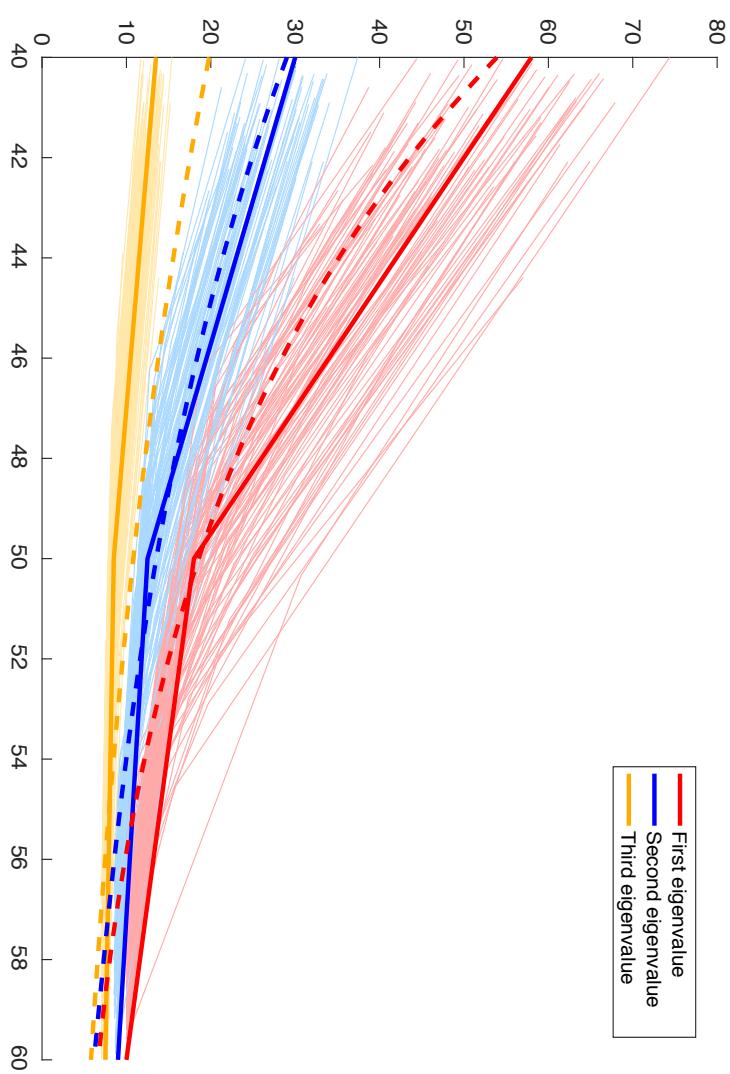


# Model of diffusion tensors

- Geodesic in the Riemannian manifold of positive definite matrices
  - Parallel transport the tensors
  - Reparametrize in time
  - Sample this curse
- 
- Average trajectory
- Parallel  $\eta^{W_i}(\gamma, t)$
- Reparametrized parallel  $\eta^{W_i}(\gamma, \psi_i(t))$
- Observations
- Time (years)

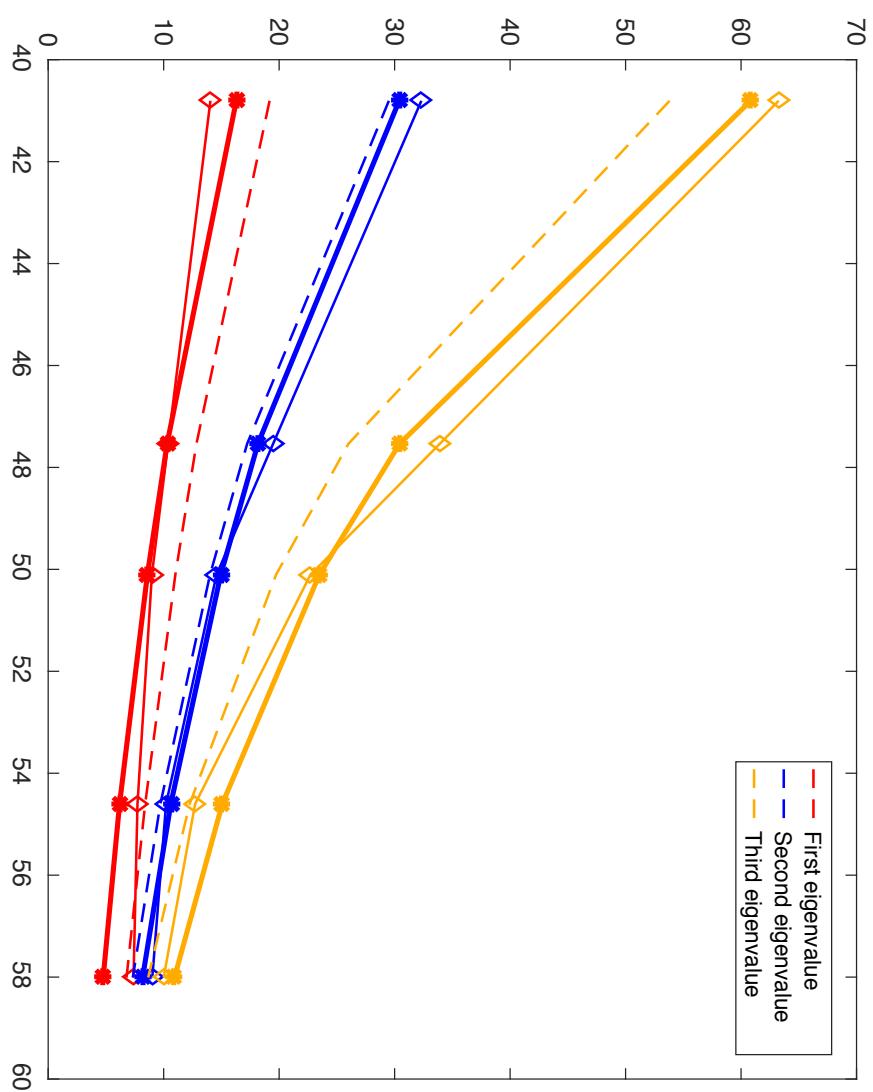
# Model of diffusion tensors

- Synthetic data not generated from the model but imitating a non smooth evolution
- 100 subjects
- 5 time points in average



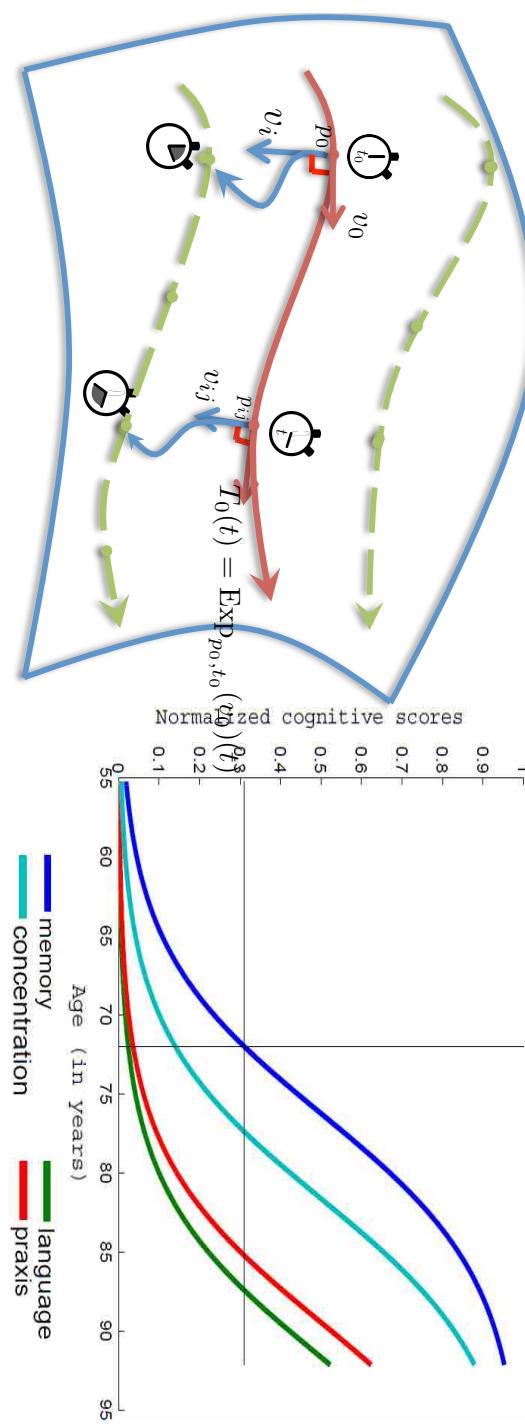
# Model of diffusion tensors

- Fitting the model to a new patient



# Conclusion

- **Generic** statistical model to learn **spatiotemporal distribution of trajectories** on **manifolds**:
  - Calibrated on **longitudinal** data sets using **MCMC-SAEM**
  - Automatically finds **temporal correspondences** among similar events that may happen at different age/time
  - Estimates the **variability** of the data at the corresponding events
- It allows us to position disease progression within the life and history of the patient
- **Future work:**
  - Derive instances of the model for more complex manifold-valued data (*e.g. spatially distributed data, shape data, etc..*)



Thank you!

