

# Bayesian life-course modelling of Alzheimer's Disease progression

Dave Lunn, Oana Petrof, Aris Perperoglou PSI 2025 Conference, London, June 8-11

### **Acknowledgments**

- The following work is proof-of-concept, inspired by...
- Raket, LL (2020) Statistical Disease Progression Modeling in Alzheimer Disease, Frontiers in Big Data, 3
- Oana Petrof (SDS-IH) currently carrying the work forwards



#### **ADNI** data

- The Alzheimer's Disease Neuroimaging Initiative (ADNI) is a longitudinal multicenter study designed to develop clinical, imaging, genetic, and biochemical biomarkers for the early detection and tracking of Alzheimer's disease (AD)...
- We focus on ADAS-Cog 13 (85 point score) as measure of disease progression:
  - ~11,000 longitudinal observations
  - ~2400 individuals
  - Between 1 and 17 observations each
- Five baseline-diagnosis groups:
  - 1. Cognitively Normal
  - 2. Significant Memory Concern
  - 3. Early Mild Cognitive Impairment
  - 4. Late Mild Cognitive Impairment
  - 5. Alzheimer's Disease

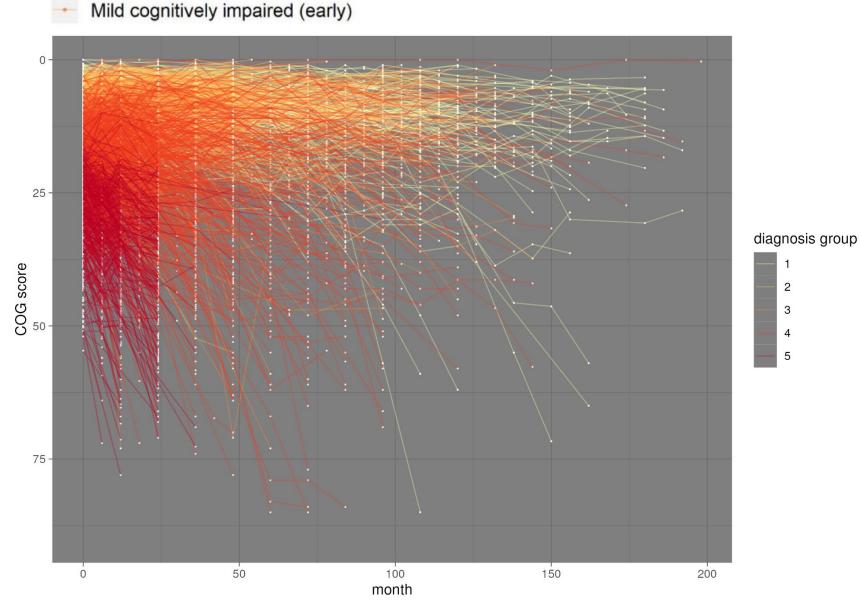


#### Raw data

- Larger scores and steeper slopes for more severe baseline diagnoses
- Some "curvature"
   apparent, so linear model
   may not be appropriate

#### Patient baseline status

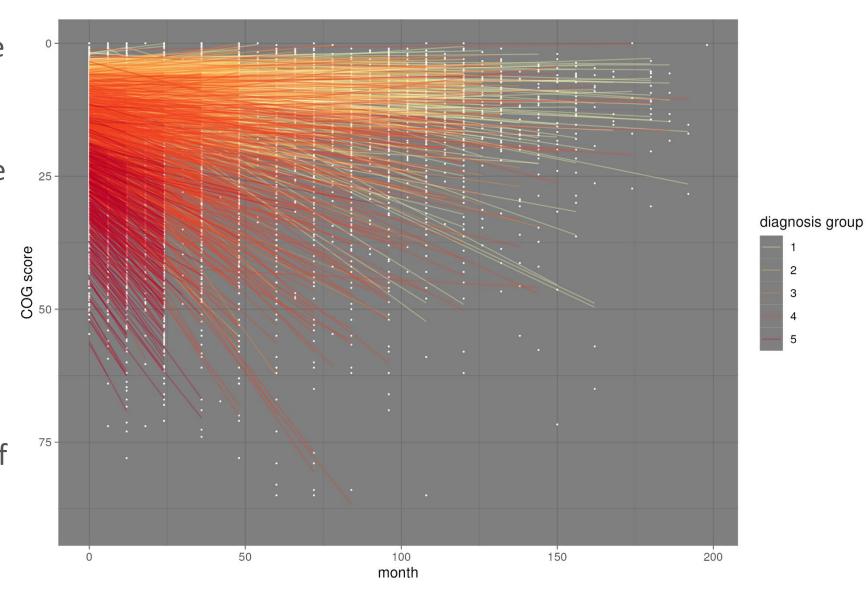






#### **Linear Mixed Effects model**

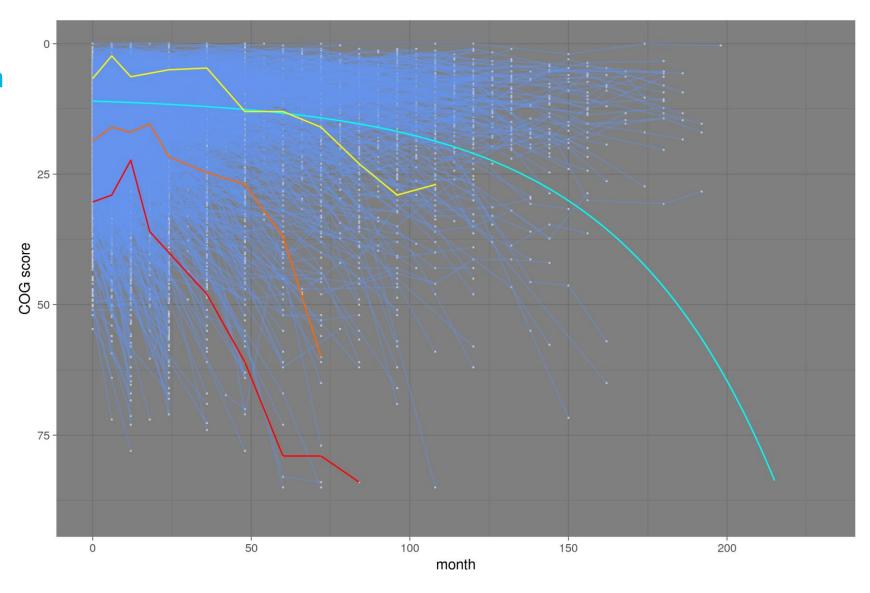
- Model assumes everyone following a different trajectory
- Perhaps better to assume everyone following a single, non-linear trajectory...
- ... but they are observed at different points along that trajectory
- Model framed in terms of disease time rather than study time





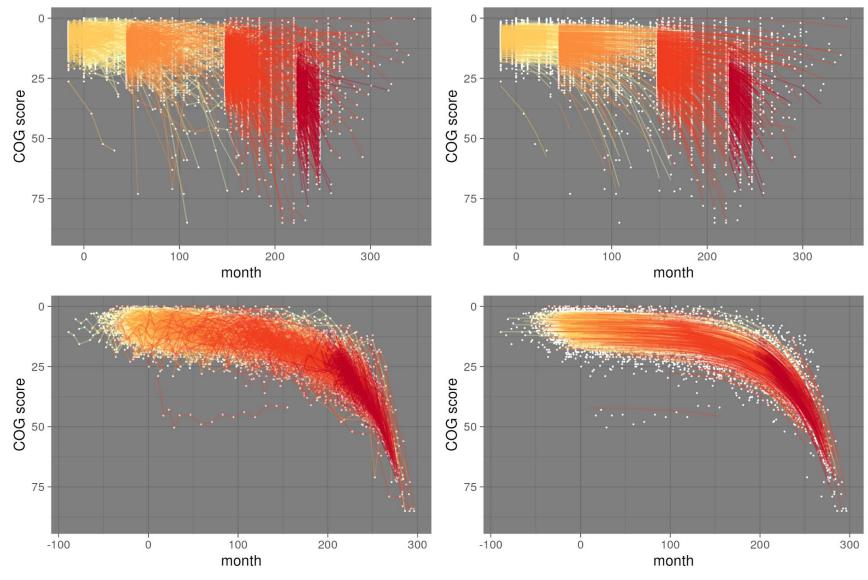
#### Disease-time (life-course) model

- Random intercepts
   model, but with a random
   x-intercept as well as a
   random y-intercept
- Each patient's data moved up/down and across onto disease-time trajectory
- Trajectory fitted simultaneously
- $\mu_{ij} = \alpha_i + \exp(\beta(\theta_i + t_{ij}))$  $\alpha_i = \text{y-shift}, \ \theta_i = \text{time-shift}$



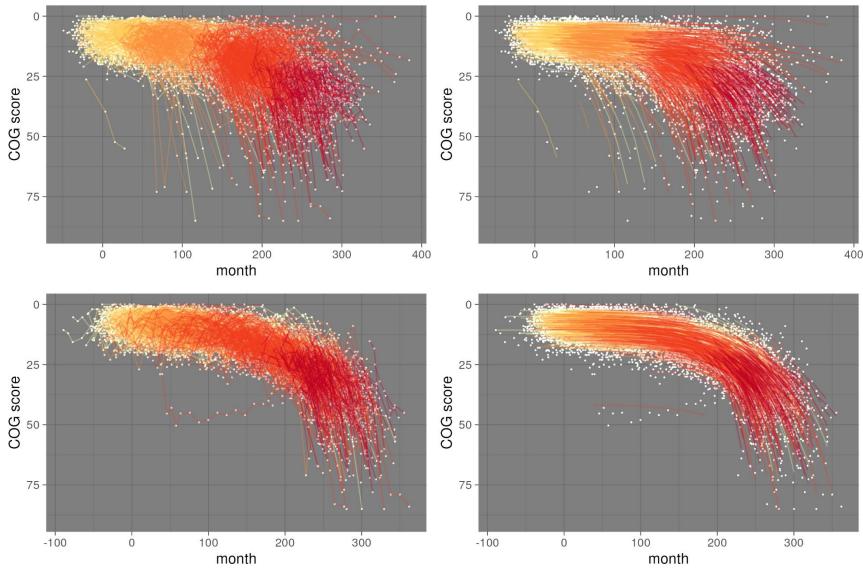


# **Outputs from Stan**



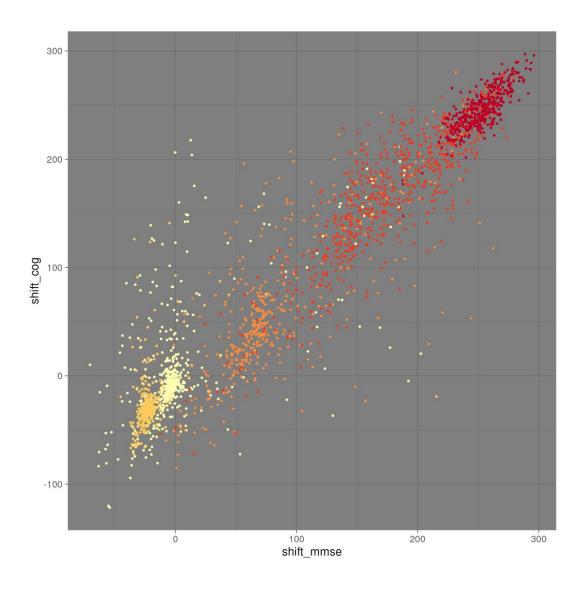


## Stan model: with baseline age, sex, education





# Different/multiple endpoints: ADAS-Cog 13 vs MMSE





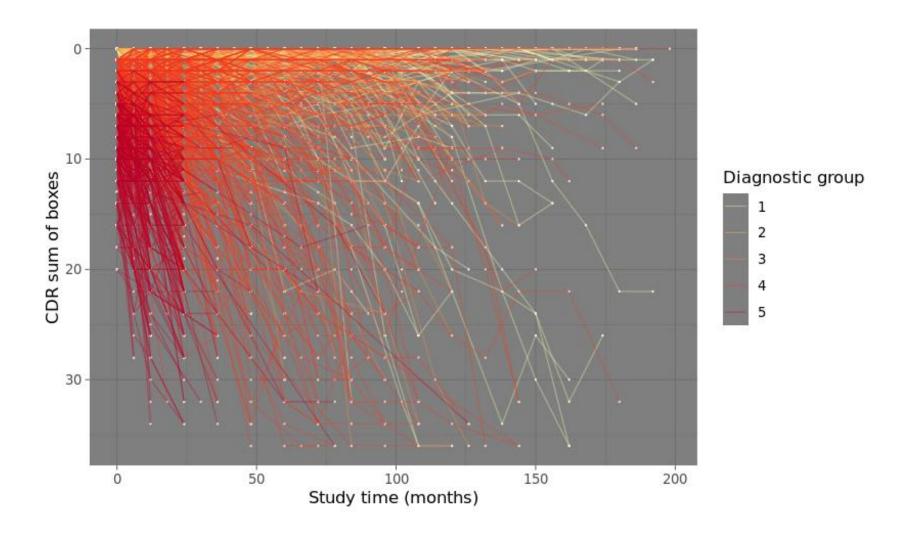
#### CDR Sum of Boxes (CDR-SB) = sum over 6 domains...

CDR Sum of Boxes	CDR Function	Community affairs
		Home and hobbies
		Personal care
	CDR Cognition	Memory
		Orientation
		Judgement/Problem-solving

- Total score between 0 and 18 with many zeros + half-integers
- Propose doubling scores and fitting negative-binomial model
- Start with Total Score; then fit Function + Cognition; and so on...

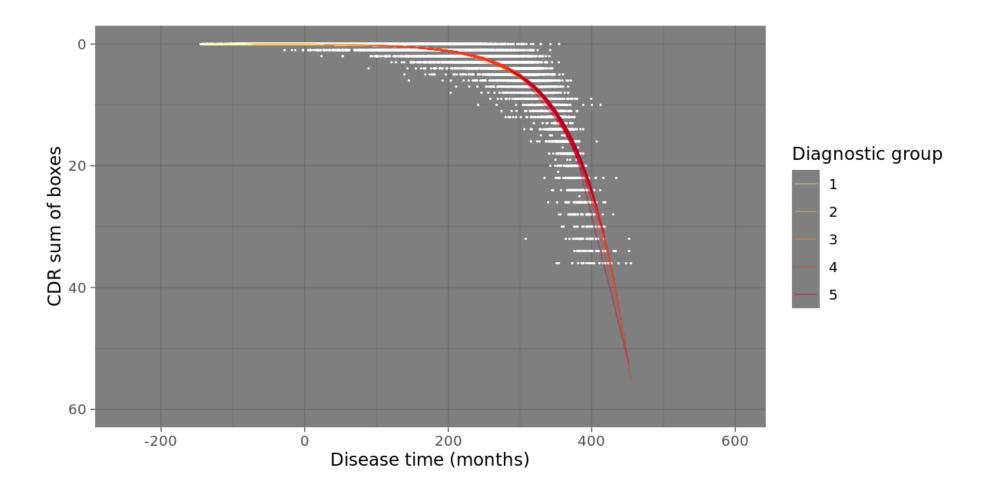


# **CDR-SB Total Score (x2)**



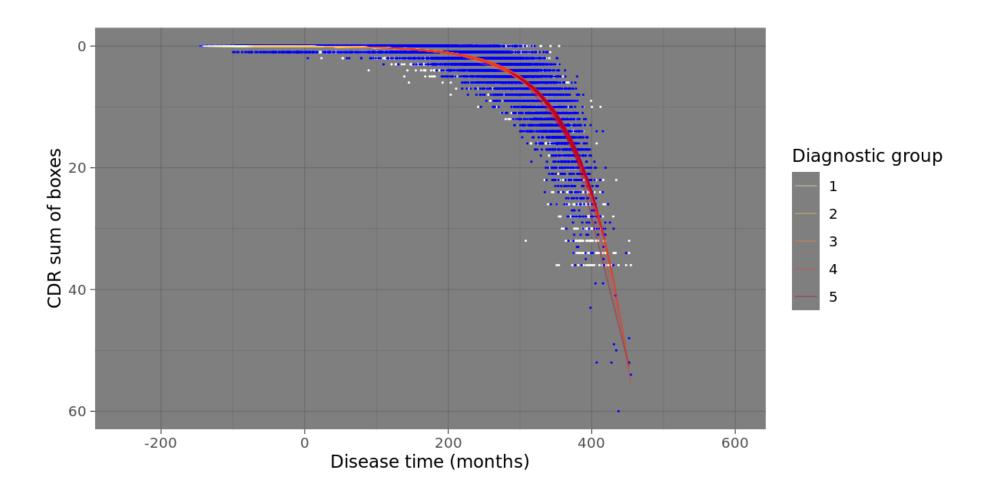


#### **CDR-SB Total Score**



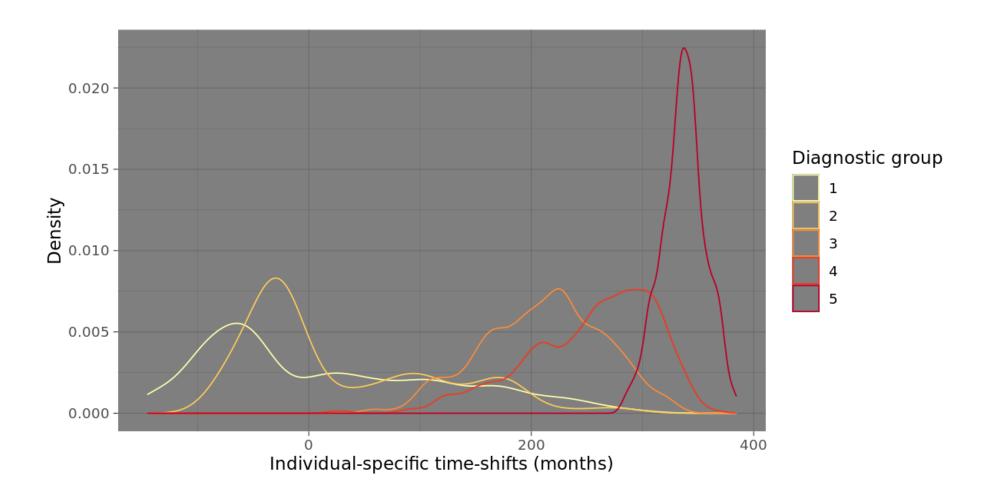


#### **CDR-SB Total + simulated "noise"**



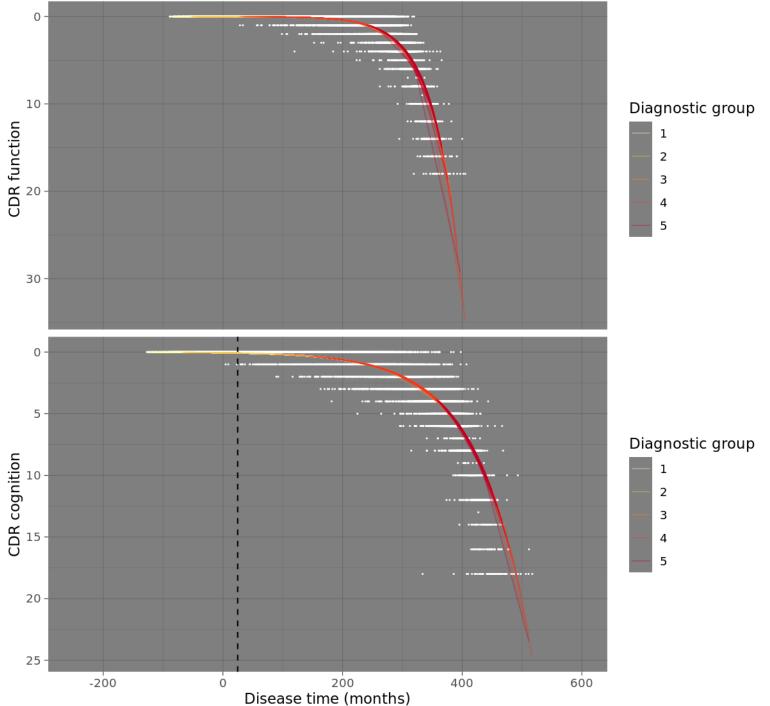


# **CDR-SB** Heterogeneity in individual-level time-shifts





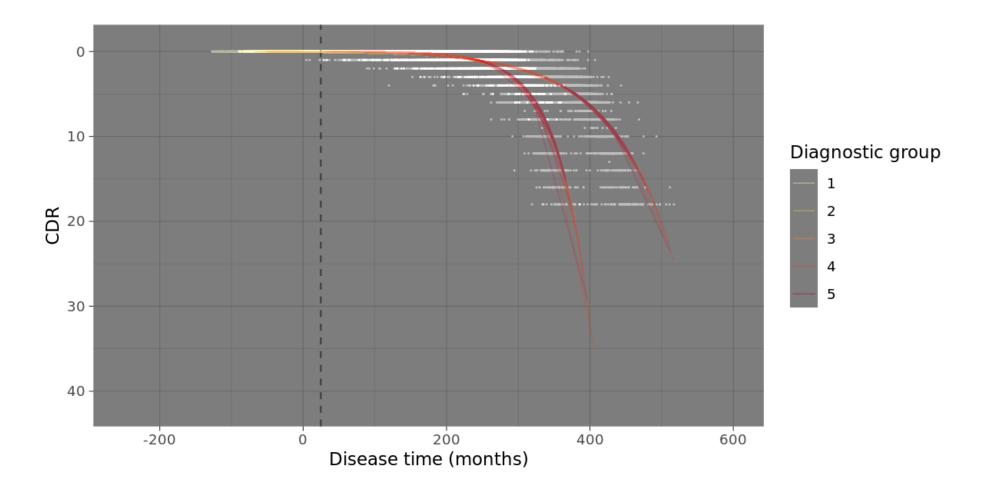
# **CDR-SB Function vs Cognition Separate models**





## **CDR-SB Function vs Cognition superimposed**

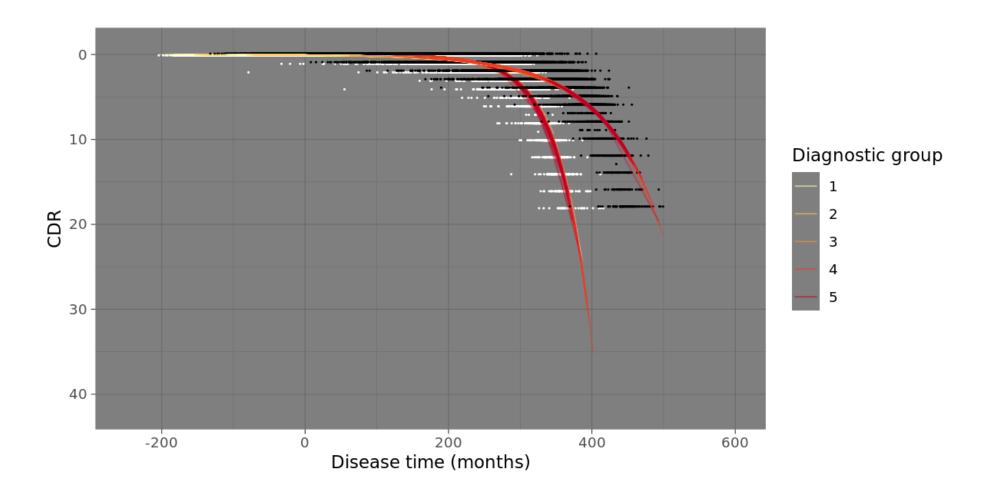
Can this be modelled using a common "shift" random effect?





### **CDR-SB Function vs Cognition: Joint model**

Cognition shift = linear transform of Function shift  $[\theta_{Ci} = \eta + \lambda \theta_{Fi}]$ 





#### **Overview**

- Summary
  - Model synthesises all data into coherent whole: "population view" of full time-course
  - Understand/simulate rate of decline for different sub-populations, at different stages of disease
- Ongoing/future work [short term]
  - Build joint "natural history" model that reflects progression in a number of domains, and accounts for differences in the timing of progression within those domains
  - Identify patient characteristics (e.g. age, sex, p-tau217) that explain heterogeneity
    - Variable selection / ML model
    - Enables prediction of disease-age (DA) in trial populations
  - Natural history model can serve as "prior" for analysis of trial data
    - Joint nature allows evaluation of treatment effects beyond just cognition
  - Broader application: other data sources + disease areas (e.g. COPD)



#### **Overview continued**

- Ongoing/future work [longer term]
  - Simulate realistic trial data
  - Virtual populations/cohorts with characteristics (e.g. disease-stage, covariates) of interest
    - Refine inclusion criteria
  - Integrate/align with other models, e.g. enrollment, disease-state, QSP
    - End-to-end simulation
  - Hypothesise longitudinal treatment effects:
    - Explore how timing of treatment (and/or the observation schedule) and the type of trial population impact on the identification of treatment effects
    - Different ways of measuring treatment effects, e.g. residence time



### Thank you for your attention

- $y_{dij} \sim D(\mu_{dij}, s_d)$ , i = patient, j = visit, d = domain;
- $\mu_{dij} = \alpha_{di} + \exp\left(\beta_d \left(\delta_d + \theta_{di} + t_{dij}\right)\right)$ ,  $\alpha_{di} = \text{y-shift}$ ,  $\theta_{di} = \text{time-shift}$ ;
- $\theta_{Fi} \sim N(\gamma_g, \phi_g^2)$ , g = diagnosis group;
- $\theta_{Ci} = \eta + \lambda \theta_{Fi}$  [for example]

