

On the Analysis of Longitudinal Clinical Lab Data with Latent Mixture Models

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Outline

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Motivating
example

Flexible
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Maximum
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- 2 Motivating example
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- 5 Summary

Pre-marketing analysis of safety data

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- Towards reporting to governing agencies and on label inserts, rates of adverse events (AE) over the course of followup during pre-marketing trials are used
- Often, the binary AEs are derived from continuous longitudinal clinical laboratory data
 - Liver function: alanine aminotransferase (ALT)) elevations are used to characterize liver damage.
 - An hepatotoxic event may be defined by ALT concentrations crossing some threshold value (e.g. 3X ULN) at some time during follow-up.

• Considerations

- Continuous data are dichotomized
 - Information loss
 - The dichotomization point (3X ULN) has no intrinsic meaning
 - Reference ranges: uncertainty / multiple labs and transformations
- Longitudinal data are ignored.
 - Ignoring the added information by taking repeated measures on individuals.
 - Dynamic treatment effects cannot be captured (does ALT elevations at 28 days mean the same thing as ALT elevations at 7 days?)
- Lack of power: combine multiple studies on the same product or on the same class of products
- There is little effort to characterize the real biological impact of the products on typical subjects.

Motivating Example: Impact of drug X on liver function

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	Placebo	Low Dose	High Dose
N	135	66	76
Female (%)	48	21	57
Ethnicity (%)			
White	81	85	84
Black	10	6	8
Other	9	9	8
Age (years)	50 (27, 65)	36 (24, 64)	53 (36, 66)
Weight (kilograms)	82 (60, 106)	83 (64, 105)	80 (56, 98)
Log-transformed, baseline ALT	2.8 (2.2, 3.5)	2.9 (2.4, 3.5)	2.6 (1.9, 3.4)

Motivating Example: Impact of drug X on liver function, *cont.*

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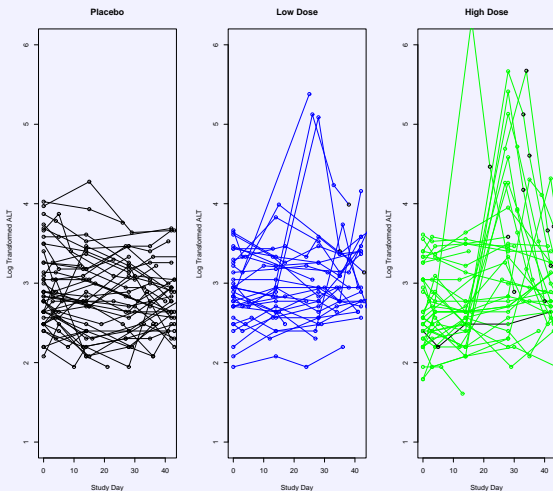
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A longitudinal data analysis approach

$$Y_i(t) = \mathbf{X}_i(t) \cdot \boldsymbol{\beta}(t) + \epsilon_i(t)$$

- $Y_i(t)$: response value for subject i at time t
- $\mathbf{X}_i(t)$: p -vector of covariates subject i at time t
- $\epsilon_i(t)$: mean-0 error process
 - Assuming a distributional form \rightarrow parametric estimation
 - Not assuming a distributional form \rightarrow semi-parametric estimation
- $\boldsymbol{\beta}(t)$ parameter vector that is the target of inference
 - Flexibility in the functional form of these parameter is critical (parametrically, semi-parametrically, or non-parametrically)

Selection mechanisms

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- Schildcrout JS et.al, *Statistics in Medicine* (DOI: 10.1002/SIM.3071)
- Potentially, a large number of selection mechanisms... many of which may be response history dependent

Type	Approach
Dropout	IPW-GEE
	ML
Visit rate	IPW-GEE
	ML
Tx discontinuation	IPTW-GEE
	Drop subsequent follow-up + GEE
	Drop subsequent follow-up + ML

Dynamic treatment effects

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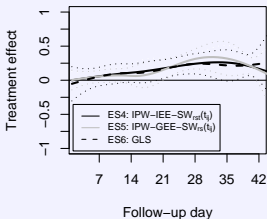
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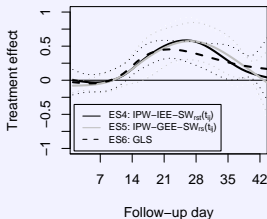
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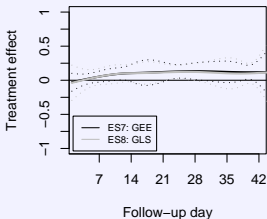
a) Low dose vs. placebo



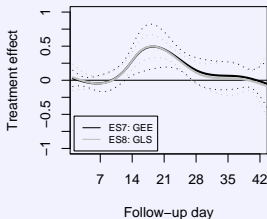
b) High dose vs. placebo



c) Low dose vs. placebo: lagged response



d) High dose vs. placebo: lagged response



Selection mechanisms (*cont.*)

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- Non-ignorable
 - Patients in clinical trials may be substantially different from those to whom we would like to generalize results
 - Exclusion criteria: counter-indicated medications, lifestyle choices
 - Post-marketing, medications are prescribed to unstudied patient populations
 - Evaluation strategies
 - Posit selection mechanisms and perform sensitivity analyses
 - Weighted estimating equations
 - Weighted resampling based approaches (e.g., tilted bootstrap)

Sensitivity Analysis

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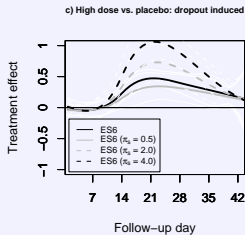
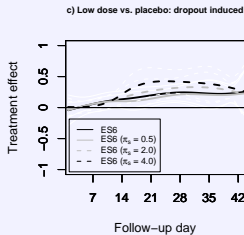
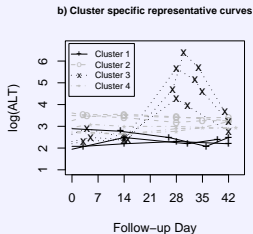
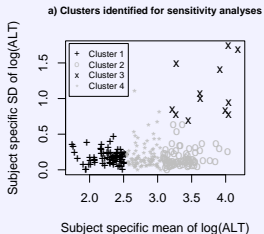
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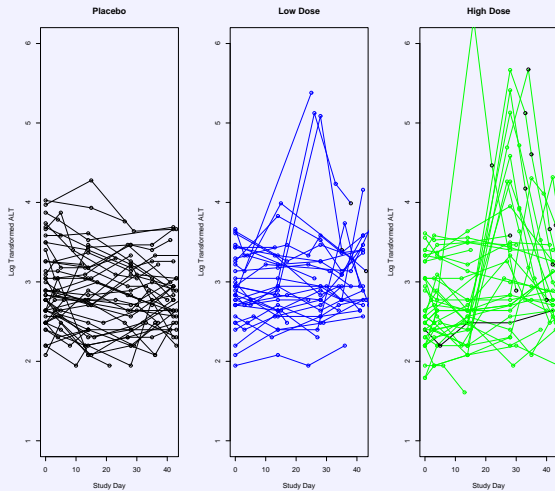
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The underlying model assuming two levels of susceptibility

- Let R_i be an indicator that subject i is someone who is susceptible to the effects of treatment if given and r_i is the realized value if we knew it.

$$Y_i(t) = (\beta_0 + \beta_1 tx_i + \beta_2 r_i + \beta_3 tx_i r_i) \\ + (\beta_4 + \beta_5 tx_i + \beta_6 r_i + \beta_7 tx_i r_i) \cdot f(t) + \epsilon_i(t)$$
$$\mu_{i,tx}^r(t) = E(Y_i(t) \mid tx_i, r_i)$$

- Treatment effect for non-susceptible subjects

$$\mu_{i,1}^0(t) - \mu_{i,0}^0(t) = \beta_1 + \beta_5 f(t)$$

- Treatment effect for susceptible subjects

$$\mu_{i,1}^1(t) - \mu_{i,0}^1(t) = (\beta_1 + \beta_3) + (\beta_5 + \beta_7) \cdot f(t)$$

The underlying model assuming two levels of susceptibility

- By randomization,

$$\pi_i \equiv p(R_i = 1) = p(R_i = 1 \mid tx_i = 1) = p(R_i = 1 \mid tx_i = 0)$$

- Marginal mean

$$\mu_{i,tx}(t) = \mu_{i,tx}^1(t)\pi_i + \mu_{i,tx}^0(t)(1 - \pi_i)$$

- Marginal treatment effect

$$\mu_{i,1}(t) - \mu_{i,0}(t) = (\mu_{i,1}^1(t) - \mu_{i,0}^1(t))\pi_1 + (\mu_{i,1}^0(t) - \mu_{i,0}^0(t))(1 - \pi_1)$$

- If it is reasonable to assume $\mu_{i,1}^0(t) = \mu_{i,0}^0(t)$,

$$\mu_{i,1}^1(t) - \mu_{i,0}^1(t) = \frac{\mu_{i,1}(t) - \mu_{i,0}(t)}{\pi_i}$$

- We may then be interested in π_i and $\mu_{i,1}^1(t) - \mu_{i,0}^1(t)$
- The challenge: R_i is unknown

Mixture models and (ML) estimation

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- π_k = overall probability of membership in class k
- The mixture model density is given by,

$$g(y_i(t) | \mathbf{x}_i(t), \theta) = \sum_{k=1}^K \pi_k f(y_i(t) | \mathbf{x}_i(t), \theta_k)$$

where $\theta = \{\theta_1, \theta_2, \dots, \theta_k, \pi_1, \pi_2, \dots, \pi_k\}$

- With N subjects and n_i repeated measures for subject i , we may consider maximum likelihood estimation with the log-likelihood

$$l = \sum_{i=1}^N \sum_t \log[g(y_i(t) | \mathbf{x}_i(t), \theta)],$$

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Summary

- This is very similar to a missing data problem where r_i is missing for each subject, and $(\mathbf{x}_i, \mathbf{y}_i, \mathbf{r}_i)$ would be the complete data
- The EM algorithm is generally used for the maximization.
- Expectation step
 - Given the parameter estimates at the $m - 1^{th}$ iteration, $\theta^{(m-1)}$ calculate the (*posterior*) probabilities of group membership

$$p_{ik}^{(m)} = \frac{\pi_k^{(m-1)} f(\mathbf{y}_i | \mathbf{x}_i, \theta_k^{(m-1)})}{\sum_{w=1}^K \pi_w^{(m-1)} f(\mathbf{y}_i | \mathbf{x}_i, \theta_w^{(m-1)})}$$

and calculate overall class membership probabilities (prior probability at iteration $m + 1$),

$$\pi_k^{(m)} = \frac{1}{N} \sum_{i=1}^N p_{ik}^{(m)}$$

Mixture models and (ML) estimation

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- Maximization step
 - Given p_{ik}^m for all i , maximize the weighted likelihood,

$$l = \sum_{i=1}^N \sum_{t_{ij}} p_{ik}^{(m)} f(y_i(t) \mid \mathbf{x}_i(t), \theta_k)$$

w.r.t. θ_k for each of the k classes.

- Notice the number of estimated parameters estimated with large K .

The model being used

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- r_i is categorical (and not observed)

$$E(Y_i(t)) = (\beta_0 + \beta_1 tx_i + \beta_2 r_i + \beta_3 tx_i r_i) \\ + (\beta_4 + \beta_5 tx_i + \beta_6 r_i + \beta_7 tx_i r_i) \cdot ns(t)$$

- ns : natural spline matrix with knots at days 14,28,35, and 42.
- Two factors to describe the three levels of Tx_i :
 $I(Tx_i = low)$ and $I(Tx_i = high)$
- The number of classes: use objective measures to determine an appropriate number of classes while acknowledging the limited sample size.

Number of Classes

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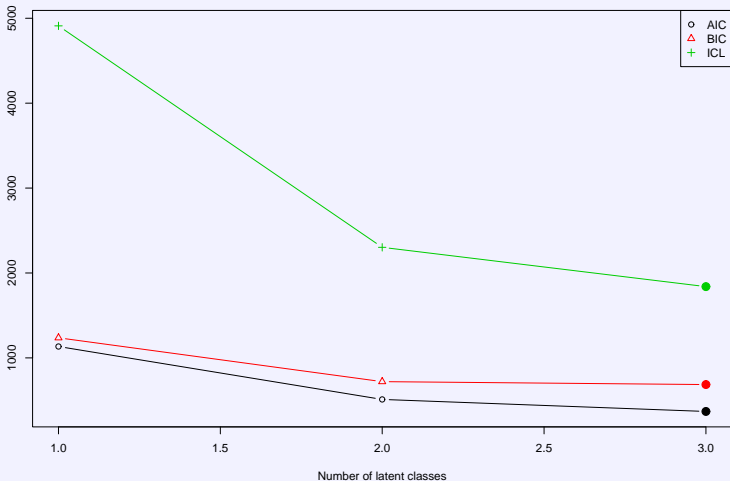
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Two latent class model

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- Prior class membership (π_k):

① 0.14

② 0.86

Two latent class model

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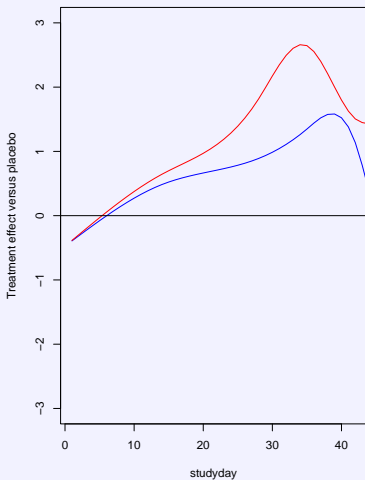
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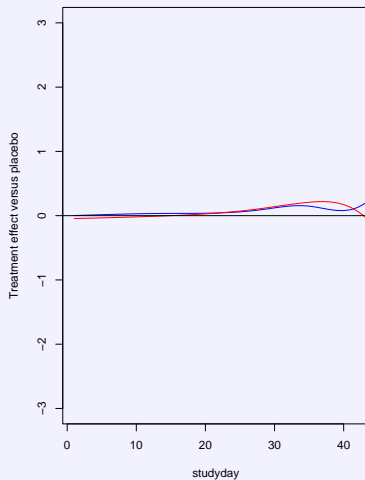
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Class 1 treatment effects



Class 2 treatment effects



Three latent class model

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- Prior class membership (π_k):

① 0.098

② 0.852

③ 0.051

Three latent class model

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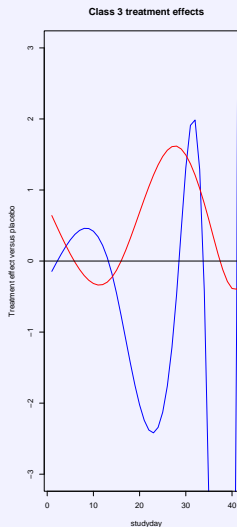
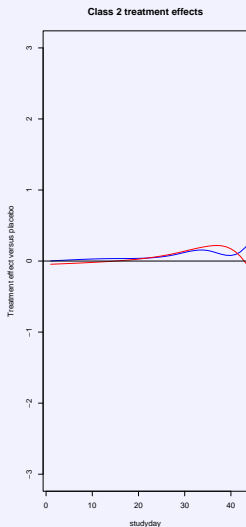
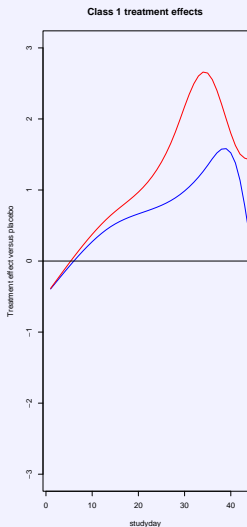
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Bayesian implementation

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$$Y_i(t) \sim N(\mu_i(t), \tau)$$

$$\mu_i(t) = (\beta_0 + \beta_1 tx_i + \beta_2 r_i + \beta_3 tx_i r_i) +$$
$$(\beta_4 + \beta_5 tx_i + \beta_6 r_i + \beta_7 tx_i r_i) \cdot ns(t)$$

$$R_i | p \sim \text{bernoulli}(p_i)$$

$$p_i \sim \text{beta}(\alpha, \beta)$$

$$\sigma^2 \sim U(0, 100)$$

$$\tau = 1/\sigma^2$$

$$\beta_j | \mu_j, \tau_j \sim N(\mu_j, \tau_j)$$

$$\mu_j \sim N(0, 100)$$

$$\sigma_j^2 \sim U(0, 100)$$

$$\tau_j = 1/\sigma_j^2$$

Treatment Effects based on means of posteriors

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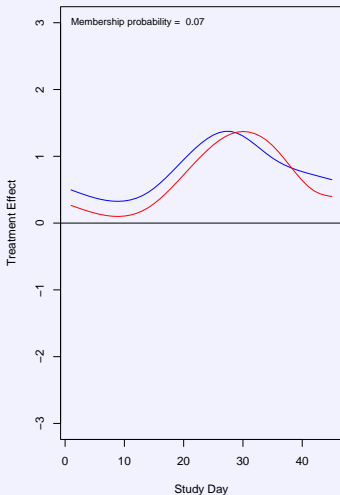
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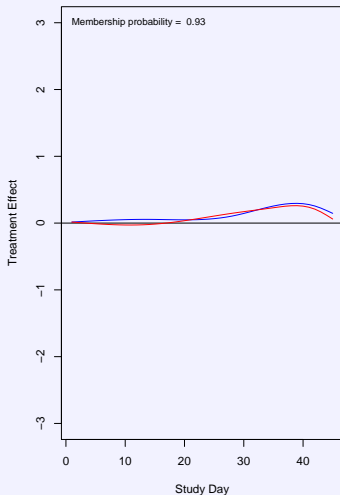
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Treatment effect in class 1



Treatment effect in class 2



Bayesian implementation (unequal variance)

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$$Y_{it} \sim N(\mu_i(t), \tau_r)$$

$$\mu_i(t) = (\beta_0 + \beta_1 tx_i + \beta_2 r_i + \beta_3 tx_i r_i) + \\ (\beta_4 + \beta_5 tx_i + \beta_6 r_i + \beta_7 tx_i r_i) \cdot ns(t)$$

$$\sigma_r^2 \mid r \sim U(0, 100)$$

$$\tau_r \mid r = 1/\sigma_r^2$$

$$R_i \mid p \sim \text{bernoulli}(p_i)$$

$$p_i \sim \text{beta}(1, 1)$$

$$\beta_j \mid \mu_j, \tau_j \sim N(\mu_j, \tau_j)$$

$$\mu_j \sim N(0, 100)$$

$$\sigma_j^2 \sim U(0, 100)$$

$$\tau_j = 1/\sigma_j^2$$

Treatment Effects based on means of posteriors

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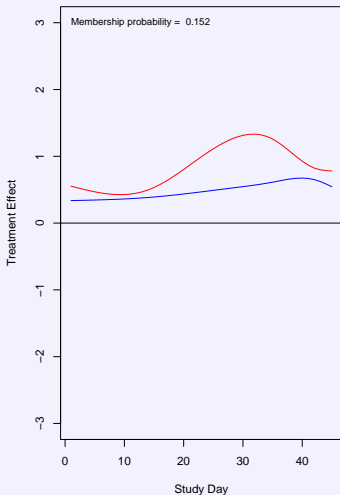
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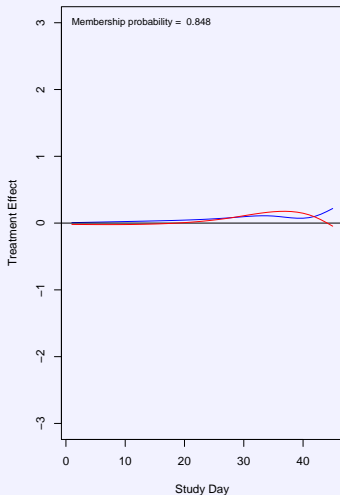
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Treatment effect in class 1



Treatment effect in class 2



Classification Probabilities

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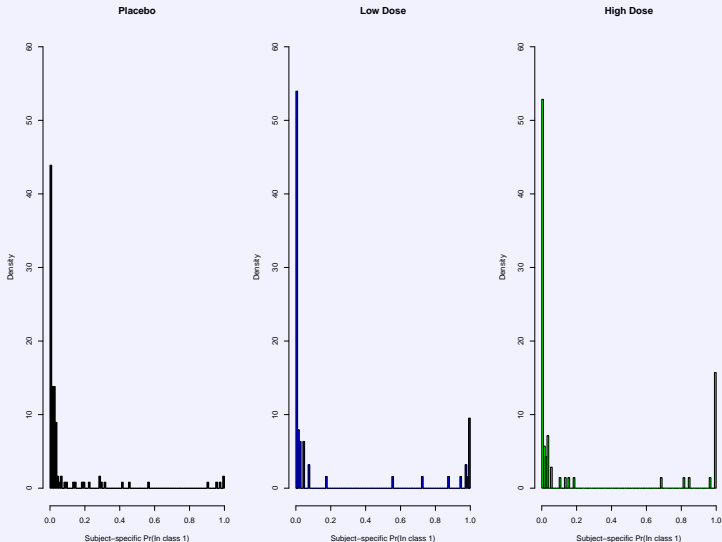
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Profiles for subjects classified with certainty

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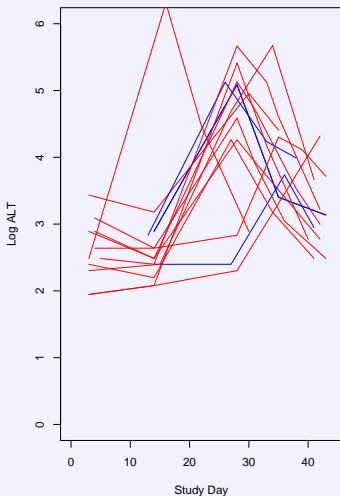
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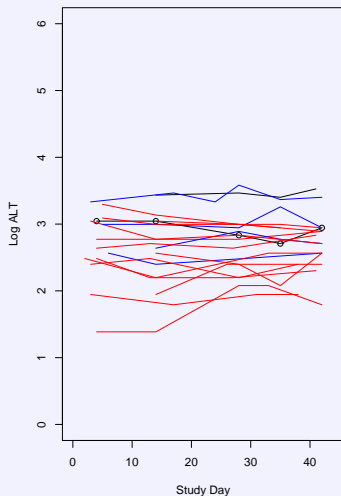
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In class 1 at every MCMC iteration



In class 2 at every MCMC iteration



Identifiability

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- Maximum Likelihood
 - Overfitting: Number of classes
 - Can be dealt with by requiring $\pi_k > 0$ and $\theta_k \neq \theta_{k'}$
 - Component relabelling
 - Component labels are interchangeable e.g., there are $K!$ label combinations that lead to a common maximized likelihood
 - Affects interpretation and not fitting of the EM algorithm... or we can impose restrictions
- Bayesian approach
 - Label reshuffling
 - No real way to discriminate between components of the mixture belonging to the same parametric family
 - During MCMC, labels can be permuted which can be very problematic (e.g., bimodal posterior distributions)
 - Post-processing may be recommended

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- Routinely collected laboratory data are not utilized effectively
- Longitudinal data analysis (acknowledging mechanisms of selection) improves our ability to characterize pharmaceutical safety
- Latent class regression seems to have the potential to improve this characterization in a very meaningful way.
- There are a number of challenges with it practically: primarily associated with the fact that class membership is not observed