

# Bayesian Statistics

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October 7, 2014

# GP-LVM for density estimation (Kundu & Dunson, 2013, Biometrika)

- ▶ Consider the latent variable model,

$$y_i = \mu(\eta_i) + \epsilon_i, \quad \epsilon_i \sim N(0, \sigma^2), \quad (i = 1, \dots, n)$$
$$\mu \sim GP(0, c), \quad \sigma \sim IG(a, b), \quad \eta_i \sim U(0, 1),$$

- ▶  $\eta_i$ 's are subject specific latent variables,  $\mu \in C[0, 1]$  is a *transfer function* relating the latent variables to the observed variables.
- ▶ The density of  $y$  conditional on the transfer function  $\mu$  and scale  $\sigma$  is obtained on marginalizing out the latent variable as

$$f(y; \mu, \sigma) \stackrel{\text{def}}{=} f_{\mu, \sigma}(y) = \int_0^1 \phi_\sigma\{y - \mu(x)\} dx \approx \frac{1}{T} \sum_{j=1}^T \phi_\sigma\left\{y - \mu\left(\frac{j}{T}\right)\right\}.$$

- ▶ Let  $F_0(t) = \int_{-\infty}^t f_0(x)dx$ .
- ▶ Letting  $\mu_0(x) = F_0^{-1}(x)$ , one obtains

$$f_{\mu_0, \sigma}(y) = \int_0^1 \phi_{\sigma}(y - F_0^{-1}(x))dx = \int_{-\infty}^{\infty} \phi_{\sigma}(y - t)f_0(t)dt,$$

where the second equality follows from the change of variable theorem.

- ▶  $\|\phi_{\sigma} * f_0 - f_0\| \rightarrow 0$
- ▶ Posterior computation: i)  $\mu \mid \mathbf{y}, \eta, \sigma$  is Gaussian ii)  $\eta \mid \mathbf{y}, \mu, \sigma$  Metropolis Hastings iii)  $\sigma \mid \mathbf{y}, \eta, \sigma$  is Inverse Gamma

# Some applications of the Dirichlet process Mixture models

# Hierarchical Modeling

- ▶  $\theta_i$  = random effects specific to “subject”  $i$
- ▶ Hierarchical models let  $\theta_i \sim P$
- ▶  $P$  = random effects distribution
- ▶ Choice of  $P$  critical in controlling borrowing of information

# Some Classical Applications

- ▶ Meta Analysis: combine data from multiple studies to make overall conclusion (e.g., drug is effective)
- ▶ Multi-level Designs: subjects are nested in schools, regions or study centers
- ▶ Longitudinal Data: data collected for subject over time - important to accommodate within-subject dependence

# Some Emerging Applications

- ▶ Joint modeling of data from different domains
  1. Images and captions
  2. Diagnostic images or functional predictors & health responses
  3. Multiple types of omics data (sequence & expression)
- ▶ Multi-task learning: borrow strength across tasks
  1. Multiple images, music pieces, security videos
  2. Compressive sensing
  3. User preferences in different domains (film, books, etc)

# Application 1 - Multinational Bioassay

- ▶ Increasing concern about adverse effects of environmental estrogens on human development
- ▶ Rodent uterotrophic bioassay: system for identifying suspected agonists or antagonists of estrogen.
- ▶ OECD study: collected data from 19 laboratories to investigate consistency of effects of known agonist (EE) & antagonist (ZM)
- ▶  $y_{ij}$  = uterus weight for rat  $j$  in lab  $i$
- ▶  $x_{ij}$  = lab indicator, dose of EE, dose of ZM



- ▶ Can potentially fit normal random effects model,

$$y_{ij} = \mathbf{x}'_{ij}\mathbf{b}_i + \epsilon_{ij}, \epsilon_{ij} \sim N(0, \sigma^2)$$
$$\boldsymbol{\theta}_i \sim N_p(\boldsymbol{\theta}, \boldsymbol{\Sigma})$$

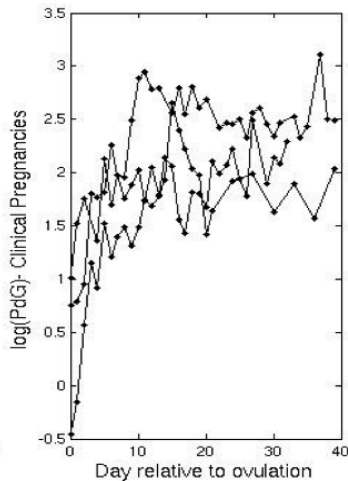
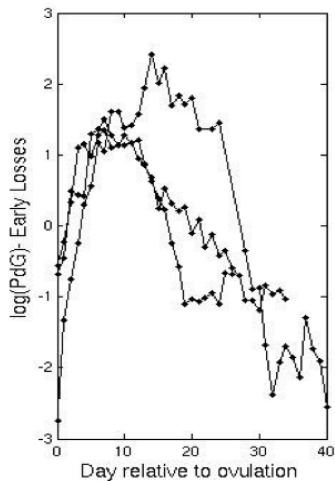
- ▶ Normal distribution has light tails & does not allow outlying labs or clusters of labs
- ▶ Conclusions may be sensitive to violations of normality
- ▶ Appealing to have a more flexible approach available

- ▶ A simple case corresponds to the linear mixed effects model

$$y_{ij} = \mathbf{x}_{ij}\boldsymbol{\beta} + \mathbf{z}_{ij}\mathbf{b}_i + \epsilon_{ij}, \epsilon_{ij} \sim N(0, \sigma^2)$$
$$\mathbf{b}_i \sim P, \quad P \sim DP(\alpha P_0)$$

- ▶ DP prior on  $P$ , the distribution of the random effects
- ▶ Useful semiparametric model for longitudinal & correlated data
- ▶ Bush & MacEachern (1996), Müller & Rosner (1997), Kleinman & Ibrahim (1998), Ishwaran & Takahara (2002), etc

# Application 2 - longitudinal data (log PdG trajectories (Bigelow & Dunson, JASA, 08))



- ▶ Interest in estimating a collection of functions,  $\{f_i\}_{i=1}^n$ .
- ▶ Longitudinal trajectories for different individuals
- ▶ We will focus on the following model:

$$y_{ij} = f_i(t_{ij}) + \epsilon_{ij}, \quad \epsilon_{ij} \sim t_\nu(\sigma^2)$$
$$f_i(t) = \sum_{j=1}^P \beta_{ij} b_j(t) = \mathbf{b}(t)' \boldsymbol{\beta}_i$$
$$\boldsymbol{\beta}_i \sim P$$

$\mathbf{b} = \{b_j\}$  = basis functions,  $\boldsymbol{\beta}_i$  = basis coefficients

- ▶ Subject-specific basis coefficients,  $\beta_i$ , allow variability in the functional trajectories for different individuals
- ▶ Heterogeneity among subjects controlled by the random effects distribution,  $P$
- ▶ Number of basis functions,  $p$ , is not small ( $p \geq 20$ )

- ▶ Characterize variability in growth curves & cluster subjects having similar trajectories
- ▶ Can be accomplished using DPM linear mixed model with

$$f_i(t_{ij}) = \sum_{l=1}^p \beta_{il} b_l(t_{ij})$$
$$\beta_i \sim P = \sum_{h=1}^{\infty} \pi_h \delta_{\beta_h^*}$$

- ▶ Recalling the DP stick-breaking property (Sethuraman, 1994):

$$\beta_i \sim P = \sum_{h=1}^{\infty} V_h \prod_{l < h} (1 - V_l) \delta_{\beta_h^*}, V_h \stackrel{i.i.d}{\sim} \text{Beta}(1, \alpha), \beta_h^* \sim P_0$$

- ▶ Hence, the  $n$  subjects are grouped into  $k \leq n$  clusters
- ▶ Subjects in cluster  $l$  all have  $\beta_i = \beta_l^*$ .
- ▶ Provides a semiparametric Bayes version of latent trajectory class or growth mixture models.
- ▶ Avoids fixing the number of clusters in advance

- ▶ The curve in cluster  $l$  is  $f(t) = \mathbf{b}(t)' \beta_l^*$ .
- ▶ The number of functional clusters in  $n$  growth curves is treated as unknown
- ▶ Gibbs samplers are straightforward to generalize
- ▶ Number of clusters and configuration of subjects into clusters varies across the MCMC iterations
- ▶ Problem: label switching!



- ▶ Problem arises because the labels on the cluster-specific parameters are ambiguous, so vary in meaning across the iterations
- ▶ Not meaningful to calculate posterior summaries of  $\theta$  across the iterations
- ▶ Strategies:
  1. Relabeling algorithms that align the clusters after running MCMC (Stephens, 00);
  2. Define clusters as individuals that are grouped together with high posterior probability
  3. Estimate optimal clustering (Dahl, 06; Lau & Green, 97)
  4. Ignore problem & avoid cluster-specific inferences