Peter Tonner

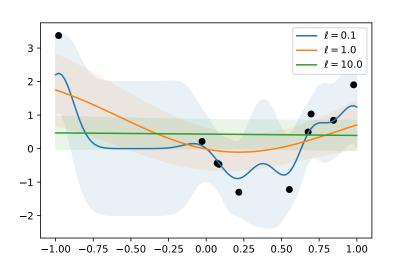
Computational Biology and Bioinformatics **Duke University**

October 13, 2017

Gaussian processes for Computational Biology: Theory

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Hyperparameters change model interpretation



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Hierarchical Models
Basic GP model
Functional Linear
Model

NA-seq

1. Maximize likelihood

- gradient optimization, point estimate
- **pros:** many existing implementations (e.g. *GPy*), often gets answer the fastest
- **cons:** requires "conjugacy" b/w f and y for analytical sol'n

2. Model hyperparameter uncertainty

- Posterior sampling (MCMC)
- **pros:** Doesn't care about form of p(y), can be placed in larger model easily
- cons: sampling time (can be long)

$$\underbrace{p(\theta|y)}_{\text{posterior}} = \underbrace{\frac{p(y|\theta)}{p(\theta)} \underbrace{p(\theta)}_{\text{evidence}}}_{\text{evidence}}$$

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likelihood prior posterior evidence

$$p(y) = \int p(y|\theta)p(\theta)\partial\theta$$

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$$p(y) = \int p(y|\theta)p(\theta)\partial\theta$$

evidence

- ▶ In general, computing p(y) is quite difficult
- MCMC sampling:
 - Gibbs sampling
 - Stan

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Markov Chain Monte Carlo: the (extremely) short version

 $\overbrace{p(\theta|y)}^{\text{posterior}} \propto \overbrace{p(y|\theta)}^{\text{likelihood prior}} \overbrace{p(\theta)}^{\text{prior}}$

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Markov Chain Monte Carlo: the (extremely) short version

$$\overbrace{p(\theta|y)}^{\text{posterior}} \propto \overbrace{p(y|\theta)}^{\text{likelihood prior}} \overbrace{p(\theta)}^{\text{prior}}$$

Generate samples:

$$\boldsymbol{\theta} = \{ \tilde{\theta} \mid \tilde{\theta} \text{ drawn from } p(\theta|y) \}$$

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Markov Chain Monte Carlo: the (extremely) short version

$$\overbrace{p(\theta|y)}^{\text{posterior}} \propto \overbrace{p(y|\theta)}^{\text{likelihood prior}} \overbrace{p(\theta)}^{\text{prior}}$$

Generate samples:

$$\boldsymbol{\theta} = \{ \tilde{\theta} \mid \tilde{\theta} \text{ drawn from } p(\theta|y) \}$$

Quantities of interest:

$$E[\theta] \approx \frac{1}{n} \sum_{i=1}^{n} \tilde{\theta}_{i}$$

▶ In general (for any f):

$$E[f(\theta)] \approx \frac{1}{n} \sum_{i=1}^{n} f(\tilde{\theta}_i)$$

▶ There are many (MCMC) algorithms to generate θ .

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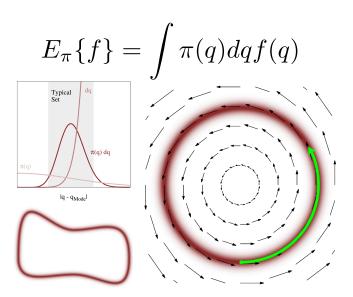
RNA-seq

Reid et al

"a state-of-the-art platform for statistical modeling and high-performance statistical computation" http://mc-stan.org/

- ► Hamiltonian monte-carlo (HMC)
- Has other inference methods as well: maximum likelihood, variational inference
- Probabilitic programming language
- Quite fast (relatively speaking and when used properly)

Hamiltonian Monte-Carlo



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functions: user defined functions

data: input to the model

transformed data: generated from data

parameters: quantities of interest

- transformed parameters: similar to parameters, derived from other parameters, these can still be used in the model block
- ▶ model: relationship b/w data and parameters
- generated quantities: similar to transformed parameters, but not used in model. e.g. posterior predictive checking



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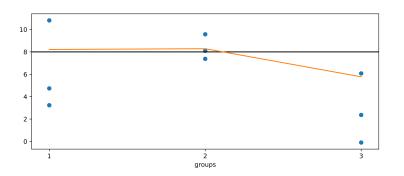
Functional Linear Mode

Single-cell RNA-sec

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Note on hierarchical models

$$y_i \sim \textit{N}(\theta_i, \sigma_y^2)$$
 and $\theta_i \sim \textit{N}(\mu, \tau^2)$



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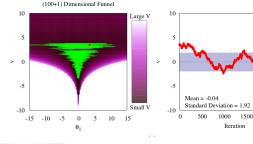
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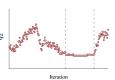
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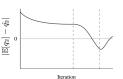
Hierarchical models confound MCMC

 $y_i \sim \textit{N}(heta_i, \sigma_{\textit{v}}^2)$ and $heta_i \sim \textit{N}(\mu, au^2)$









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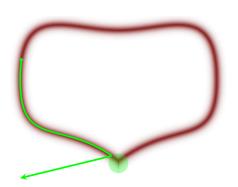
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HMC can identify problems in model

$$y_i \sim N(\theta_i, \sigma_y^2)$$
 and $\theta_i \sim N(\mu, \tau^2)$



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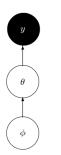
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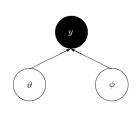
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Solution: non-centered parameterization

$$y_i \sim \textit{N}(\vartheta_i \tau + \mu, \sigma_y^2)$$
 and $\vartheta_i \sim \textit{N}(0, 1)$
 $\Rightarrow \vartheta_i \tau \sim (0, \tau^2)$





("Hamiltonian Monte Carlo for Hierarchical Models", Michael Betancourt and Mark Girolam)

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$$y(x) \sim N(f(x), \sigma_y^2)$$
 $f(x) \sim GP(\mu(x), \kappa(x, \alpha, \ell))$
 $\sigma_y^2 \sim Ga(\cdot, \cdot)$
 $\alpha \sim Ga(\cdot, \cdot)$
 $\ell \sim InvGa(\cdot, \cdot)$

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Functional Linear Model

$$\Sigma = LL^T$$

- ▶ L: lower triangular matrix
- ▶ allows for fast solving of $\Sigma x = y$, e.g. compute $\Sigma^{-1}y$
- ▶ if L is a Cholesky factor of Σ and $z \sim N(0, I)$, then

$$x = \mu + Lz \sim N(\mu, \Sigma)$$

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f(x), ℓ , and α are highly related - certain values of one influence the probability of the others and vice-versa.

Non-centered implementation

$$f_{\eta}(x) \sim N(0,1)$$

$$\kappa(x, \alpha, \ell) = LL^T$$
 and $f(x) = L \cdot f_{\eta}(x)$
 $\Rightarrow f(x) \sim N(0, \kappa(x, \alpha, \ell))$

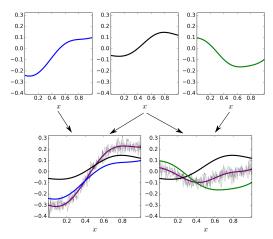
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Functional Linear Model

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Functional Linear Model

$$y_r(x) = \sum_{i=1}^k M_{r,i} \cdot \beta_i(x) + \epsilon(x)$$



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$$y_r(x) = \sum_{i=1}^k M_{r,i} \cdot \beta_i(x) + \epsilon(x)$$

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$$y_r(x) = \sum_{i=1}^k M_{r,i} \cdot \beta_i(x) + \epsilon(x)$$
 $y(x): n \times p$ observations $M: p \times k$ design matrix $g \in \{1, \dots, L\}^k$ group assignment

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Functional Linear Model

$$y_r(x) = \sum_{i=1}^k M_{r,i} \cdot \beta_i(x) + \epsilon(x)$$
 $y(x) : n \times p$ observations $M : p \times k$ design matrix $g \in \{1, \dots, L\}^k$ group assignment

Each group j has a GP prior with hyperparameters σ_i^2 , ℓ_i

$$\beta(\mathbf{x}) = \{\beta_1(\mathbf{x}), \dots, \beta_{m_1}(\mathbf{x}), \beta_{m_1+1}(\mathbf{x}), \dots, \beta_{m_1+m_2}(\mathbf{x}), \dots, \beta_{\sum_g m_g}(\mathbf{x})\}$$

$$GP(\mu_1(x), K_1(x_1, x_2) \mid \theta_1) \quad GP(\mu_2(x), K_g(x_1, x_2) \mid \theta_2) \quad \cdots$$

$$\sigma_1^2, \ell_1 \qquad \sigma_2^2, \ell_2$$

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Functional Linear Model

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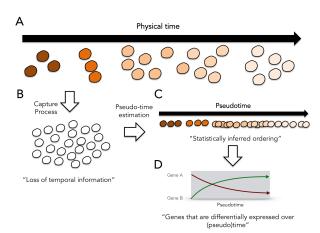
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Reid et al.

for Computational

Single-cell RNA-seq Reid et al.

Single-cell RNA-seq and pseudotime



"Order Under Uncertainty: Robust Differential Expression Analysis Using Probabilistic Models for Pseudotime Inference", Cambpell $\it et al.$, 2016

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$$y_{g} \sim N(\phi_{g}, \Sigma_{g})$$

$$\Sigma_{g}(\tau_{1}, \tau_{2}) = \psi_{g} \kappa(\tau_{1}, \tau_{2}) + \omega_{g} \delta(\tau_{1} = \tau_{2})$$

$$log(\psi_g) \sim \textit{N}()$$
 and $log(\omega_g) \sim \textit{N}()$

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

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