## Japanese Joint Statistical Meeting 2018

2018/09/09 (Sun.) - 2018/09/13 (Thu.)

# Stochastic Variational Inference of Mixture Models in Phylogenetics

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2018年度

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■E会場 (5333教室) 10:00 - 12:00

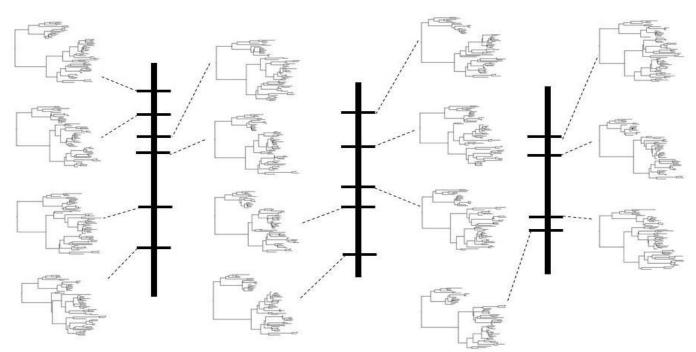
【一般講演】English Session (4): Medical Statistics and Biostatistics

[Chair] Ryuji Uozumi (Kyoto University)

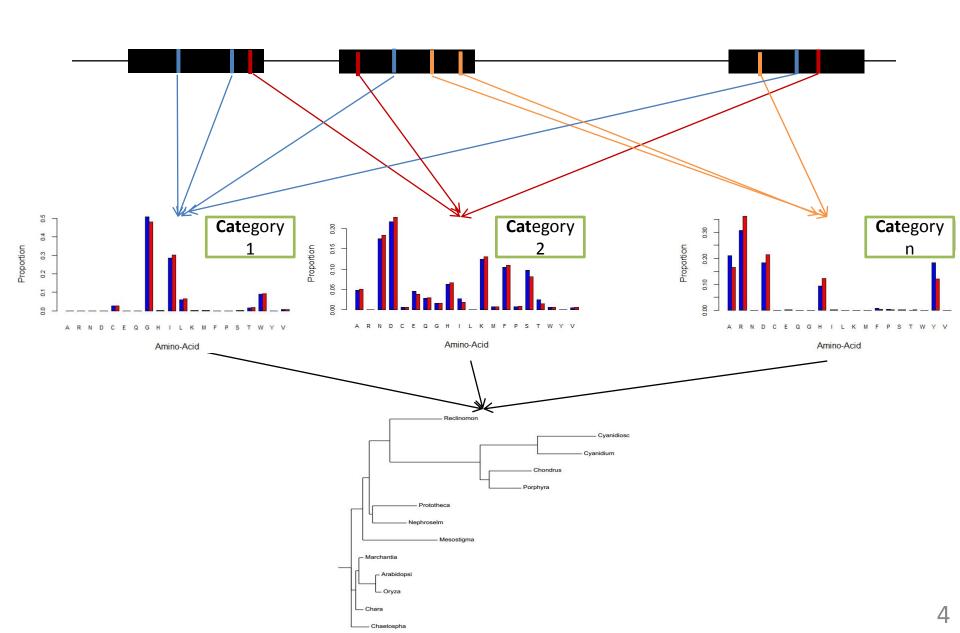
	講演タイトル	発表者 (所属)	共著者 (所属)	報告集
1	Use of external information for assessing efficacy equivalence in biosimilar clinical trials	Ryuji Uozumi (Kyoto University)	Shinjo Yada (A2 Healthcare)	<u> </u>
2	Bartlett-type corrections for the confidence interval of a treatment effect of the multivariate random effects meta- analysis model via analytical approach	Masahiro Kojima (Kyowa Hakko Kirin)		<u> </u>
3	The impact of unobserved heterogeneity and competing risks with shared frailty in radiation risk assessment	Kyoji Furukawa (Kurume University)		<u> </u>
4	Modelling life history under varying temperature conditions	Hideyasu Shimadzu (Loughborough University)		
5	Sufficient dimension reduction via random-partitions for the large-p-small-n problem	Hung Hung (National Taiwan University)		
6	Stochastic Variational Inference of Mixture Models in Phylogenetics	Tung Dang (University of Tokyo)	Hirohisa Kishino (University of Tokyo)	

### Problem of Phylogenomics

- The pattern of molecular evolution varies among gene sites and genes in a genome.
- By taking into account the complex heterogeneity of evolutionary processes among sites in a genome, Bayesian infinite mixture models of genomic evolution enable robust phylogenetic inference.



### CAT model (Lartillot et al 2004)



#### The likelihood of CAT model

$$p(\Xi_{ij} \mid \pi_{ka}, r_i, l_j) = \prod_{k=1}^{\infty} \prod_{a=1}^{20} \left( \pi_{ka} p(\mathbf{n}_{ij} \mid r_i, l_j) \right)^{I[Z_i = k]}$$

$$p(\Xi_{ij} \mid \pi_{ka}, r_i, l_j) = \left(\prod_{k=1}^{\infty} \prod_{a=1}^{20} \pi_{ka}^{w_{ka}}\right)^{\prod_{i \neq i} \sum_{j} n_{ij}} \left(\prod_{i} r_i^{\sum_{j} n_{ij}}\right) \left(\prod_{j} l_j^{\sum_{i} n_{ij}}\right) \left(\prod_{ij} \frac{e^{-r_i l_j}}{n_{ij}!}\right)$$

 $l_i$ : branch lengths

 $r_i$ : rate of substitution

 $\pi_{ka}$  : equilibrium frequency profile

A stick-breaking construction

 $V_{\nu}$  : unit length of the stick

 $I[Z_i=k]$ : allocation variable

 $\Xi_{ij}$ : substitution mapping data

 $n_{ij}$ : number of substitutions

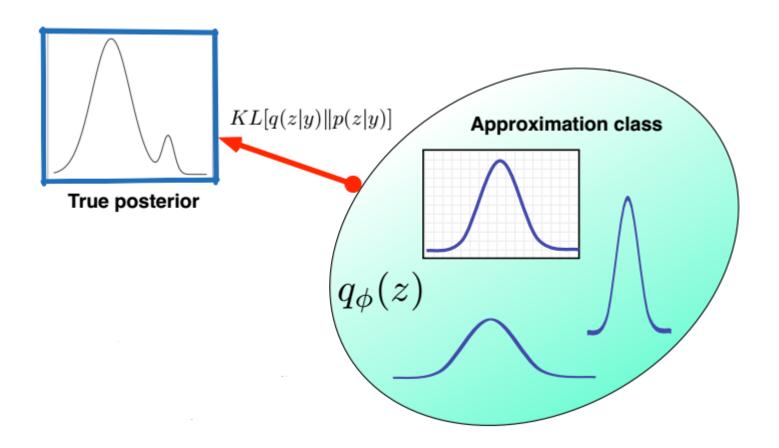
 $W_{ka}$ : number of type of substitutions

### MCMC becomes infeasible for large datasets

- The computational burden of MCMC is prohibitive for large data sets.
- Even well-designed sampling schemes needs a large sample to achieve convergence.
- Diagnosis of convergence is difficult for high dimensional parameter space.

#### Variational Method

approximate complicated densities by a simpler class of densities, called **variational distribution**.



### Evidence Lower Bound (ELBO)

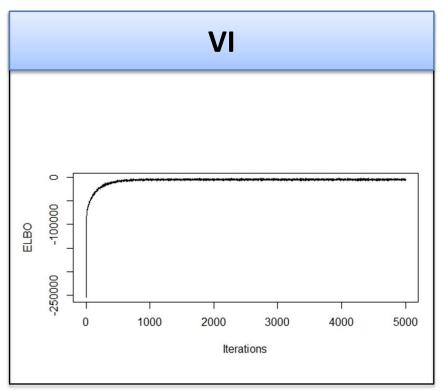
$$\text{KL}[q(\boldsymbol{\theta}; \boldsymbol{\Theta}) \parallel p(\boldsymbol{\theta}|\mathbf{X})]$$

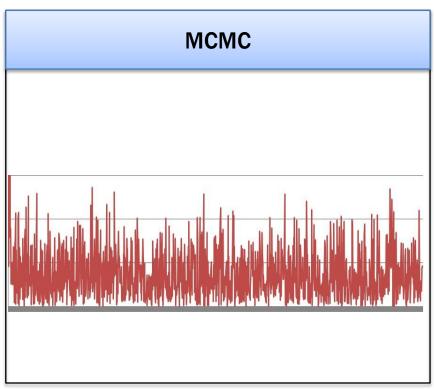
$$= E_q[\log q(\boldsymbol{\theta}; \boldsymbol{\Theta})] - E_q[\log p(\mathbf{X}, \boldsymbol{\theta})] + \log p(\mathbf{X})$$

-ELBO: computable

Computational headache
But constant !!

### Variational Inference and MCMC





Maximizing ELBO

Monte Carlo simulation with proposal and acceptance steps

## Example: Variational Inference of Bayesian Ridge Regression

The likelihood is

$$p(t|x, w, \beta) = \prod_{n=1}^{N} \mathcal{N}(t_n|w^Tx_n, \beta^{-1})$$

- The regression coefficient  $p(w|\alpha) = \mathcal{N}(w|0, \alpha^{-1}I)$
- The extent of shrinkage  $p(\alpha) = Gam(\alpha|a_0, b_0)$
- The variational mean-field representation

$$q(w, \alpha) = q(w) q(\alpha)$$

The practical variational distributions

$$q(w) = \mathcal{N}(w|m_N, S_N)$$
  
 $q(\alpha) = Gam(\alpha|a_N, b_N)$ 

## Example: Variational Inference of Bayesian Ridge Regression

• The ELBO for Bayesian ridge regression model.

$$\mathcal{L}\left[q(w, \alpha | m_N, S_N, a_N, b_N)\right] = \mathcal{E}_q\left[\log p\left(t | w\right)\right] + \mathcal{E}_q\left[\log p\left(w | \alpha\right)\right] + \mathcal{E}_q\left[\log p\left(\alpha\right)\right]$$
$$-\mathcal{E}_q\left[\log q\left(w | m_N, S_N\right)\right] - \mathcal{E}_q\left[\log q\left(\alpha | a_N, b_N\right)\right]$$

• Update  $m_N, S_N$ : Given  $a_N = a_N^0, b_N = b_N^0, m_N = m_N^0, S_N = S_N^0$ 

$$m_N = \beta S_N^0 X^T t$$

$$S_N = \left( \mathbb{E}_q \left[ \alpha \right] + \beta X^T X \right)^{-1} I = \left( \frac{a_N^0}{b_N^0} + \beta X^T X \right)^{-1} I$$

• Update  $a_N, b_N$ : Given  $a_N = a_N^0, b_N = b_N^0, m_N = m_N^0, S_N = S_N^0$ 

$$a_N = a_0 + \frac{M}{2}$$
  
 $b_N = b_0 + \frac{1}{2} E_q \left[ w^T w \right] = b_0 + \frac{1}{2} \left( m_N^{0^T} m_N^0 + S_N^0 \right)$ 

The PDF of a DMM can be represented

$$f(\mathbf{X}; \mathbf{\Pi}, \mathbf{U}) = \prod_{n=1}^{N} \sum_{i=1}^{I} \pi_i \operatorname{Dir}(\mathbf{x}_n; \mathbf{u}_i), \quad \pi_i > 0, \quad \sum_{i=1}^{I} \pi_i = 1$$

The mixture weights  $\Pi = [\pi_1, ..., \pi_I]^T$ 

$$\mathbf{\Pi} = [\pi_1, ..., \pi_I]^{\mathrm{T}}$$

The parameter matrix 
$$\mathbf{U} = [\mathbf{u}_1, ..., \mathbf{u}_I]$$

The joint distribution of the observation X and all the latent variables

$$f(\mathbf{X}, \mathcal{Z}) = f(\mathbf{X}, \mathbf{U}, \mathbf{\Pi}, \mathbf{Z})$$

$$= f(\mathbf{X}|\mathbf{Z}, \mathbf{U}) f(\mathbf{Z}|\mathbf{\Pi}) f(\mathbf{\Pi}) f(\mathbf{U})$$

$$= \prod_{n=1}^{N} \prod_{i=1}^{I} \left[ \pi_{i} \frac{\Gamma(\sum_{k=1}^{K+1} u_{ki})}{\prod_{k=1}^{K+1} \Gamma(u_{ki})} \prod_{k=1}^{K+1} x_{kn}^{u_{ki}-1} \right]^{z_{ni}} \times \frac{\Gamma(\sum_{i=1}^{I} c_{i_{0}})}{\prod_{i=1}^{I} \Gamma(c_{i_{0}})} \prod_{i=1}^{I} \pi_{i}^{c_{i_{0}}-1}$$

$$\times \prod_{i=1}^{I} \prod_{k=1}^{K+1} \frac{\alpha_{ki_{0}}^{\mu_{ki_{0}}}}{\Gamma(\mu_{ki_{0}})} u_{ki}^{\mu_{ki_{0}}-1} e^{-\alpha_{ki_{0}} u_{ki}}.$$

The ELBO for Dirchlet Mixture model

$$\mathcal{L} = \mathbb{E}_{\mathcal{Z}}[\ln f(\mathbf{X}, \mathcal{Z})] - \mathbb{E}_{\mathcal{Z}}[\ln f(\mathcal{Z})]$$

The optimal solution to the posterior distribution of uki is

$$\ln f^{*}(u_{ki}; \mu_{ki}, \alpha_{ki}) \\
= \sum_{n=1}^{N} \mathbb{E}[z_{ni}] \times \mathbb{E}_{Z \setminus u_{ki}} \left[ \ln \frac{\Gamma(\sum_{k=1}^{K+1} u_{ki})}{\prod_{k=1}^{K+1} \Gamma(u_{ki})} \right] \\
+ u_{ki} \sum_{n=1}^{N} \mathbb{E}[z_{ni}] \ln x_{kn} + (\mu_{ki_{0}} - 1) \ln u_{ki} - \alpha_{ki_{0}} u_{ki} + \text{const.}$$

The optimal solution to the posterior distribution

$$\ln f^*(\pi_i; c_i) = \mathbb{E}_{\mathcal{Z} \setminus \pi_i}[\ln f(\mathbf{X}, \mathcal{Z})] = \ln \pi_i \times \sum_{n=1}^N \mathbb{E}[z_{ni}] + \ln \pi_i(c_{i_0} - 1) + \text{const.}$$

For the variable zni, the optimal approximation to the posterior distribution is

$$\ln f^{*}(z_{ni}) = \mathbb{E}_{\mathcal{Z}\setminus z_{ni}}[\ln f(\mathbf{X}, \mathcal{Z})]$$

$$= z_{ni} \times \left[\mathbb{E}[\ln \pi_{i}] + \sum_{k=1}^{K+1} (u_{ki} - 1)\ln x_{kn}\right]$$

$$+ z_{ni} \times \mathbb{E}\left[\ln \frac{\Gamma(\sum_{k=1}^{K+1} u_{ki})}{\prod_{k=1}^{K+1} \Gamma(u_{ki})}\right] + \text{const.}$$

#### Definition [edit]

The Taylor series of a real or complex-valued function f(x) that is infinitely differentiable at a real or complex number a is the power series

-0.5

-1.5

-2.5

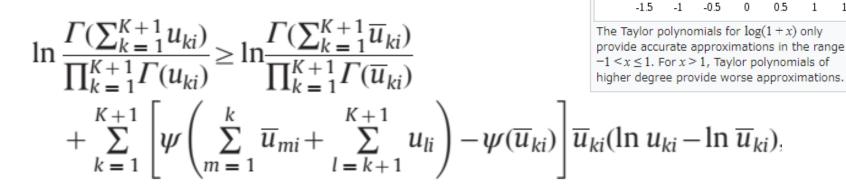
-3.5

$$f(a) + \frac{f'(a)}{1!}(x-a) + \frac{f''(a)}{2!}(x-a)^2 + \frac{f'''(a)}{3!}(x-a)^3 + \cdots,$$

which can be written in the more compact sigma notation as

$$\sum_{n=0}^{\infty} \frac{f^{(n)}(a)}{n!} (x-a)^n,$$

A lower-bound approximation can be obtained as



 $\psi(\cdot)$  is the digamma function defined as  $\psi(x) = \partial \ln \Gamma(x)/\partial x$ .

1.5

The optimal solution to the posterior distribution of uki is

$$\ln f^*(u_{ki}; \mu_{ki}, \alpha_{ki}) \approx \mathbb{E}_{\mathbb{Z}\setminus u_{ki}} \left[\ln \widetilde{f}(\mathbf{X}, \mathbb{Z})\right]$$

$$= \sum_{n=1}^{N} \mathbb{E}[z_{ni}] \times \mathbb{E}_{\mathbb{Z}\setminus u_{ki}} \left[\ln \frac{\Gamma(\sum_{k=1}^{K+1} u_{ki})}{\prod_{k=1}^{K+1} \Gamma(u_{ki})}\right] = \sum_{n=1}^{N} \mathbb{E}[z_{ni}] \times \left[\psi\left(\sum_{k=1}^{K+1} \overline{u}_{ki}\right) - \psi(\overline{u}_{ki})\right] \overline{u}_{ki} \ln u_{ki} - \ln \overline{u}_{ki}$$

$$+ u_{ki} \sum_{n=1}^{N} \mathbb{E}[z_{ni}] \ln x_{kn} + (\mu_{ki_0} - 1) \ln u_{ki} - \alpha_{ki_0} u_{ki} + \text{const.}$$

$$+ u_{ki} \sum_{n=1}^{N} \mathbb{E}[z_{ni}] \ln x_{kn} + (\mu_{ki_0} - 1) \ln u_{ki} - \alpha_{ki_0} u_{ki} + \text{const.},$$

For the variable zni, the optimal approximation to the posterior distribution is

$$\ln f^{*}(z_{ni}) = \mathbb{E}_{\mathcal{Z}\setminus z_{ni}}[\ln f(\mathbf{X}, \mathcal{Z})] \qquad \approx \mathbb{E}_{\mathcal{Z}\setminus z_{ni}}[\ln f(\mathbf{X}, \mathcal{Z})]$$

$$= z_{ni} \times \left[\mathbb{E}[\ln \pi_{i}] + \sum_{k=1}^{K+1} (u_{ki} - 1) \ln x_{kn}\right] = z_{ni} \times \left[\mathbb{E}[\ln \pi_{i}] + \sum_{k=1}^{K+1} (u_{ki} - 1) \ln x_{kn}\right]$$

$$+ z_{ni} \times \mathbb{E}\left[\ln \frac{\Gamma(\sum_{k=1}^{K+1} u_{ki})}{\prod_{k=1}^{K+1} \Gamma(u_{ki})}\right] + \text{const.} \qquad + z_{ni} \times \sum_{k=1}^{K+1} \left[\psi\left(\sum_{k=1}^{K+1} \overline{u}_{ki}\right) - \psi(\overline{u}_{ki})\right] \overline{u}_{ki} \mathbb{E}_{u_{ki}}[\ln u_{ki}] - \ln \overline{u}_{ki}) + \text{const.}$$

#### **Algorithm 1.** Variational DMM.

```
Input: observation X, number of mixture components I
Initialize \alpha_{ki_0}, \mu_{ki_0}, c_{i_0}, for i = 1,..., I, k = 1,..., K+1^3;
repeat
      for each k, i
      \alpha_{ki}^* = \alpha_{ki_0} - \sum_{n=1}^N \mathbb{E}[z_{ni}] \ln x_{kn}
      \mu_{ki}^* = \mu_{ki_0} + \sum_{n=1}^{N} \mathbb{E}[z_{ni}] \overline{u}_{ki} [\psi(\sum_{k=1}^{K+1} \overline{u}_{ki}) - \psi(\overline{u}_{ki})]
      c_i^* = c_{i_0} + \sum_{n=1}^{N} \mathbb{E}[z_{ni}]
until stop criteria are reached.
Output: the optimal hyperparameters \alpha_{ki}^*, \mu_{ki}^*, c_i^*.
(The quantities \overline{u}_{ki} and \mathbb{E}[z_{ni}] are calculated
          \overline{u}_{ki} = \frac{\mu_{ki}}{\alpha_{ki}}, \quad \mathbb{E}[z_{ni}] = \frac{\rho_{ni}}{\sum_{i} \alpha_{ki}},
                     \ln \rho_{ni} = \psi(c_i) - \psi(\mathbf{c}^{\mathsf{T}} \mathbf{1}_I) + P_i + (\mathbf{u}_i - 1)^{\mathsf{T}} \ln \mathbf{x}_n
```

#### Variational distribution for CAT model

The mean-field variational representation

$$\begin{split} q(\Xi,z,V,\pi,l,r|\Theta) &= \prod_{j} q\left(l_{j}|\gamma_{j},\gamma_{j}^{'}\right) \times \prod_{i} q\left(r_{i}|\zeta_{i},\zeta_{i}^{'}\right) \\ &\times \prod_{k=1}^{K_{\max}} \prod_{a=1}^{20} q\left(\pi_{a}^{k}|\lambda_{a}^{k}\right) \times \prod_{k=1}^{K_{\max}} q\left(V_{k}|\vartheta_{k},\vartheta_{k}^{'}\right) \\ &\times \prod_{i} \prod_{a=1}^{K_{\max}} q\left(z_{i}^{k}|\phi_{i}^{k}\right) \times \prod_{j} q\left(n_{ij}|\omega_{ij}\right) \\ &\times \prod_{k=1}^{K_{\max}} \prod_{a=1}^{20} q\left(w_{a}^{k}|\iota_{a}^{k}\right) \\ &\times \prod_{i} \prod_{k=1}^{K_{\max}} q\left(z_{i}^{k}|\phi_{i}^{k}\right) \times \prod_{ij} q\left(n_{ij}|\omega_{ij}\right) \\ &\times \prod_{k=1}^{K_{\max}} \prod_{a=1}^{20} q\left(w_{a}^{k}|\iota_{a}^{k}\right) \\ &\times \prod_{k=1}^{K_{\min}} \prod_{a=1}^{20} q\left(w_$$

#### Stochastic Variational Inference

These distributions are in the exponential family

$$p(\pi \mid \Xi, z, l, r) = h(\pi) \exp\left(\eta(\Xi, z, l, r)^{T} t(\pi) - a(\eta(\Xi, z, l, r))\right)$$

Natural parameter

Sufficient statistics

Log-normalizer

- The variational parameters  $q(\pi | \lambda) = h(\pi) \exp(\lambda^T t(\pi) a(\lambda))$
- The natural gradient of the ELBO [Amari, 1998]

$$\nabla_{\lambda}^{nat} ELBO(\lambda) = \left(prior + NE_{q}\left[t(\Xi, z, l, r)\right]\right) - \lambda$$

- It is good for stochastic optimization.
  - Its expectation is the exact gradient (unbiased).
  - It only depends on optimized parameters of one data point (cheap).

## Variational approximation for model of nucleotide substitution

#### Evidence Lower Bound (ELBO)

$$\mathcal{L} = \sum_{k=1}^{K_{max}} \operatorname{E}_{q} \left[ \log \left( p \left( V_{k} | 1, \kappa \right) \right) \right] - \sum_{k=1}^{K_{max}} \operatorname{E}_{q} \left[ \log \left( q \left( V_{k} | \vartheta_{k}, \vartheta_{k}^{'} \right) \right) \right]$$

$$+ \sum_{i} \sum_{k=1}^{K_{max}} \operatorname{E}_{q} \left[ \log p(Z_{i}^{k} | V_{1}, V_{2}, ..., V_{K_{max}}) \right]$$

$$- \sum_{i} \sum_{k=1}^{K_{max}} \operatorname{E}_{q} \left[ \log \left( q \left( Z_{i}^{k} | \varphi_{i}^{k} \right) \right) \right]$$

$$+ \sum_{i} \sum_{k=1}^{K_{max}} \sum_{a=1}^{20} \operatorname{E}_{q} \left[ \log p(\pi_{a}^{k} | v_{a}) \right] - \sum_{k=1}^{K_{max}} \sum_{a=1}^{20} \operatorname{E}_{q} \left[ \log \left( q \left( \pi_{a}^{k} | \lambda_{a}^{k} \right) \right) \right]$$

$$+ \sum_{i} \operatorname{E}_{q} \left[ \log \left( p \left( l_{j} | 1, \beta \right) \right) \right] - \sum_{i} \operatorname{E}_{q} \left[ \log \left( q \left( l_{j} | \gamma_{j}, \gamma_{j}^{'} \right) \right) \right]$$

$$+ \sum_{i} \operatorname{E}_{q} \left[ \log \left( p \left( r_{i} | \alpha, \alpha \right) \right) \right] - \sum_{i} \operatorname{E}_{q} \left[ \log \left( q \left( r_{i} | \zeta_{i}, \zeta_{i}^{'} \right) \right) \right]$$

$$+ \sum_{i} \int_{i} \int_{z} \sum_{n} \sum_{i} q(z) q(n) q(\pi) q(r) q(l) \log \left( p(n|D, z, \pi, r, l) \right) d(\pi) d(r) d(l)$$

$$- \sum_{i} q(u) \log \left( q(u) \right)$$

$$+ \int_{\pi} \int_{r} \int_{l} \sum_{z} \sum_{w} q(z) q(w) q(\pi) q(r) q(l) \log \left( p(w|D, z, \pi, r, l) \right) d(\pi) d(r) d(l)$$

$$- \sum_{i} q(w) \log \left( q(w) \right)$$

## Variational approximation for model of nucleotide substitution

 We consider a first-order Taylor expansion to preserve a bound, intractable expectations are avoided

The product of  $r_i l_j$  is denoted  $t_{ij}$ , firstly, we consider a first-order Taylor expansion of  $\log (p(a, b | \pi, t_{ij}))$  for  $\pi_a$  and  $t_{ij}$  at  $\pi'_a = \frac{v_a}{\sum_{a'=1}^{20} v_{a'}}$  and  $t'_{ij} = \frac{1}{\beta} \frac{\alpha}{\alpha} = \frac{1}{\beta}$ 

$$\log \left[ e^{-t_{ij}} + (1 - e^{-t_{ij}}) \pi_{a} \right] \approx \log \left[ e^{-t'_{ij}} + (1 - e^{-t'_{ij}}) \pi'_{a} \right]$$

$$+ \frac{\partial \log \left[ e^{-t_{ij}} + (1 - e^{-t_{ij}}) \pi'_{a} \right]}{\partial t_{ij}} \left( t_{ij} - t'_{ij} \right)$$

$$+ \frac{\partial \log \left[ e^{-t'_{ij}} + (1 - e^{-t'_{ij}}) \pi_{a} \right]}{\partial \pi_{a}} \left( \pi_{a} - \pi'_{a} \right)$$

$$(40)$$

#### Stochastic Variational Inference for CAT model

Iterates t times to update local variational parameters  $\Theta_l = \left\{\mathcal{G}, \mathcal{G}, \phi\right\}$  of local variables  $\Phi_l = \left\{V, z\right\}$  based on mapping data

$$\Theta_l^* = \mathrm{E}_{\Theta_g} \left\{ \eta \left[ \Phi_g, \Xi \right] \right\}$$

By using the natural gradient, iterates t times to update global variational parameters  $\Theta_g = \left\{ \gamma , \gamma', \zeta, \zeta', \lambda, \omega, \iota \right\}$  of global variables  $\Phi_g = \left\{ \Xi, \pi, l, r \right\}$  based on mapping data with step size

$$\begin{split} \widehat{\nabla_{\Theta_g}} \mathcal{L} &= prior + N\{E_{\Theta_t}[t(\Phi_n, \Xi_n), 1]\} - \Theta_g \\ \Theta_g^{(t)} &= \Theta_g^{(t-1)} + \rho_t \widehat{\nabla_{\Theta_g}} \mathcal{L} \end{split}$$

### Checking the performance

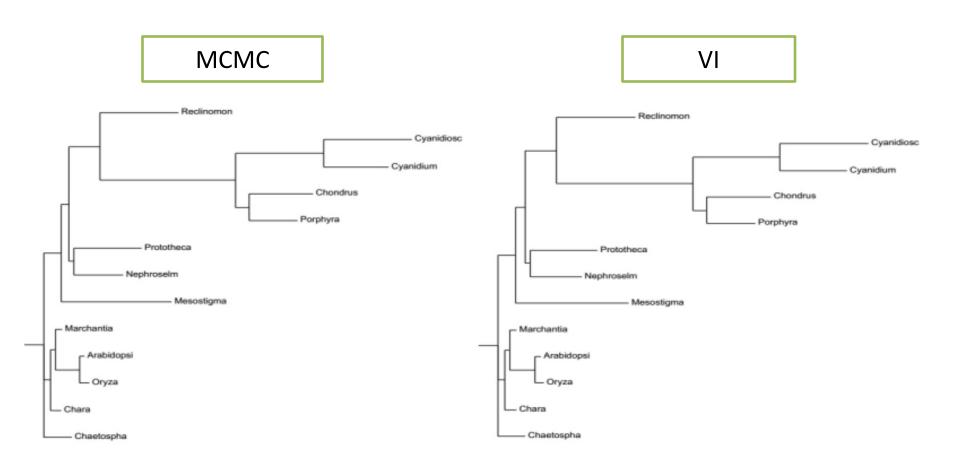
- the mitochondrial data set which consisted of 33 proteins, a total of 6,622 amino acid positions, from 13 species (data set A).
- the plastid data set which consisted of 50 plastidencoded proteins, a total of 10,137 amino acid positions, from 28 species (data set B).
- mitochondrial protein sequences, a large alignment from EST and genome data, which consists of 197 genes, a total of 38,330 amino-acid positions from 66 species (data set C).

### **CPU** time

Run times of variational inference and MCMC algorithms on real data

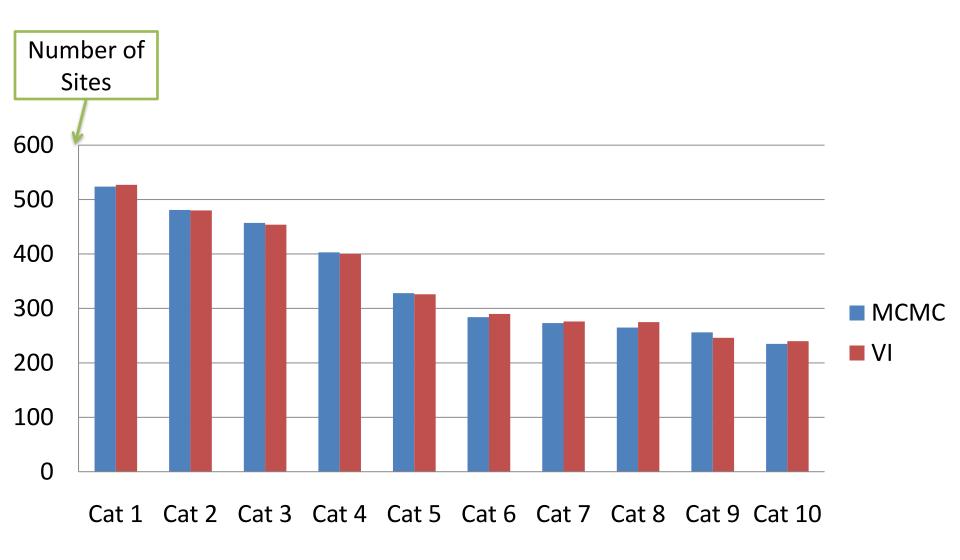
	Data set	Taxa	Sites	States		
	Data Set A	13	6,622	20		1
	Data Set B	28	10,137	20		
Days	Data Set C	66	38,330	20	<u></u>	
30						
25						
20						
15						■ MCMC
10						■ VI
5						
0						
Da	ata Set A I	Data Se	et B	Data S	et C	

### Reconstructed tree

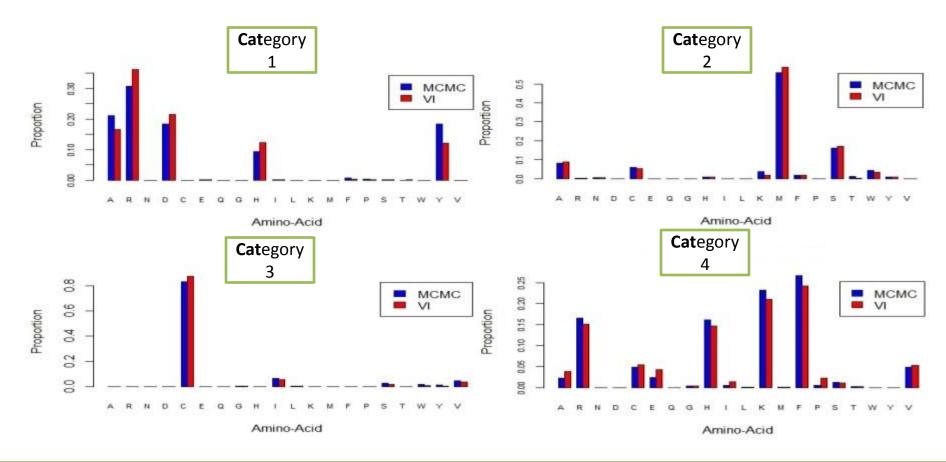


A mitochondrial data set (13 taxa and 6,622 amino acid positions (Rodr´ıguez-Ezpeleta et al. 2006))

## Size of profile categories



### Look into the profile of each category



A mitochondrial data set (13 taxa and 6,622 amino acid positions (Rodr´ıguez-Ezpeleta et al. 2006))

### Summary

- The pattern of molecular evolution varies among gene sites and genes in a genome.
- By taking into account the complex heterogeneity of evolutionary processes among sites in a genome, Bayesian infinite mixture models of genomic evolution enable robust phylogenetic inference.
- With large modern data sets, however, the computational burden of Markov chain Monte Carlo sampling techniques becomes prohibitive.
- Here, we have developed a variational Bayesian procedure to speed up the widely used PhyloBayes MPI program, which deals with the heterogeneity of amino acid propensity.