

Modern Computational Statistics

Lecture 1: Introduction



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School of Mathematical Sciences, Peking University

September 9, 2019

- ▶ Class times:
 - ▶ Monday 6:40-8:30pm, odd Wednesday 8:00-9:50pm
 - ▶ Classroom Building No.3, Room 504
- ▶ Tentative office hours:
 - ▶ Wednesday 10:00-11:00am
 - ▶ By appointment
- ▶ Website:
<https://zcrabbit.github.io/courses/msc-f19.html>
- ▶ Join us at Piazza:
https://piazza.com/peking_university/fall2019/00113730



- ▶ A branch of mathematical sciences focusing on efficient numerical methods for statistically formulated problems
- ▶ The focus lies on computer intensive statistical methods and efficient modern statistical models.
- ▶ Developing rapidly, leading to a broader concept of computing that combines the theories and techniques from many fields within the context of statistics, mathematics and computer sciences.



- ▶ Become familiar with a variety of modern computational statistical techniques and knows more about the role of computation as a tool of discovery
- ▶ Develop a deeper understanding of the mathematical theory of computational statistical approaches and statistical modeling.
- ▶ Understand what makes a good model for data.
- ▶ Be able to analyze datasets using a modern programming language (e.g., python).



- ▶ Optimization Methods
 - ▶ Gradient Methods
 - ▶ Expectation Maximization
- ▶ Approximate Bayesian Inference Methods
 - ▶ Markov chain Monte Carlo
 - ▶ Variational Inference
 - ▶ Scalable Approaches
- ▶ Applications in Machine Learning
 - ▶ Variational Autoencoder
 - ▶ Generative Adversarial Networks
 - ▶ Flow-based Generative Models



Familiar with at least one programming language (with python preferred!).

- ▶ All class assignments will be in python (and use numpy).
- ▶ You can find a good Python tutorial at

<http://www.scipy-lectures.org/>

You may also find another shorter python+numpy tutorial useful at **here**

Familiar with the following subjects (better if have taken related courses)

- ▶ Probability and Statistical Inference
- ▶ Stochastic Processes



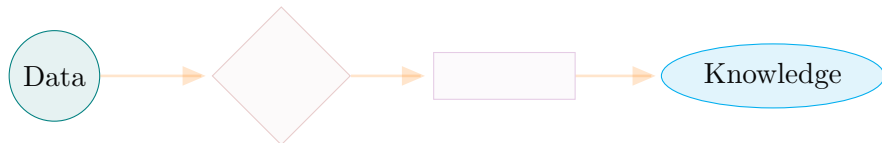
- ▶ 4 Problem Sets: $4 \times 15\% = 60\%$
- ▶ Final Course Project: 40%
 - ▶ Midterm proposal: 5%
 - ▶ Final write-up: 35%
 - ▶ Bonus point for exceptional oral presentation
- ▶ Late policy
 - ▶ 7 free late days, use them in your ways
 - ▶ Afterward, 25% off per late day
 - ▶ Not accepted after 3 late days per PS
 - ▶ Does not apply to Final Course Project
- ▶ Collaboration policy
 - ▶ Finish your work independently, verbal discussion allowed

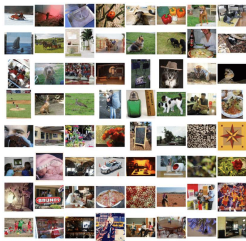


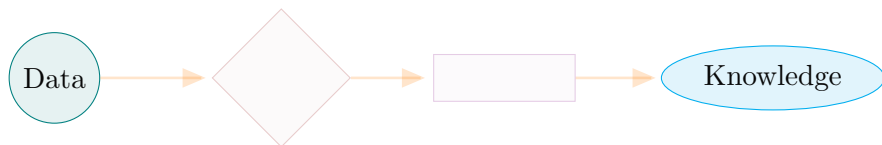
- ▶ You may structure your project exploration around a general problem type, algorithm, or data set, but should explore around your problem, testing thoroughly or comparing to alternatives.
- ▶ You should submit a project proposal that briefly describe your project concept and goals in one page by 11/04.
- ▶ There will be in class project presentation at the end of the term. Not presenting your projects will be taken as voluntarily giving up the opportunity for the final write-ups.
- ▶ You should turn in a write-up (< 10 pages) describing your project and its outcomes, similar to a research-level publication.

- ▶ A brief overview of statistical approaches
- ▶ Basic concepts in statistical computing







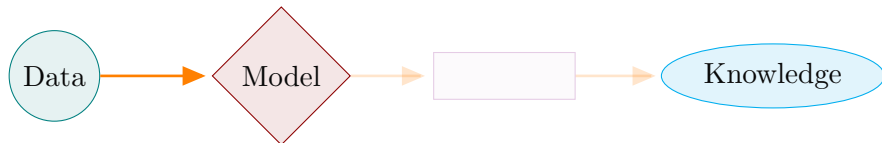
 \mathcal{D} 

Linear Models

Neural Networks

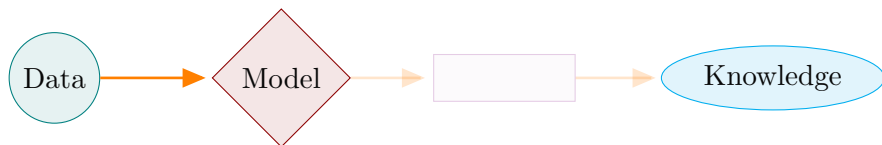
Bayesian Nonparametric Models

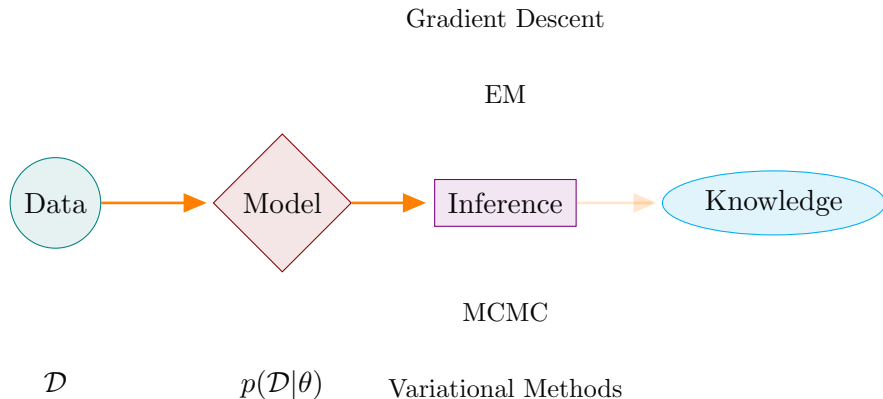
Generalized Linear Models

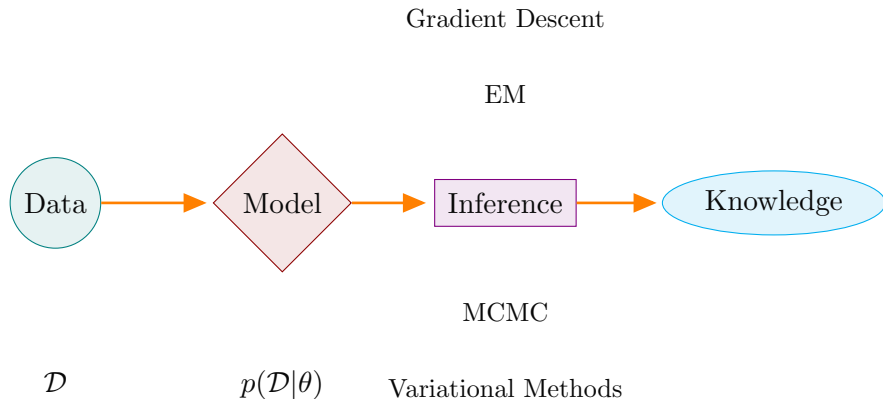


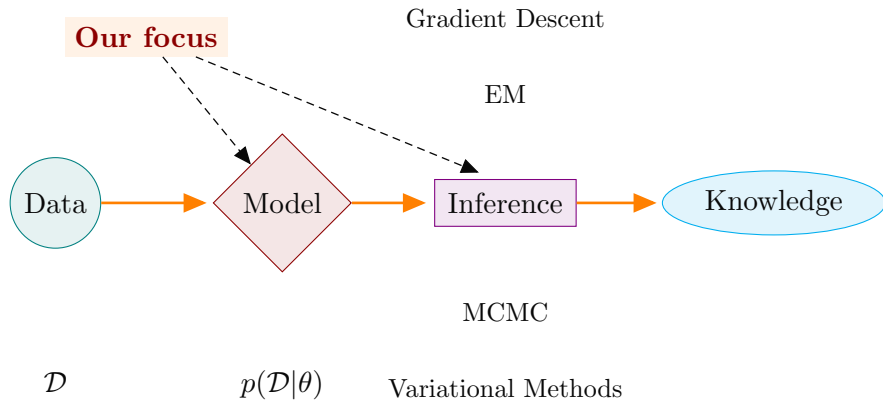
\mathcal{D}



 \mathcal{D} $p(\mathcal{D}|\theta)$ 







“All models are wrong, but some are useful.”

George E. P. Box

Models are used to describe the data generating process, hence prescribe the probabilities of the observed data \mathcal{D}

$$p(\mathcal{D}|\theta)$$

also known as the **likelihood**.

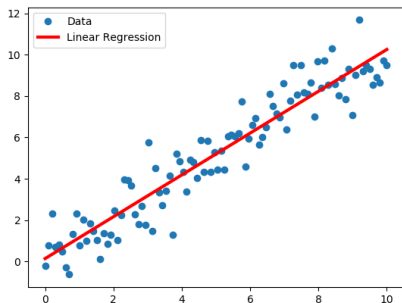


Data: $\mathcal{D} = \{(x_i, y_i)\}_{i=1}^n$

Model:

$$Y = X\theta + \epsilon, \epsilon \sim \mathcal{N}(0, \sigma^2 I_n)$$

$$\Rightarrow Y \sim \mathcal{N}(X\theta, \sigma^2 I_n)$$



$$p(Y|X, \theta) = (2\pi\sigma^2)^{-n/2} \exp\left(-\frac{\|Y - X\theta\|_2^2}{2\sigma^2}\right)$$



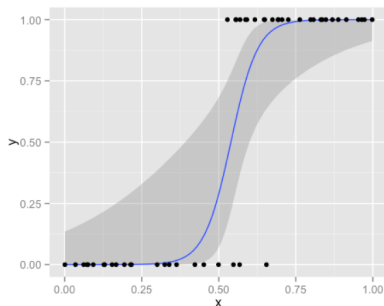
Data:

$$\mathcal{D} = \{(x_i, y_i)\}_{i=1}^n, \quad y_i \in \{0, 1\}$$

Model:

$$Y \sim \text{Bernoulli}(p)$$

$$p = \frac{1}{1 + \exp(-X\theta)}$$



$$p(Y|X, \theta) = \prod_{i=1}^n p_i^{y_i} (1 - p_i)^{1-y_i}$$

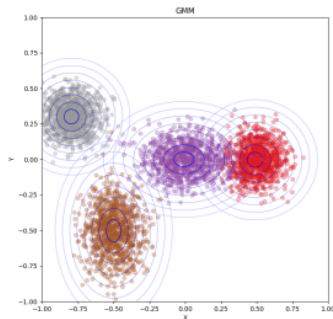


Data: $\mathcal{D} = \{y_i\}_{i=1}^n, y_i \in \mathbb{R}^d$

Model:

$$y|Z = z \sim \mathcal{N}(\mu_z, \sigma_z^2 I_d)$$

$$Z \sim \text{Categorical}(\alpha)$$



$$p(Y|\mu, \sigma, \alpha) = \prod_{i=1}^n \sum_{k=1}^K \alpha_k (2\pi\sigma_k^2)^{(-d/2)} \exp\left(-\frac{\|y_i - \mu_k\|_2^2}{2\sigma_k^2}\right)$$



Data: DNA sequences $\mathcal{D} = \{y_i\}_{i=1}^n$

CTTTTC AAGG	AGTATT TCCT	ATGAAC GAGT	TAGACGG CAT
CATTGC AAAG	GGAA TAATCT	ATGAAC GCAA	TAATTAT TGA
CATTTTC AGG	ATAACT TTCT	ATGAAA GTAA	ACTTAAT ACT
GAAAAG AAAAT	CGAGGC AAAA	ATGAGC AAAAG	TCAGACT CGC
TGCAAAAAA A	GGAA GACCAT	ATGCTT GACG	CTCAAAC CAT
TTTTTG TGG A	GAAG AC GCGT	GTGATT GTTA	AACGACC CGT
GTTATT AAGG	ATAT GTTCAT	ATGTTTT TCA	AAAAGA ACCT
TACCCAC CGG	ATTTT TACCC	ATGCTC ACCG	TTAAGC AGAT
AATCAAA ATG	GAAT AAAATC	ATGCTA CCAT	CTATTT CAAT
ATCACAG GGG	AAGGT GAGAT	ATGCACT CTC	AAATCT GGGT
ACATCC AGTG	AGAG AGACCG	ATGCAT CCGA	TGCTGA ACAT



Phylogenetic tree showing relationships between *Plasmodium* species, with bootstrap values indicated at the nodes. The tree is rooted at the top left. Bootstrap values are shown at the nodes. Species names are color-coded: African Cercopithecoidea (black), Asian Cercopithecoidea (blue), and Hominidae (green). Silhouettes of representative species are shown to the right. A scale bar of 0.005 is at the bottom left.

- P. gonderi* (African Cercopithecoidea)
- Plasmodium* sp. (African Cercopithecoidea)
- P. fragile* (Asian Cercopithecoidea)
- P. coatneyi* (Asian Cercopithecoidea)
- P. knowlesi* (Asian Cercopithecoidea)
- P. simiovale* (Asian Cercopithecoidea)
- P. fieldi* - N-3 (Asian Cercopithecoidea)
- P. inui* - Taiwan II (Asian Cercopithecoidea)
- P. inui* - Leaf Monkey II (Asian Cercopithecoidea)
- Plasmodium* sp. (VM82) (Asian Cercopithecoidea)
- P. hylobati* (Asian Cercopithecoidea)
- P. cynomolgi* - Berok (Asian Cercopithecoidea)
- P. cynomolgi* Ceylonensis (Asian Cercopithecoidea)
- P. vivax* (Hominidae)

Scale bar: 0.005

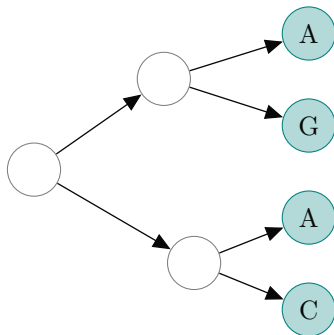
Data: DNA sequences $\mathcal{D} = \{y_i\}_{i=1}^n$

Model: Phylogenetic tree: (τ, q) .

Substitution model:

- ▶ stationary distribution: $\eta(a_\rho)$.
- ▶ transition probability:

$$p(a_u \rightarrow a_v | q_{uv}) = P_{a_u a_v}(q_{uv})$$



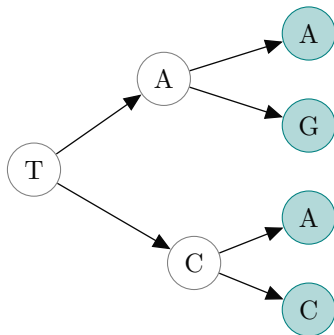
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$$\eta(a_\rho^i) \prod_{(u,v) \in E(\tau)} P_{a_u^i a_v^i}(q_{uv})$$



Data: DNA sequences $\mathcal{D} = \{y_i\}_{i=1}^n$

Model: Phylogenetic tree: (τ, q) .

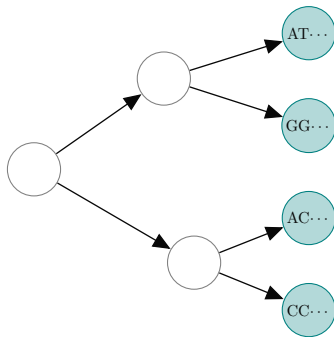
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- ▶ stationary distribution: $\eta(a_\rho)$.
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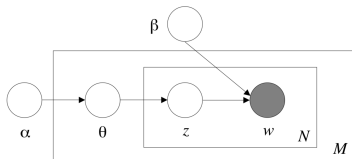
$$p(a_u \rightarrow a_v | q_{uv}) = P_{a_u a_v}(q_{uv})$$

$$p(Y|\tau, q) = \prod_{i=1}^n \sum_{a^i} \eta(a_\rho^i) \prod_{(u,v) \in E(\tau)} P_{a_u^i a_v^i}(q_{uv})$$

where a^i agree with y^i at the tips.



Data: a corpus $\mathcal{D} = \{\mathbf{w}_i\}_{i=1}^M$



Model: for each document \mathbf{w} in \mathcal{D} ,

- ▶ choose a mixture of topics $\theta \sim \text{Dir}(\alpha)$
- ▶ for each of the N words w_n ,

$$z_n \sim \text{Multinomial}(\theta), \quad w_n | z_n, \beta \sim p(w_n | z_n, \beta)$$

$$p(\mathcal{D} | \alpha, \beta) = \prod_{d=1}^M \int p(\theta_d | \alpha) \prod_{n=1}^{N_d} \sum_{z_{dn}} p(z_{dn} | \theta_d) p(w_{dn} | z_{dn}, \beta) d\theta_d$$



Many well-known distributions take the following form

$$p(y|\theta) = h(y) \exp(\phi(\theta) \cdot T(y) - A(\theta))$$

- ▶ $\phi(\theta)$: natural/canonical parameters
- ▶ $T(y)$: sufficient statistics
- ▶ $A(\theta)$: log-partition function

$$A(\theta) = \log \left(\int_y h(y) \exp(\phi(\theta) \cdot T(y)) dy \right)$$



$Y = \{y_i\}_{i=1}^n$, $y_i \sim p(y_i|\theta)$, the Log-likelihood

$$L(\theta; Y) = \sum_{i=1}^n \log p(y_i|\theta)$$

The gradient of L with respect to θ is called the **score**

$$s(\theta) = \frac{\partial L}{\partial \theta}$$

The expected value of the score is zero

$$\mathbb{E}(s) = n \int \frac{\partial \log p(y|\theta)}{\partial \theta} p(y|\theta) dy = n \frac{\partial}{\partial \theta} \int p(y|\theta) dy = 0$$



Fisher information is the variance of the score.

$$\mathcal{I}(\theta) = E(ss^T)$$

Under mild assumptions (e.g., exponential families),

$$\mathcal{I}(\theta) = -\mathbb{E} \left(\frac{\partial^2 L}{\partial \theta \partial \theta^T} \right)$$

Intuitively, **Fisher information** captures the variability of the **score**. Therefore, it reflects the sensitivity of model about the parameter at its current value.

$$\hat{\theta}_{MLE} = \arg \max_{\theta} L(\theta)$$

- ▶ **Consistency.** Under weak regularity condition, $\hat{\theta}_{MLE}$ is consistent: $\hat{\theta}_{MLE} \rightarrow \theta_0$ in probability as $n \rightarrow \infty$, where θ_0 is the “true” parameter
- ▶ **Asymptotical Normality.**

$$\sqrt{n}(\hat{\theta}_{MLE} - \theta_0) \rightarrow \mathcal{N}(0, \mathcal{I}^{-1}(\theta_0))$$

See Rao 1973 for more details.



$$L(\theta; y) = y \log \theta - \theta - \log y!$$

$$s(\theta) = \frac{y}{\theta} - 1, \quad \mathcal{I}(\theta) = \frac{1}{\theta}$$

$$\hat{\theta}_{MLE} = \arg \max_{\theta} \sum_{i=1}^n y_i \log \theta - n\theta = \frac{\sum_{i=1}^n y_i}{n}$$

By the **Law of large numbers**

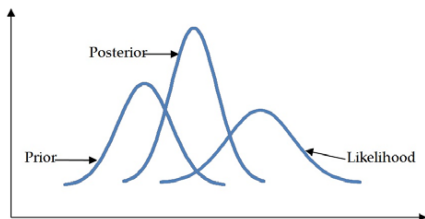
$$\hat{\theta}_{MLE} \xrightarrow{p} \theta_0$$

By **central limit theorem**

$$\sqrt{n}(\hat{\theta}_{MLE} - \theta_0) \xrightarrow{d} \mathcal{N}(0, \theta_0)$$



In Bayesian statistics, besides specifying a model $p(y|\theta)$ for the observed data, we also specify our **prior** $p(\theta)$ for the model parameters.



Bayes rule for inverse probability

$$p(\theta|\mathcal{D}) = \frac{p(\mathcal{D}|\theta) \cdot p(\theta)}{p(\mathcal{D})} \propto p(\mathcal{D}|\theta) \cdot p(\theta)$$

known as the **posterior**.



- ▶ uncertainty quantification, provides more useful information
- ▶ reducing overfitting. **Regularization** \iff **Prior**.

Prediction

$$p(x|\mathcal{D}) = \int p(x|\theta, \mathcal{D})p(\theta|\mathcal{D})d\theta$$

Model Comparison

$$p(m|\mathcal{D}) = \frac{p(\mathcal{D}|m)p(m)}{p(\mathcal{D})}$$

$$p(\mathcal{D}|m) = \int p(\mathcal{D}|\theta, m)p(\theta|m) d\theta$$



- ▶ **Subjective Priors.** Priors should reflect our beliefs as well as possible. They are subjective, but not arbitrary.
- ▶ **Hierarchical Priors.** Priors of multiple levels.

$$\begin{aligned} p(\theta) &= \int p(\theta|\alpha)p(\alpha) d\alpha \\ &= \int p(\theta|\alpha) d\alpha \int p(\alpha|\beta)p(\beta) d\beta \end{aligned}$$

- ▶ **Conjugate Priors.** Priors that ease computation, often used to facilitate the development of inference and parameter estimation algorithms.



- ▶ **Conjugacy:** prior $p(\theta)$ and posterior $p(\theta|Y)$ belong to the same family of distribution
- ▶ Exponential family

$$p(Y|\theta) \propto \exp \left(\phi(\theta) \cdot \sum_i T(y_i) - nA(\theta) \right)$$

- ▶ Conjugate prior

$$p(\theta) \propto \exp (\phi(\theta) \cdot \nu - \eta A(\theta))$$

- ▶ Posterior

$$p(\theta|Y) \propto \exp \left(\phi(\theta) \cdot (\nu + \sum_i T(y_i)) - (n + \eta)A(\theta) \right)$$



Data: $\mathcal{D} = \{\mathbf{x}_i\}_{i=1}^m$. For each \mathbf{x} in \mathcal{D}

$$p(\mathbf{x}|\theta) \propto \exp \left(\sum_{k=1}^K x_k \log \theta_k \right)$$

Use $\text{Dir}(\alpha)$ as the **conjugate** prior

$$p(\theta) \propto \exp \left(\sum_{k=1}^K (\alpha_k - 1) \log \theta_k \right)$$

$$p(\theta|\mathcal{D}) \propto \exp \left(\sum_{k=1}^K \left(\alpha_k - 1 + \sum_{i=1}^M x_{ik} \right) \log \theta_k \right)$$



Consider random variables $\{X_t\}, t = 0, 1, \dots$ with state space \mathcal{S}

Markov Property

$$p(X_{n+1} = x | X_0 = x_0, \dots, X_n = x_n) = p(X_{n+1} = x | X_n = x_n)$$

Transition Probability

$$P_{ij}^n = p(X_{n+1} = j | X_n = i), \quad i, j \in \mathcal{S}.$$

A Markov chain is called *time homogeneous* if $P_{ij}^n = P_{ij}, \forall n$.

A Markov chain is governed by its transition probability matrix.



- Stationary Distribution.

$$\pi^T P = \pi^T.$$

- Ergodic Theorem. If the Markov chain is irreducible and aperiodic, with stationary distribution π , then

$$X_n \xrightarrow{d} \pi$$

and for any function h

$$\frac{1}{n} \sum_{t=1}^n h(X_t) \rightarrow \mathbb{E}_{\pi} h(X), \quad n \rightarrow \infty$$

given $\mathbb{E}_{\pi}|h(X)|$ exists.



- ▶ In general, finding MLE and posterior analytically is difficult. We almost always have to resort to computational methods.
- ▶ In this course, we'll discuss a variety of computational techniques for numerical optimization and integration, approximate Bayesian inference methods, with applications in statistical machine learning, computational biology and other related field.

Signup in Piazza:

https://piazza.com/peking_university/fall2019/00113730



- ▶ J. Felsenstein. Evolutionary trees from DNA sequences: a maximum likelihood approach. J. Mol. Evol. 17, 368–376 (1981)
- ▶ D. M. Blei, A. Y. Ng, and M. I. Jordan. Latent dirichlet allocation. JMLR 3, 2003.
- ▶ C. R. Rao. Linear Statistical Inference and its Applications. 2nd edition. New York: Wiley, 1973.
- ▶ S. M. Ross. Introduction to Probability Models, 7th ed. Academic, 2000.

