

# 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 8:00-9:50am
  - ▶ Classroom Building No.3, Room 504
- ▶ Tentative office hours:
  - ▶ 1279 Science Building No.1
  - ▶ Thursday 3:00-5:00pm or by appointment
- ▶ Website:  
<https://zcrabbit.github.io/courses/mcs-f19.html>
- ▶ Join us at Piazza:  
[https://piazza.com/peking\\_university/fall2019/00113730](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 find a shorter python+numpy tutorial useful at

<http://cs231n.github.io/python-numpy-tutorial/>

Familiar with the following subjects

- ▶ Probability and Statistical Inference
- ▶ Stochastic Processes



- ▶ 4 Problem Sets:  $4 \times 15\% = 60\%$
- ▶ Final Course Project: 40%
  - ▶ 2-3 people (recommended) for each team
  - ▶ Teams should be formed by the end of week 4
  - ▶ 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

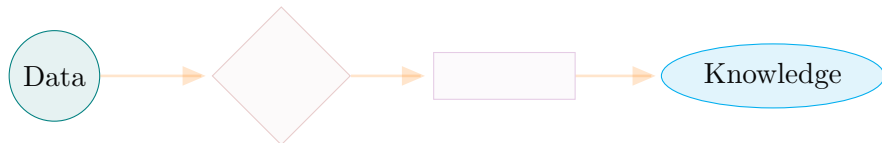


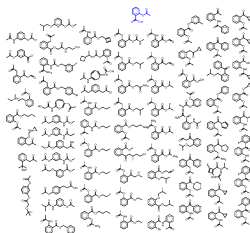
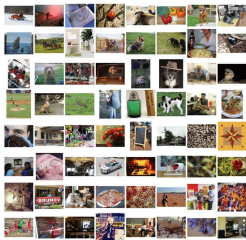
- ▶ Structure your project exploration around a general problem type, algorithm, or data set, but should explore around your problem, testing thoroughly or comparing to alternatives.
- ▶ Submit a project proposal that briefly describe your teams' project concept and goals in one page by 11/04.
- ▶ There 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.
- ▶ Turn in a write-up ( $< 10$  pages) describing your project and its outcomes, similar to a research-level publication.

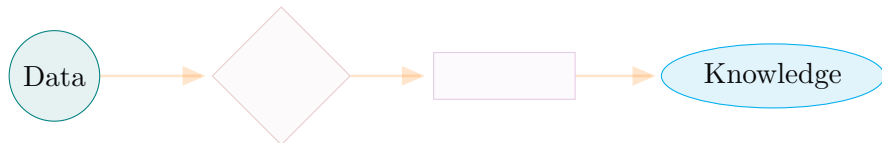


- ▶ A brief overview of statistical approaches
- ▶ Basic concepts in statistical computing







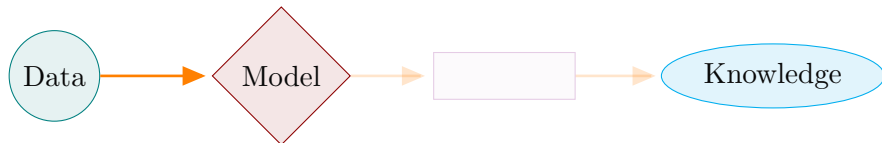
 $\mathcal{D}$ 

Linear Models

Neural Networks

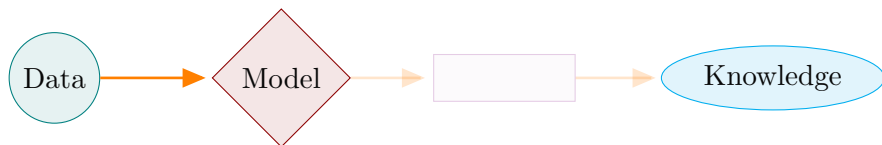
Bayesian Nonparametric Models

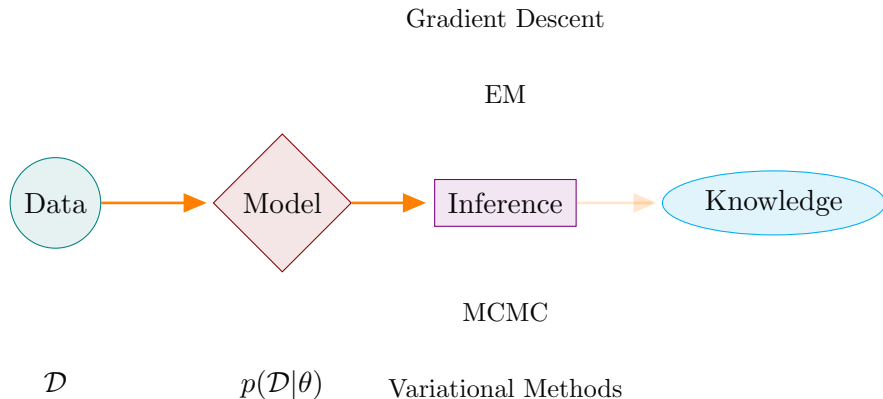
Generalized Linear Models

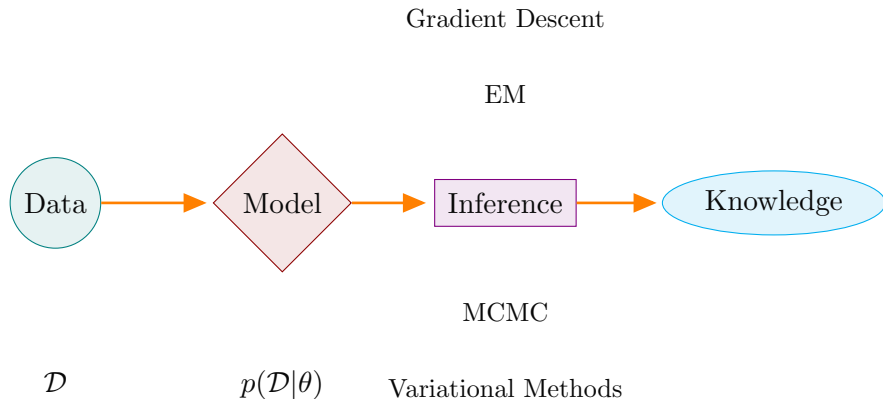


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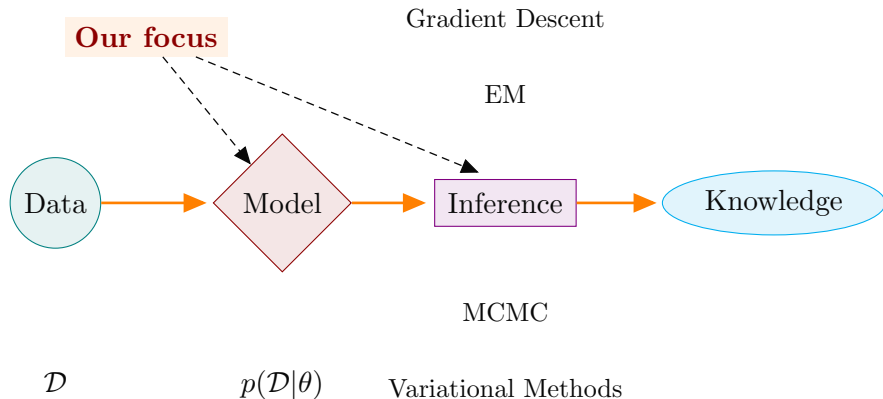


 $\mathcal{D}$  $p(\mathcal{D}|\theta)$ 









“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**.

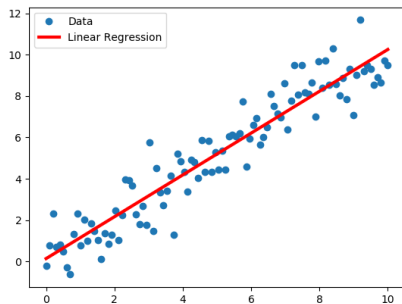


**Data:**  $\mathcal{D} = \{(x_i, y_i)\}_{i=1}^n$

**Model:**

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

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



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



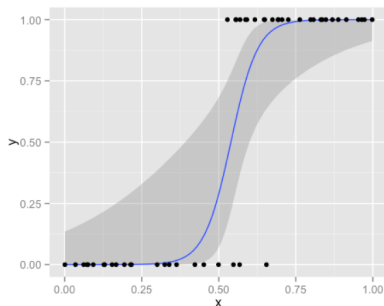
**Data:**

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

**Model:**

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

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



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

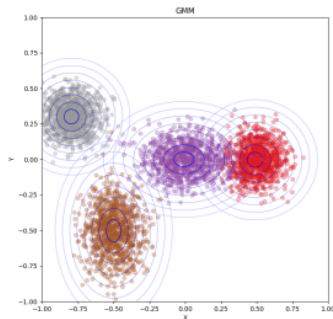


**Data:**  $\mathcal{D} = \{y_i\}_{i=1}^n, y_i \in \mathbb{R}^d$

**Model:**

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

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



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



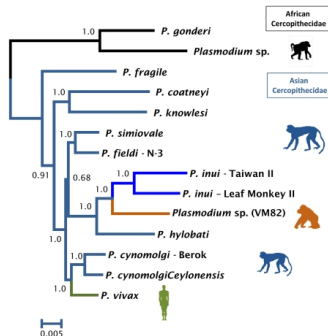
**Data:** DNA sequences  $\mathcal{D} = \{y_i\}_{i=1}^n$

CTTTTC AAGG	AGTATTT CCT	ATGAACGAGT	TAGACGGCAT
CATTGCA AAG	GGAAATAATCT	ATGAACGCAA	TAATTATTGA
CATTTTCAGG	ATAACTTTCT	ATGAAAGTAA	ACTTAATACT
GAAAAGAAAT	CGAGGC AAAA	ATGAGCAAAG	TCAGACTCGC
TGCAAAAAAA	GG AAGACCAT	ATGCTTGACG	CTCAAACCAT
TTTTTGTGGA	GAAGACGCGT	GTGATTGTTA	AACGACCCGT
GTTATTAAGG	ATATGTT CAT	ATGTTTTTCA	AAAAGAACCT
TACCCACCGG	ATTTTACCC	ATGCTCACC	TTAAGCAGAT
AATCAAAATG	GAATAAAATC	ATGCTACCAT	CTATTTCAAT
ATCACAGGGG	AAGGTGAGAT	ATGCACTCTC	AAATCTGGGT
ACATCCAGTG	AGAGAGACCG	ATGCATCCGA	TGCTGAACAT



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

CTTTTCAAGG	AGTATTTTCCT	ATGAACGAGT	TAGACGGCAT
CATTGCAAAAG	GGAATAATCT	ATGAACGCAA	TAATTATTGA
CATTTTCAGG	ATAACTTTCT	ATGAAAGTAA	ACTTAATACT
GAAAAGAAAAT	CGAGGC AAAA	ATGAGCAAAG	TCAGACTCGC
TGCAAAAAAA	GGAGACCAT	ATGCTTGACG	CTCAAACCAT
TTTTTGTGGA	GAAGACGCGT	GTGATTGTTA	AACGACCCGT
GTTATTAAGG	ATATGTTTCAT	ATGTTTTTCA	AAAAGAACCT
TACCCACCGG	ATTTTTACCC	ATGCTCACCG	TTAAGCAGAT
AATCAAAATG	GAATAAAATC	ATGCTACCAT	CTATTTCAAT
ATCACAGGGG	AAGGTGAGAT	ATGCACTCTC	AAATCTGGGT
ACATCCAGTG	AGAGAGACCG	ATGCATCCGA	TGCTGAACAT



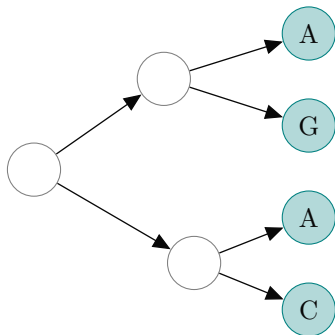
**Data:** DNA sequences  $\mathcal{D} = \{y_i\}_{i=1}^n$

**Model:** Phylogenetic tree:  $(\tau, q)$ .

Substitution model:

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

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





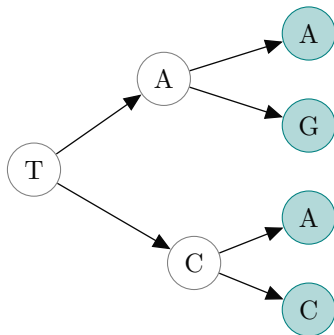
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$$\eta(a_\rho^i) \prod_{(u,v) \in E(\tau)} P_{a_u^i a_v^i}(q_{uv})$$



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

**Model:** Phylogenetic tree:  $(\tau, q)$ .

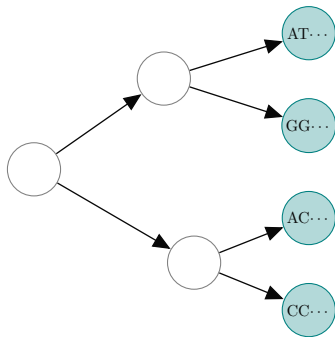
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- ▶ stationary distribution:  $\eta(a_\rho)$ .
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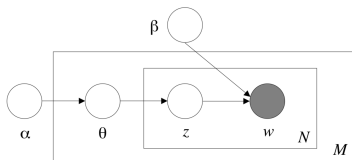
$$p(a_u \rightarrow a_v | q_{uv}) = P_{a_u a_v}(q_{uv})$$

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

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  $w_n$ ,

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

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



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

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

The gradient of  $L$  with respect to  $\theta$  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** is a measure of the **curvature** of the **score**. Therefore, it reflects the sensitivity of model about the parameter at its current value.

- ▶ Kullback-Leibler divergence or KL divergence is a measure of statistical distance between two distributions  $p(x)$  and  $q(x)$

$$D_{KL}(q||p) = \int q(x) \log \frac{q(x)}{p(x)} dx$$

- ▶ KL divergence is non-negative

$$D_{KL}(q||p) = - \int q(x) \log \frac{p(x)}{q(x)} \geq - \log \int p(x) dx = 0$$

- ▶ Consider a family of distributions  $p(x|\theta)$ , Fisher information is Hessian of KL-divergence between two distributions  $p(x|\theta)$  and  $p(x|\theta')$  with respect to  $\theta'$  at  $\theta' = \theta$

$$\nabla_{\theta'}^2 D_{KL}(p(x|\theta)||p(x|\theta'))|_{\theta'=\theta} = \mathcal{I}(\theta)$$



$$\begin{aligned}\hat{\theta}_{MLE} &= \arg \max_{\theta} L(\theta) \approx \arg \max_{\theta} \mathbb{E}_{y \sim p_{data}} \log \frac{p(y|\theta)}{p_{data}(y)} \\ &= \arg \min_{\theta} D_{KL}(p_{data}(y) || p(y|\theta))\end{aligned}$$

- **Consistency.** Under weak regularity condition,  $\hat{\theta}_{MLE}$  is consistent:  $\hat{\theta}_{MLE} \rightarrow \theta_0$  in probability as  $n \rightarrow \infty$ , where  $\theta_0$  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**

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

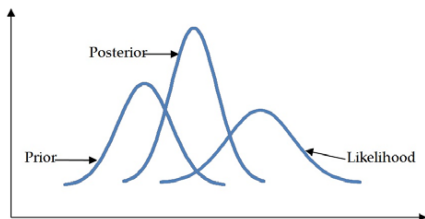
By **central limit theorem**

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





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**  $\Longleftrightarrow$  **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.



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

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



- ▶ **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  $\pi$ , 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:

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- ▶ 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.

