# Markov Chain Monte-Carlo (MCMC)

What for is it and what does it look like?

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#### Monte Carlo method: a figure square

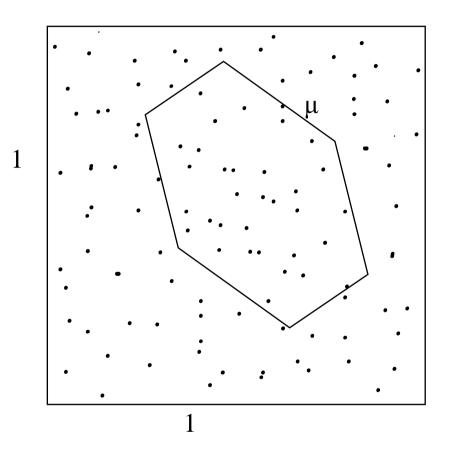
The value  $\mu$  is unknown.

Let's sample a random value (**r.v.**)  $\xi$ :

 $\{x, y\}: \text{ i.i.d. as flat} [0,1]$  $\{\xi = 1 \Leftrightarrow (x, y) \in \mu \\ \xi = 0 \Leftrightarrow (x, y) \notin \mu$ 

Clever notation:  $\xi = I_{\mu}(x, y)$ **i.i.d.** is "Identically Independently Distributed"

Expectation of  $\xi: E\{\xi\} = \overline{\xi} = S(\mu) = S$ 



#### Monte Carlo method: efficiency

Large Numbers Law: 
$$S \approx \hat{S}_m = \frac{1}{m} \sum_{i=1}^m \xi_i$$

Central Limit Theorem: 
$$S - \hat{S}_m \rightarrow \frac{1}{\sqrt{m}} \cdot N(0, \operatorname{var}\{\xi\})$$

Variance var 
$$\{\xi\} = E\left(\left[\xi - E(\xi)\right]^2\right)$$
, also notated as  $\sigma^2$ .

#### Monte Carlo Integration

We are evaluating  $I = \int_{D} f(x) dx$ . *D* is domain of f(x) or its subset. We can sample **r.v.**  $x_i \in D$ :  $x_i$  are **i.i.d.** uniformly in D:  $E[f(x_i)] = \frac{1}{|D|} \int_{D} f(x) dx = I$ .

The Monte Carlo estimation:  $\widehat{I_m} = \frac{|D|}{m} \sum_{i=1}^m f(x_i)$ ,

$$I - \widehat{I_m} \to \frac{|D|}{\sqrt{m}} \cdot N\left(0, \operatorname{var}_D\left\{f\left(x\right)\right\}\right)$$

f(x)D

Advantage:

• The multiplier ~  $m^{-\frac{1}{2}}$  does not depend on the space dimension.

Disadvantage:

 $\circ$  a lot of samples are spent in the area where f(x) is small;

• the variation value  $\operatorname{var}_{D} \{f(x)\}$  that determine convergence time can be large.

#### Monte Carlo importance sampling

We are evaluating  $I = \int_{D} f(x) dx$ 

Let's sample  $x_i \in D$  from a "trial" distribution g(x) that "looks like" f(x) and  $|f(x)| > 0 \Rightarrow g(x) > 0$ .  $x_i$  **i.i.d.** in *D* as g(x) that "resembles" f(x)

Thus 
$$E_g\left(\frac{f(x_i)}{g(x_i)}\right) = \int_D \frac{f(x)}{g(x)}g(x)dx = \int_D f(x)dx.$$
  
MC evaluation:  $\widehat{I_m} = \frac{1}{m}\sum_{i=1}^m \frac{f(x_i)}{g(x_i)}$ ;  $I - \widehat{I_m} \to \frac{1}{\sqrt{m}} \cdot N\left(0, \operatorname{var}_D\left\{\frac{f(x)}{g(x)}\right\}\right)$ 

"More uniform" means "better".

#### Another example of importance sampling

We are evaluating  $\mu = E_{\pi} \{h(x)\} = \int h(x)\pi(x)dx$ , where  $\pi(x)$  is a distribution, e.g.  $\int \pi(x)dx = 1$ 

Solution sample  $x_i$  from a distribution g(.) so that  $\pi(x) > 0 \Rightarrow g(x) > 0$ 

> Importance weight  $w_i = \pi(x_i)/g(x_i)$ ;  $E_g\{w(x)\} = \int \frac{\pi(x)}{g(x)}g(x)dx = 1$ 

$$\hat{\mu}_{m} = \frac{1}{m} \sum_{i=1}^{m} \frac{\pi(x_{i})}{g(x_{i})} h(x_{i}) = \frac{1}{m} \sum_{i=1}^{m} w(x_{i}) h(x_{i}) = \sum_{i=1}^{m} w_{i} h(x_{i}) / \sum_{i=1}^{m} w_{i}$$

$$\hat{\mu}_{m} = \frac{1}{m} \sum_{i=1}^{m} w(x_{i}) h(x_{i}) = \sum_{i=1}^{m} w_{i} h(x_{i}) / \sum_{i=1}^{m} w_{i}$$

$$\hat{\mu}_{m} = \frac{1}{m} \sum_{i=1}^{m} h(x_{i})$$

# Rejection sampling (Von Neumann, 1951)

We have a distribution  $\pi(x)$  and we want to sample from it.

We are able to calculate  $f(x) = c \cdot \pi(x)$  for  $\forall x$ . Any *c*.

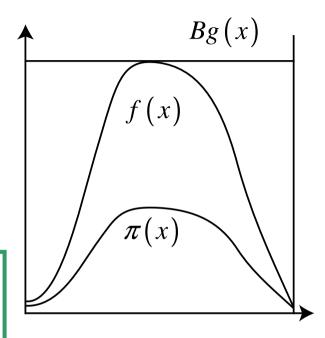
We are able to sample  $g(x), \exists B : Bg(x) \ge f(x)$ .

Thus, we can sample  $\pi(x)$ :

 $\succ$  Draw a value x from g(x).

Accept the value x with the probability f(x)/Bg(x).

$$P(accept) = \int P(accept \mid x) P(x) \cdot dx = \int \frac{c \cdot \pi(x)}{Bg(x)} \cdot g(x) \cdot dx = \frac{c}{B}$$
$$P(x \mid accept) = \frac{P(accept \mid x) \cdot P(x)}{P(accept)} = \frac{c \cdot \pi(x)}{Bg(x)} \cdot g(x) \cdot \frac{B}{c} = \pi(x)$$



#### Metropolis algorithm (1953)

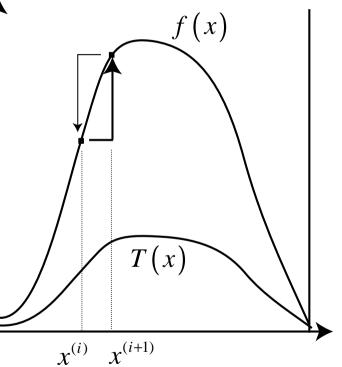
We want to be able to draw  $x^{(i)}$  from a distribution  $\pi(x)$ . We know how to compute the value of a function f(x) so that  $f(x) \sim \pi(x)$  at each point and we are able to draw x from flat distribution.

Let's denote the *i*-th step result as  $x^{(i)}$ .

Draw  $y^{(i)}$  from flat. It is an analog of g in importance sampling.

Transition probability 
$$\varphi(y^{(i)} | x^{(i)}) = \min\left(1, \frac{f(y^{(i)})}{f(x^{(i)})}\right).$$

The new value is accepted  $x^{(i+1)} = y^{(i)}$  with probability  $\varphi(y^{(i)} | x^{(i)})$ . Otherwise, it is rejected and  $x^{(i+1)} = x^{(i)}$ .



# Metropolis-Hastings algorithm (1953,1970)

We want to be able to draw  $x^{(i)}$  from a distribution  $\pi(x)$ . We know how to compute the value of a function f(x) so that  $f(x) \sim \pi(x)$  at each point and we are able to draw x from T(x | y) (instrumental distribution, transition kernel). Let's denote the *i*-th step result as  $x^{(i)}$ .

Draw 
$$y^{(i)}$$
 from  $T(y | x^{(i)})$ .  $T(y | x^{(i)})$  is flat in pure

Metropolis. It is an analog of g in importance sampling.

Transition probability  

$$\varphi\left(y^{(i)} \mid x^{(i)}\right) = \min\left(1, \frac{T\left(x^{(i)} \mid y^{(i)}\right) \cdot f\left(y^{(i)}\right)}{T\left(y^{(i)} \mid x^{(i)}\right) \cdot f\left(x^{(i)}\right)}\right).$$

f(x) T(x) T(x)

The new value is accepted  $x^{(i+1)} = y^{(i)}$  with probability  $\varphi(y^{(i)} | x^{(i)})$ . Otherwise, it is rejected  $x^{(i+1)} = x^{(i)}$ .

#### Why does it work: the local balance

Let's show that if x is already distributed as  $\pi(\cdot) \sim f(\cdot)$ , then the MH algorithm keeps

the distribution.



Local balance condition for two points x and y :  $flux(x \rightarrow y) = flux(y \rightarrow x)$ 

Let's check it:

$$flux(x \to y) = f(x) \cdot T(y \mid x) \cdot \varphi(y \mid x); \ flux(y \to x) = f(y) \cdot T(x \mid y) \cdot \varphi(x \mid y)$$

$$flux(x \to y) = f(x) \cdot T(y|x) \cdot \varphi(y|x) = f(x) \cdot T(y|x) \cdot \min\left(1, \frac{T(x|y) \cdot f(y)}{T(y|x) \cdot f(x)}\right) = \min\left(T(y|x) \cdot f(x), T(x|y) \cdot f(y)\right) = f(y) \cdot T(x|y) \cdot \varphi(x|y) = flux(y \to x)$$

#### Why does it work: the local balance stability

Let's suppose a deviation from the f(x) distribution:  $f_{real}(x) = f(x) + \Delta$ .

What happen with the fluxes?

$$flux_{new}(y \to x) = f(y) \cdot T(x \mid y) \cdot \varphi(x \mid y) = flux(y \to x)$$
  

$$flux_{new}(x \to y) = f_{new}(x) \cdot T(y \mid x) \cdot \varphi(y \mid x)$$
  

$$= f_{real}(x) \cdot T(y \mid x) \cdot \varphi(y \mid x)$$
  

$$= flux(y \to x) + \Delta \cdot T(y \mid x) \cdot \varphi(y \mid x)$$
  

$$= flux_{new}(y \to x) + \Delta \cdot T(y \mid x) \cdot \varphi(y \mid x)$$

The change in flux compensate the deviation. The balance is stable. f(x) distribution is a stable distribution for the MH Markov chain.

The stable local balance is enough (BTW, it is not a necessary condition).

# Markov chains, Maximization, Simulated Annealing

 $x_i$  created as described above is a Markov chain (MC) with transition kernel  $\varphi(x^{(i+1)} | x^{(i)}) \cdot T(x^{(i+1)} | x^{(i)})$ . The fact that the chain has a stationary distribution and the

convergence of the chain to the distribution can be proved by the MC theory methods.

**Minimization.** 
$$C(x)$$
 is a cost (a fine).  $f(x) = \exp\left(-\frac{C(x) - C_{\min}}{t}\right)$ 

We can characterize the transition kernel with a temperature. Then we can decrease the temperature step-by-step (simulated annealing). MCMC and SA are very effective for optimization since gradient methods use to be locked is a local maximum while pure MC is extremely ineffective.

## MCMC prior and Bayesian paradigm

$$P(M \mid D) = \frac{P(D \mid M) \cdot P(M)}{P(D)} \propto P(D \mid M) \cdot P(M)$$
 here, evidence posterior  $\propto$  likelihood  $\cdot$  prior

MCMC and its variations are often used for the best model search .

Let's can formulate some requirements for the algorithm and thus for the transition kernel:

- We want it not to depend on the current data.
- $\circ$  We want to minimize the rejection rate.

So, an effective transition kernel is so that the prior P(M) is its stationary distribution.

#### Terminology: names of relative algorithms

- MCMC, Metropolis, Metropolis-Hastings, hybrid Metropolis, configurational bias Monte-Carlo, exchange Monte-Carlo, multigrid Monte-Carlo (MGMC), slice sampling, RJMCMC (samples the dimensionality of the space), Multiple-Try Metropolis, Hybrid Monte-Carlo.....
- Simulated annealing, Monte-Carlo annealing, statistical cooling, umbrella sampling, probabilistic hill climbing, probabilistic exchange algorithm, parallel tempering, stochastic relaxation....

o Gibbs algorithm, successive over-relaxation...

# Gibbs Sampler (Geman and Geman, 1984)

Now, x is a k-dimensional variable  $(x_1, x_2, ..., x_k)$ .

Let's denote  $x_{-m} = (x_1, x_2, .., x_{m-1}, x_{m+1}, .., x_k), 1 \le m \le k$ 

On each step of the Markov Chain we choose the "current coordinate"  $m_i$ .

Then, we calculate the distribution  $f(x_{m_i} | x_{-m_i}^{(i)})$  and draw the next value  $y_{m_i}^{(i)}$  from the

distribution.

All other coords are the same as on the previous step,  $y_{-m_i}^{(i)} = x_{-m_i}^{(i)}$ .

For such a transition kernel,

$$\varphi(y^{(i)} | x^{(i)}) = \min\left(1, \frac{T(x^{(i)} | y^{(i)}) \cdot f(y^{(i)})}{T(y^{(i)} | x^{(i)}) \cdot f(x^{(i)})}\right) = 1.$$

o We have no rejects, so the procedure is very effective.

• The "temperature" decreases rather fast .

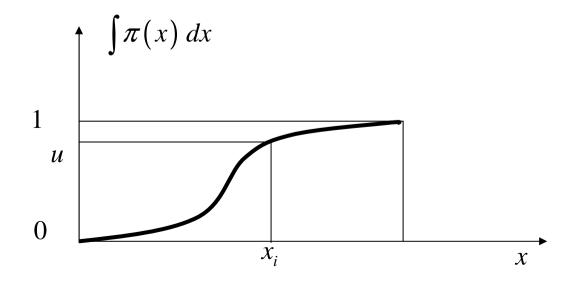
### Inverse transform sampling (well-known)

We want to sample from the density  $\pi(x)$ . We know how to calculate the inverse

function for the cumulative distribution.

Solution Generate a random number from the [0,1] uniform distribution; call this  $u_i$ . Compute the value  $x_i$  such that  $\int_{-\infty}^{x_i} \pi(x) dx = u_i$ 

 $\succ x_i$  is the random number that is drawn from the distribution described by  $\pi(x)$ .



$$[x, x + \Delta x] \leftrightarrow [u, u + \Delta u]$$
  

$$p(x)\Delta x = uniform(u) \times \Delta u$$
  

$$p(x) = uniform \times \frac{\Delta u}{\Delta x} = \pi(x)$$

# Slice sampling (Neal, 2003)

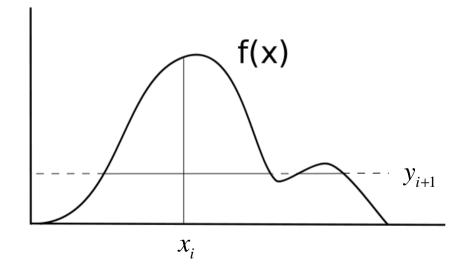
Sampling of x from f(x) is equivalent to sampling of (x, y) pairs from they area.

So, we introduce an auxiliary variable *y* and iterate as follows:

For a sample  $x_t$  we choose  $y_t$  uniformly from the interval  $[0, f(x_t)]$ 

Solution  $y_t$  we choose  $x_{i+1}$  uniformly at random from  $\{x: f(x) > y_t\}$ 

the sample of x distributed as f(x) is obtained by ignoring the y values.



#### Literature

Liu, J.S. (2002) Monte Carlo Strategies in Scientific Computing. Springer-Verlag, NY, Berlin, Heidelberg.

Robert, C.P. (1998) Discretization and MCMC Convergence Assessment, Springer-Verlag.

Laarhoven, van, P.M.J. and Aarts, E.H.L (1988) Simulated Annealing: Theory and Applications. Kluwer Academic Publishers.

Geman, S and Geman, D (1984). *Stochastic relaxation, Gibbs distribution and the Bayesian restoration of images.* IEEE Transactions on Pattern Analysis and Machine Intelligence. **6**, 621-641.

Besag, J., Green, P., Higdon, D., and Mengersen, K. (1996) *Bayesian computation and Stochastic Sytems*. Statistical Science, **10**, 1, 3-66.

Lawrence, C.E., Altschul, S.F., Boguski, M.S., Liu, J.S., Neuwald, A.F., and Wootton, J.C. (1993). *Detecting subtle sequence signals: a Gibbs sampling strategy for multiple alignment*. Science **262**, 208-214.

Sivia, D.S. (1996) Data Analysis. A Bayesian tutorial. Clarendon Press, Oxford.

Neal, Radford M. (2003) Slice Sampling. The Annals of Statistics 31(3):705-767.

http://civs.ucla.edu/MCMC/MCMC\_tutorial.htm

Sheldon Ross. A First Course in Probability

Соболь И.М. Метод Монте-Карло

### Sometimes, it works ©

Favorov, A.V., Andreewski, T.V., Sudomoina, M.A., Favorova O.O., Parmigiani, G. Ochs, M.F. (2005). A Markov chain Monte Carlo technique for identification of combinations of allelic variants underlying complex diseases in humans. Genetics **171**(4): 2113-21.

Favorov, A.V., Gelfand, M.S., Gerasimova, A.V. Ravcheev, D.A., Mironov, A.A., Makeev, V. J. (2005). A Gibbs sampler for identification of symmetrically structured, spaced DNA motifs with improved estimation of the signal length. Bioinformatics **21**(10): 2240-2245.