

*Year 2020-2021*  
*Estimation and filtering*

**Bayesian estimation  
using stochastic simulation:  
theory e applications**

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# SUMMARY

- Fisherian vs Bayesian estimation
- Bayesian estimation using Monte Carlo methods
- Bayesian estimation using Markov chain Monte Carlo
- On-line Bayesian estimation (particle filters)

# FISHER VS BAYES

Let us consider the model:  $y = G(x) + v$

*Fisher approach:*  $x$ , which admits a true deterministic value, is estimated using only the experimental data  
e.g. Maximum Likelihood:  $\hat{x} = \arg \max p_{y|x}(y|x)$

*Bayes approach:*  $x$  is random and we estimate one realization using not only the experimental data (posteriori information), but also the a priori information (independent of the data)

# Fisher approach to parametric estimation



## ADVANTAGES

- require optimization algorithms (e.g. conjugate gradient/Newton) often not so computational expensive

## DRAWBACKS

- They are minimum variance estimators only using linear models and Gaussian measurement errors
- They often return non realistic confidence intervals (e.g. containing negative values due to Gaussian approximations of the estimates)

# Bayes approach to parametric estimation (1/7)

The starting point is that we have some information on  $x$ , independent of the data (i.e. “before seeing the data”=*a priori*), and these expectations are summarized in the *a priori* probability density function

$$p_x(x)$$

Such expectations are then modified after seeing the data  $y$ , hence one speaks of a posteriori probability density function (=conditional on  $y$ )

$$p_{x|y}(x|y)$$

This is the key function obtained by Bayes.

From it, one can obtain point estimates and confidence intervals.

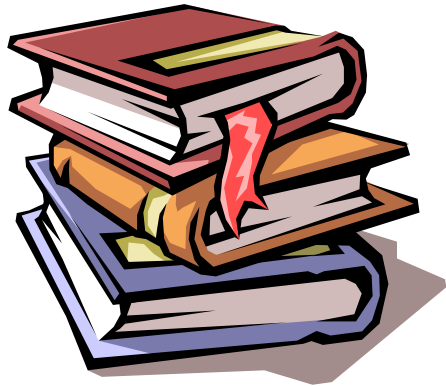
# Bayes approach to parametric estimation (2/7)

## Why using Bayesian priors

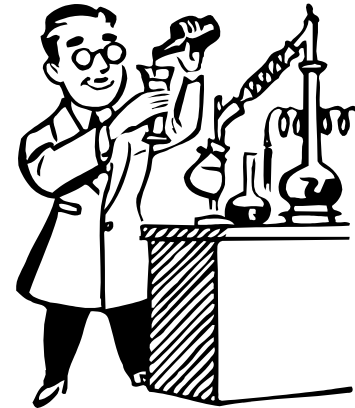
- To include all the available information in the estimation process
- To extend the complexity of the model
  - Priors on all the unknown parameters
- To improve the parameter estimates
  - Use of population or individual information
- To analyze sparse data set/high measurement noise
  - “Weak” Likelihood, “strong” prior

# How to obtain the prior?

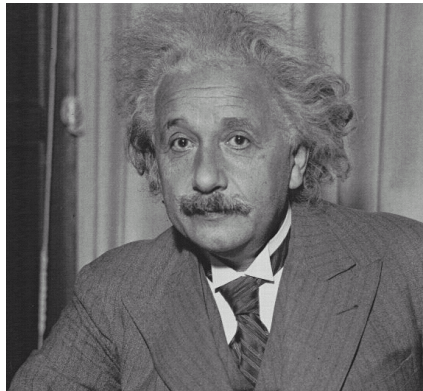
Literature



Previous experiments



Experts



Population studies



# Bayes approach to parametric estimation (3/7)

## Examples of Bayesian estimators

From  $p_{x|y}(x|y)$  one can obtain different estimators.  
The most used are:

**Posterior mean (minimum variance error)**

$$\hat{x} = E[x|y] = \int xp_{x|y}(x|y)dx$$

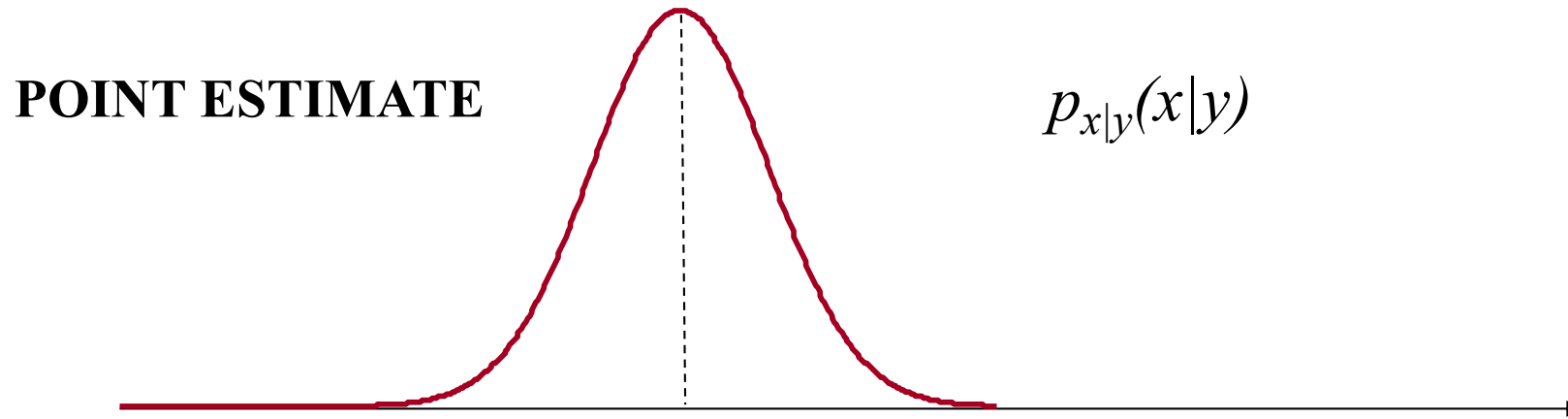
**Maximum a posteriori (MAP)**

$$\hat{x} = \arg \max p_{x|y}(x|y)$$



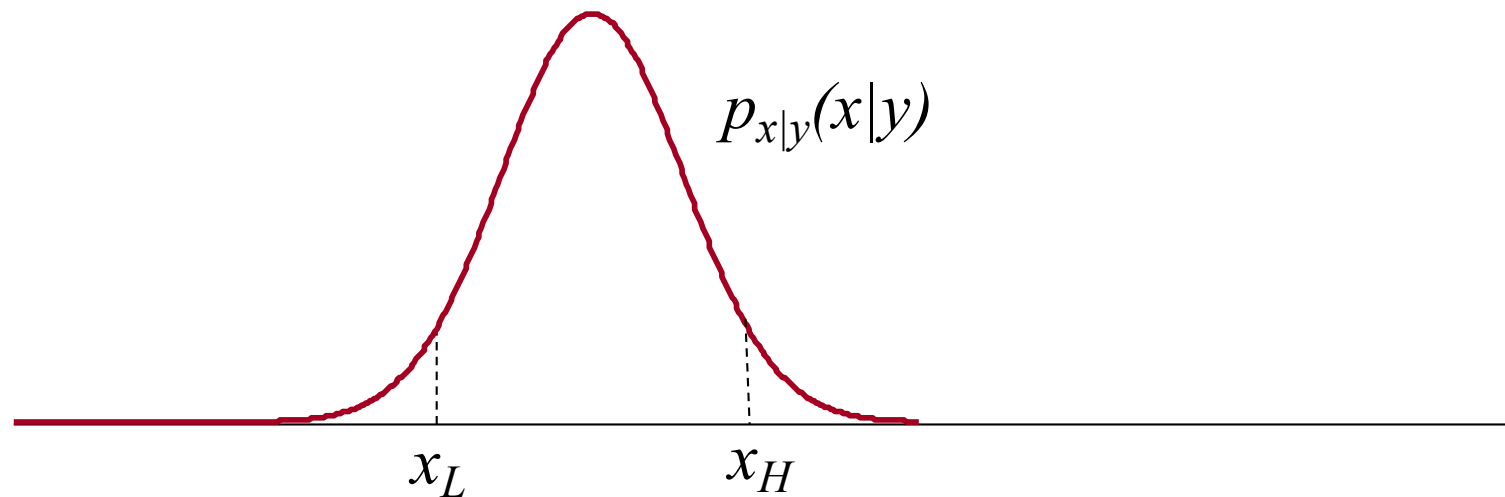
# Bayes approach to parametric estimation (4/7)

## Use of the posterior: example with scalar $x$



Here MAP (Maximum a Posteriori) estimate coincides with minimum variance estimate

### CONFIDENCE INTERVALS



95% CI (mean  $\pm$  2SD if  $x|y$  is Gaussian)

# Bayes approach to parametric estimation (5/7)

We can estimate  $x$  from the posterior  $p_{x|y}(x|y)$ .  
But how can we obtain it?

Bayes rule:

$$p_{x|y}(x|y) = \frac{p_{yx}(y|x)p_x(x)}{p_y(y)}$$

To determine  $p_{x|y}(x|y)$  we need:

- the prior density of  $x$ ,  $p_x(x)$
- the likelihood  $y$ ,  $p_{y|x}(y|x)$ , computable from the model  $G(x)$  and from the statistics of the error  $v$  ( $y=G(x)+v$ )

# Bayes approach to parametric estimation (6/7)

**PARTICULAR CASE:  $x$  e  $v$  independent Gaussian,  
linear  $G$  ( $G(x)=Gx$ )**

$$p_x(x) = \frac{1}{[(2\pi)^M \det(\Sigma_x)]^{1/2}} \exp\left(-\frac{1}{2}(x - \mu)^T \Sigma_x^{-1}(x - \mu)\right) \quad \text{Prior density}$$

$$p_{y|x}(y | x) = \frac{1}{[(2\pi)^N \det(\Sigma_v)]^{1/2}} \exp\left(-\frac{1}{2}[y - Gx]^T \Sigma_v^{-1}[y - Gx]\right) \quad \text{Likelihood}$$

The posterior is also Gaussian and we have:

$$\hat{x}_{MAP} = E[x|y] = \arg \min_x \left[ \underbrace{[y - Gx]^T \Sigma_v^{-1}[y - Gx]}_{\text{Posterior information = data}} + \underbrace{(x - \mu)^T \Sigma_x^{-1}(x - \mu)}_{\text{A priori information}} \right]$$

# Bayes approach to parametric estimation (7/7)



## ADVANTAGES

- Return all the distribution of the estimates (from which e.g. minimum variance estimates and realistic confidence intervals can be obtained)

## DRAWBACKS

- Computation of Bayesian point estimates and relative confidence may require solutions of computationally intractable integrals

# Bayes approach: computational difficulties (1/2)

Integration plays a fundamental role in Bayesian estimation

- determination of the normalization factor

$$p_{x|y}(x|y) = \frac{p_{yx}(y|x)p_x(x)}{p_y(y)} \rightarrow \int p_{y|x}(y|x)p_x(x) dx$$

- distribution synthesis  $\int g(x)p_{x|y}(x|y) dx$

Esempi:

$$x = [x_1 \ x_2 \ \dots \ x_d]^T$$

$g(x) = x_i$  : minimum variance estimate of  $x_i$

$$A \subset \mathfrak{R}^d$$

$$\chi(p \in A) = \begin{cases} 1 & \text{if } p \in A \\ 0 & \text{otherwise} \end{cases}$$

$g(x) = \chi(x \in A)$  : probability that  $x$  assumes values in  $A$

## Bayes approach: computational difficulties (2/2)

- Vector  $x$  may assume values in high-dimensional spaces and its prior distribution can be non Gaussian
- Nonlinear models may be needed
- Data set size may be poor and the signal to noise ratio can be small



Posterior may be complex,  
far from Gaussianity,  
hence difficult to integrate

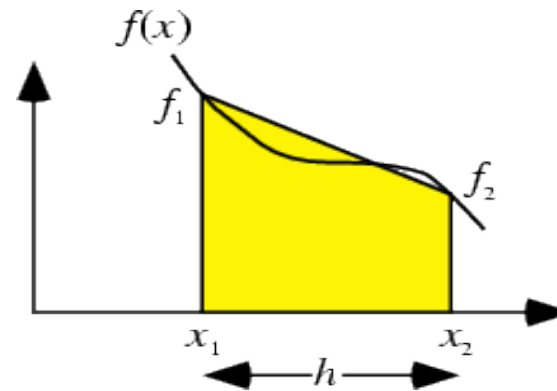
# DETERMINISTIC APPROACHES TO THE PROBLEM (1/4)

- **Classical numerical methods**

Use quadrature rules which approximate the integral using sums of areas of polygons

Dimension 1: the integration interval is divided in pieces of length  $h$

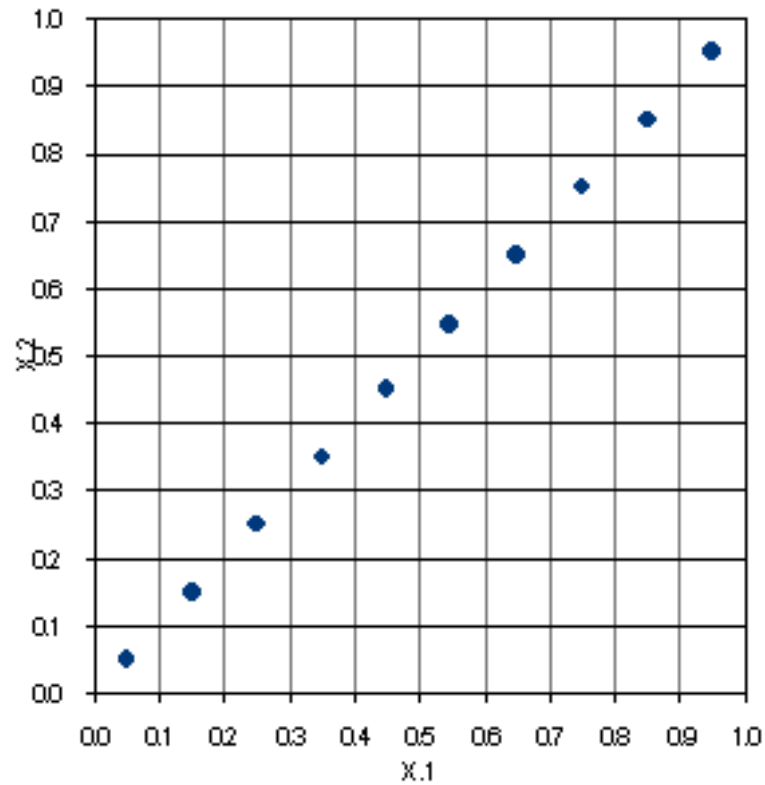
One obtains polygons which approximate the function (e.g. lines, Lagrange polynomials) and then we obtain the area



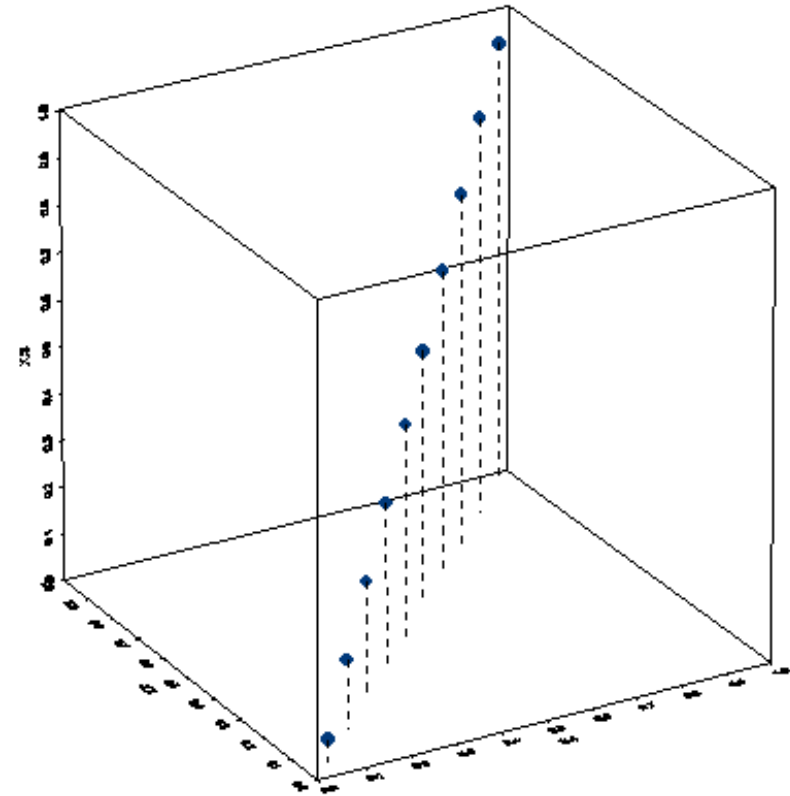
Limits: even if they can provide very accurate results, they are numerical procedures which can be used only in low-dimensional spaces, in practice 2- or 3-dimensional (due to the “curse of dimensionality”)

# DETERMINISTIC APPROACHES TO THE PROBLEM (2/4)

## Curse of dimensionality



**10% of coverage**



**1% of coverage**

The number of points has to exponentially increase to maintain a certain coverage accuracy



# DETERMINISTIC APPROACHES TO THE PROBLEM (3/4)

- Asymptotic Laplace approximation

The posterior  $\pi(x)$  is approximated by a Gaussian distribution by computing its maximum and its Hessian around the maximum of the log-posterior

$$\hat{x} = \arg \max_x \log(\pi(x))$$

$$\log \pi(x) \approx \log \pi(\hat{x}) + \frac{1}{2}(x - \hat{x})^T \times \left[ \frac{\partial^2 \log \pi}{\partial x^T \partial x} \Big|_{\hat{x}} \right] \times (x - \hat{x})$$

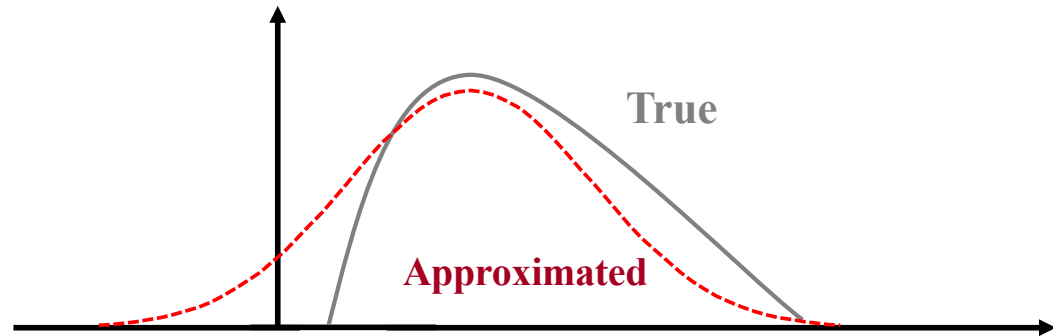
$$\pi(x) \approx \frac{1}{\sqrt{\det(2\pi\Sigma)}} e^{-\frac{1}{2}(x-\hat{x})^T \Sigma^{-1}(x-\hat{x})} \doteq N(\hat{x}, \Sigma)$$

$$\Sigma = - \left[ \frac{\partial^2 \log \pi}{\partial x^T \partial x} \Big|_{\hat{x}} \right]^{-1}$$

# DETERMINISTIC APPROACHES TO THE PROBLEM (4/4)

$$\pi(x) \approx N(\hat{x}, \Sigma)$$

$$\Sigma = - \left[ \frac{\partial^2 \log \pi}{\partial x^T \partial x} \Big|_{\hat{x}} \right]^{-1}$$



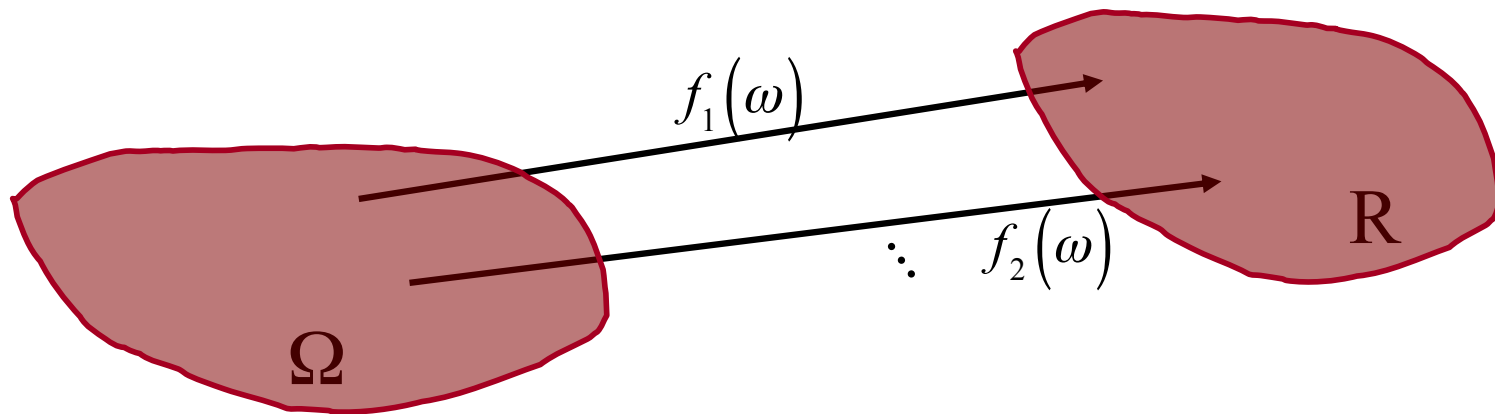
**Limits:** results are often not so reliable and it is hard to evaluate the goodness of the approximation

# SUMMARY

- Fisherian vs Bayesian estimation
- Bayesian estimation using Monte Carlo methods
- Bayesian estimation using Markov chain Monte Carlo
- On-line Bayesian estimation (particle filters)

# CONVERGENCE OF RANDOM VARIABLES (1/2)

Consider a sequence of random variables  $f_n$   
on a sample space  $\Omega$  with generic element  $\omega$

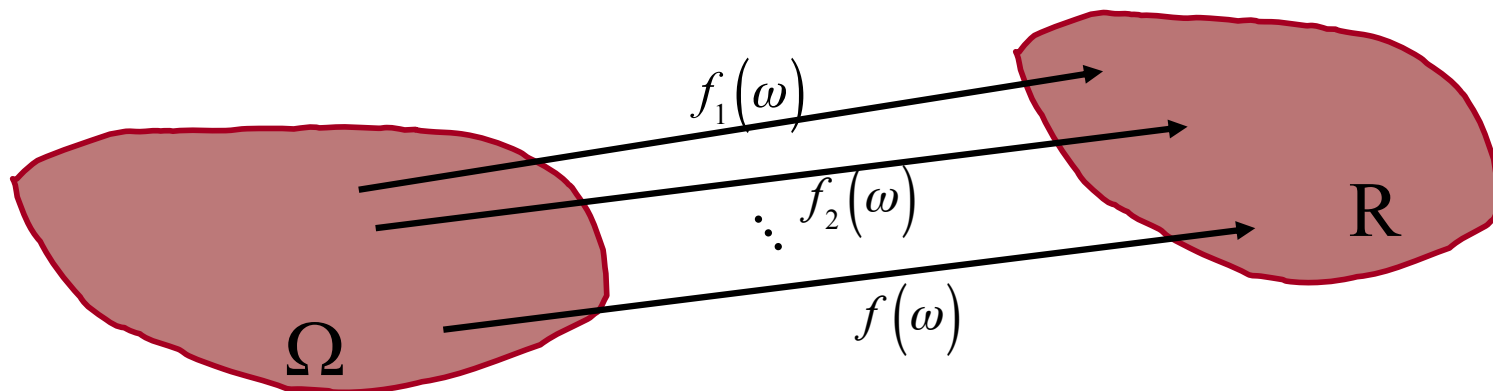


# CONVERGENCE OF RANDOM VARIABLES (2/2)

$$\lim_{n \rightarrow \infty} \overset{\text{almost surely}}{f_n} = f$$

if

$$\Pr(\omega: \lim_{n \rightarrow \infty} f_n(\omega) = f(\omega)) = 1$$



# STOCHASTIC APPROACHES: MONTE CARLO SIMULATION

Let us use  $\pi(x)$  to denote the posterior:

we are interested in  $E_{\pi}(g) \doteq \int g(x)\pi(x)dx$

We have  $x^1, x^2, \dots, x^n$  realizations i.i.d. from  $\pi$

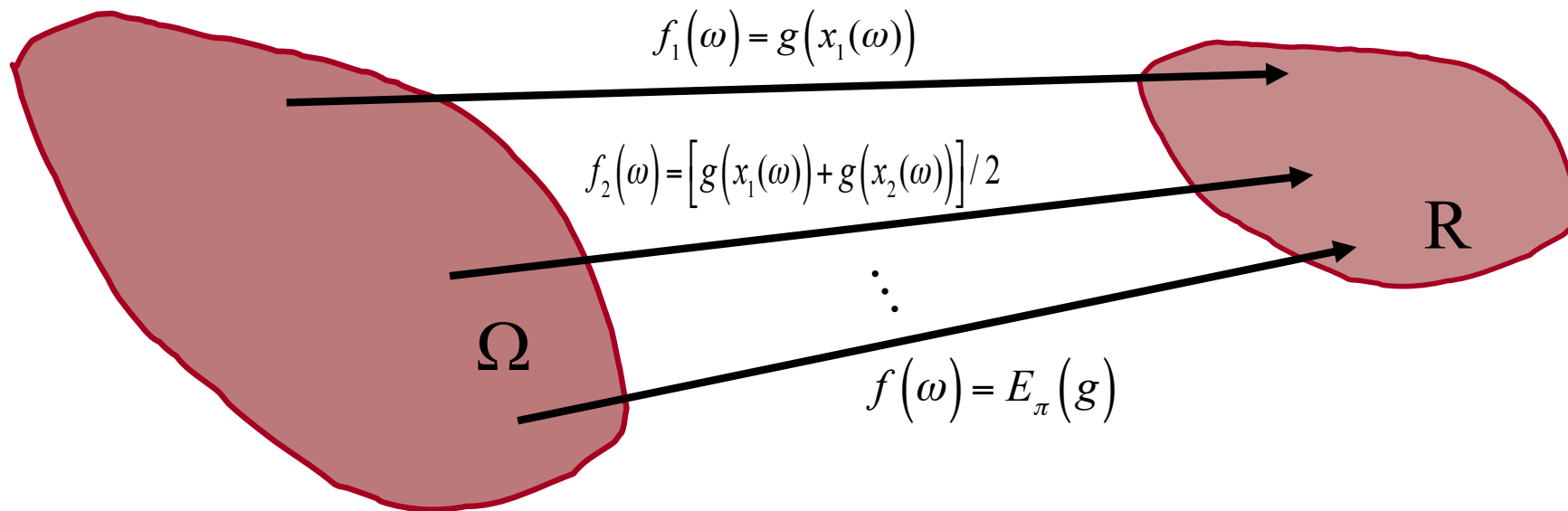
Let us define the following Monte Carlo approximation of the integral:

$$E_{\pi}(g) \approx \frac{1}{n} \sum_{i=1}^n g(x_i)$$

# CONVERGENCE OF A MONTE CARLO ESTIMATOR (1/2)

Strong law of large numbers holds:

$$\lim_{n \rightarrow \infty} \frac{1}{n} \sum_{i=1}^n g(x_i) \stackrel{\text{almost surely}}{=} E_{\pi}(g)$$



# CONVERGENCE OF A MONTE CARLO ESTIMATOR (2/2)

One has:

$$E[g(x_i)] = E_\pi[g]$$
$$\text{var}\left(\frac{1}{n} \sum_{i=1}^n g(x_i)\right) = \frac{1}{n} \int (g(x) - E_\pi(g))^2 \pi(x) dx \doteq \frac{\sigma^2}{n}$$

- difference from the true integral value has standard deviation going to zero as  $n^{-1/2}$  (independent of dimension of  $x$ )
- good approximation of the integral requires generation of a large number of realizations/samples from  $\pi$

Question: is it easy to draw independent samples from  $\pi$ ?



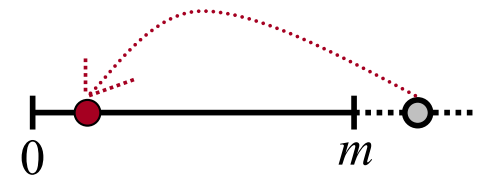
# MONTE CARLO SIMULATION: COMPUTATIONAL DIFFICULTIES

**Obtaining independent realizations from  $\pi$  is in general simple if we consider univariate distributions**

- One obtains samples from uniform random variables over  $[0, m]$  using recursive methods by computer

$$x_{i+1} = (ax_i + c) \bmod(m) \quad a, c \in \mathbb{N}$$

$$x_0 = \text{generator seed}$$



- Then one uses the **inversion method**:

$$F(a) = \int_{-\infty}^a \pi(x) dx$$

If  $x$  has generic but invertible probability distribution  $F$ , and  $u$  is drawn from an uniform random variable over  $[0, 1]$ ,

$F^{-1}(u)$  is a sample drawn from  $\pi$ .

In fact:

$$\Pr(x := F^{-1}(u) \leq a) = \Pr(u \leq F(a)) = F(a)$$

# **MONTE CARLO SIMULATION: COMPUTATIONAL DIFFICULTIES**

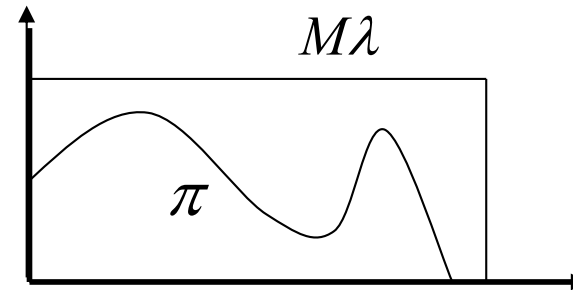
**Drawing independent samples from  $\pi$  is in general a very hard problem if one considers multivariate and non standard probability density functions**

- Sample/resample methods
- Ratio of uniform method
- ....
- **Rejection sampling**

# Rejection sampling (acceptance/rejection method)

- 1) One first obtains samples from a density  $\lambda(x)$  different from that of interest assuming that there exists a scalar  $M$  such that:

$$M\lambda(x) \geq \pi(x)$$



- 2) Then one obtains a sample from a uniform  $u$  in  $[0,1]$  and accepts the realization  $x$  from  $\lambda$  if

$$u \leq \frac{\pi(x)}{M\lambda(x)}$$

Accepted realizations are  
i.i.d. samples from  $\pi$

# Rejection sampling: observations

- Two-step method: use of an auxiliary density and then a correction method
- Choice of  $\lambda$  is crucial.  
It must be:
  - easy to simulate
  - easy to evaluate pointwise
  - such that it leads to a small probability of rejecting the sample (similar to  $\pi$ )

# Rejection sampling: limitations (1/2)

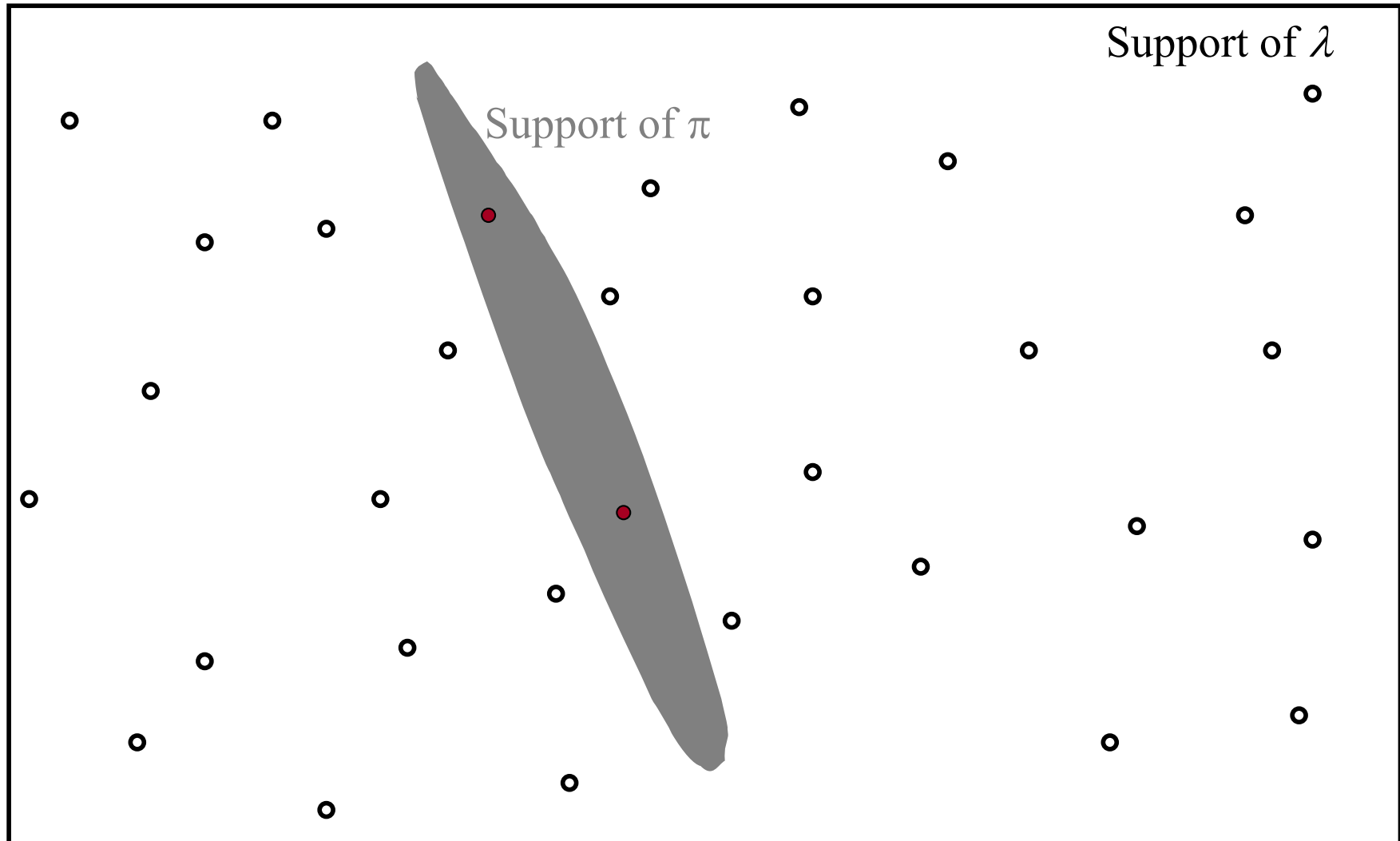
Probability of accepting the sample from  $\lambda$ :

$$\int \Pr\left(u \leq \frac{\pi(x)}{M\lambda(x)} \mid x\right) \lambda(x) dx =$$
$$\int \frac{\pi(x)}{M\lambda(x)} \lambda(x) dx = \frac{1}{M}$$

In practice  $M\lambda$  has to be a nice cover of  $\pi$   
but its choice is difficult in high-dimension

# Rejection sampling: limitations (2/2)

## CURSE OF DIMENSIONALITY



# Rejection sampling: proof of correctness

Recall that we proved that, if  $A$  is the event  
`the sample from  $\lambda$  is accepted`,  
then  $\Pr(A) = M^{-1}$

$$\Pr(x|A) = \frac{\Pr(x \cap A)}{\Pr(A)} = M \Pr(x \cap A)$$

Infinitesimal probability of  
generating and accepting  $x$   
using rejection sampling

$$\Pr(x \cap A) = \lambda(x) dx \Pr\left(U \leq \frac{\pi(x)}{M\lambda(x)}\right) = \frac{\lambda(x) dx \pi(x)}{M\lambda(x)}$$

**Hence, we can conclude that**

$$\Pr(x|A) = M \frac{\lambda(x) dx \pi(x)}{M\lambda(x)} = \pi(x) dx$$

# GENERALIZATION OF MONTE CARLO SIMULATION

The target is  $E_{\pi}(g) \doteq \int g(x)\pi(x)dx$

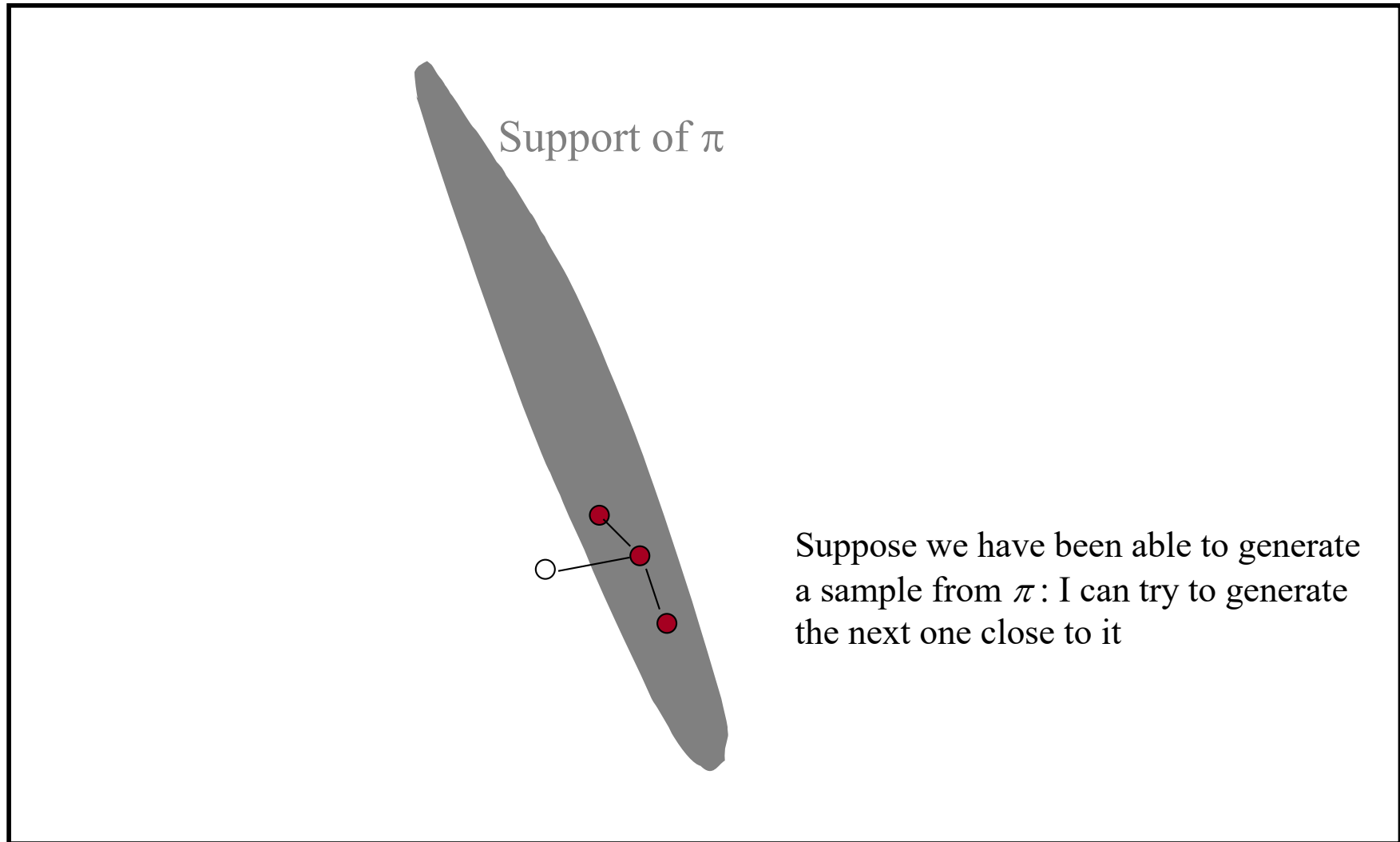
We try to extend the use of this estimator

$$E_{\pi}(g) \approx \frac{1}{n} \sum_{i=1}^n g(x_i)$$

To the case where  $x^1, x^2, \dots, x^n$  are non independent realizations from  $\pi$



# Advantages



This concept is the basis of the simulation technique called  
Markov chain Monte Carlo (MCMC)

# SUMMARY

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- Bayesian estimation using Monte Carlo methods
- Bayesian estimation using Markov chain Monte Carlo
- On-line Bayesian estimation (particle filters)

# MARKOV CHAINS

Let us consider a collection of random vectors of dimension  $d$

$$\{X_t, t = 0, 1, 2, \dots\}$$

We say it is a Markovian collection if, considering

$$X_t \mid X_{t-1} = x_{t-1}, X_{t-2} = x_{t-2}, \dots, X_0 = x_0$$

it holds that

$$\Pr(X_t \in A \mid X_{t-1} = x_{t-1}, X_{t-2} = x_{t-2}, \dots, X_0 = x_0) = \Pr(X_t \in A \mid X_{t-1} = x_{t-1})$$

$$\forall A \in \mathcal{B}, \forall t, \forall x$$

$\mathcal{B}$ =sigma-algebra

# STATIONARY MARKOV CHAINS

The chain is stationary if the conditional probability distributions do not vary over time

$$\Pr(X_1 \in A | X_0 = x) = \Pr(X_t \in A | X_{t-1} = x) \doteq P(A, x)$$

$$\forall A \in \mathcal{B}, \forall t, \forall x$$

# TRANSITION KERNEL OF A STATIONARY MARKOV CHAIN (1/3)

The transition kernel of the  
chain is that function  $k(a,x)$  s.t.:

$$P(A, x) = \int_A k(a, x) da$$

$$k(\cdot, \cdot) = p_{X_{t+1}|X_t}(\cdot | \cdot)$$

## TRANSITION KERNEL OF A STATIONARY MARKOV CHAIN (2/3)

$\pi_0$  (initial probability density) and  
 $k(.,.)$  completely define the  
probability laws of the chain

### Example

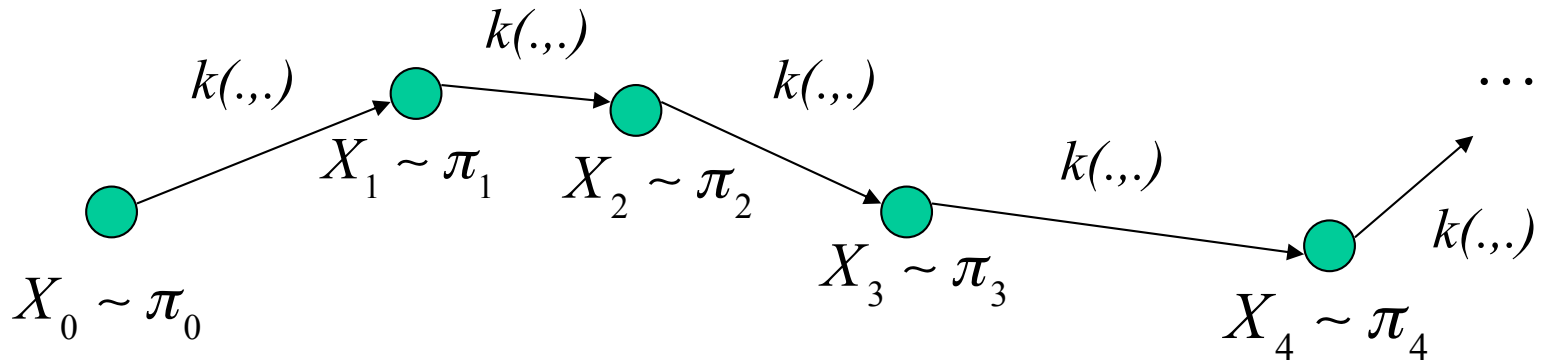
$$\begin{aligned} p_{x_0, x_1, x_2} (x_0, x_1, x_2) &= p_{x_0} (x_0) p_{x_1|x_0} (x_1|x_0) p_{x_2|x_1, x_0} (x_2|x_1, x_0) \\ &= \pi_0 (x_0) k(x_1, x_0) k(x_2, x_1) \end{aligned}$$

For any n-uple of vectors from the chain , the joint  
probability density can be computed

# TRANSITION KERNEL OF A STATIONARY MARKOV CHAIN (3/3)

Assume  $X_{t-1}$  has probability density  $\pi_{t-1}$   
If  $\pi_t$  is the probability density of  $X_t$ , one has:

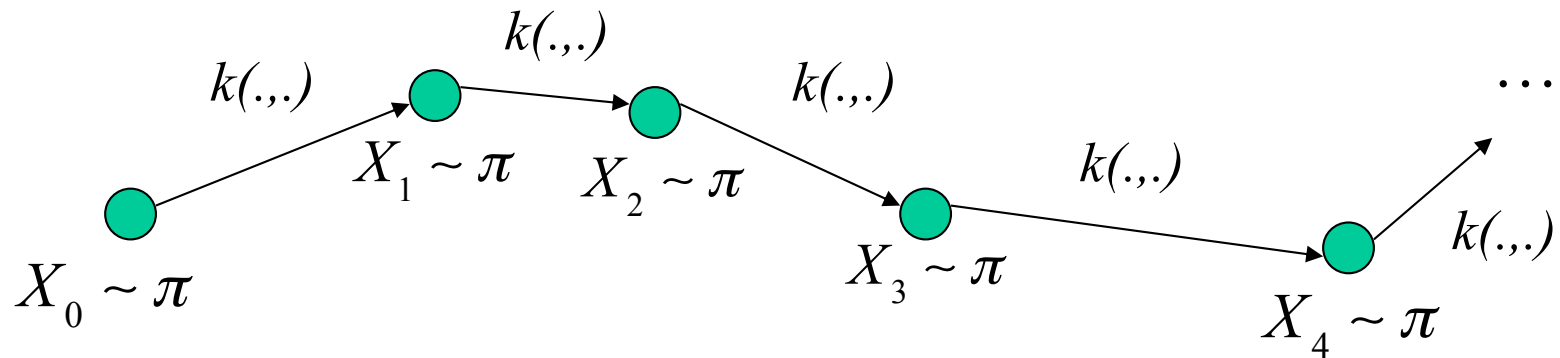
$$\pi_t(a) = \int k(a, x) \pi_{t-1}(x) dx$$



# INVARIANT DENSITY OF A STATIONARY MARKOV CHAIN

$\pi$  is an **invariant probability density**  
for the chain if:

$$\pi(a) = \int k(a, x) \pi(x) dx$$



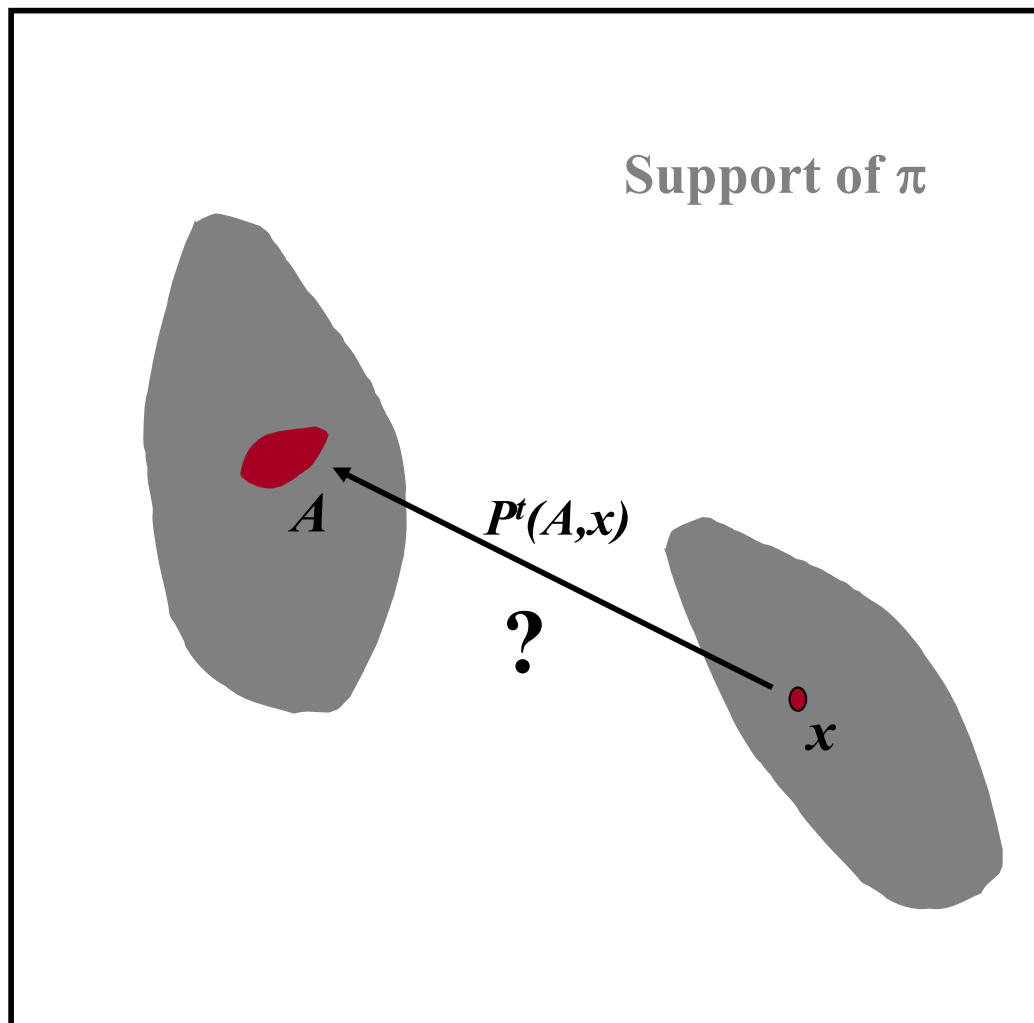


# IRREDUCIBLE MARKOV CHAINS (1/2)

Let  $\pi$  be an invariant density for the chain:  
the chain is **irreducible** if for any  $x$  and  
 $A$  in  $\mathbf{B}$ , with  $\int_A \pi(x) dx > 0$  ,  
there exists  $t > 0$  s.t.

$$\Pr(X_t \in A | X_0 = x) > 0$$

## IRREDUCIBLE MARKOV CHAINS (2/2)



Irreducibility = possibility  
of visiting all the interesting  
regions of  $\pi$  starting  
from any  $x$

# STRONG LAW OF LARGE NUMBERS FOR MARKOV CHAINS

Let  $\{X_t\}$  be an irreducible Markov chain  
having  $\pi$  as invariant density.

One has:

$$\lim_{n \rightarrow \infty} \frac{1}{n} \sum_{t=0}^n g(X_t) \stackrel{q.c.}{=} E_{\pi}(g)$$

for any initial state  
(except a set of probability zero)

# MARKOV CHAIN MONTE CARLO

- Builds an irreducible Markov chain with invariant density equal to the posterior
- Uses Monte Carlo integration to obtain the quantities of interest

The first step of the algorithm can be obtained by using the Metropolis-Hastings algorithm

# METROPOLIS-HASTINGS ALGORITHM (1/2)

Current chain state:  $X_t = x$

- We propose a new sample  $c \sim q(\cdot|x)$   
where  $q(\cdot|.)$  is the proposal density of the chain
- with a certain probability  $\alpha(c,x)$  we accept the candidate  $c$ ,  
i.e.  $X_{t+1} = c$
- otherwise  $X_{t+1} = x$

## ALGORITMO DI METROPOLIS-HASTINGS (2/2)

If the acceptance probability is:

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$

$\pi$  becomes the invariant density  
of the generated Markov chain

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Preliminary lemma

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$



$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Preliminary lemma

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$



$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$

**Proof**

Let us show that the equality holds  
for any possible couple  $(X_t, X_{t+1})$



# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Preliminary lemma

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$



$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$

**Proof**

Let us divide all the possible  
couples  $(X_t, X_{t+1})$   
into two groups

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Preliminary lemma

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$



$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$

**Proof**

Group 1:  $\frac{\pi(X_{t+1})q(X_t|X_{t+1})}{\pi(X_t)q(X_{t+1}|X_t)} \leq 1$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Preliminary lemma

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$



$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$

**Proof**

Group 1: 
$$\frac{\pi(X_{t+1})q(X_t|X_{t+1})}{\pi(X_t)q(X_{t+1}|X_t)} \leq 1$$

This implies 
$$\alpha(X_{t+1}, X_t) = \frac{\pi(X_{t+1})q(X_t|X_{t+1})}{\pi(X_t)q(X_{t+1}|X_t)} \text{ e } \alpha(X_t, X_{t+1}) = 1$$

and the equality immediately follows

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Preliminary lemma

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$



$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$

**Proof**

Group 2:  $\frac{\pi(X_t)q(X_{t+1}|X_t)}{\pi(X_{t+1})q(X_t|X_{t+1})} < 1$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Preliminary lemma

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)}\right)$$



$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$

**Proof**

Group 2:  $\frac{\pi(X_t)q(X_{t+1}|X_t)}{\pi(X_{t+1})q(X_t|X_{t+1})} < 1$

This implies  $\alpha(X_t, X_{t+1}) = \frac{\pi(X_t)q(X_{t+1}|X_t)}{\pi(X_{t+1})q(X_t|X_{t+1})}$  e  $\alpha(X_{t+1}, X_t) = 1$

and the equality immediately follows

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) + \delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)$$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$\underbrace{k(X_{t+1}|X_t)} = q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) + \delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)$$

Kernel of the Markov chain  
describing the infinitesimal  
probability of going from  
 $X_t$  to  $X_{t+1}$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

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Infinitesimal probability of  
proposing as candidate  $X_{t+1}$   
if the current state is  $X_t$



# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = q(X_{t+1}|X_t) \underbrace{\alpha(X_{t+1}, X_t)} + \delta(X_{t+1} = X_t) \left(1 - \int q(c|X_t) \alpha(c, X_t) dc\right)$$

Probability of  
accepting as candidate  $X_{t+1}$   
if the current state is  $X_t$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

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Infinitesimal probability  
of going to  $X_{t+1}$  from  $X_t$   
through the acceptance  
of the candidate

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = \underbrace{q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t)}_{\text{Infinitesimal probability of going to } X_{t+1} \text{ from } X_t \text{ through the acceptance of the candidate}} + \delta(X_{t+1} = X_t) \underbrace{\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)}_{\text{Probability of accepting a sample (before generating it!) If the current state is } X_t \text{ (generated by } q \text{ with acceptance probability given by } \alpha)}$$

Infinitesimal probability  
of going to  $X_{t+1}$  from  $X_t$   
through the acceptance  
of the candidate

Probability of accepting a  
sample (before generating it!)  
If the current state is  $X_t$   
(generated by  $q$  with  
acceptance probability  
given by  $\alpha$ )

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = \underbrace{q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t)}_{\text{Infinitesimal probability of going to } X_{t+1} \text{ from } X_t \text{ through the acceptance of the candidate}} + \delta(X_{t+1} = X_t) \underbrace{\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)}_{\text{Probability of remaining at } X_t}$$

Infinitesimal probability  
of going to  $X_{t+1}$  from  $X_t$   
through the acceptance  
of the candidate

Probability of  
remaining at  $X_t$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = \underbrace{q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t)} + \underbrace{\delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)}$$

Infinitesimal probability  
of going to  $X_{t+1}$  from  $X_t$   
through the acceptance  
of the candidate

And also Dirac delta area  
which is equal to the probability  
of going from  $X_t$  to  $X_{t+1}$   
by refusing the candidate:  
contribution to  $k(X_{t+1}|X_t)$   
only if  $X_{t+1} = X_t$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = \underbrace{q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t)}_{\text{Infinitesimal probability of going to } X_{t+1} \text{ from } X_t \text{ through the acceptance of the candidate}} + \underbrace{\delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)}_{\text{Hence, the second contribution is the Dirac delta with that area and centred on } X_t}$$

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Infinitesimal probability of going to  $X_{t+1}$  from  $X_t$  through the acceptance of the candidate

Hence, the second contribution is the Dirac delta with that area and centred on  $X_t$

Symmetric term in  $X_{t+1}$  and  $X_t$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) + \underbrace{\delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)}_{\text{Symmetric term in } X_{t+1} \text{ and } X_t}$$

+ (lemma)

$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$



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Symmetric term in  $X_{t+1}$  and  $X_t$

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$$\pi(X_t)k(X_{t+1}|X_t) = \pi(X_{t+1})k(X_t|X_{t+1})$$

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$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$



$$\pi(X_t)k(X_{t+1}|X_t) = \pi(X_{t+1})k(X_t|X_{t+1})$$

Immediately derives from the symmetry of the term  $\delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)$  that defines the kernel of the chain

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

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Symmetric term in  $X_{t+1}$  and  $X_t$

+ (lemma)

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$$\pi(X_t)k(X_{t+1}|X_t) = \pi(X_{t+1})k(X_t|X_{t+1})$$

$$\int \pi(X_t)k(X_{t+1}|X_t)dX_t = \pi(X_{t+1})\int k(X_t|X_{t+1})dX_t$$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

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$$\pi(X_t)k(X_{t+1}|X_t) = \pi(X_{t+1})k(X_t|X_{t+1})$$

$$\int \pi(X_t)k(X_{t+1}|X_t)dX_t = \pi(X_{t+1}) \int k(X_t|X_{t+1})dX_t = 1$$

# METROPOLIS-HASTINGS ALGORITHM: PROOF OF CORRECTNESS

Kernel of the chain

$$k(X_{t+1}|X_t) = q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) + \underbrace{\delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)}_{\text{Symmetric term in } X_{t+1} \text{ and } X_t}$$

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$$\int \pi(X_t)k(X_{t+1}|X_t)dX_t = \pi(X_{t+1})$$

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$$\pi(X_t)q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) = \pi(X_{t+1})q(X_t|X_{t+1})\alpha(X_t, X_{t+1})$$



$$\int \pi(X_t)k(X_{t+1}|X_t)dX_t = \pi(X_{t+1})$$

Hence,  $\pi$  is indeed the invariant density

## OBSERVATIONS (1/2)

- differently from the rejection sampling:
  - the chain always moves  
(if the sample is refused, the next state is equal to the previous one)
  - in general, the algorithm is able to return correlated  
(but not independent) samples from  $\pi$

## OBSERVATIONS (2/2)

- the target density  $\pi$  can be known apart from a normalization factor

$$\alpha(c, x) = \min \left( 1, \frac{\pi(c)q(x|c)}{\pi(x)q(c|x)} \right) \quad \pi(x) \propto p_{y|x}(y|x)p_x(x)$$

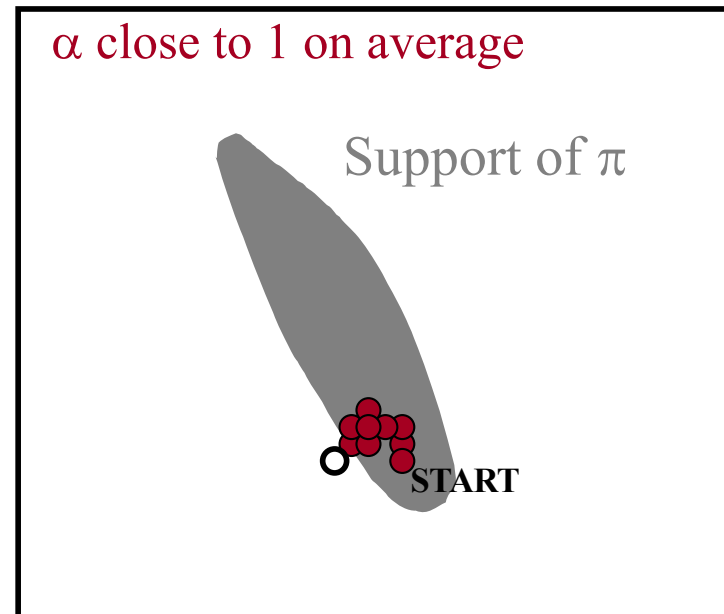
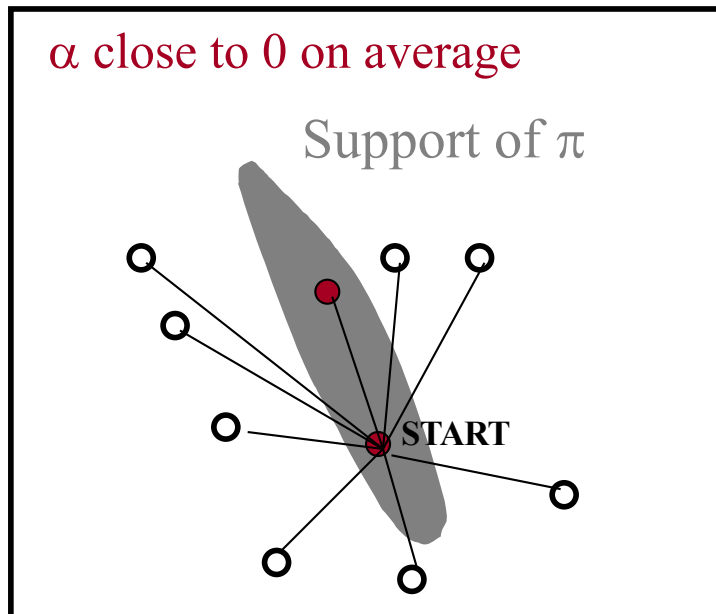
- theoretically, the algorithm works for any  $q(\cdot|\cdot)$  (if the chain is irreducible), but in practice the choice of  $q$  is crucial



# CHOICE OF $q(.|.)$ (1/2)

$q(.|.)$  must

- be easy to sample
- be simple to be evaluated pointwise
- able to quickly explore the support of  $\pi$



## CHOICE OF $q(\cdot|\cdot)$ (2/2)

Often, it is useful to adopt random-walk proposals

$$q(c|x) = f(|c-x|) = q(x|c)$$

$$\left. \begin{array}{l} c = x_t + \varepsilon \\ \varepsilon \sim N(0, \Sigma) \end{array} \right\} q(c|x) = N(x, \Sigma)$$

- $\Sigma$  provides information as how to move locally around the current point
- the acceptance probability becomes

$$\alpha(c, x) = \min\left(1, \frac{\pi(c)}{\pi(x)}\right)$$

## Strategies to choose $\Sigma(1/2)$ :

In high-dimension it is worth performing an explorative analysis of  $\pi$

### Example #1:

- Define a diagonal matrix  $\Sigma$  with small variances values

$$\Sigma_{start} = \begin{bmatrix} \sigma_1^2 & & & \\ & \sigma_2^2 & & \\ & & \dots & \\ & & & \sigma_n^2 \end{bmatrix}$$

- generate Markov chains and monitor the results.  
Change the variances so as to obtain an acceptance rate around 30-40%
- generate the Markov chain using the matrix  $\Sigma$  obtained by the pilot analysis

## Strategies to choose $\Sigma$ (2/2):

### Example #2:

- Calculate the posterior maxima and obtain information on the a posteriori correlation of the components of  $x$

$$\Sigma \propto \left[ -\frac{\partial^2 \log \pi}{\partial x^T \partial x} \Big|_{\hat{x}} \right]^{-1}$$
$$\hat{x} = \arg \min_x -\log(\pi)$$

- the scale factor is chosen so as to obtain an acceptance rate around 30-40%

# MCMC: SIMULATED EXAMPLE (1 of 4)

Aim: to reconstruct in  
sampled form a  
Gaussian distribution

**TARGET**

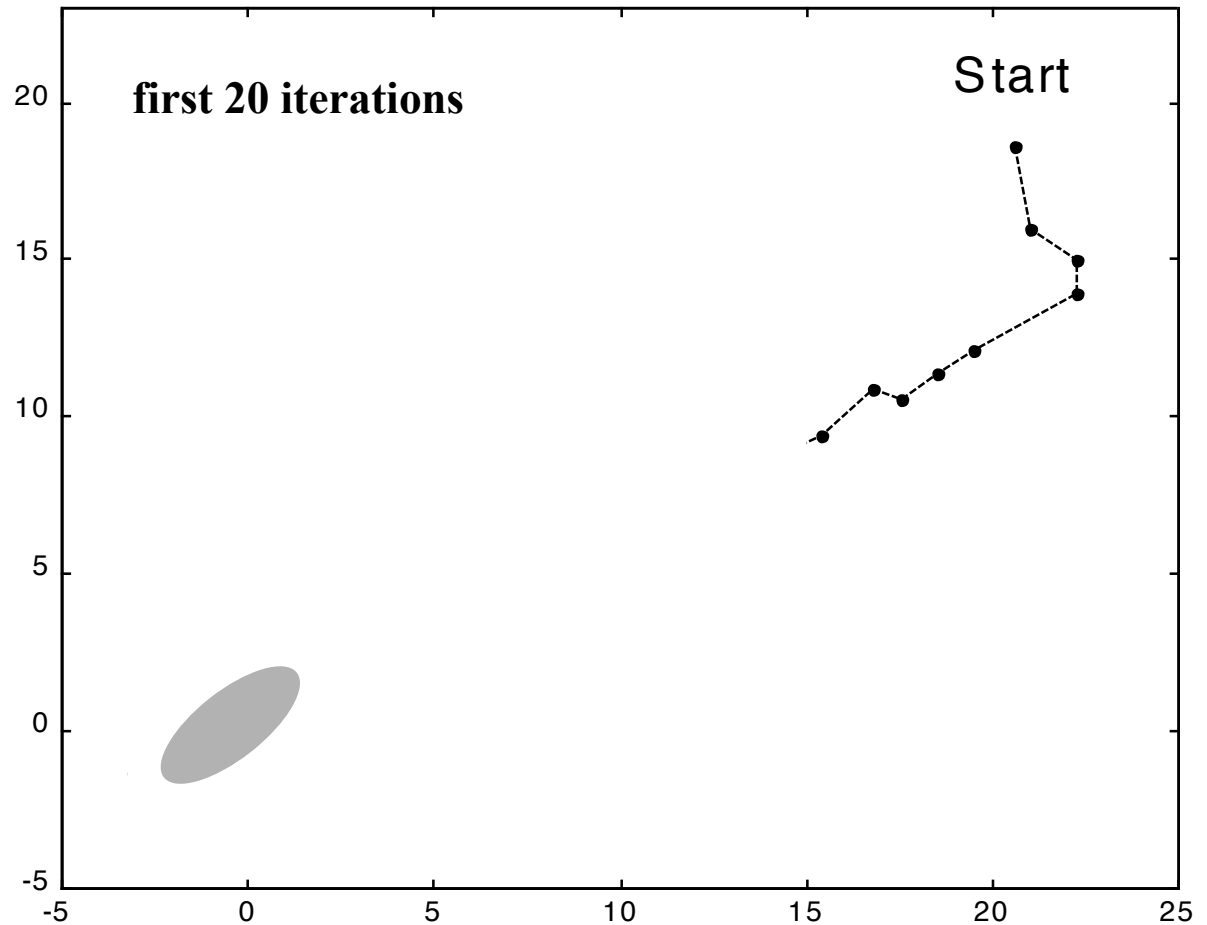
$$\pi = N(0, A)$$

$$A = \begin{pmatrix} 2 & 1 \\ 1 & 1 \end{pmatrix}$$

**PROPOSAL**

$$q(y|x) \sim N(x, B)$$

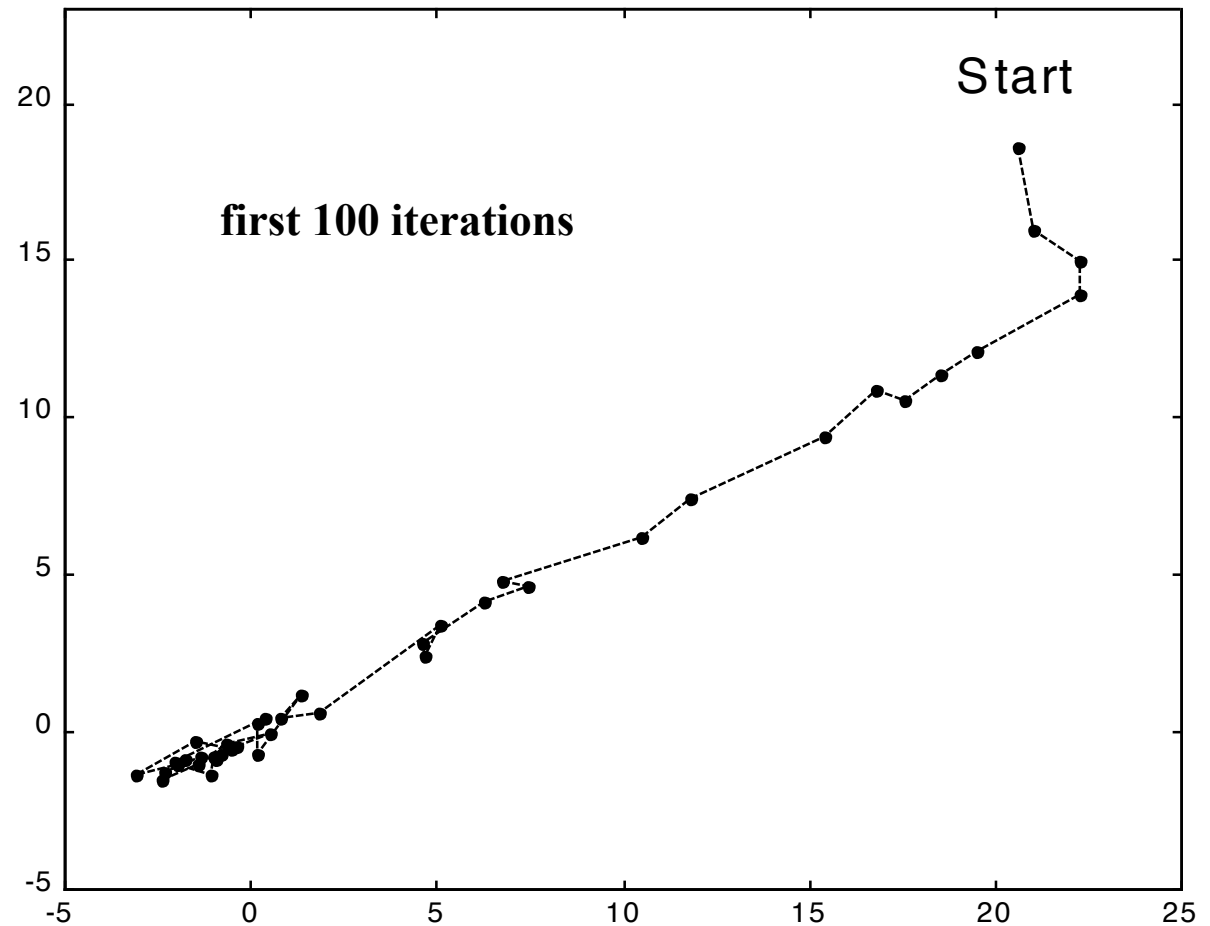
$$B = \begin{pmatrix} 2 & 0 \\ 0 & 2 \end{pmatrix}$$



# MCMC: SIMULATED EXAMPLE (2 of 4)

Aim: to reconstruct  
in sampled form a  
Gaussian distribution of  
zero mean and covariance

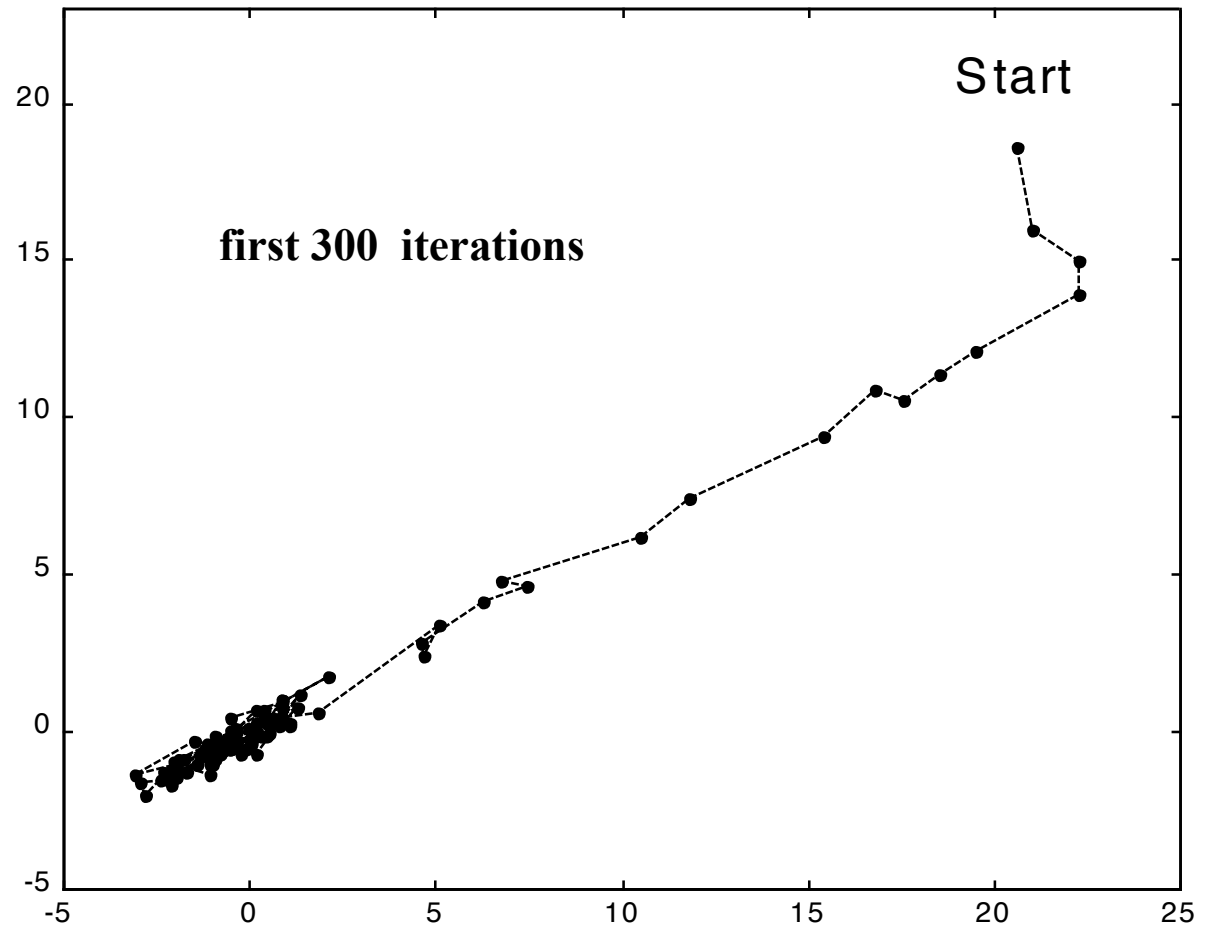
$$A = \begin{pmatrix} 2 & 1 \\ 1 & 1 \end{pmatrix}$$



# MCMC: SIMULATED EXAMPLE (3 of 4)

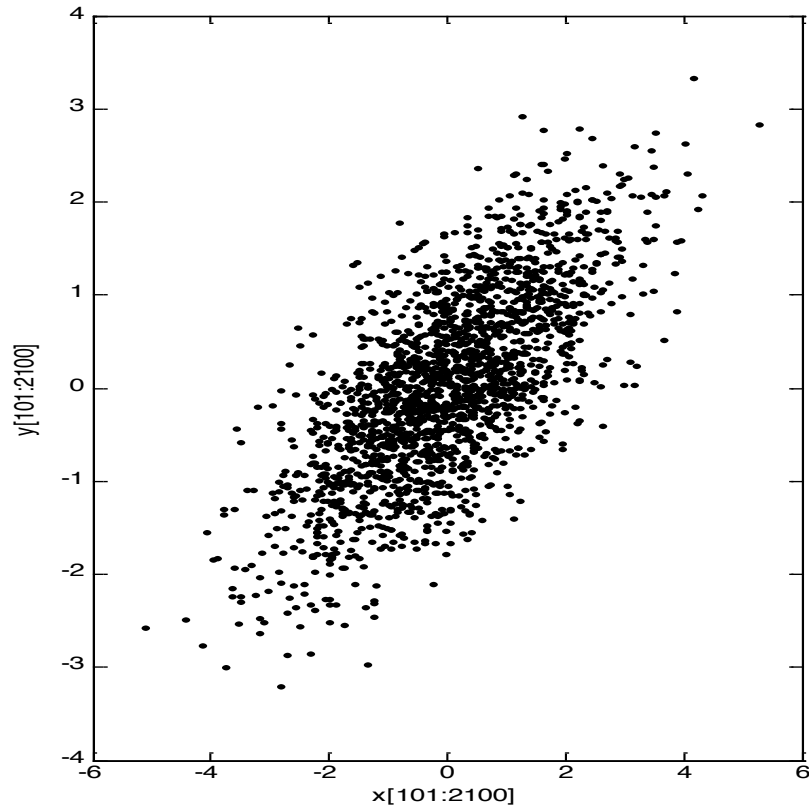
Aim: to reconstruct  
in sampled form a  
Gaussian distribution of  
zero mean and covariance

$$A = \begin{pmatrix} 2 & 1 \\ 1 & 1 \end{pmatrix}$$

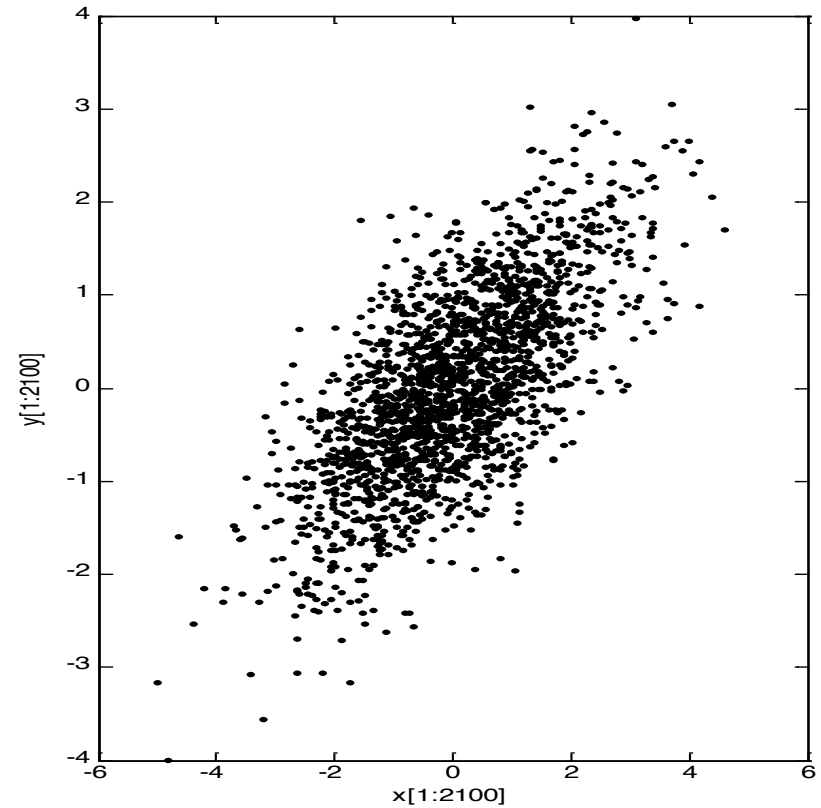


# MCMC: SIMULATED EXAMPLE (4 of 4)

2000 MCMC samples  
(iterations 101-2100)

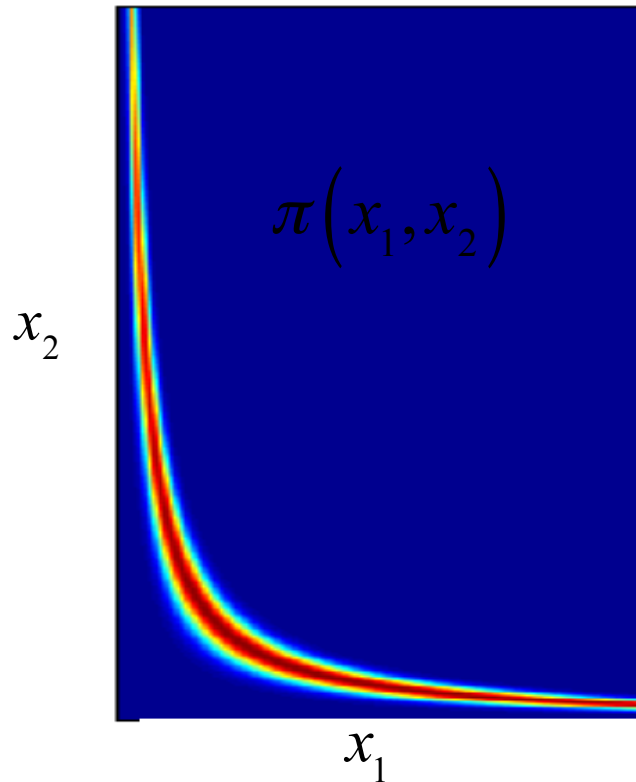


2000 independent  
samples





# CHOICE OF $q(.|.)$ : BLOCK SCHEMES

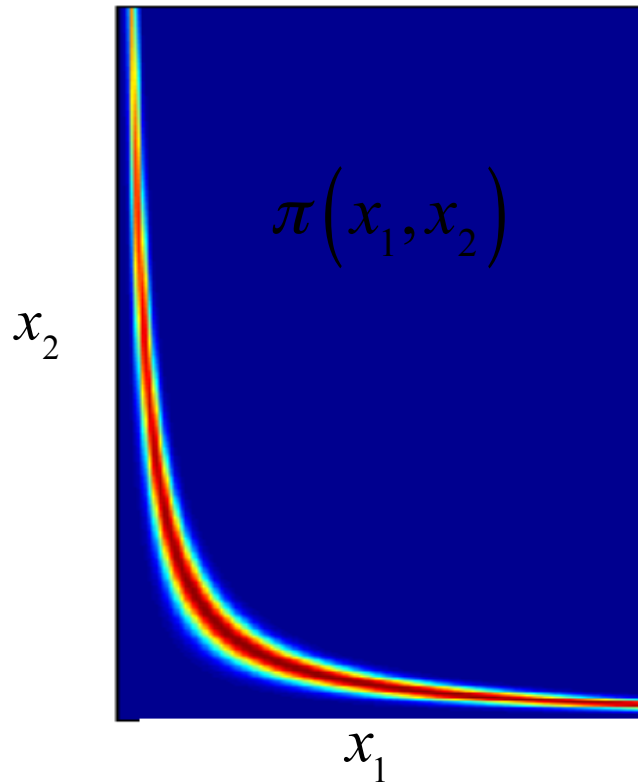


$$x = \begin{bmatrix} x_1 & x_2 \end{bmatrix}$$

Hard case:

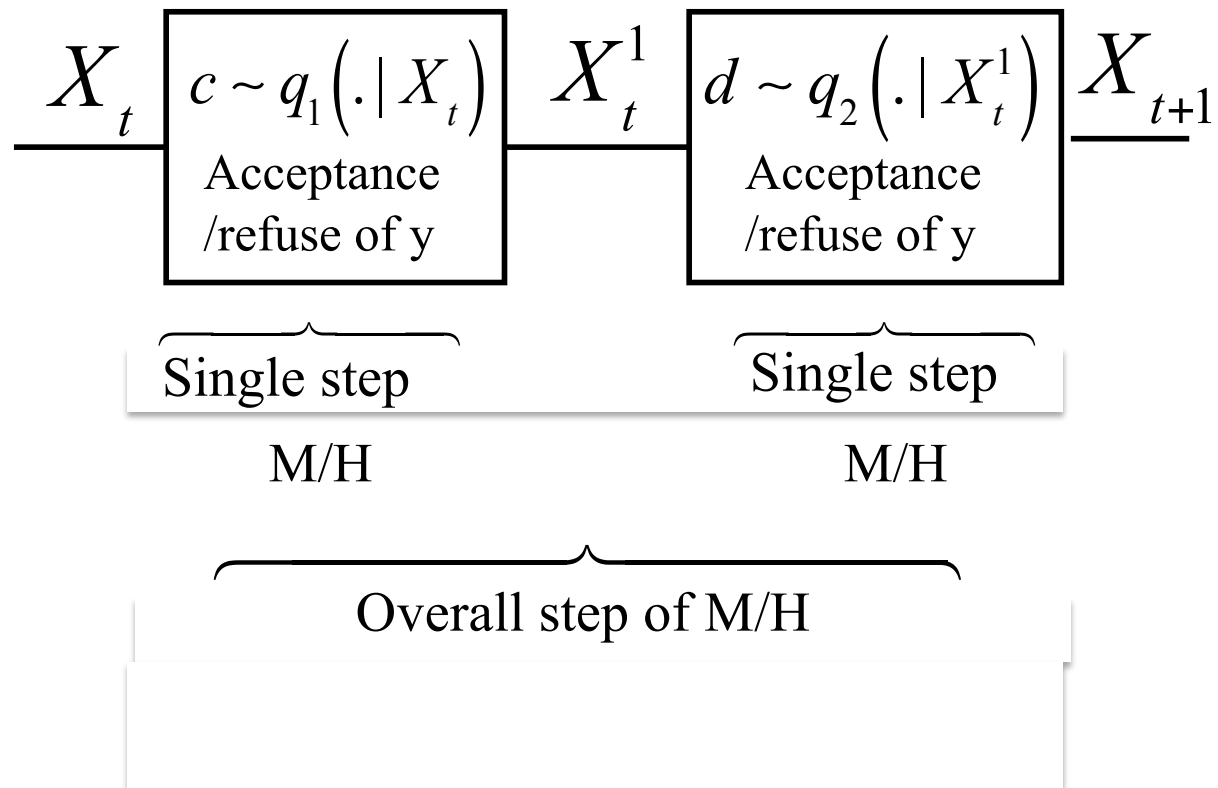
- strong a posteriori correlation
- correlation much varies along the parameter space
- difficult to move simultaneously  $x_1$  and  $x_2$  with a suitable probability  $c$  accepting the generated sample

# CHOICE OF $q(\cdot|\cdot)$ : BLOCK SCHEMES



One solution is to move separately  $x_1$  and  $x_2$  by defining two proposal densities  $q_1$  and  $q_2$

# CHOICE OF $q(\cdot|\cdot)$ : BLOCK SCHEMES



# CONVERGENCE DIAGNOSTICS (1/2)

Once an MCMC simulation starts,  
how many iterations do we need to perform?

- the chain kernel assumes a complex form

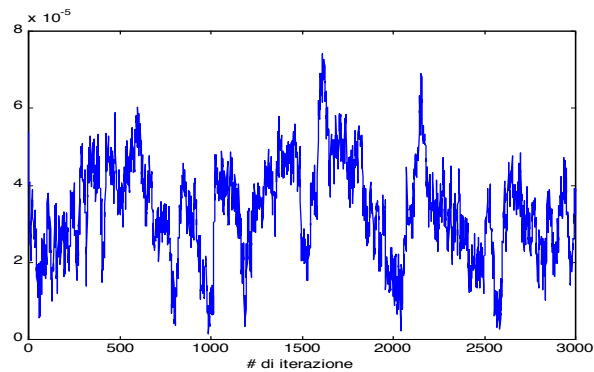
$$k(X_{t+1}|X_t) = q(X_{t+1}|X_t)\alpha(X_{t+1}, X_t) + \delta(X_{t+1} = X_t)\left(1 - \int q(c|X_t)\alpha(c, X_t)dc\right)$$

and is thus complex to analyze convergence under a theoretical viewpoint

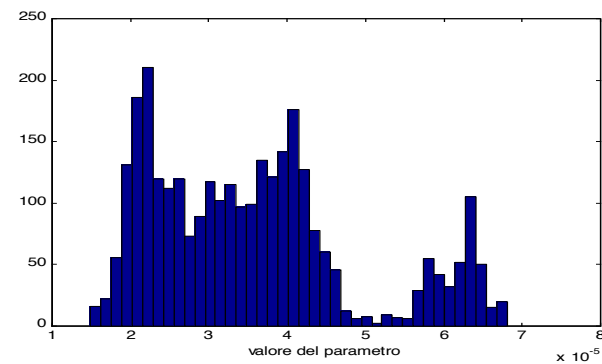
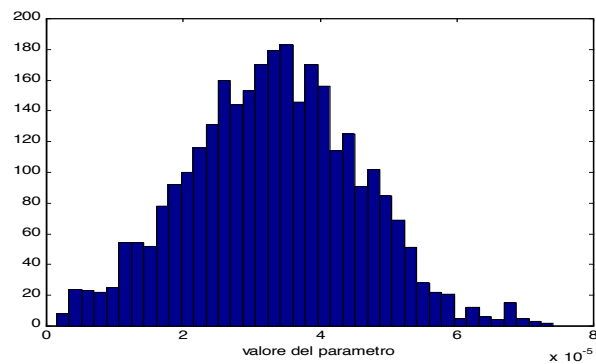
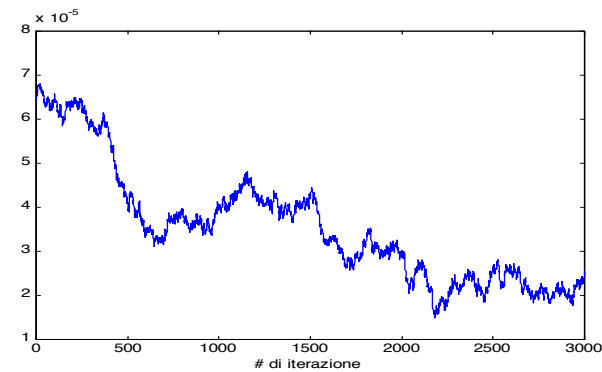
# CONVERGENCE DIAGNOSTICS (2/2)

- in practice one obtains information on the Markov chain convergence by analyzing the statistical properties of the generated samples

Good convergence



Bad convergence



# MINIMAL MODEL EQUATIONS

$G(t)$  = glucose plasma concentration

$I(t)$  = insulin plasma concentration

$$\begin{aligned}\dot{G}(t) &= -(S_G + X(t))G(t) + S_G G_b & G(0) &= G_0 \\ \dot{X}(t) &= -p_2 \{ X(t) - S_I [I(t) - I_b] \} & X(0) &= 0\end{aligned}$$

- The model contains **4 parameters** that are not directly measurable and have to be estimated from glucose samples
- $I(t)$  is assumed perfectly known by linear interpolation of its noisy samples. The model thus turns out to be a priori identifiable.

# MM PARAMETER ESTIMATION USING FISHER

$$y_i = h(t_i, x) + v_i$$

$i=1,2,\dots,N$

Glucose prediction

$$x = [S_I, p_2, S_G, G_0]$$

Gaussian error (CV%=2)

$$v \sim N(0, \Sigma_v) \quad \Sigma_v(i, i) = \sigma_i^2$$

$$L(x) = \frac{1}{(2\pi)^{N/2} \det(\Sigma_v)^{1/2}} e^{-\frac{1}{2} \sum_{i=1}^N \left( \frac{y_i - h(t_i, x)}{\sigma_i} \right)^2}$$

$$x^{ML} = \arg \max_p L(p)$$

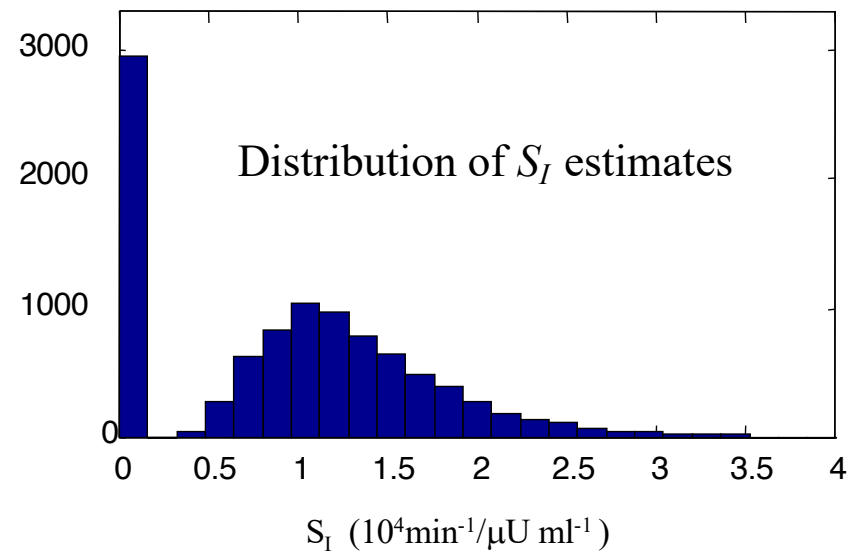
**LIKELIHOOD**

**MAXIMUM LIKELIHOOD  
ESTIMATE**

# DIFFICULTIES ENCOUNTERED BY THE FISHERIAN APPROACH (1/2)

## THE $S_I=0$ PROBLEM

In almost 40% of diabetic subjects the model  
returns an  $S_I$  estimate equal to zero





# DIFFICULTIES ENCOUNTERED BY THE FISHERIAN APPROACH (2/2)

## OTHER PROBLEMS

- $S_I$  estimate may turn out very small and much uncertain (in particular in diabetic subjects)
- $S_I$  pestimate may turn out much uncertain and not realistic, assuming very large value
- also  $p_2$  estimate may turn out much uncertain

# REPRODUCING FISHER DIFFICULTIES VIA COMPUTER SIMULATION

$$y_i = h(t_i, x) + v_i$$

$$x = [S_I, p_2, S_G, G_0]$$

Let us fix these parameters  
to realistic values  
for a diabetic subject:

$$S_I = 0.7 e - 4 \text{ min}^{-1} / \mu\text{Uml}^{-1}$$

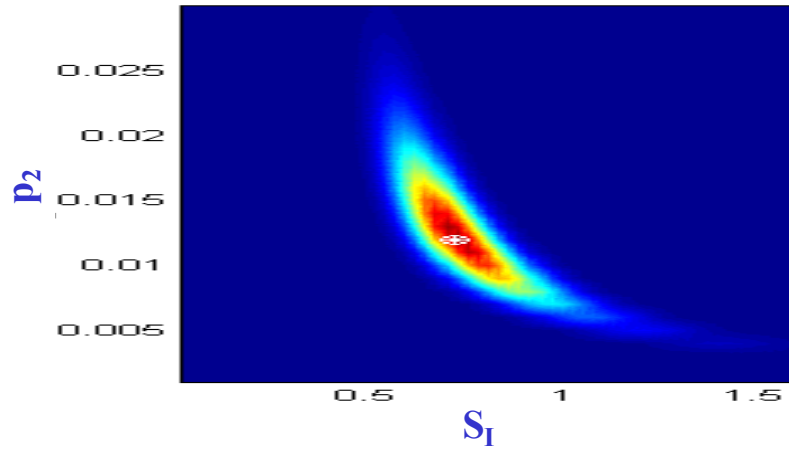
$$p_2 = 0.01 \text{ min}^{-1}$$

We generate 1000 realizations  
of the measurement error

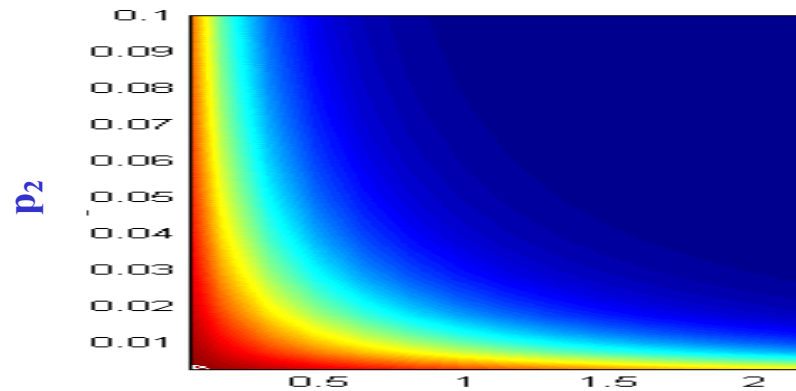
$$v \sim N(0, \Sigma_v)$$

and after each noise realization  
we obtain the maximum likelihood  
estimate of the MM parameters

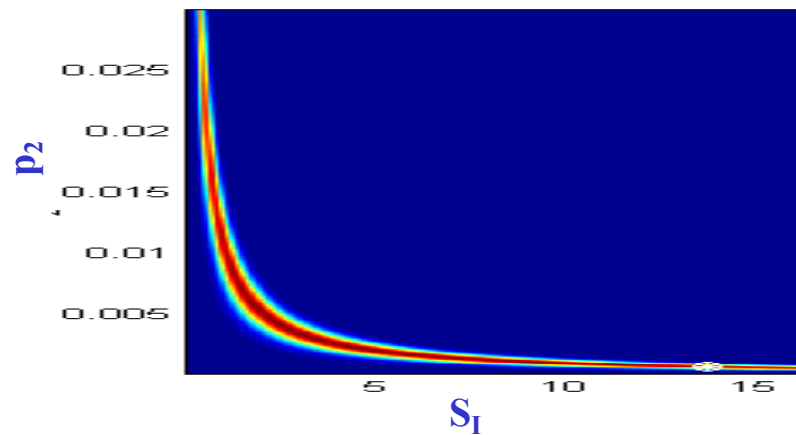
# Likelihood shapes in 3 significant cases



Works well



$S_I = 0$  and also  $p_2$   
is much uncertain

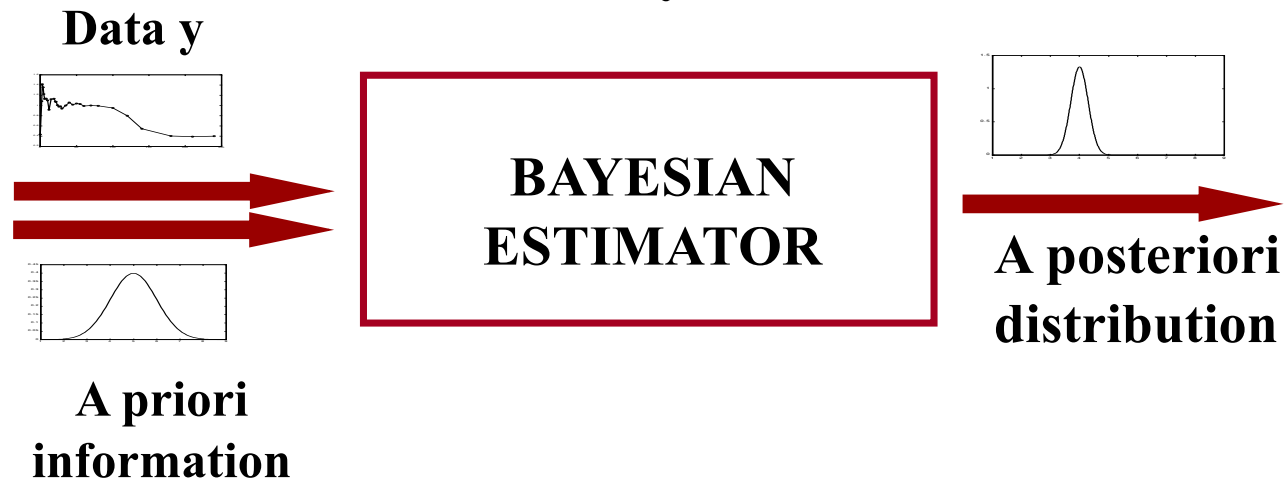


Large  $S_I$ , not realistic, and small  
 $p_2$  with large uncertainty

# Question: passing from Fisher....



to Bayes



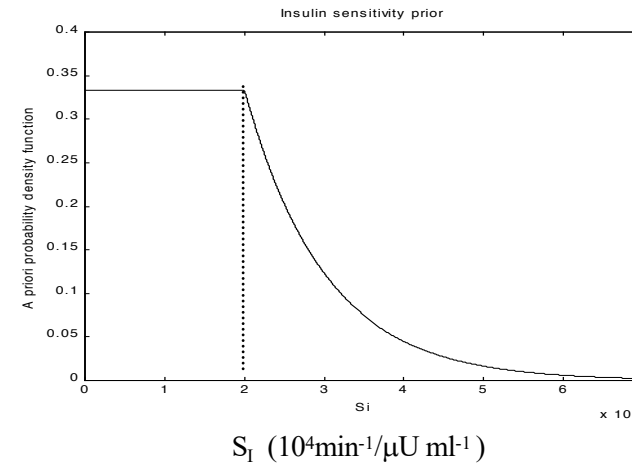
can we overcome the identification problems?

# Bayesian strategy: definition of the prior

- Let us define a prior for  $S_I$  based on the many studies reported in the literature

$$p_{S_I}(S_I) \propto \begin{cases} 0 & \text{se } S_I < 0 \\ 1 & \text{se } 0 \leq S_I \leq 2e-4 \\ e^{-\frac{(S_I - (2e-4))}{1e-4}} & \text{se } S_I > 2e-4 \end{cases}$$

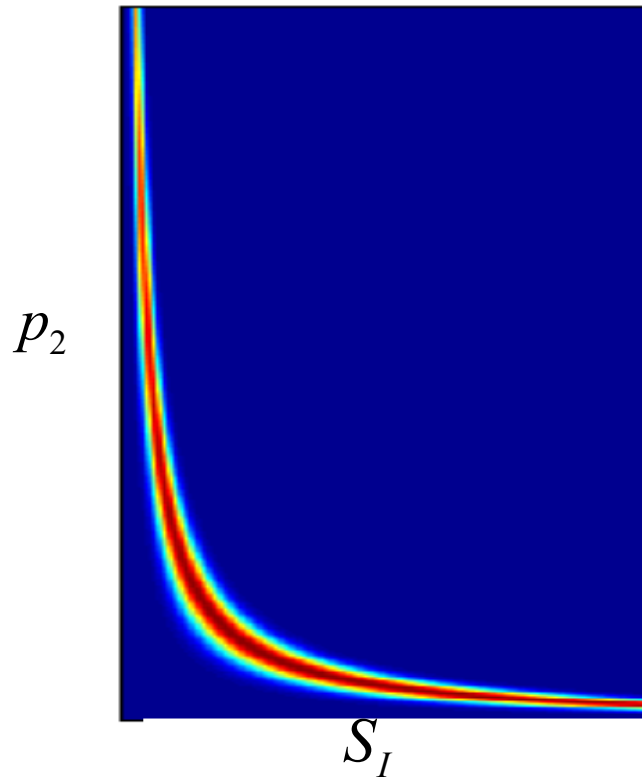
Prior for  $S_I$



- The prior is then poorly informative regarding  $S_G, p_2$  e  $G_0$  including just nonnegativity information

$$p_{S_I, S_G, p_2, G_0} \propto p_{S_I}(S_I) \chi(S_G \geq 0) \chi(p_2 \geq 0) \chi(G_0 \geq 0)$$

# Bayesian strategy: definition of the MCMC scheme



$S_I$  and  $p_2$  are often strongly correlated a posteriori. It is convenient to update them separately by defining two proposal densities:

$$\Sigma_1 = \begin{pmatrix} \sigma_{S_I}^2 & 0 & 0 \\ 0 & \sigma_{G_0}^2 & 0 \\ 0 & 0 & \sigma_{S_G}^2 \end{pmatrix}$$

$$\Sigma_2 = \left( \sigma_{p_2}^2 \right)$$

$$q_1(S_I^{new}, G_0^{new}, S_G^{new} | S_I^{old}, G_0^{old}, S_G^{old}) \\ = N([S_I^{old} \ G_0^{old} \ S_G^{old}], \Sigma_1)$$

$$q_2(p_2^{new} | p_2^{old}) \\ = N(p_2^{old}, \Sigma_2)$$

# COMPUTATIONAL COMPLEXITY

Related to the posterior evaluation at any MCMC iteration, i.e. to the cost of solving the differential equations of the model for any new proposed sample

$$\dot{G}(t) = -(S_G + X(t))G(t) + S_G G_b \quad G(0) = G_0$$

$$\dot{X}(t) = -p_2 \{ X(t) - S_I [I(t) - I_b] \} \quad X(0) = 0$$

Define:

$$Z(t) = \int_0^t X(\tau) d\tau$$

$$= \int_0^t \int_0^\tau S_I p_2 e^{-p_2(t-\tau)} (I(\tau) - I_b) d\tau dt = \int_0^t S_I (1 - e^{-p_2(t-\tau)}) (I(\tau) - I_b) d\tau$$

$$\text{One has: } G(t) = G_0 e^{-S_G t - Z(t)} + S_G G_b \int_0^t e^{-S_G(t-\tau) - Z(t) + Z(\tau)} d\tau$$

Glucose prediction in closed form

# RESULTS

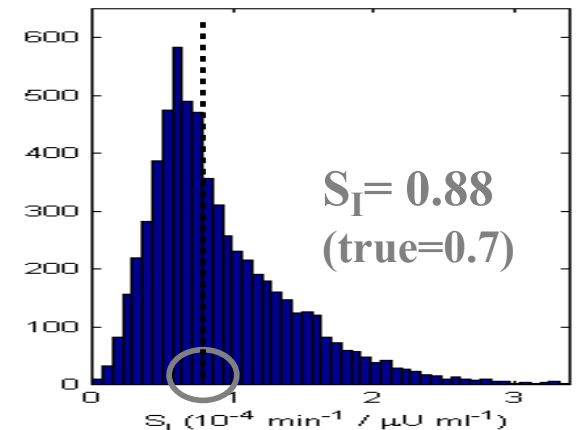
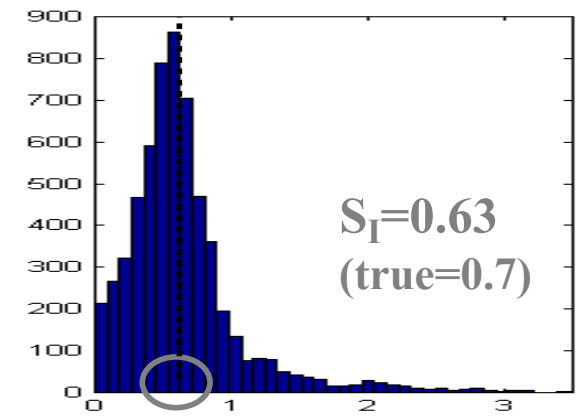
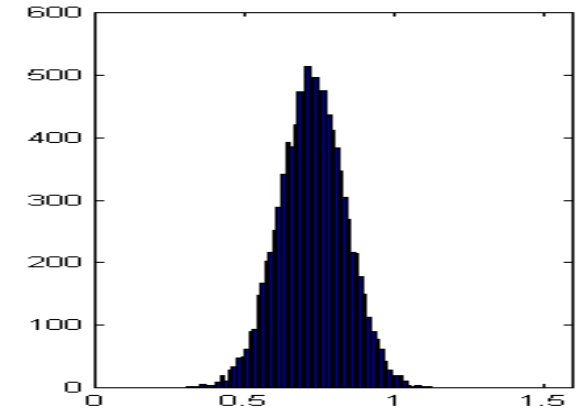
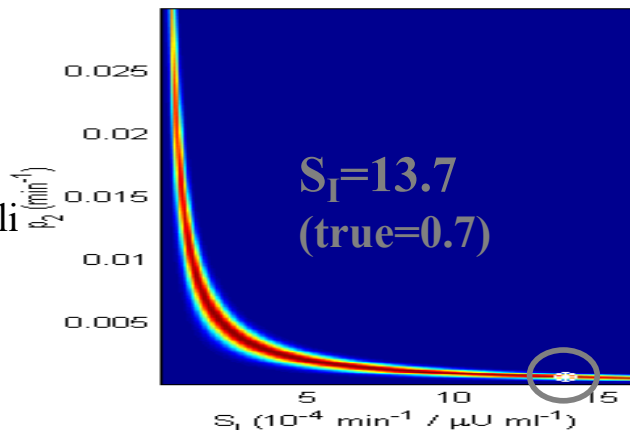
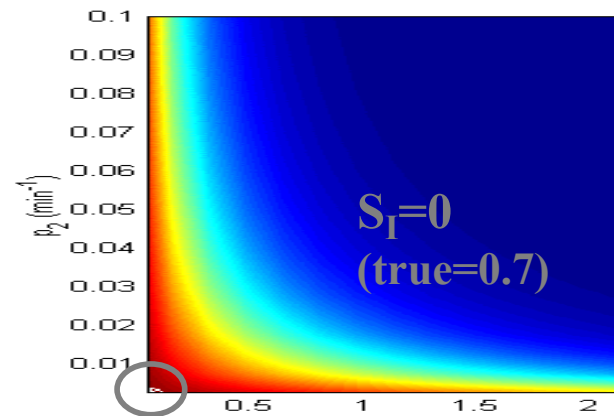
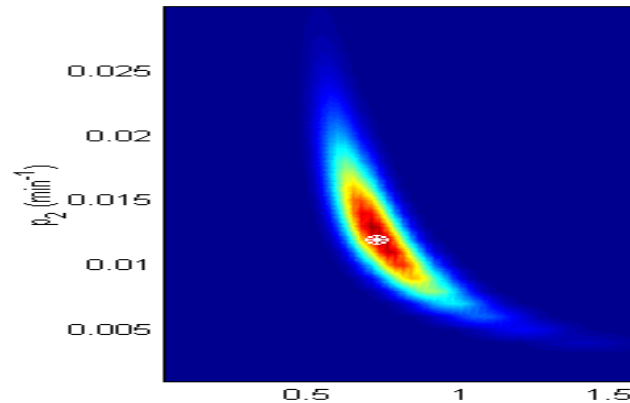
## FISHER (ML)

$$\hat{x} = \arg \max p_{y|p}(y|p)$$

## BAYES $S_I$ POSTERIOR

$$E[x|y] = \int xp_{x|y}(x|y)dx$$

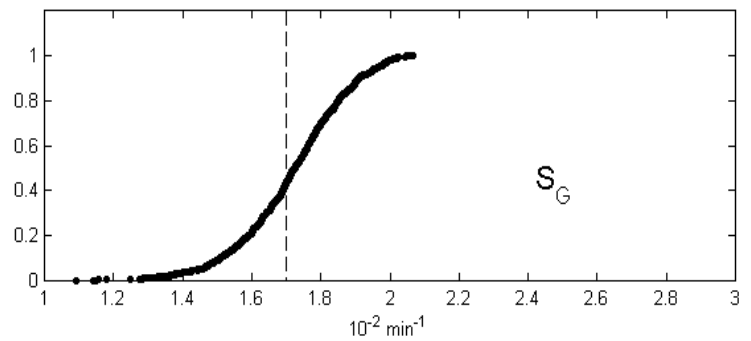
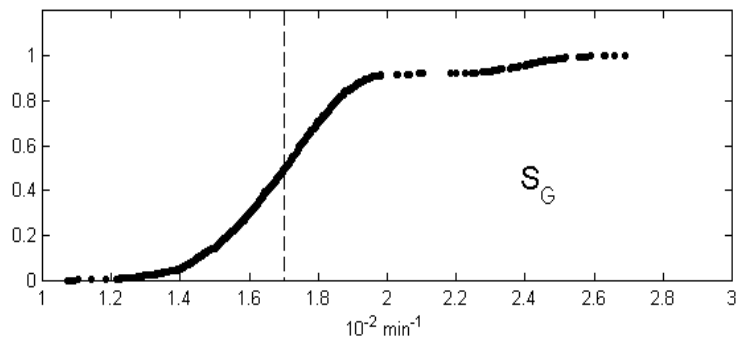
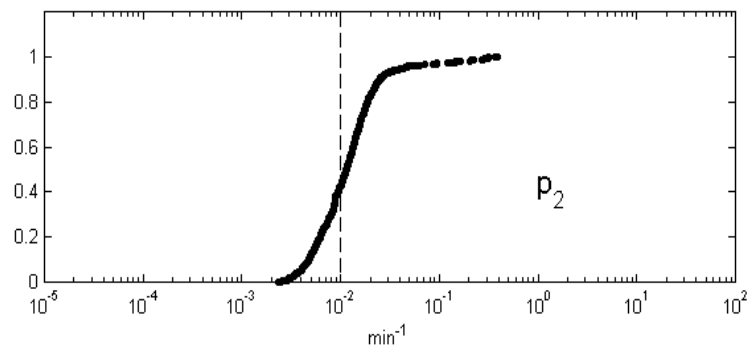
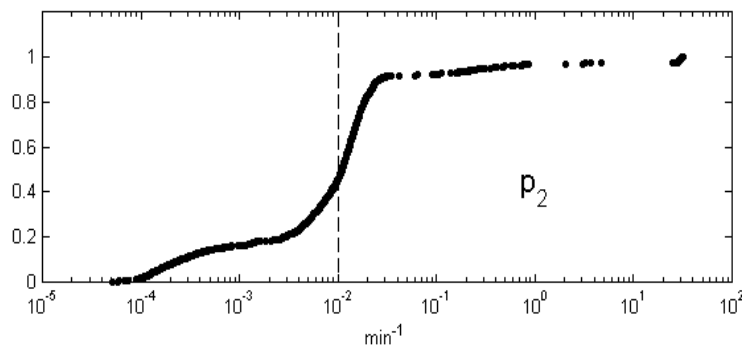
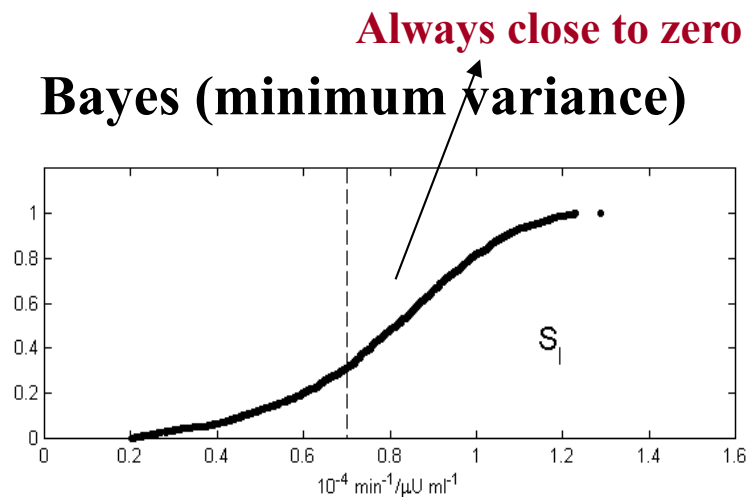
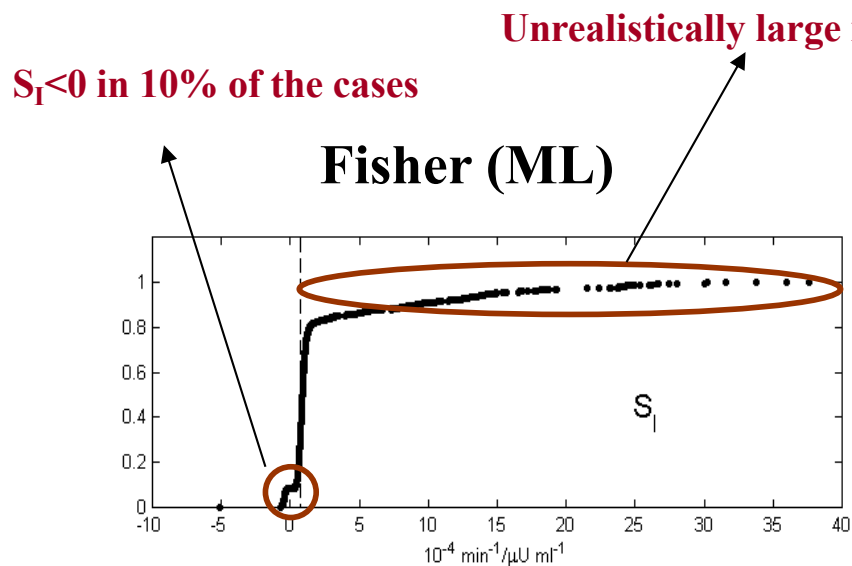
Use of a Bayesian estimator is key in the last two situations



Pillonetto G. , G. Sparacino and C. Cobelli  
*Numerical non identifiability regions of the minimal model of glucose kinetics: superiority of Bayesian estimation,*  
 Mathematical Biosciences, 2003



# SUMMARY: 1000 SYNTHETIC SUBJECTS



# CONCLUSIONI

- Mathematical description and identification of a physical system is often a complex task  
(introduction of nonlinearities complicates the estimation process, e.g. nonnegativity constraints)
- Fisher approaches sometimes are not suited to face such difficulties, differently from the Bayesian approaches which appear more powerful alternatives but also more difficult to implement
- MCMC is currently the most powerful approach to face the computational difficulties related to the use of a Bayesian estimator