

# Monte Carlo Markov Chain

**Bayesian methods**

**Simone Paradiso**

Most of the material in this presentation is taken from

**“Information Theory, Inference, and Learning Algorithms”**

by **David J. C. McKay**.

Free pdf at <https://www.inference.org.uk/itprnn/book.pdf>

Suggested reading: “Handbook of Markov chain Monte Carlo” by S. Brooks, A. Gelman, G. L. Jones and X.-L. Meng

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This is the probability of y without any given conditions; this is known as the **evidence**. It

can be written as:  $P(y) = \int p(y | x)p(x)dx$

# Monte Carlo methods

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- Generate samples  $\{\mathbf{x}_i\}_{i=1}^N$  from a probability distribution  $P(\mathbf{x})$
- Generate expectation of functions under this distribution. For instance:

$$\Phi = \langle \phi(\mathbf{x}) \rangle = \int d^N P(\mathbf{x}) \phi(\mathbf{x})$$

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Some examples of  $\phi(\mathbf{x})$  can be the first order moments of the target density, i.e. mean and variance.

So let's assume that  $P(\mathbf{x})$  is too complicated and its moments can't be evaluated in some exact way. **We want to use Monte Carlo methods.**

# Monte Carlo methods

## The sampling problem

- Let's focus on the **sampling problem**, because if we solve this, then generating the expectation function is straightforward using the random samples  $\{\mathbf{x}^{(i)}\}_{i=1}^N$  to build the estimator:

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- The estimator is unbiased as long as  $\{\mathbf{x}^{(i)}\}_{i=1}^N \sim P(\mathbf{x})$ .



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**Property of MC methods:** The accuracy of an MC estimate depends only on the variance of  $\phi$ , not on the parameter space dimension. Precisely, the variance of  $\hat{\Phi}$  decreases with the number of samples.

- However, sampling from high-dimensionality can be a problem in MC methods; drawing samples from  $P(\mathbf{x})$  is not easy in general.

# Monte Carlo methods

## The sampling problem

- Let's assume we can evaluate  $P(\mathbf{x})$  up to a normalization constant, i.e. we can evaluate  $P^*(\mathbf{x}) = P(\mathbf{x})/Z$ .
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  - A. We do not know the normalization constant  $Z = \int P^*(\mathbf{x}) d^N \mathbf{x}$ , and
  - B. Even if we knew  $Z$ , it would still be challenging to sample in a high-dimensional space without exploring most of all the possible states.

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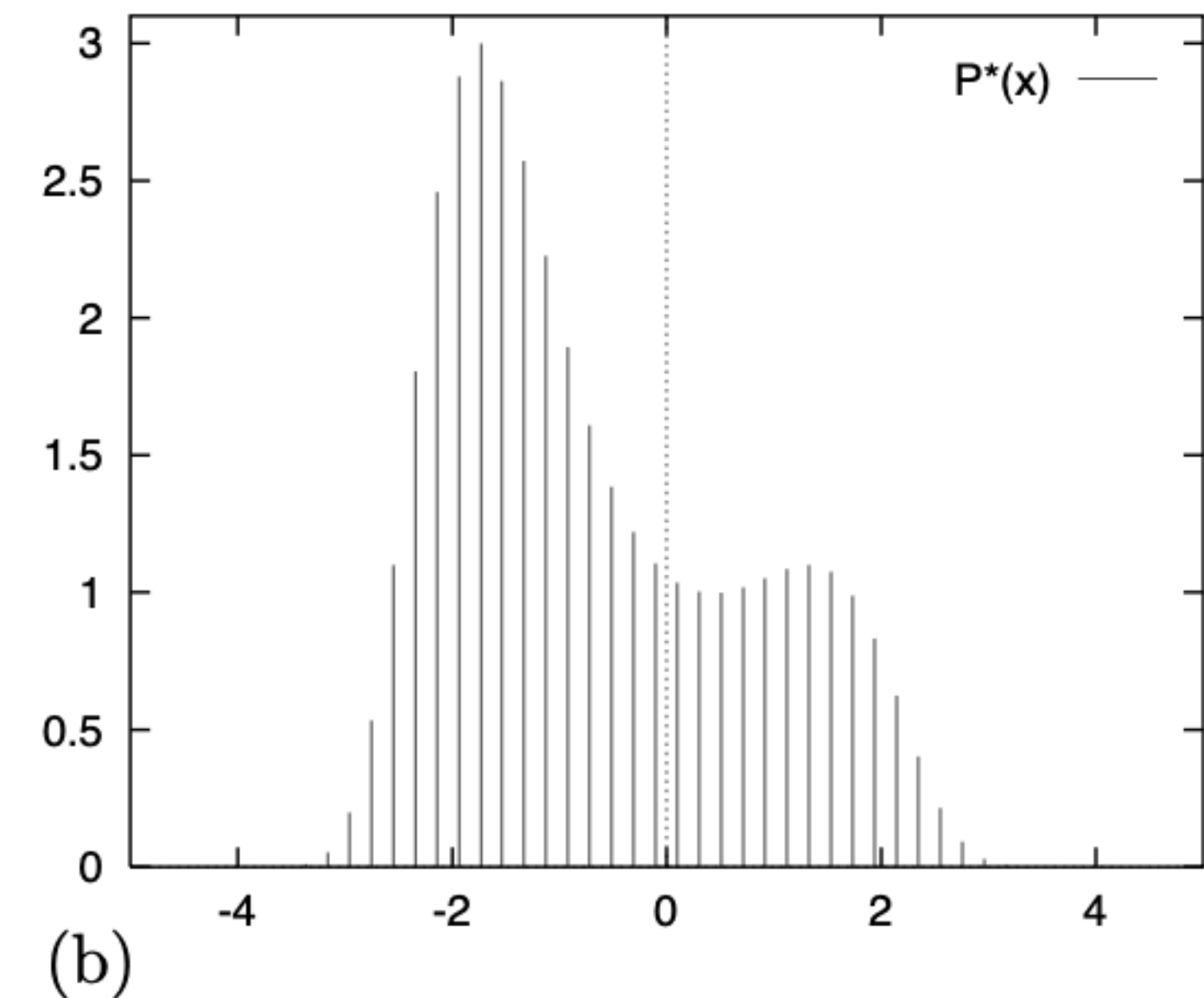
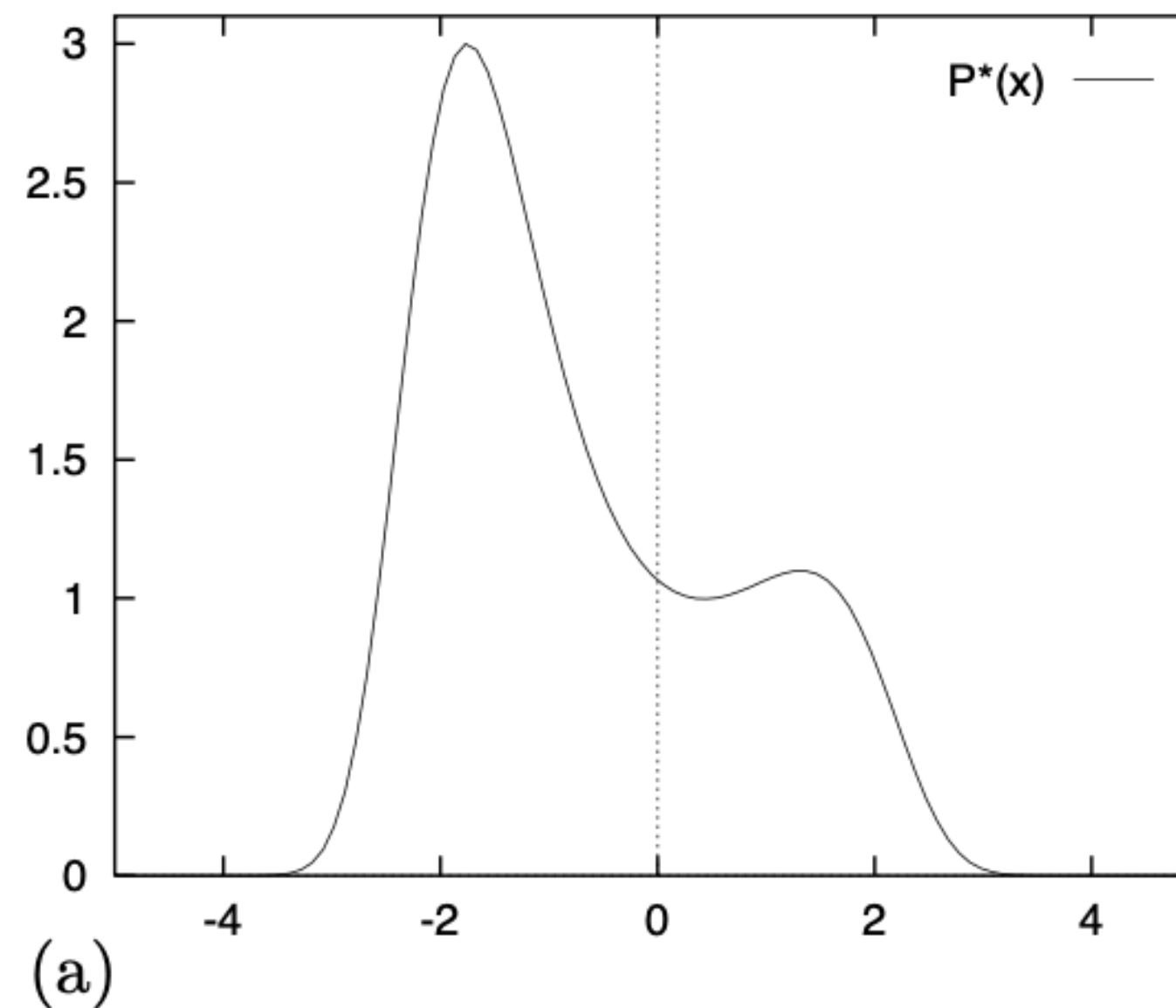
- To draw samples from  $P(\mathbf{x})$  we need to explore the space where  $P(\mathbf{x})$  is large, and we can only guess where it happens by evaluating the density *everywhere*.
- We know a convenient way to draw samples from very few distributions; the Normal distribution is of course one of these.

# Monte Carlo methods

## A simple 1D example

- We want to draw samples from  $P^*(x) = P(x)/Z$ , with:

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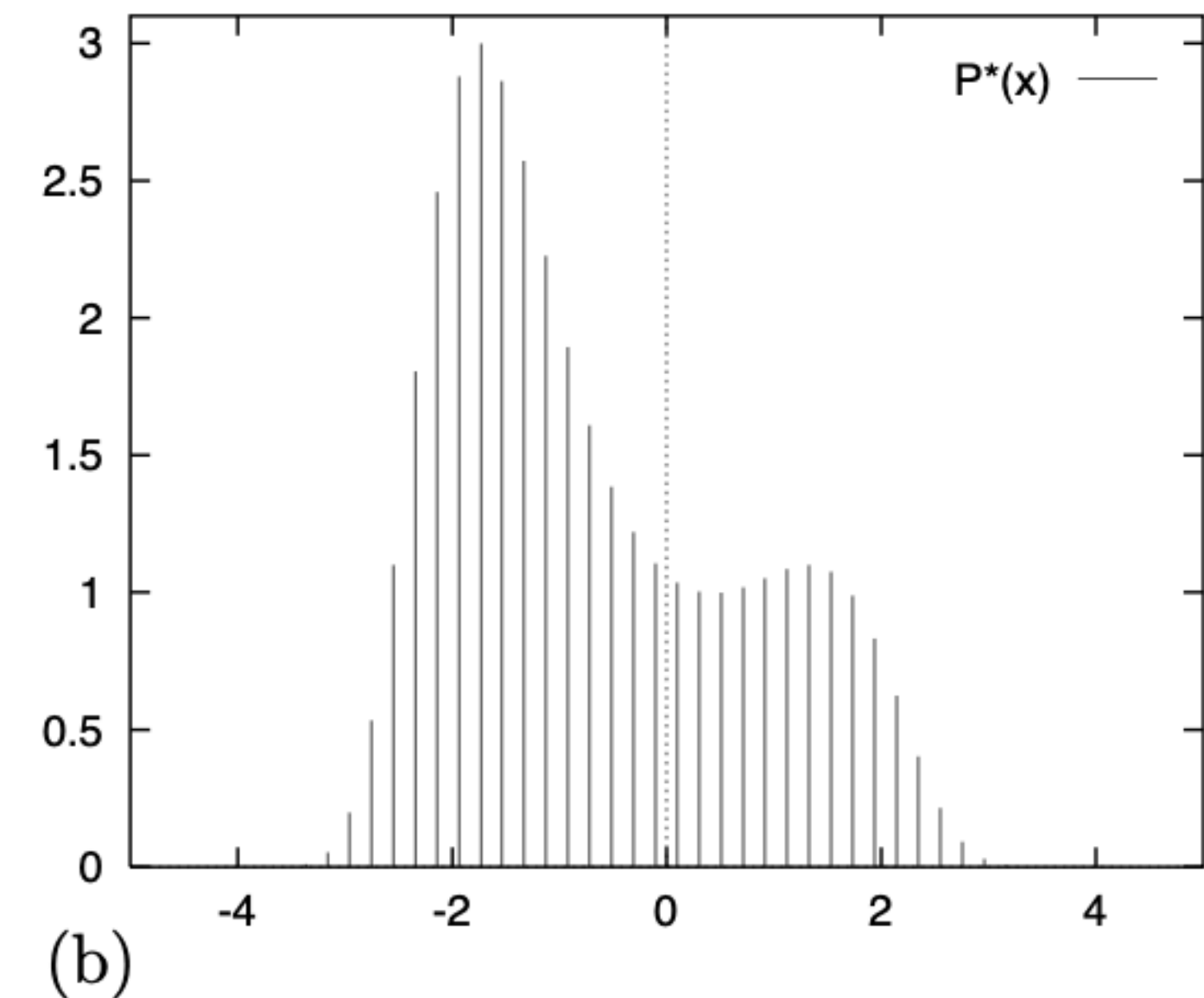
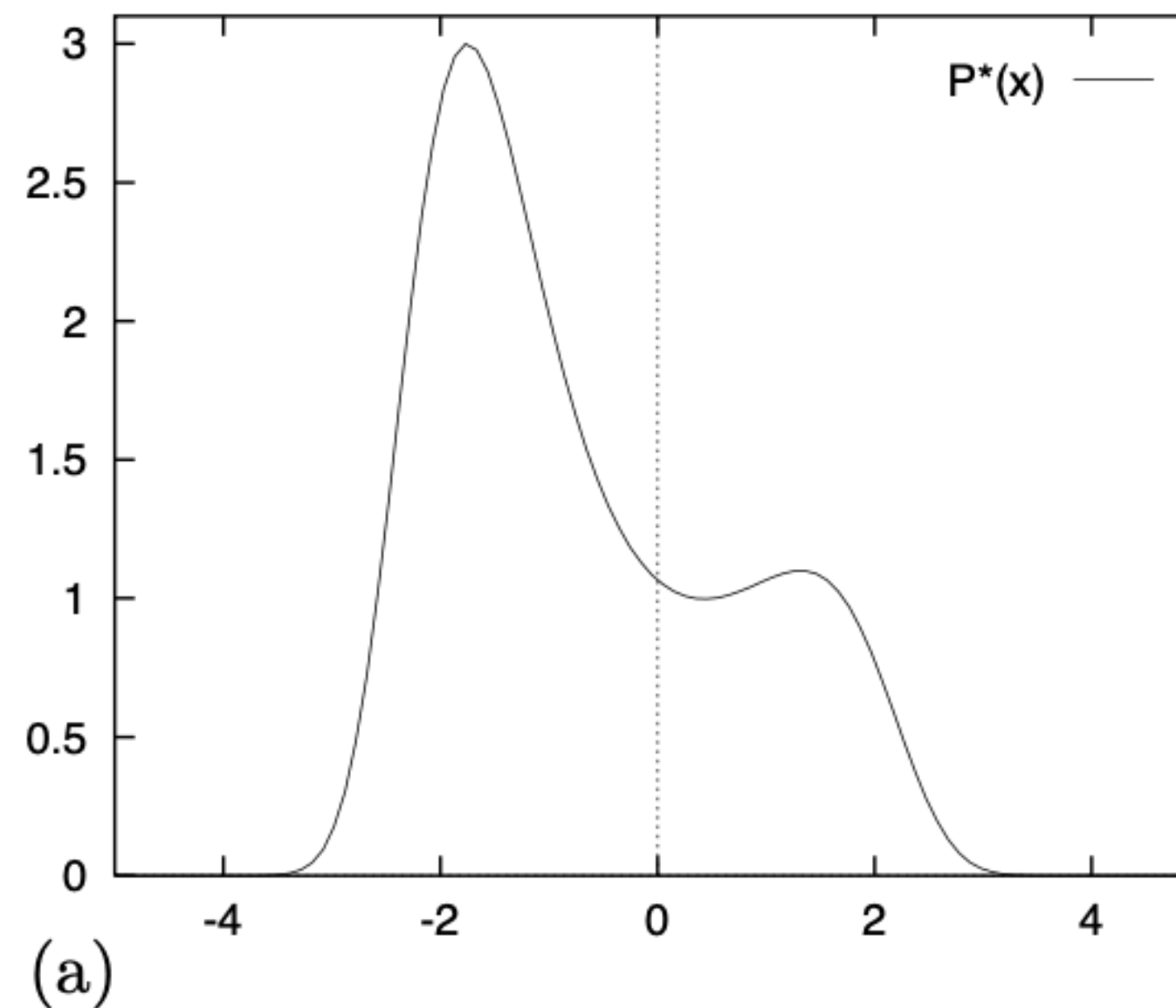
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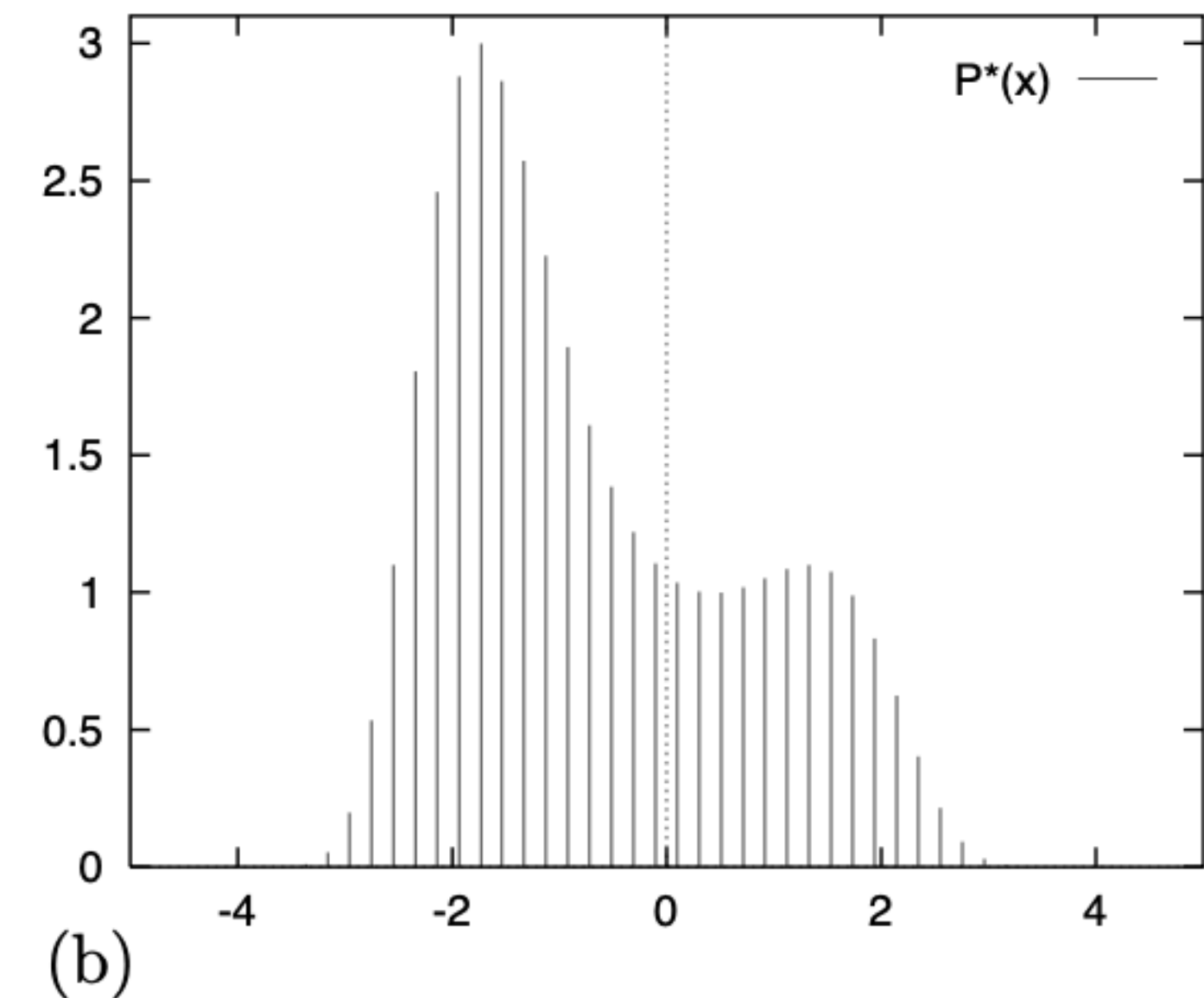
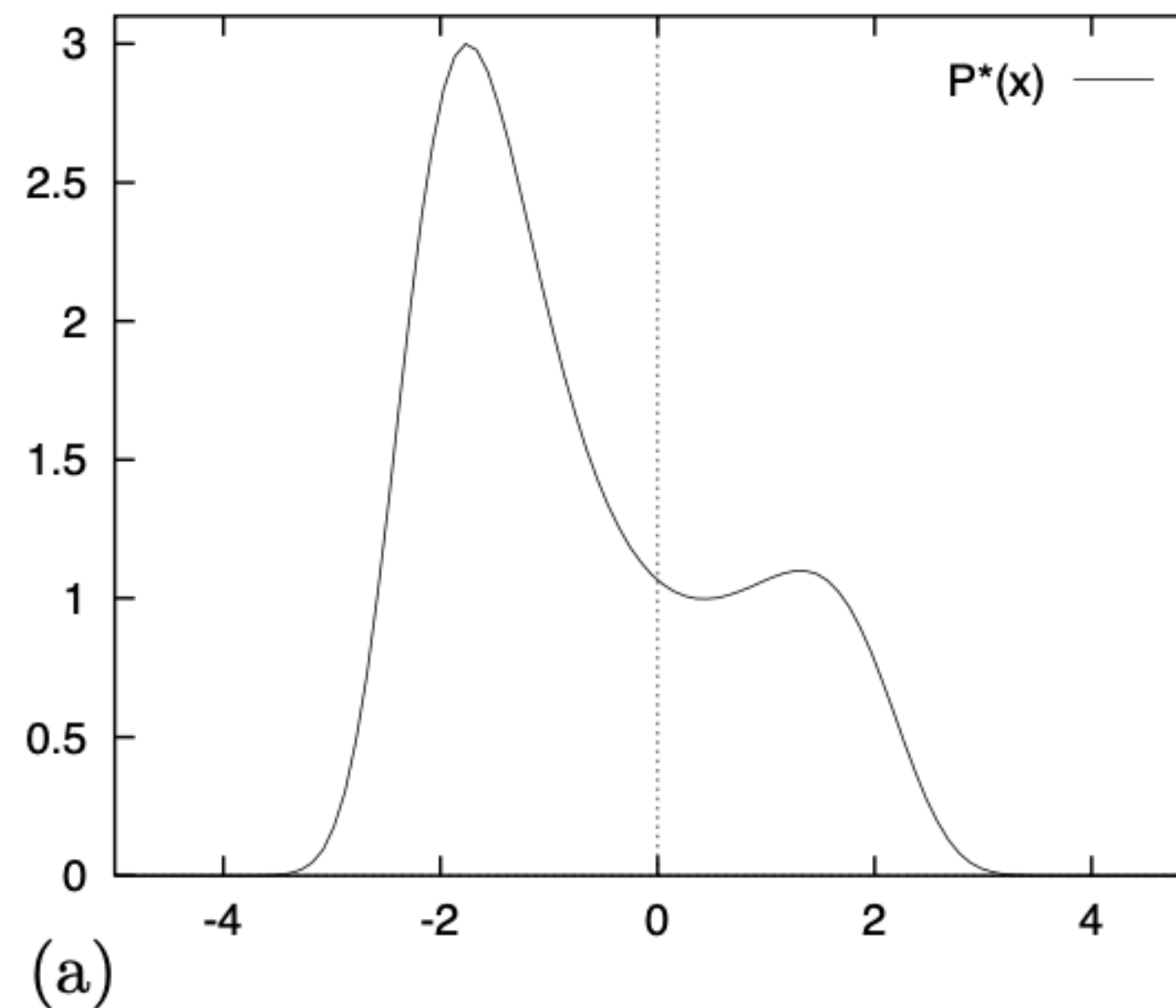
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- We first need to know  $Z$ .



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## A simple 1D example

- Let's try with a brute-force approach: we can evaluate discretize  $P^*(x)$  by evaluating it on equally spaced values  $\{x^{(i)}\}$ , and then compute:

$$Z = \sum_i P^*(x^{(i)}) \rightarrow P(x^{(i)}) = P^*(x^{(i)})/Z$$

- We can now sample from  $P(x^{(i)})$ . A basic sampling algorithm would just be to draw many times a number in  $U(0,1)$  and compare to  $P(x^{(i)})$  for each  $x_i \in \{x^{(i)}\}$ .

# Monte Carlo methods

## A simple 1D example: computational cost

- To compute  $Z$  we have to visit every point in the space. Depending on the  $x$  spacing ( $n$ ), and the number of dimensions ( $d$ ), this operation requires  $n^d$  computations.
- A typical cosmological problem involves at least 6 parameters, and the typical spacing is  $\sim 1000$  points. This means we need to perform  $1000^6 \approx 10^{18}$  operations. A theory code for cosmological purposes (CAMB, CLASS) take  $\sim 1$ s (best scenario); this means a computer would take  $10^{18}s \approx 30\text{Gyrs}$ .

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## Uniform sampling

- Acknowledged that we can't exhaustively visit every location  $x$  in the parameter space, let's try to solve the second problem: **estimating the expectation of a function  $\phi(x)$** .



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- We can then normalize by  $Z_N = \sum_{i=1}^N P^*(x^{(i)})$  and estimate  $\Phi(x) = \int \phi(x)P(x)dx$  via:

$$\hat{\Phi} = \sum_{i=1}^N \phi(x^{(i)}) \frac{P^*(x^{(i)})}{Z_N}$$

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- **This means that unless  $H \sim d$ , or  $P(x)$  is uniform, corresponding to quite boring cases, uniform sampling is unlikely to be useful, or efficient.**

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## overview

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**We need some workaround.**



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## Importance Sampling

Let's try to make the uniform sampling a little bit more general.

- Let's assume a target distribution  $P(x)$  we are able to evaluate at each  $x$ :

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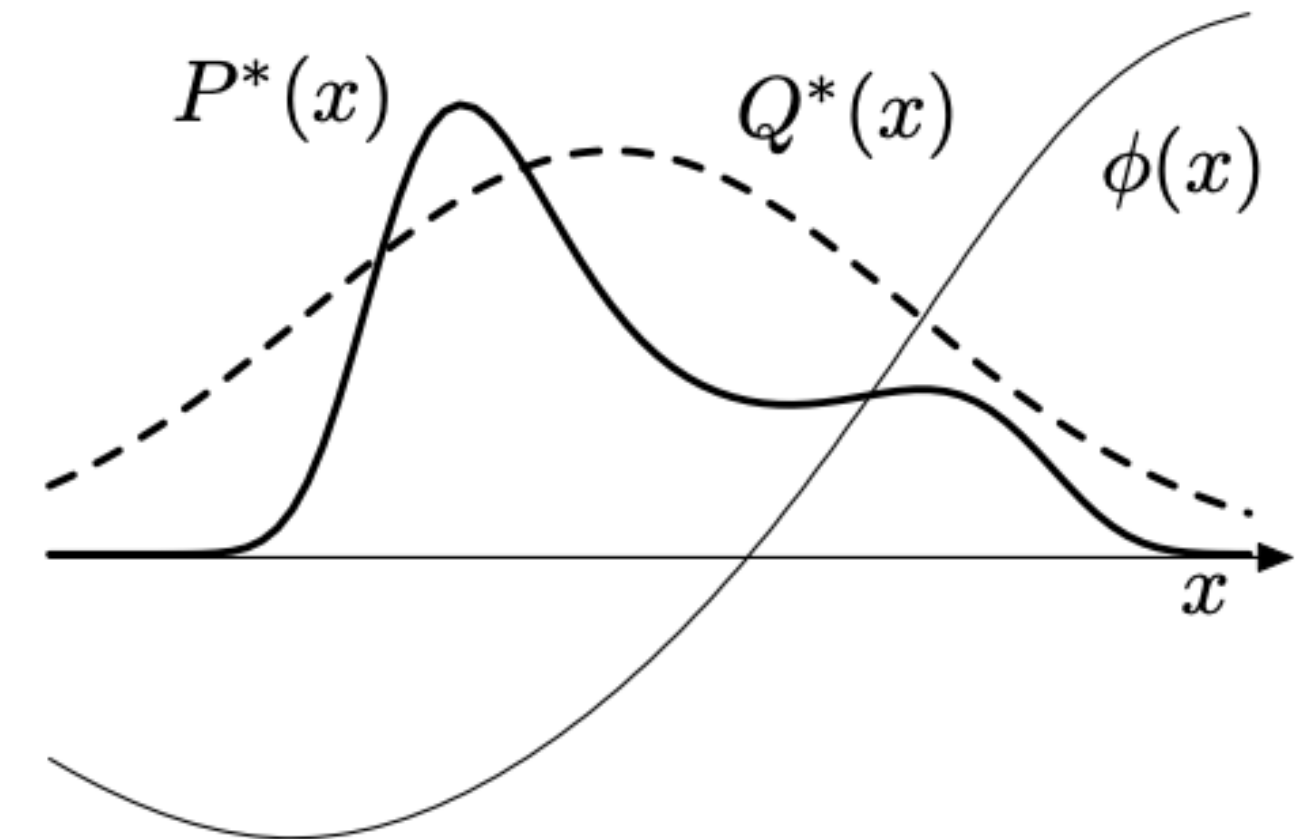
- But  $P(x)$  is too complicated to sample directly from it...
- But let's assume we have a simpler density  $Q(x)$ , from which we can generate samples and which we can evaluate up to a normalization constant:

$$Q(x) = Q^*(x)/Z$$

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- We can generate  $N$  samples from  $Q(x)$ .

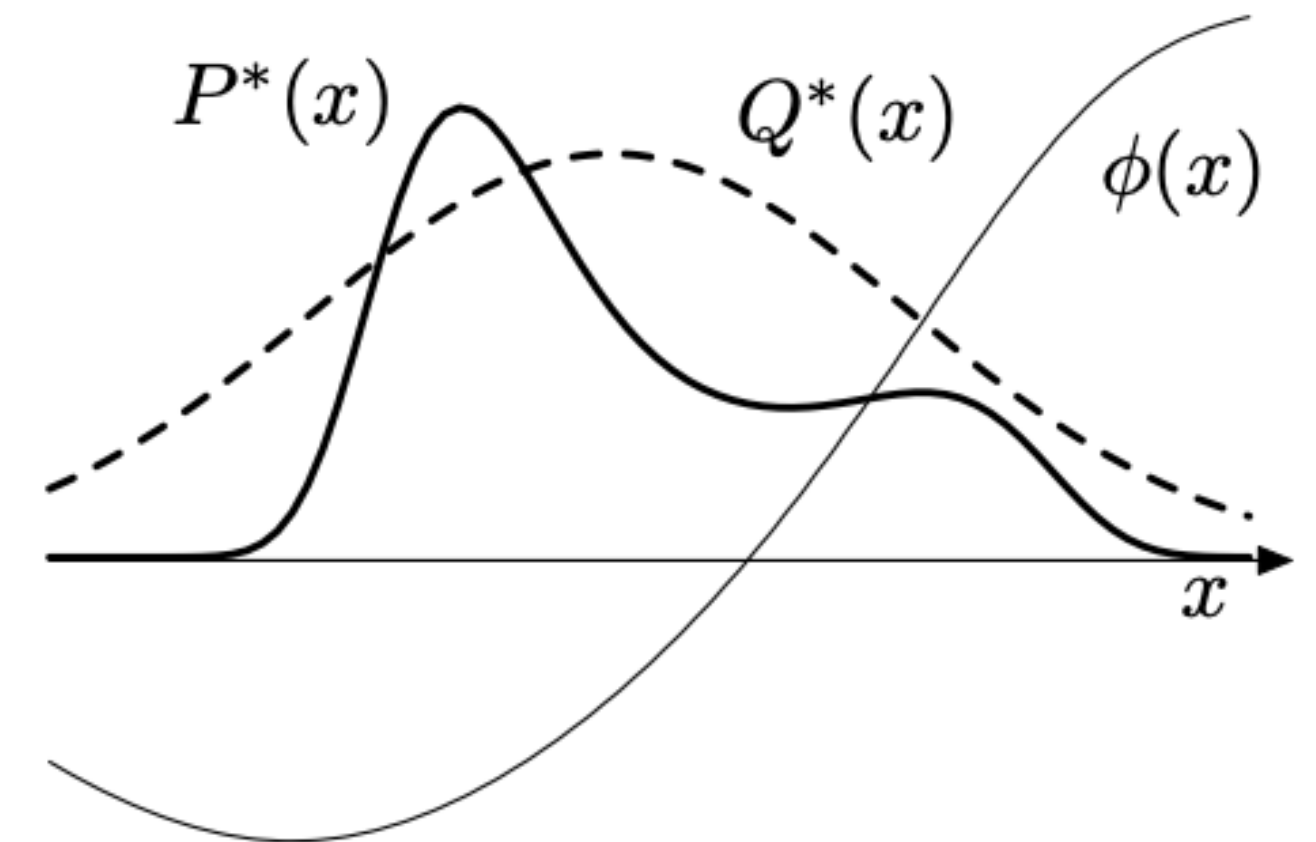


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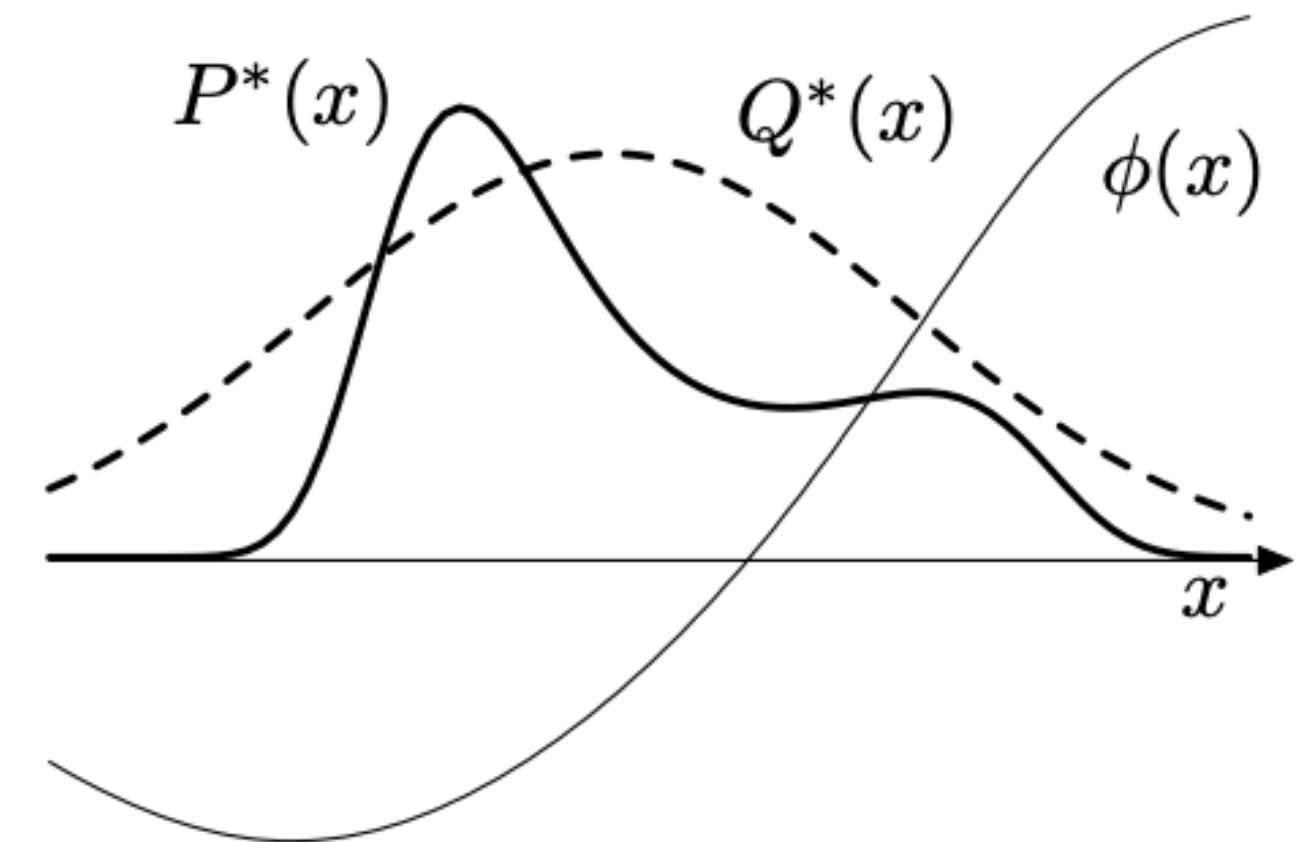
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- Which we can use to adjust the importance of each point in our estimator such that:

$$\hat{\Phi} = \frac{\sum_i w^{(i)} \phi(x^{(i)})}{\sum_i w^{(i)}}$$



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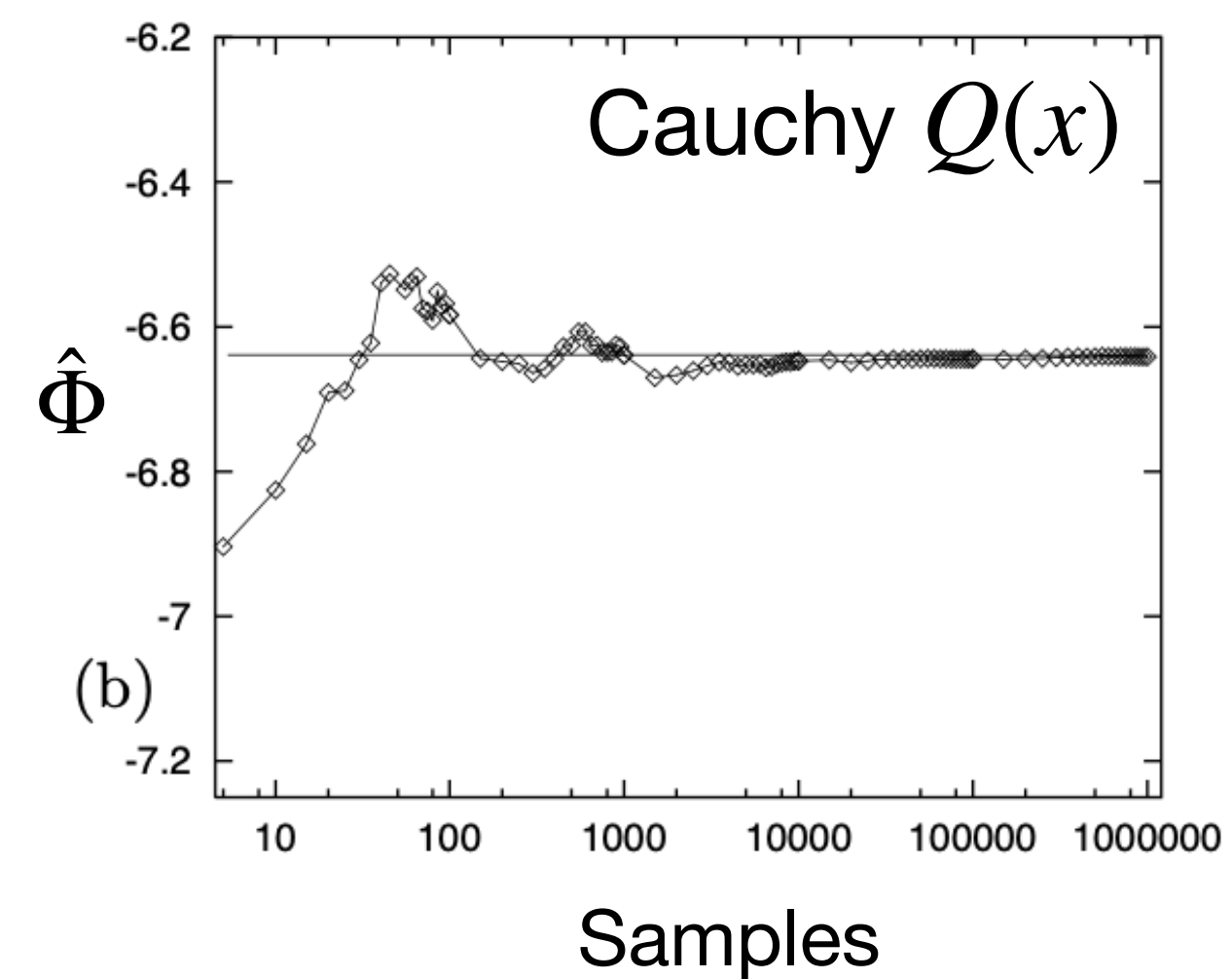
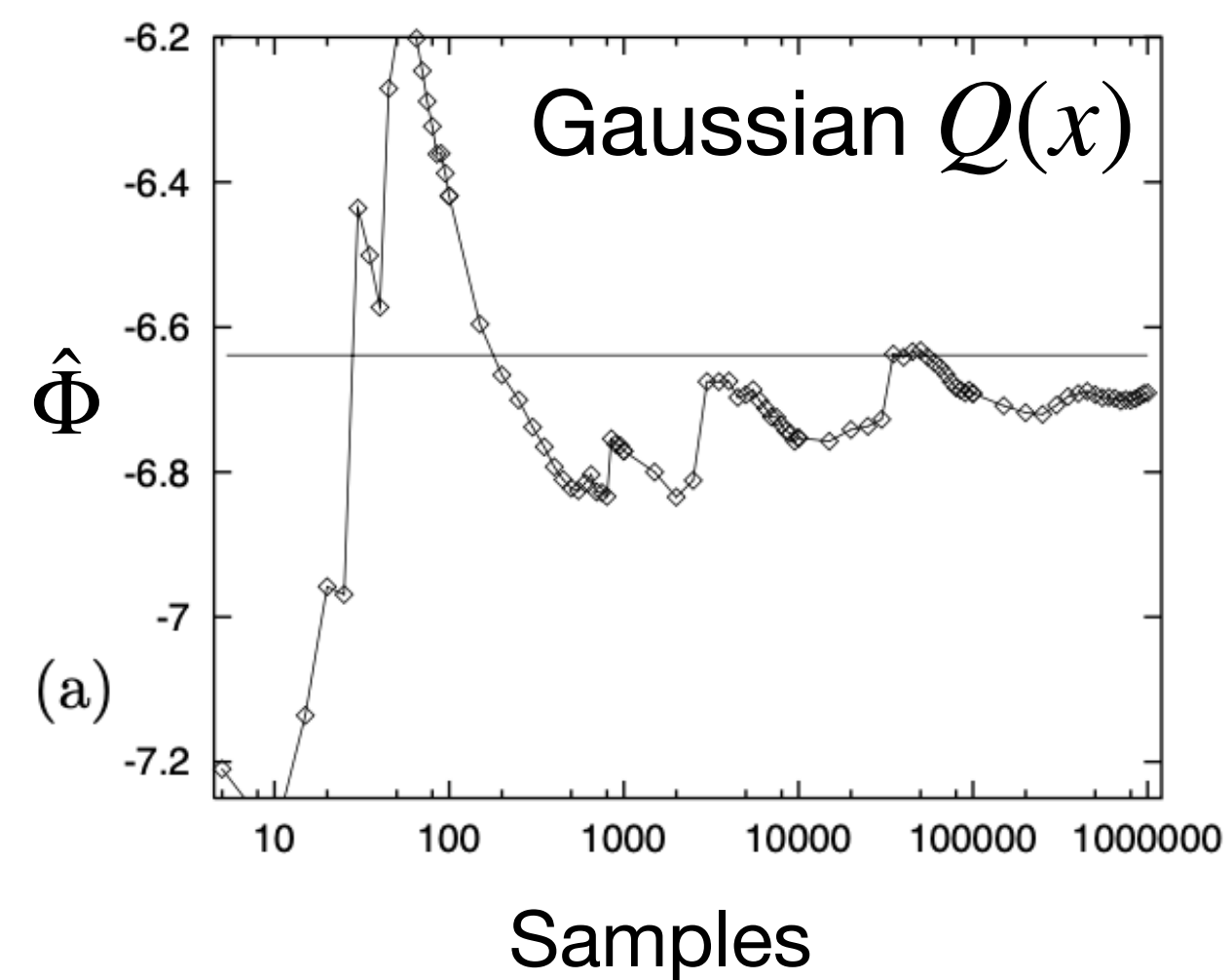
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- The variance of the estimator is hard to estimate because it depends on an integral over  $x$  and  $P^*(x)$ .
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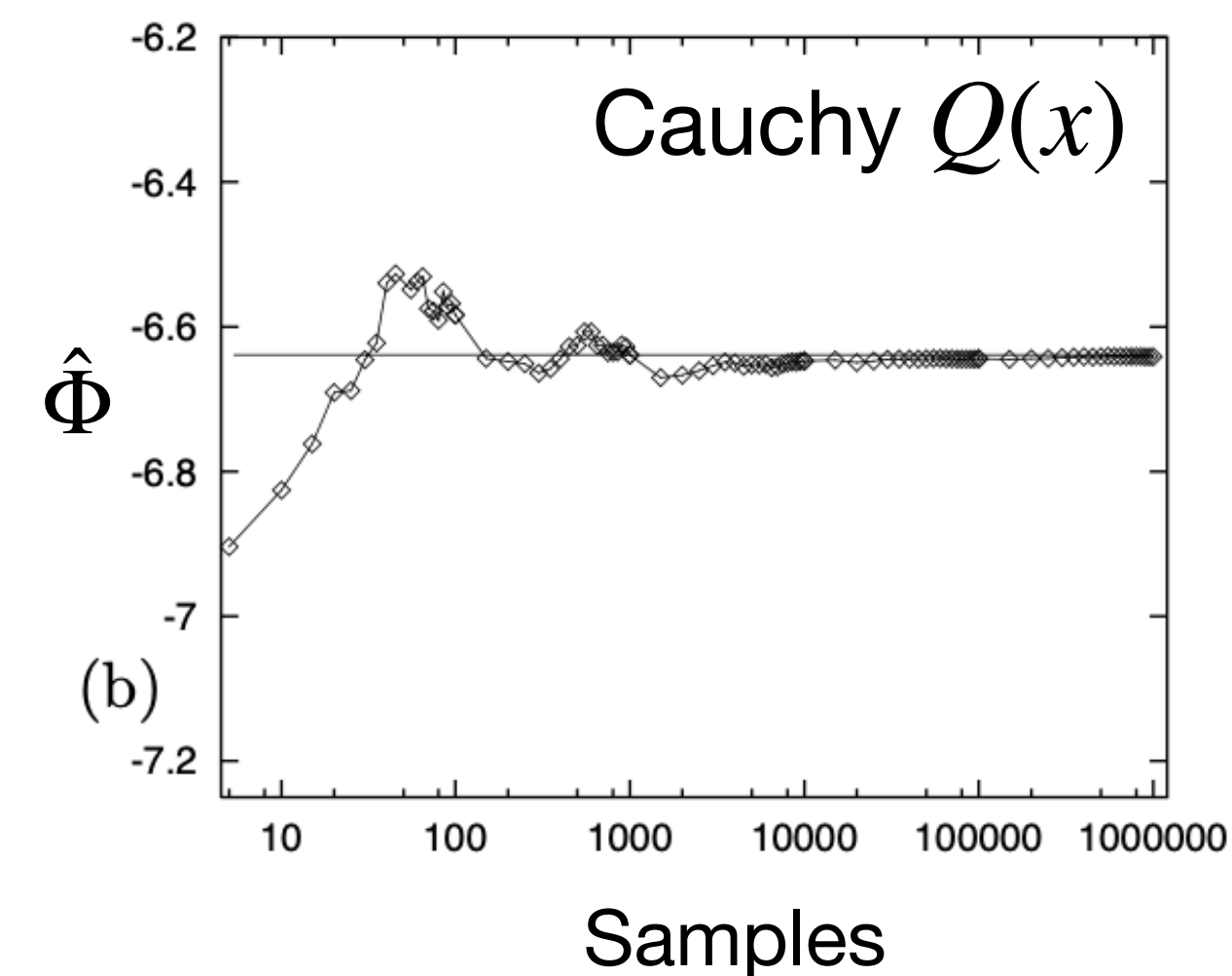
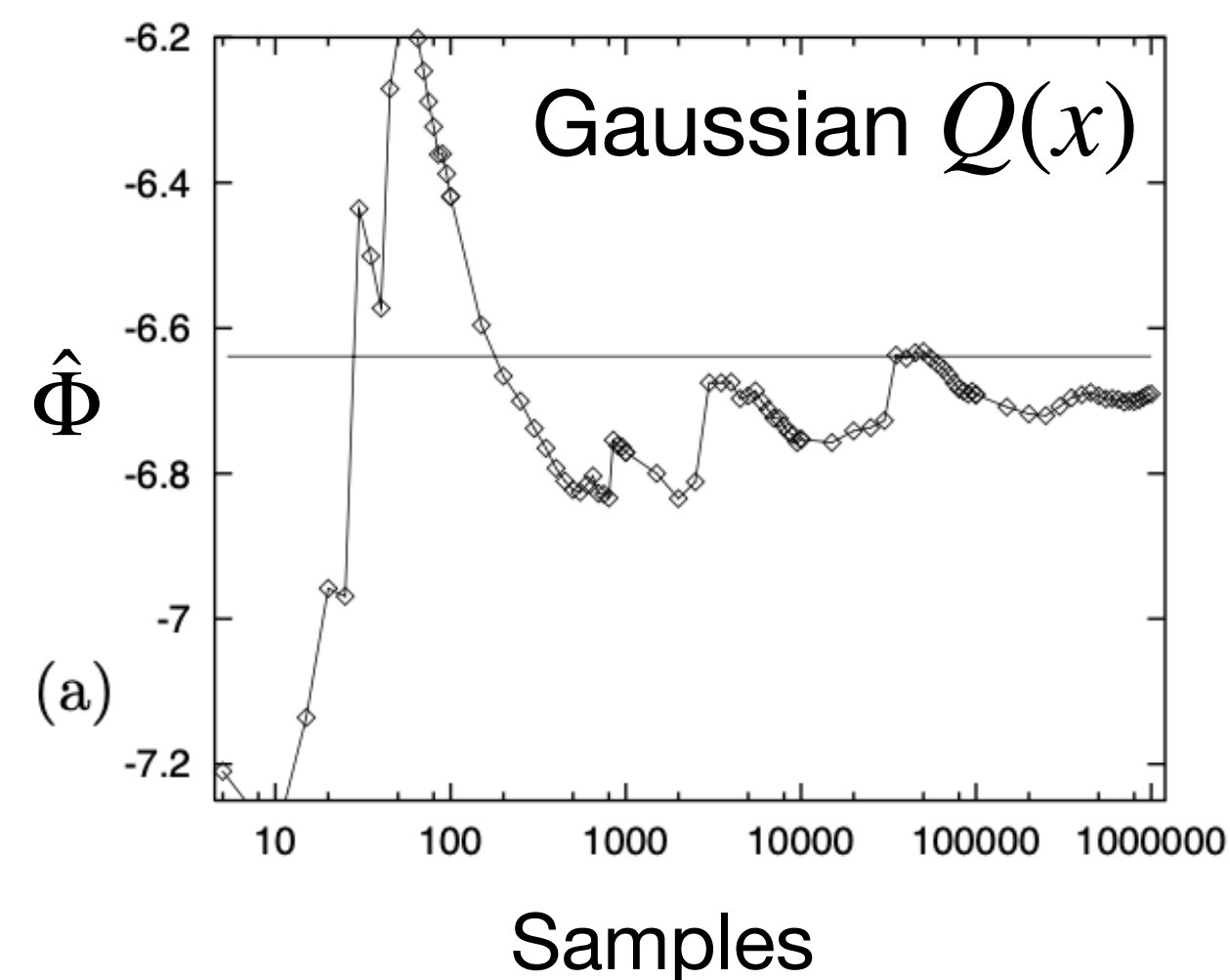
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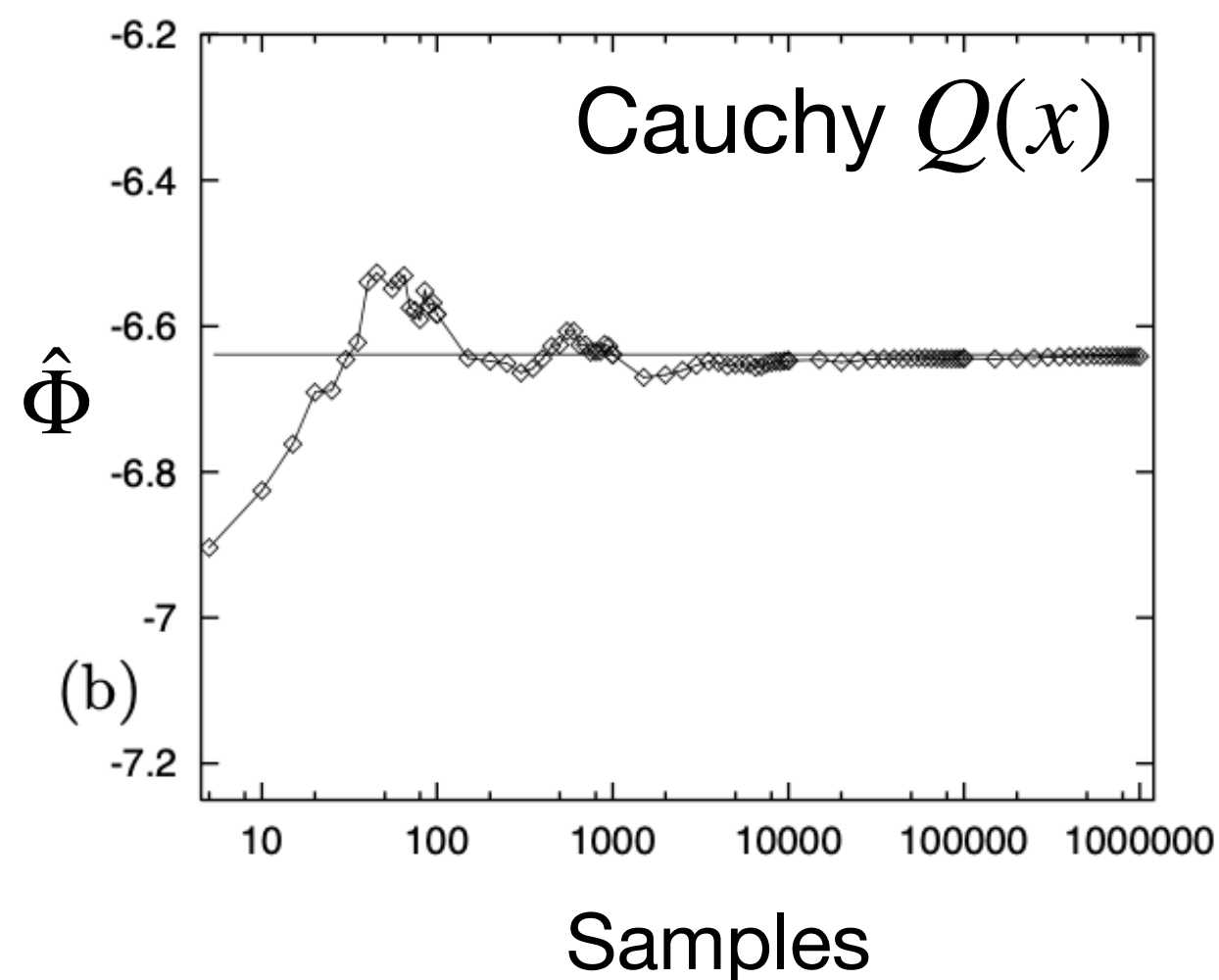
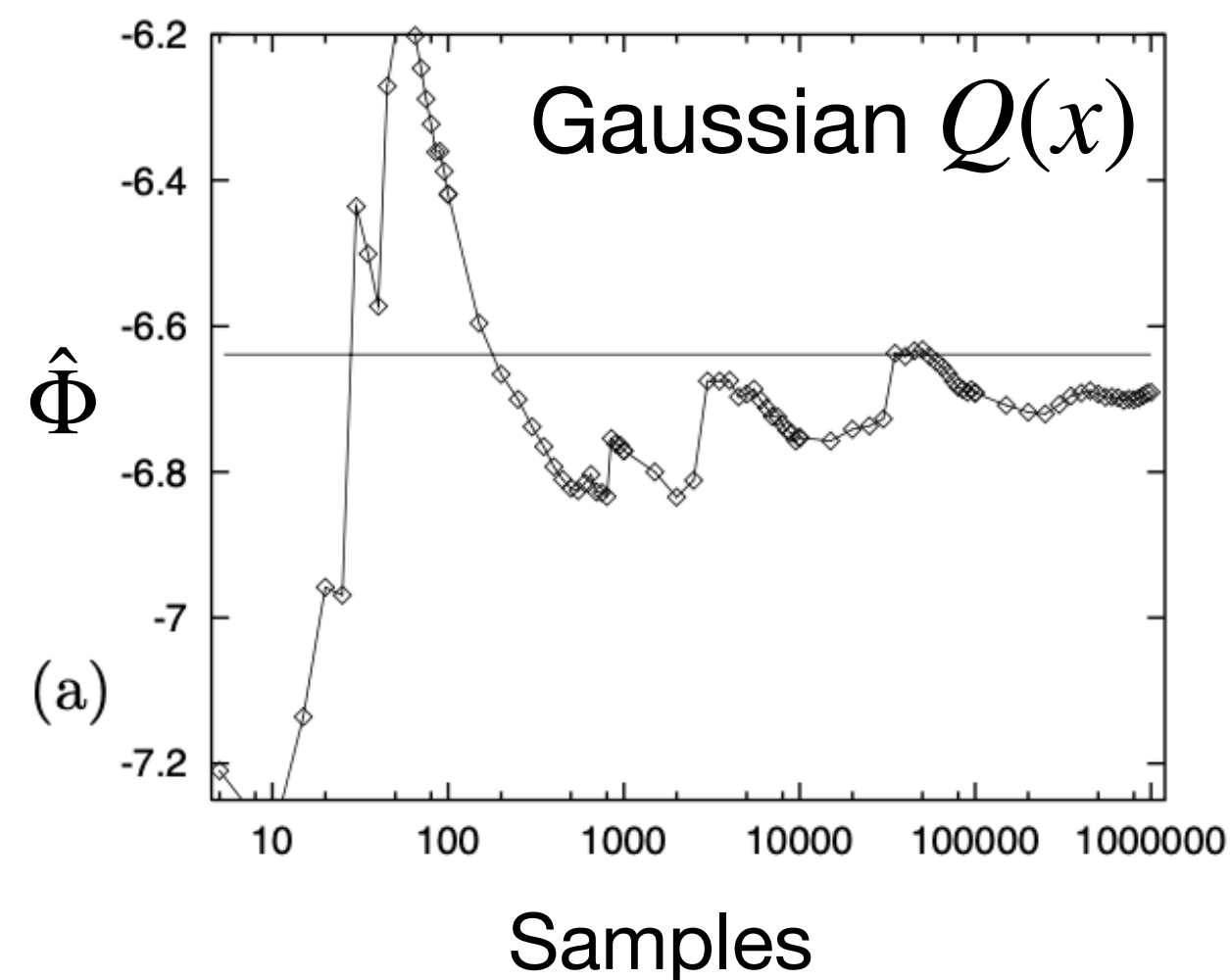
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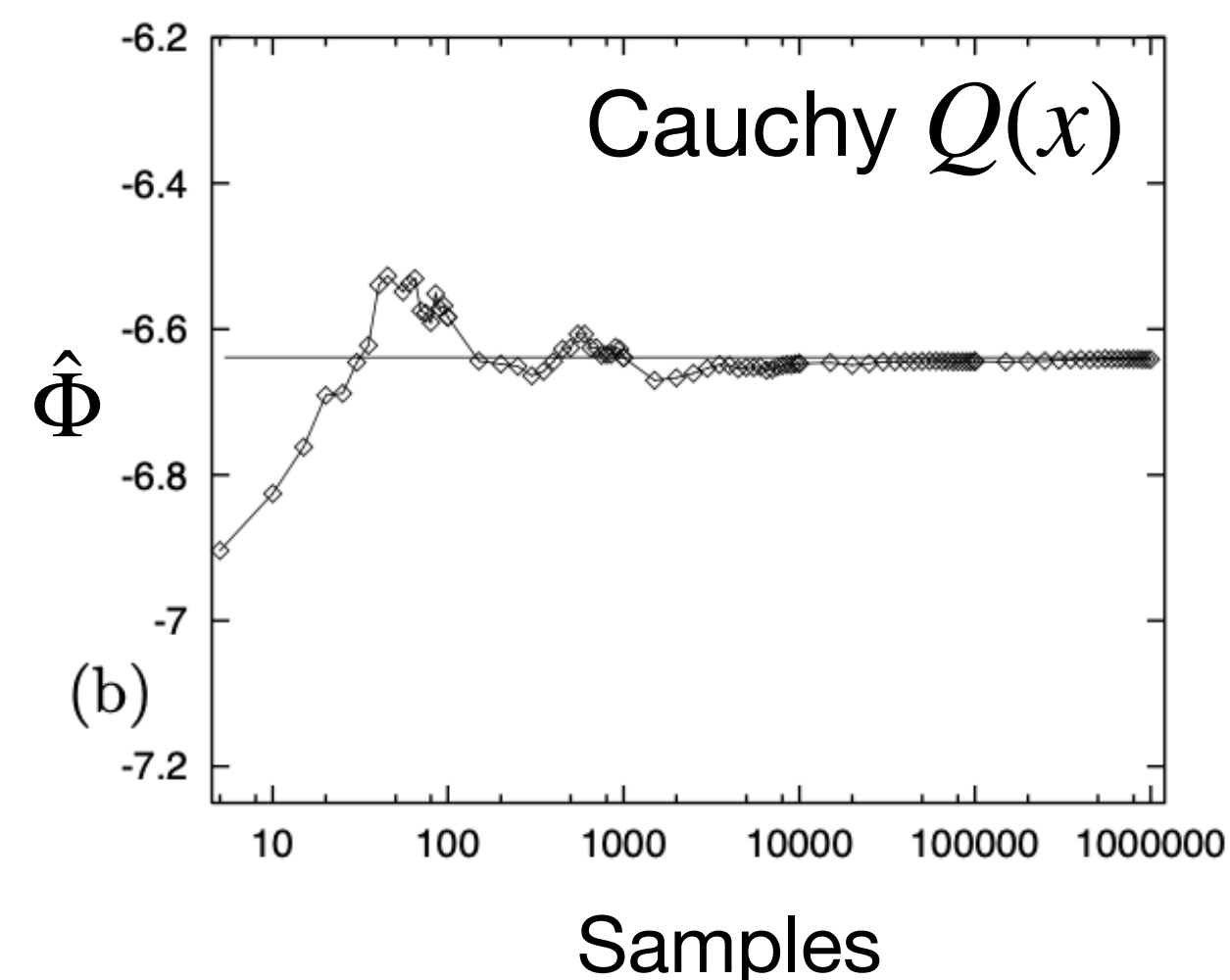
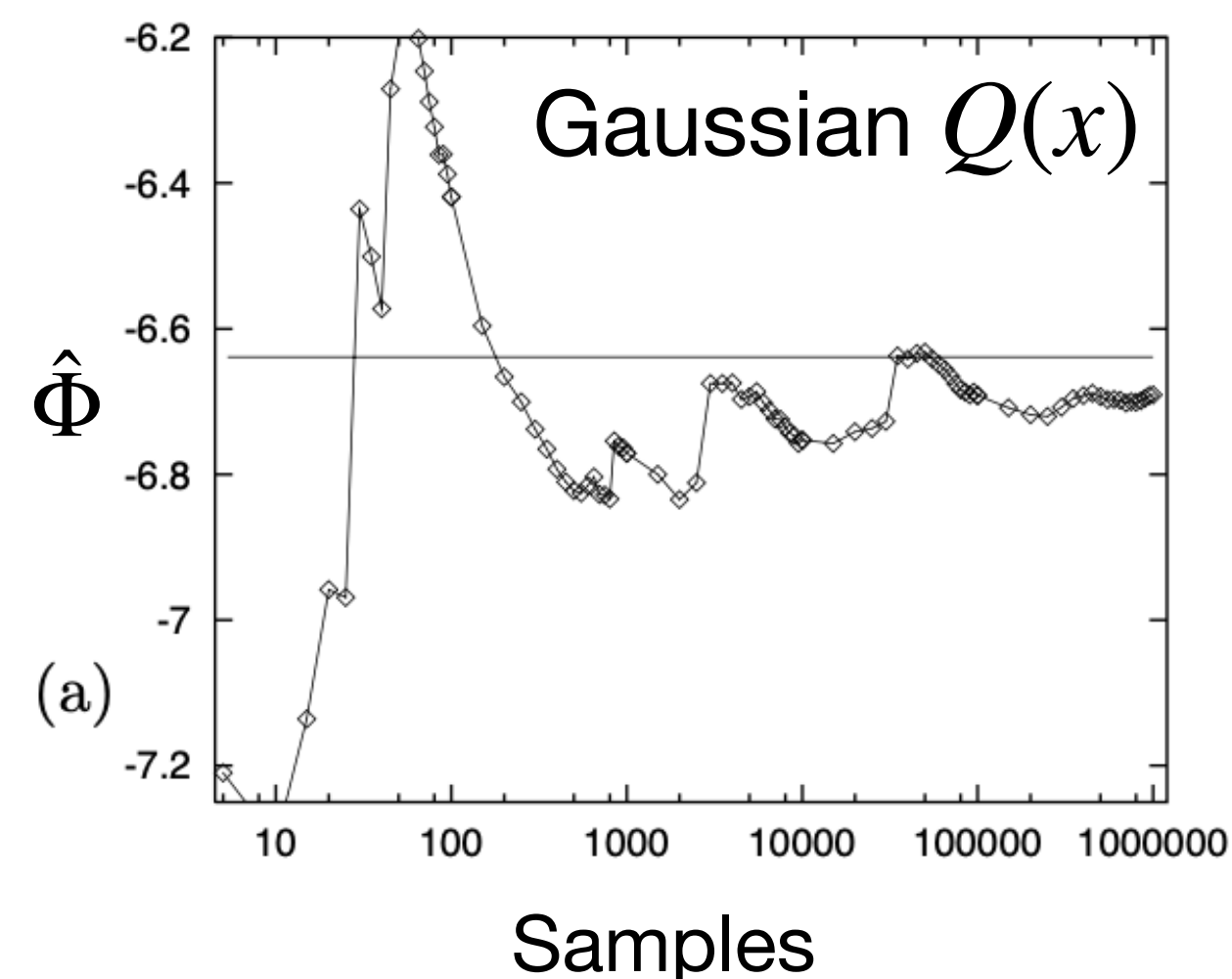
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- In this case  $\hat{\Phi}$  will be wrong, with no indication in the empirical variance variance that the true variance of  $\hat{\Phi}$  is large.





# Monte Carlo methods

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- We also assume that we know the value of a constant  $c$  such that:

$$cQ^*(x) > P^*(x)$$

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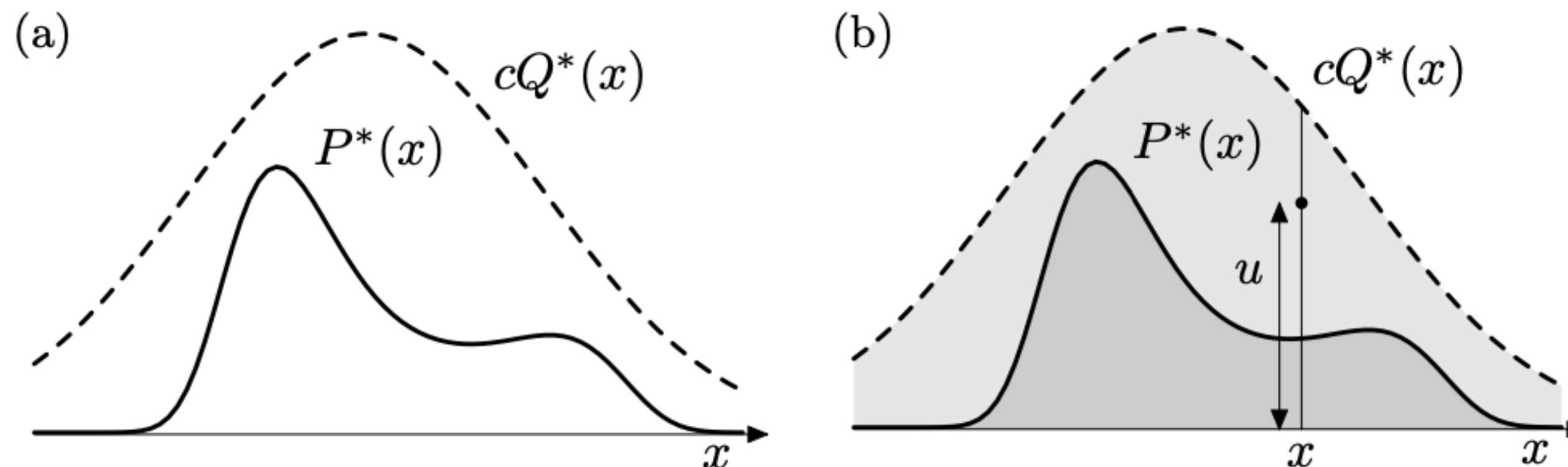
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- We evaluate  $P^*(x)$  and accept or reject  $x$  by comparing the value of  $u$  with  $P^*(x)$ . If  $u > P^*(x)$  then  $x$  is rejected, otherwise is accepted and added to our collection of samples  $\{x^{(i)}\}_N$ .



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- This method works best if  $Q$  is a good approximation to  $P$ .
- If  $Q$  and  $P$  are very different, we need a very large value of  $c$  to ensure  $cQ > P$  everywhere, and therefore the rejection frequency will be large  $\rightarrow$  need a lot of samples.

# Markov chains

## Definitions

- A sequence  $X_1, X_2, \dots, X_n$  of random elements of some set is a **Markov chain** if the conditional distribution of  $X_{n+1}$  given  $X_1, \dots, X_n$  depends on  $X_n$  only.
- A Markov chain has **stationary transition probabilities** if  $P(X_{n+1} | X_n)$  does not depend on  $n$ .



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Moreover:

- A transition probability distribution is **reversible** with respect to an initial distribution if, for the Markov chain  $X_1, X_2, \dots$ , the distribution of pairs  $(X_i, X_{i+1})$  is exchangeable.

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- The Markov chain Central Limit theorem is much sharper and conditions much simpler when reversibility applies.
- It allows for constructing efficient probability mechanisms for MCMC (we'll see shortly...).

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In the Metropolis-Hastings sampling our proposal density  $Q(x)$  depends on the current state  $x^{(i)}$ .

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In the Metropolis-Hastings sampling our proposal density  $Q(x)$  depends on the current state  $x^{(i)}$ .

- This is an MCMC process, and  $Q(x'; x^{(i)})$  does not need to be close to the true  $P(x)$  to be useful!

# MCMC algorithms

## Metropolis-Hastings

In the Metropolis-Hastings sampling our proposal density  $Q(x)$  depends on the current state  $x^{(i)}$ .

- This is an MCMC process, and  $Q(x'; x^{(i)})$  does not need to be close to the true  $P(x)$  to be useful!

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Note the difference from rejection sampling: here a rejection cause the current state to be written again into the samples list.

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## Gibbs sampling

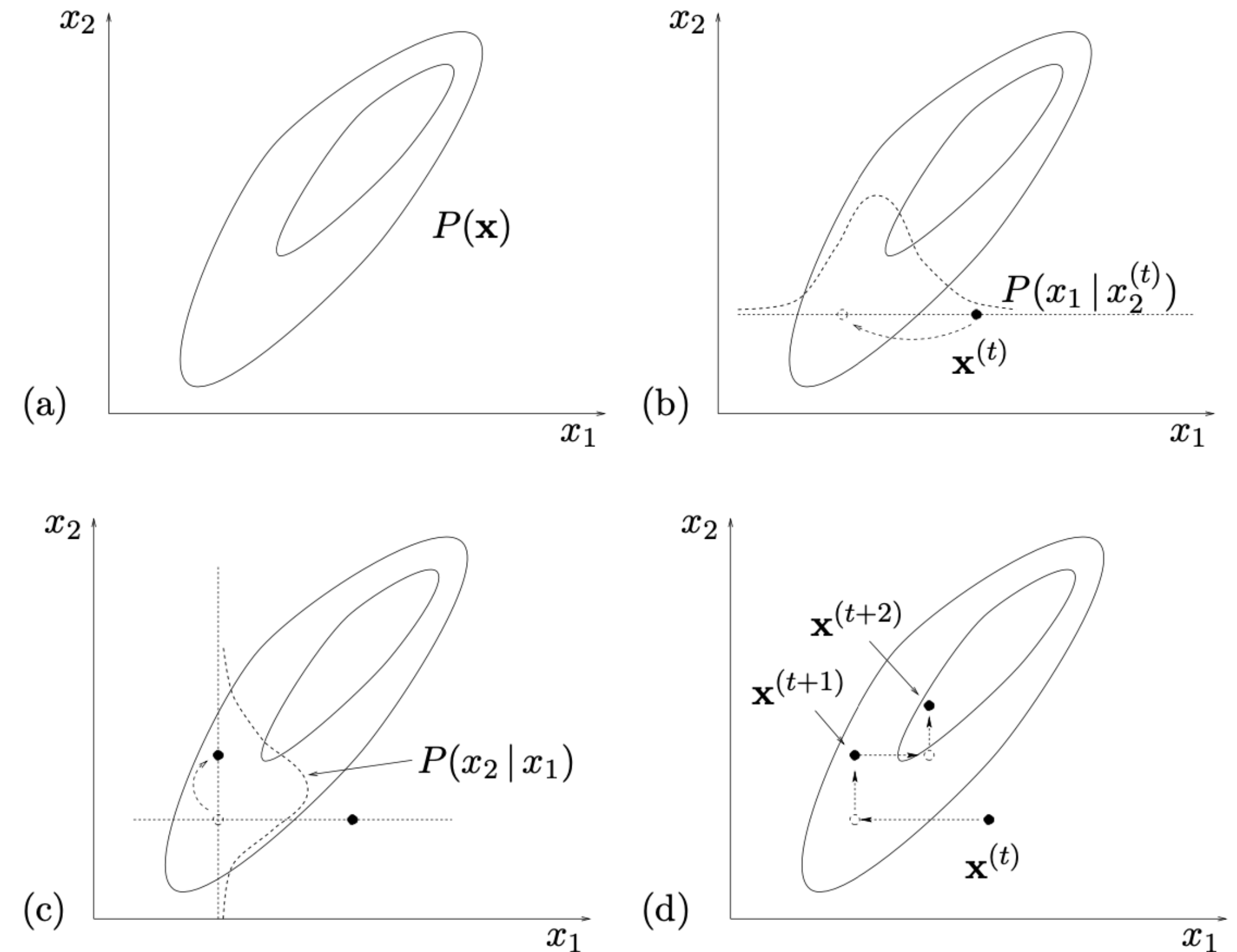
Gibbs sampling can be viewed as a MH method in which a sequence of proposal distributions  $Q$  are defined in terms of the conditional distributions of the joint distribution  $P(\mathbf{x})$ .

It is assumed that  $P(\mathbf{x})$  is too complex to draw samples from, but its conditional distributions  $P(x_i | x_{j \neq i})$  are tractable to work with.

# MCMC algorithms

## Gibbs sampling

A simple 2D example:



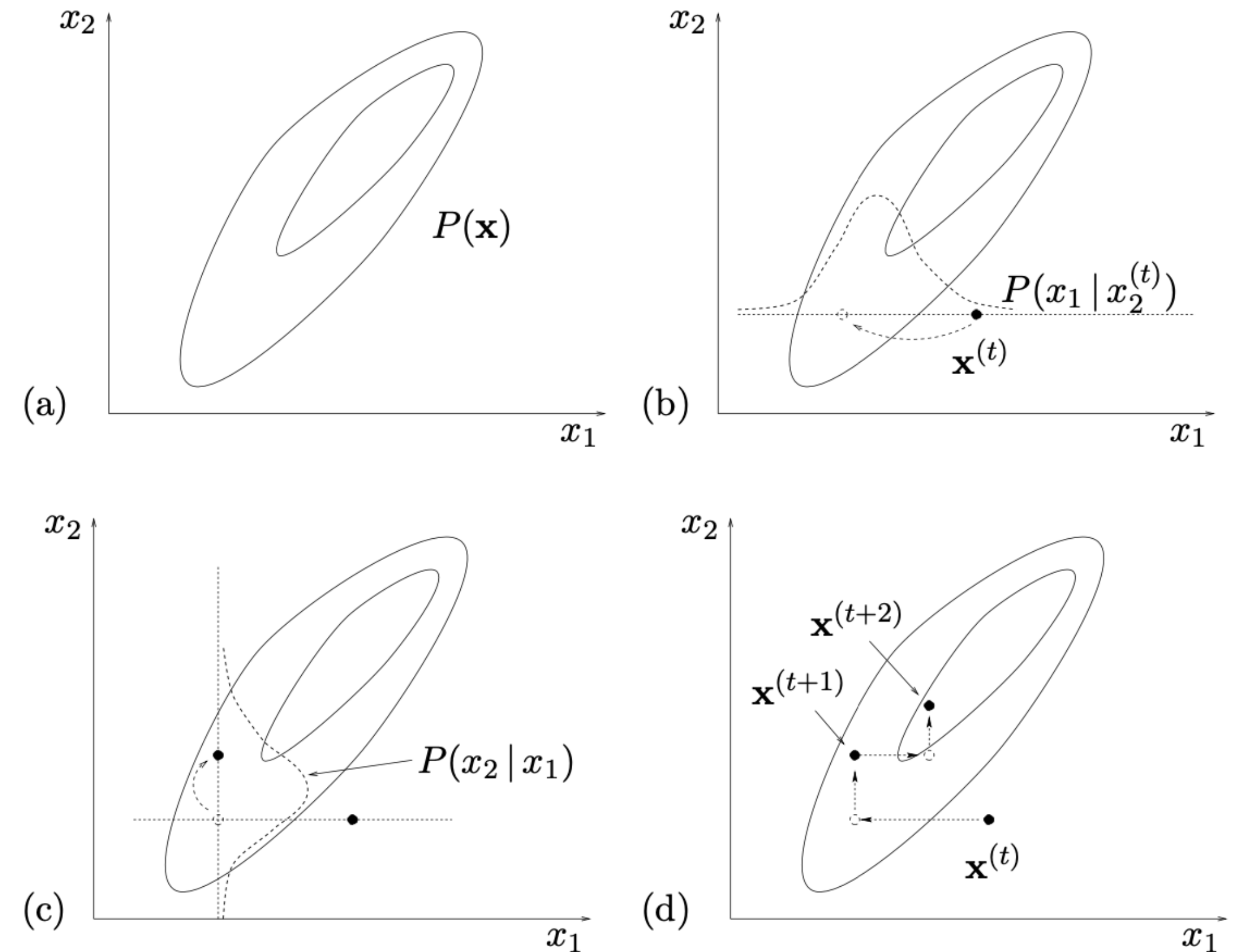
PS: The person who is teaching this class on my behalf will probably say that Gibbs sampling is obsolete. **He himself is obsolete.**

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- Two variables  $(x_1, x_2) = \mathbf{x}$



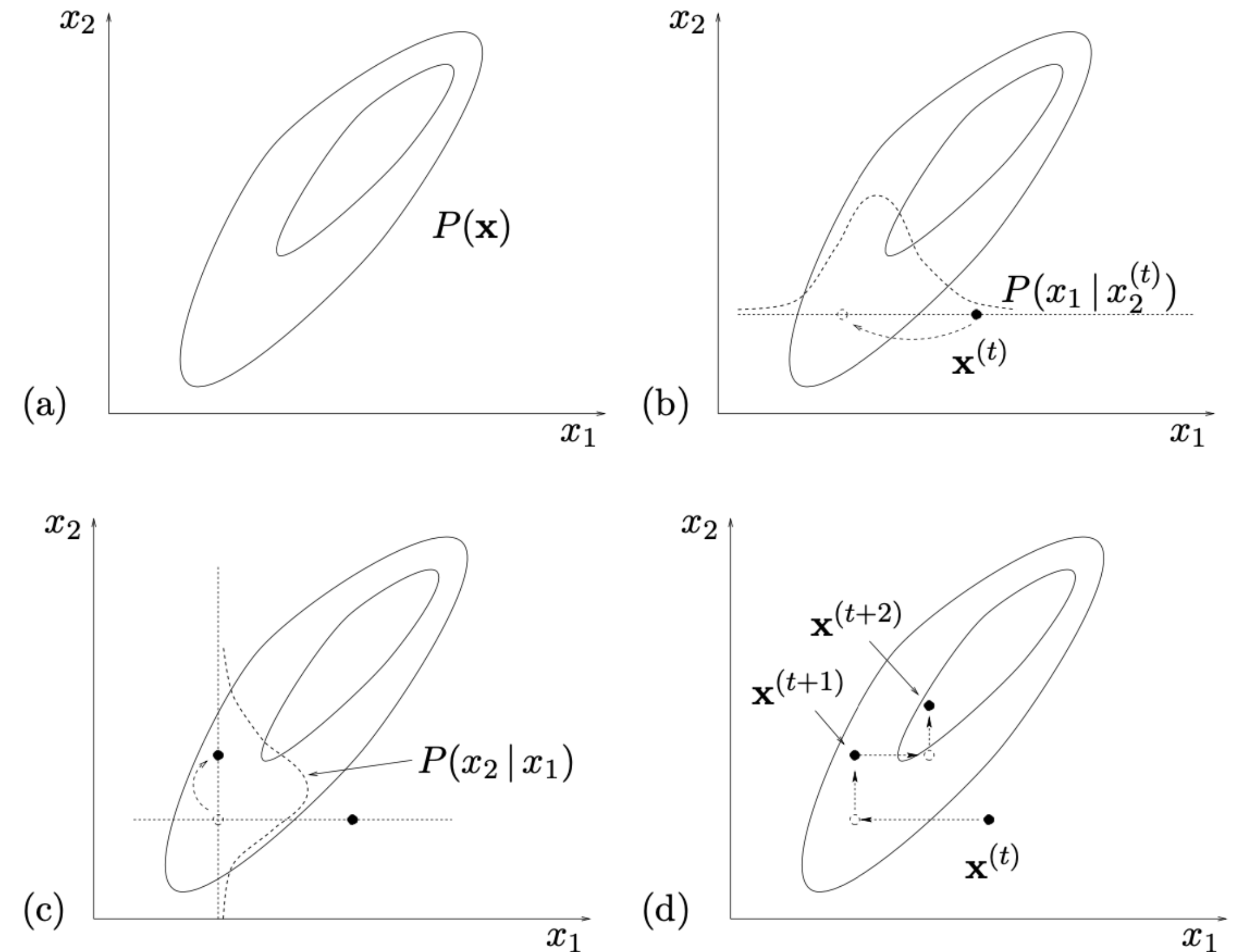


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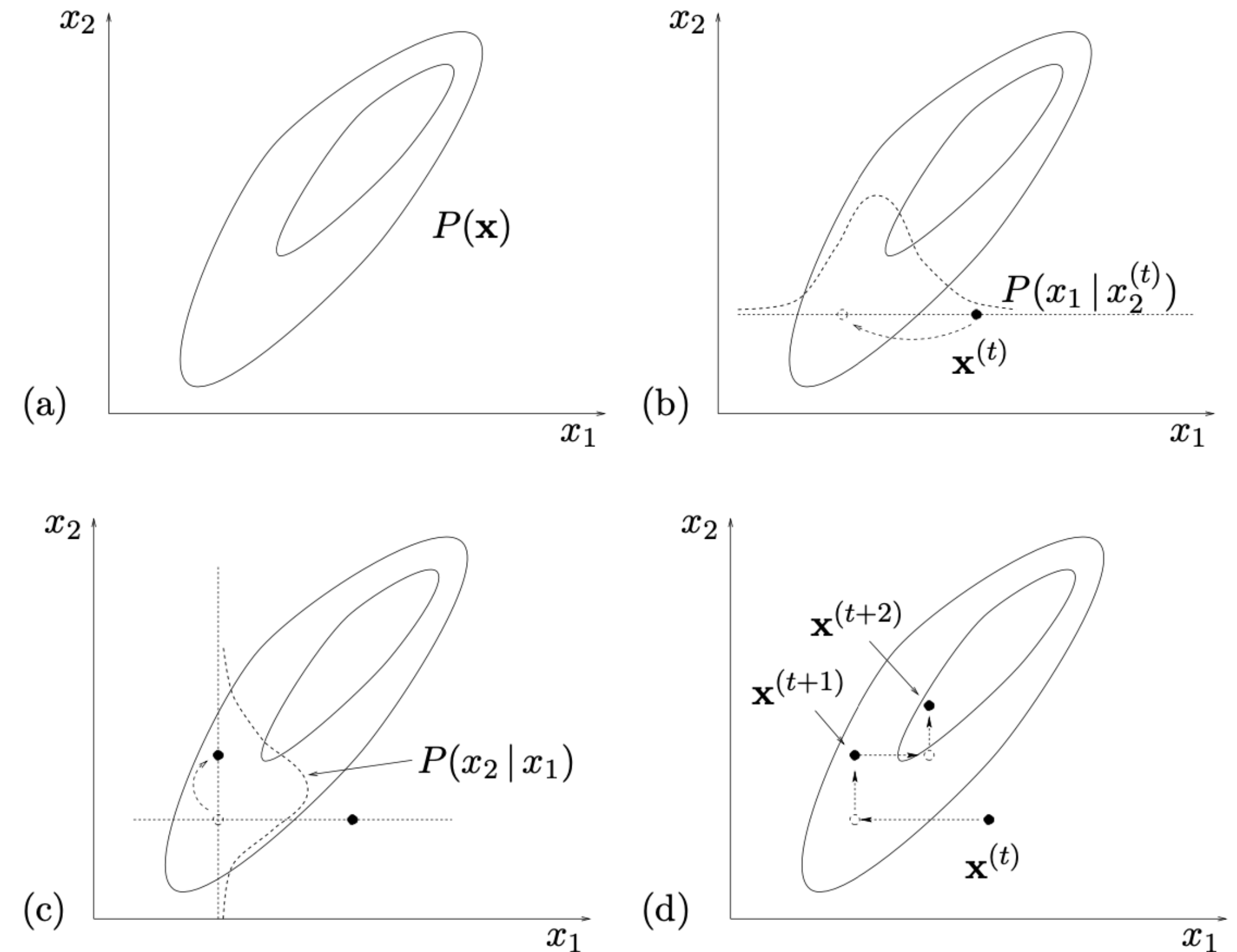


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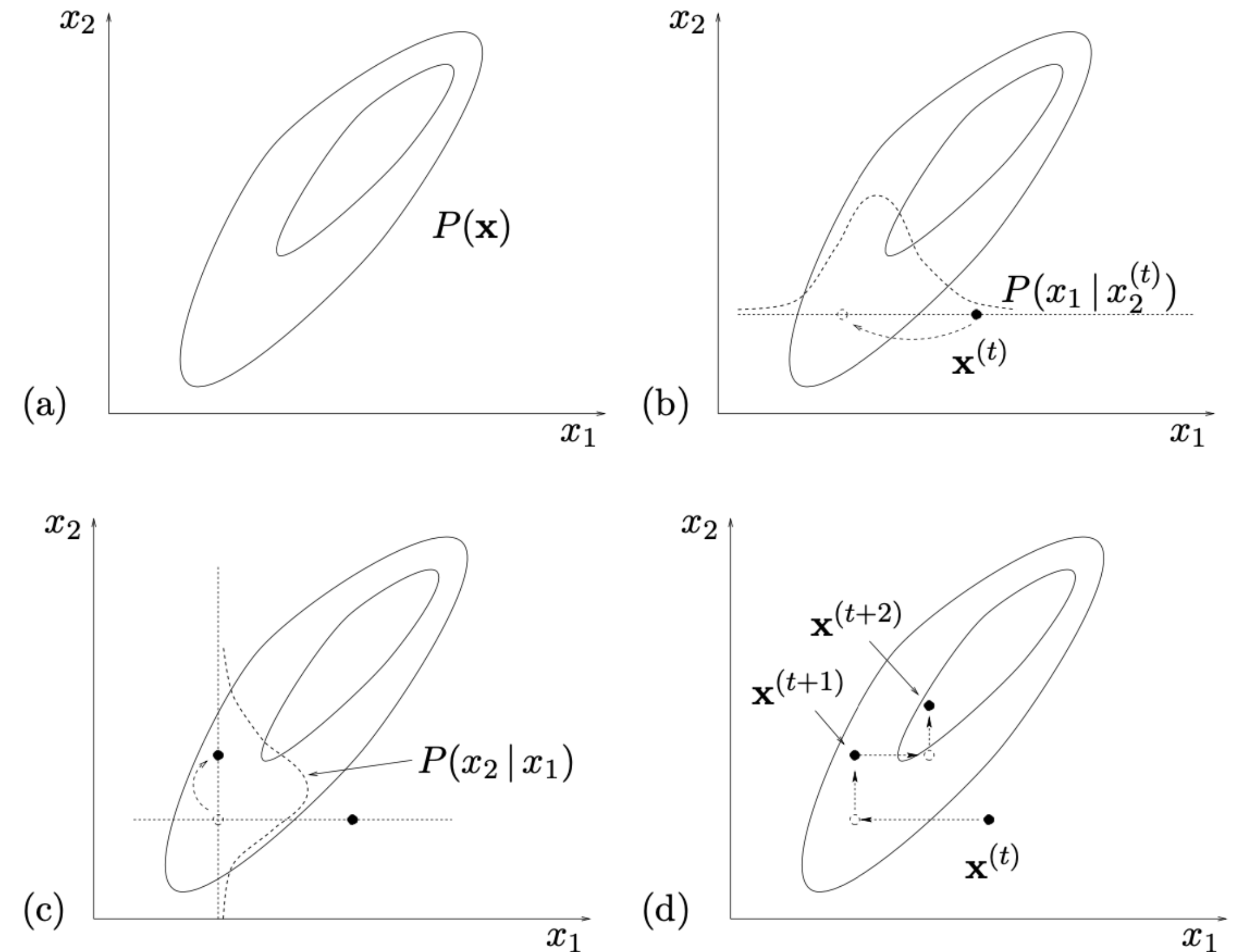


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In general, for a system of  $K$  variables, a single iteration involves sampling one parameter at a time:

$$\begin{aligned}x_1^{(t+1)} &\sim P(x_1 | x_2^{(t)}, x_3^{(t)}, \dots, x_K^{(t)}) \\x_2^{(t+1)} &\sim P(x_2 | x_1^{(t+1)}, x_3^{(t)}, \dots, x_K^{(t)}) \\x_3^{(t+1)} &\sim P(x_3 | x_1^{(t+1)}, x_2^{(t+1)}, \dots, x_K^{(t)}), \text{ etc.}\end{aligned}$$

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**Gibbs samples are always accepted!**



# MCMC algorithms

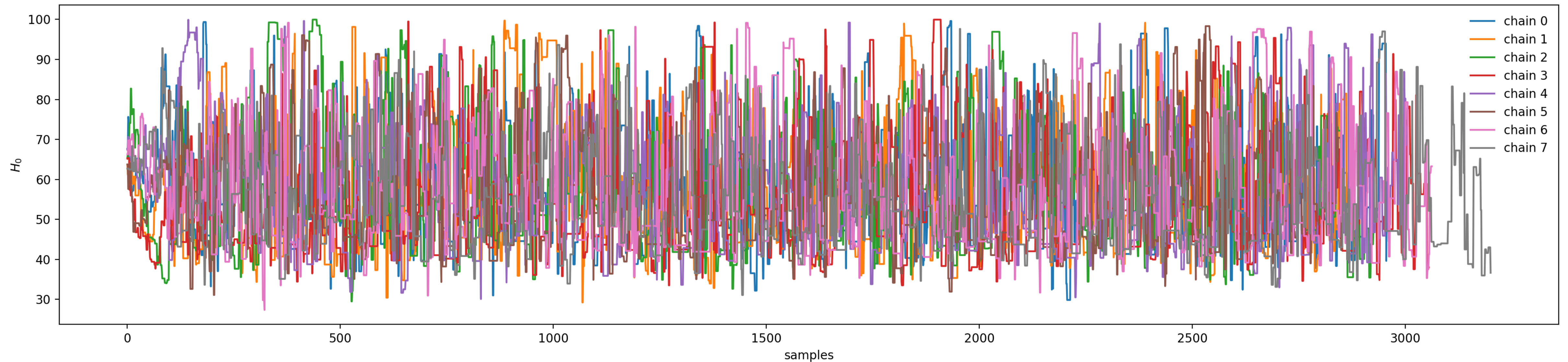
Let's play

- <https://chi-feng.github.io/mcmc-demo/app.html>



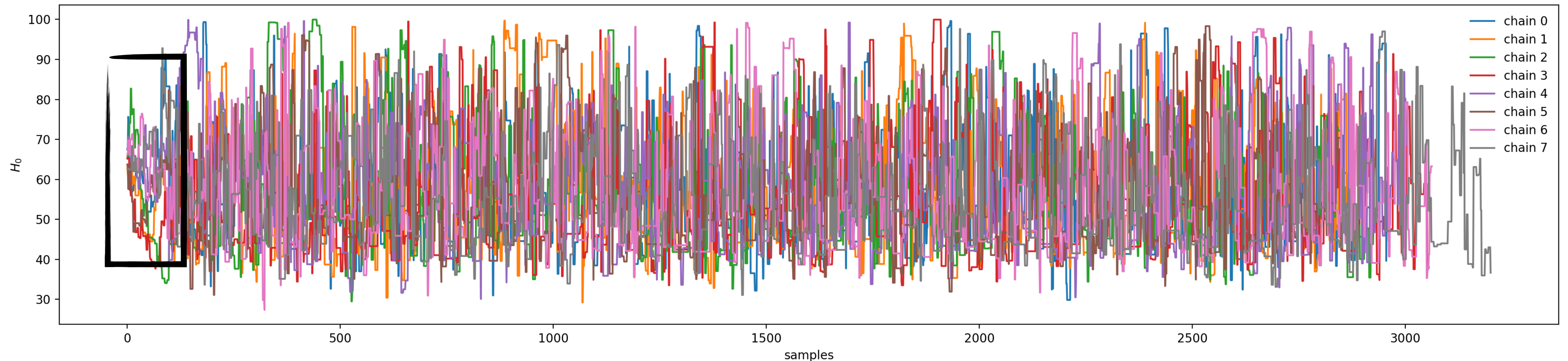
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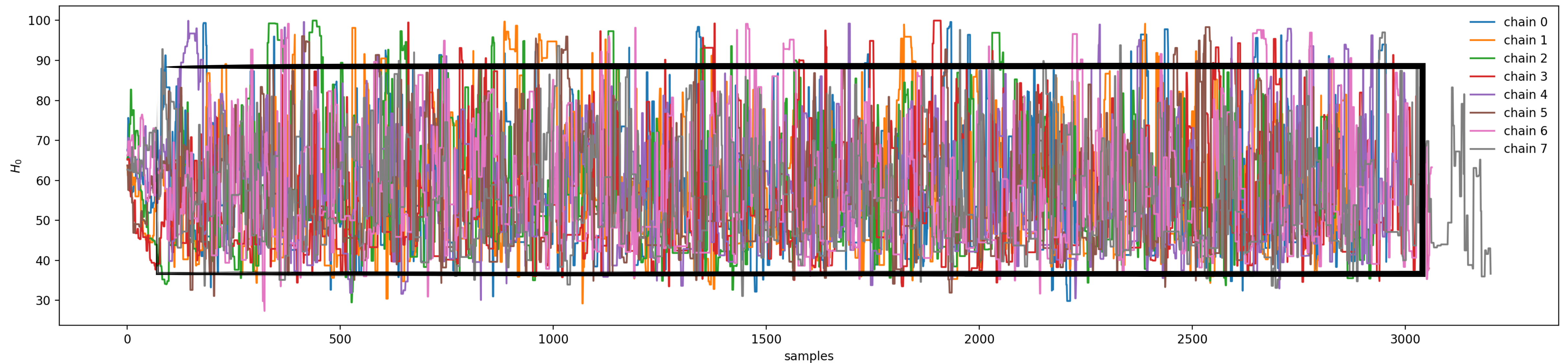
First Burn-in phase: chains leading to a stationary state from initial random points



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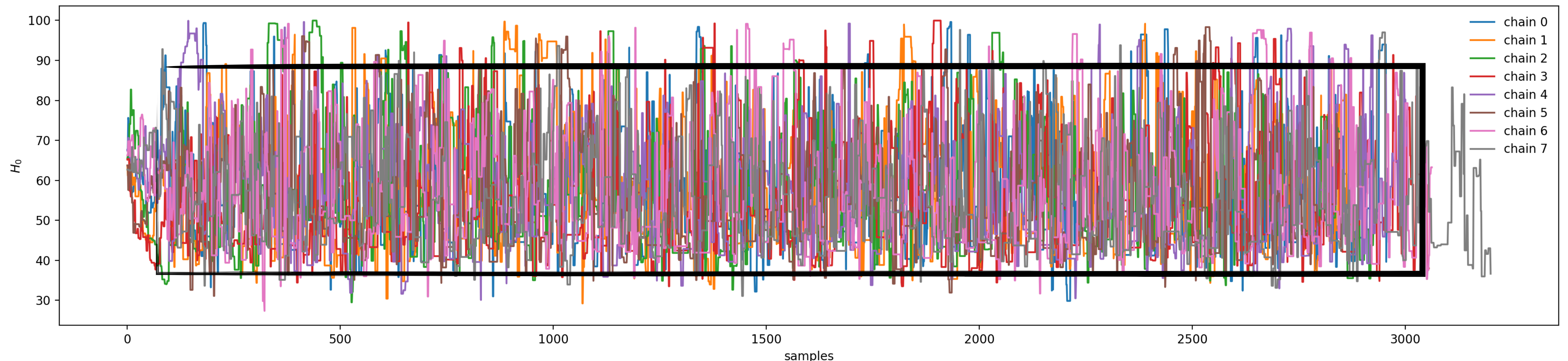
For a sufficiently long run all chains explore efficiently the parameter space.



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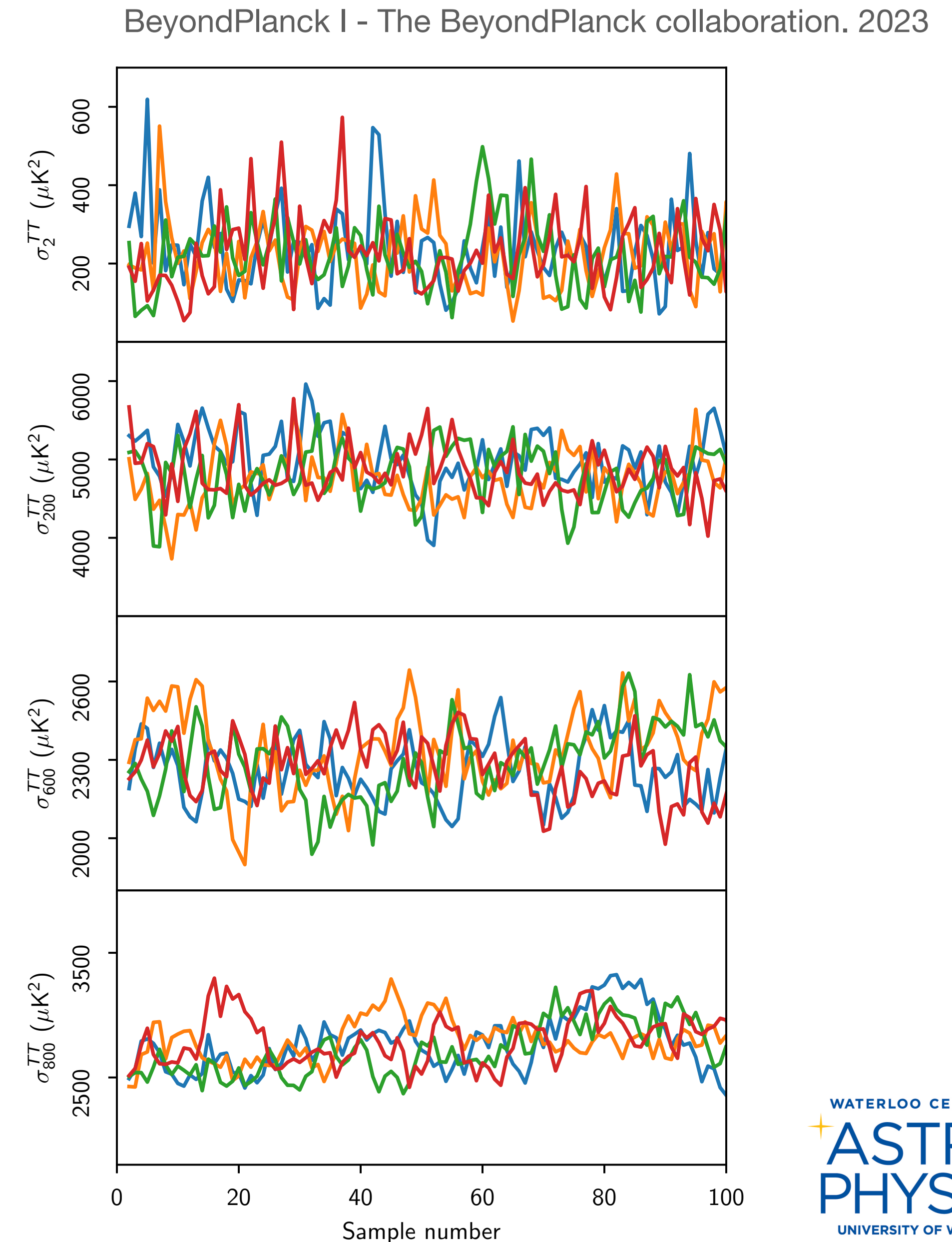
Small correlation length  $\rightarrow$  good exploration; ergodicity.



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Correlation length can be very helpful when it comes to assess quickly the convergency status of chains **individually**.

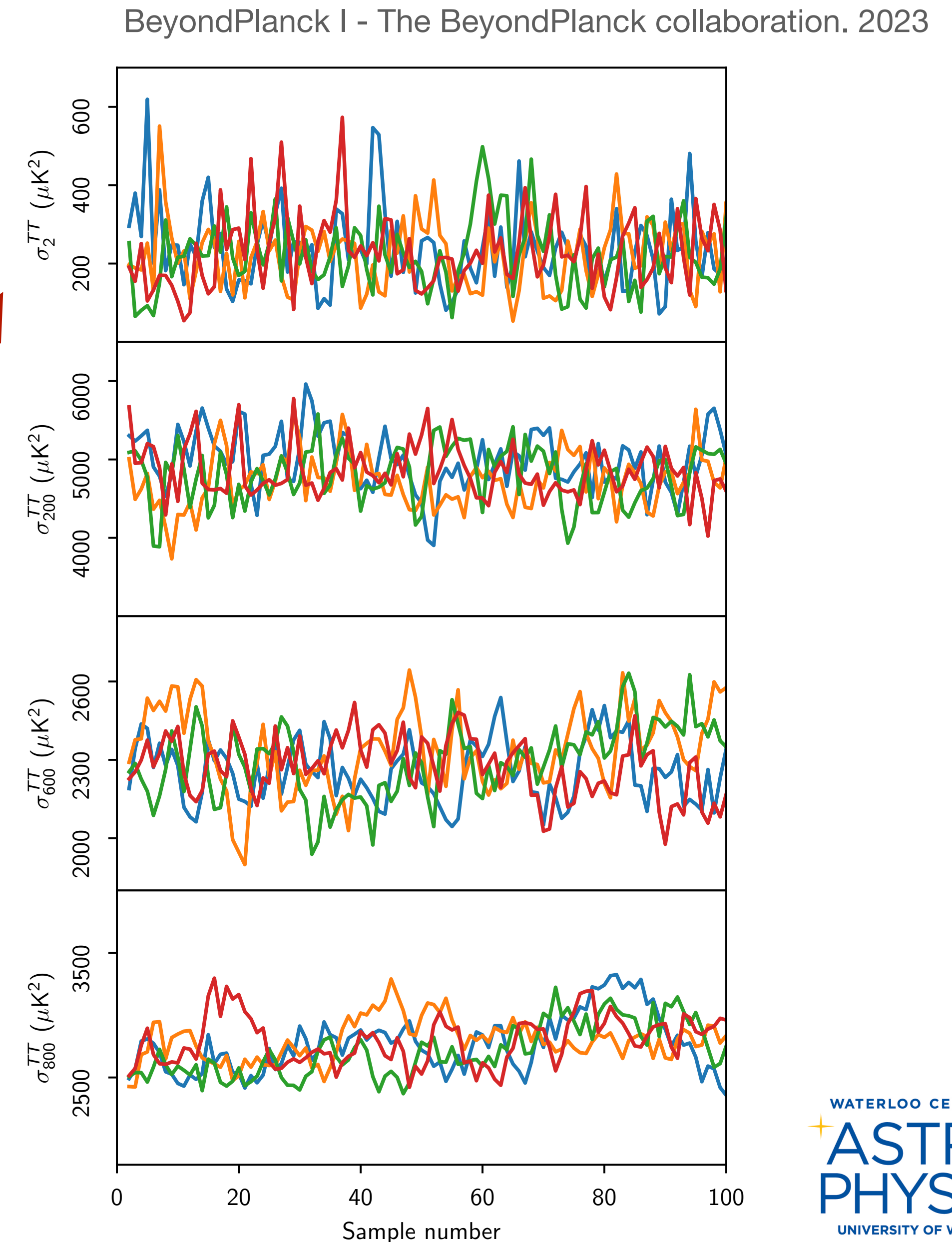


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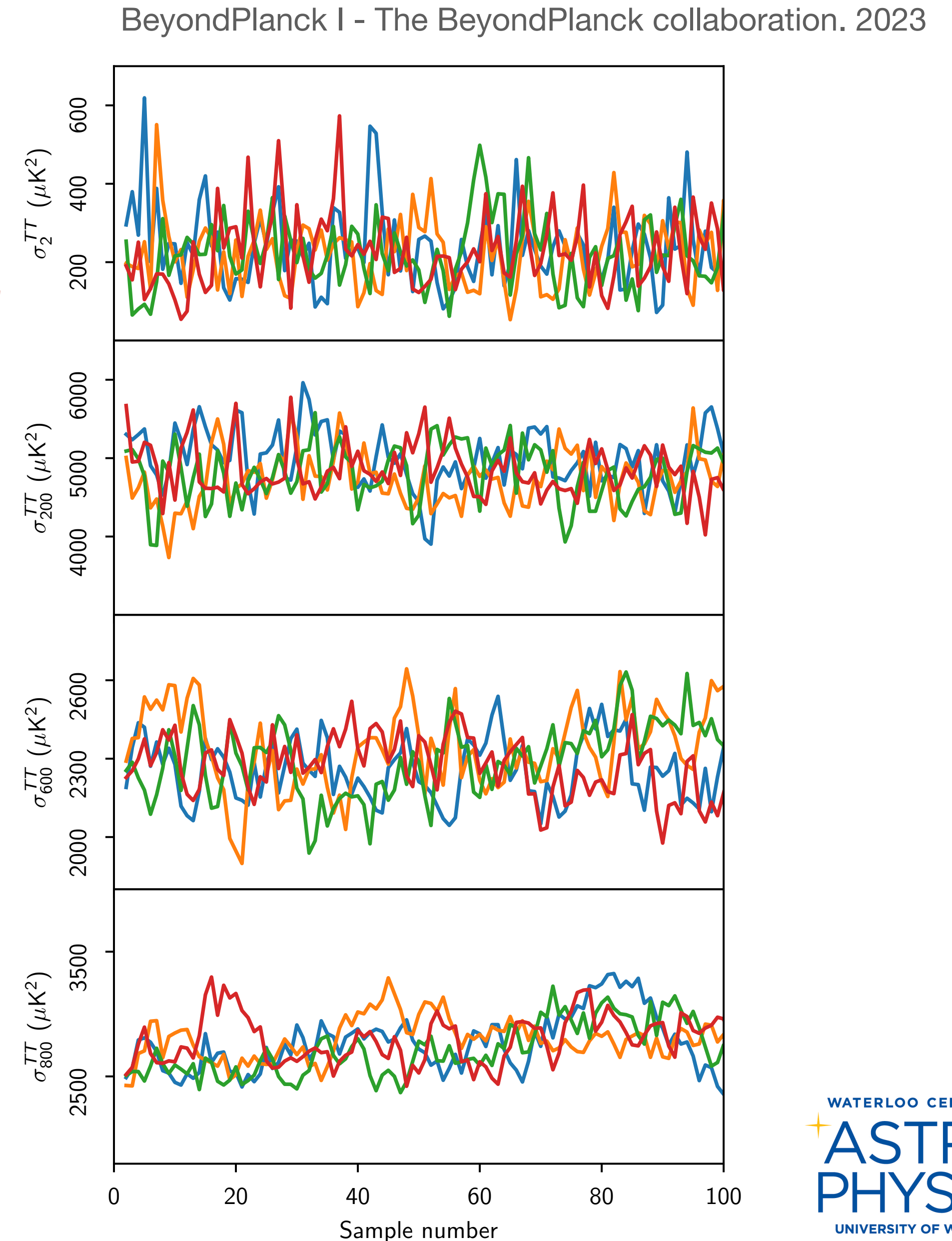


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Correlation length can be very helpful when it comes to assess quickly the convergency status of chains **individually**.

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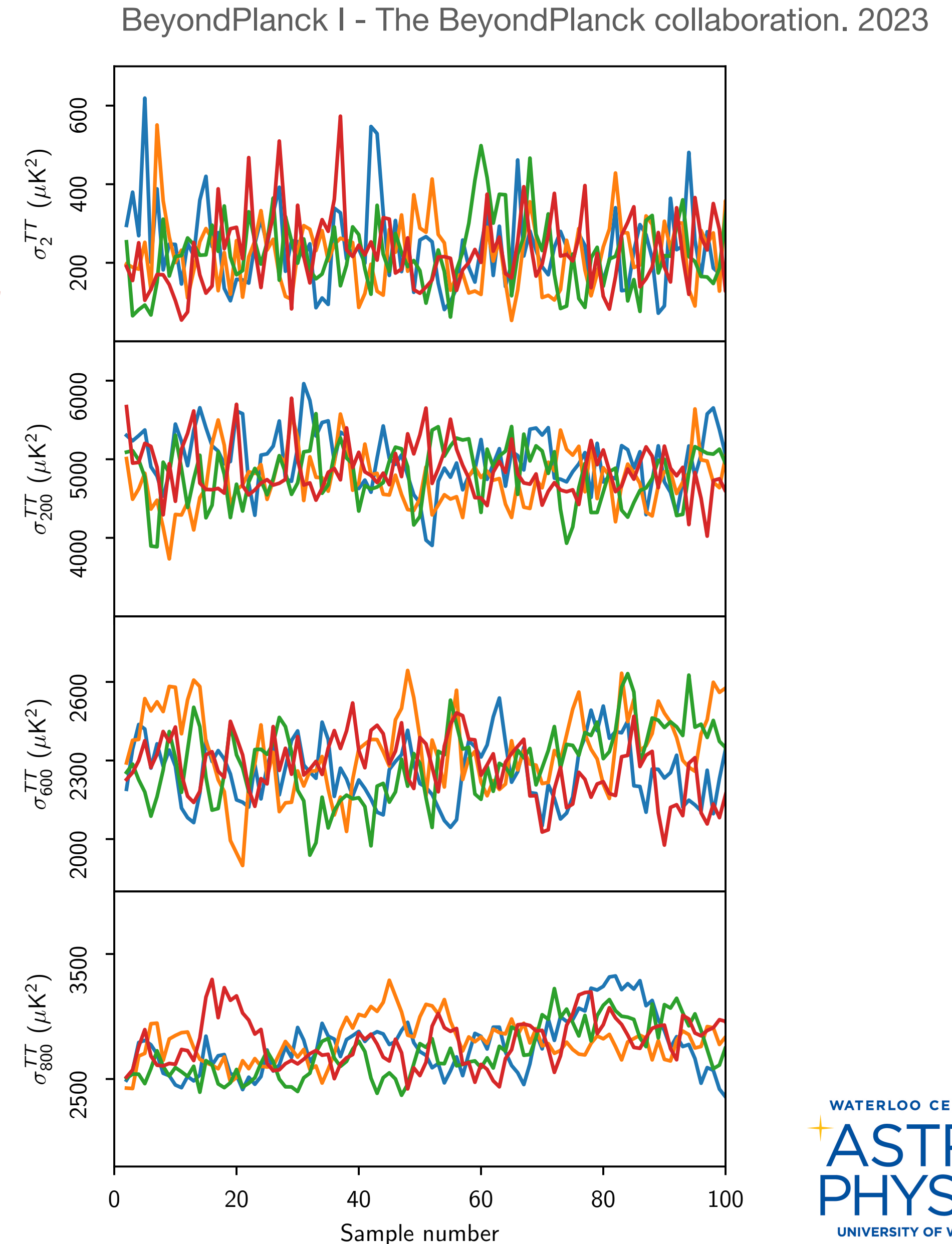
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However, parameters can be highly degenerate, and correlation length can just stay long —> **need much more samples** to properly explore the parameter space. This also **depends on the sampling algorithm**.





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This is usually referred as the Gelman-Rubin statistics for J chains of length L:

$$\bar{x}_j = \frac{1}{L} \sum_{t=1}^L x_t^{(j)} \quad (\text{chain mean})$$

$$\bar{x}_{\cdot} = \frac{1}{J} \sum_{j=1}^J \bar{x}_j \quad (\text{grand mean})$$

$$B = \frac{L}{J-1} \sum_{j=1}^J (\bar{x}_j - \bar{x}_{\cdot})^2 \quad (\text{between chain variance})$$

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The GR diagnostic suggests that a good convergency is achieved for  $R < 1.1$  or equivalently  $R - 1 < 0.1$

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