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- This lecture introduces also necessary diagnostics to check whether MCMC results are useful

# Chapter 11

- 11.1 Gibbs sampler
- 11.2 Metropolis and Metropolis-Hastings
- 11.3 Using Gibbs and Metropolis as building blocks
- 11.4 Inference and assessing convergence (important)
  - potential scale reduction  $\widehat{R}$  (R-hat)
- 11.5 Effective number of simulation draws (important)
  - effective sample size (ESS /  $S_{\text{eff}}$ )
- 11.6 Example: hierarchical normal model (quick glance)

## Chapter 11 demos

- demo11\_1: Gibbs sampling
- demo11\_2: Metropolis sampling
- demo11\_3: Convergence of Markov chain
- demo11\_4: split- $\hat{R}$  and effective sample size (ESS or  $S_{\text{eff}}$ )
- demo11\_5: Diagnostics with posterior and bayesplot packages

It's all about expectations (reminder)

$$E_{p(\theta|y)}[f(\theta)] = \int f(\theta)p(\theta | y)d\theta,$$

$$\text{where } p(\theta | y) = \frac{p(y | \theta)p(\theta)}{\int p(y | \theta)p(\theta)d\theta}$$

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- Grid (equal spacing) evaluation with self-normalization

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- Monte Carlo methods which can sample from  $p(\theta^{(s)} | y)$  using only  $q(\theta^{(s)} | y)$

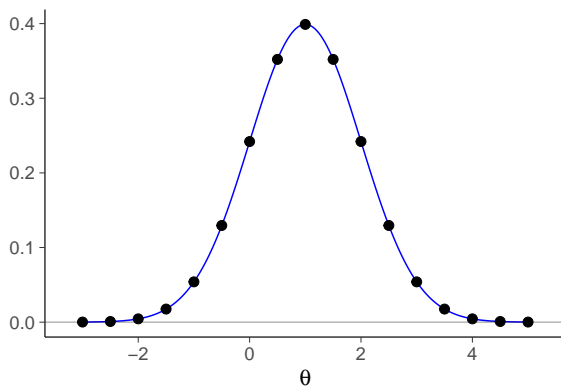
$$E_{p(\theta|y)}[f(\theta)] \approx \frac{1}{S} \sum_{s=1}^S f(\theta^{(s)})$$

# Monte Carlo

- Monte Carlo methods we have discussed so far
  - Inverse CDF works for 1D
  - Analytic transformations work for only certain distributions
  - Factorization works only for certain joint distributions
  - Grid evaluation and sampling works in a few dimensions
  - Rejection sampling works mostly in 1D (truncation is a special case)
  - Importance sampling is reliable only in special cases

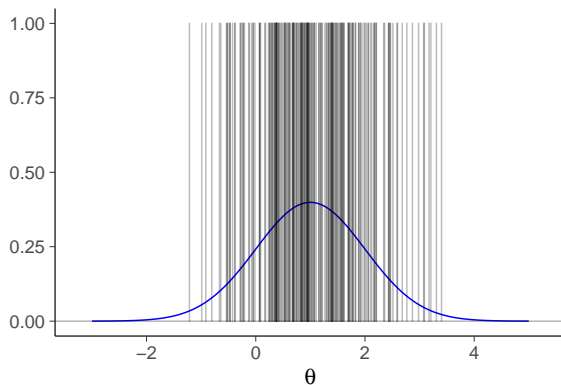
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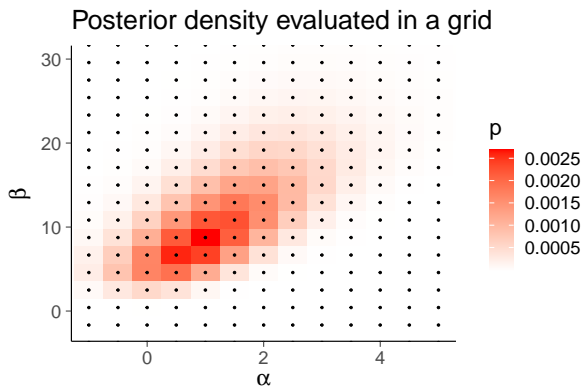
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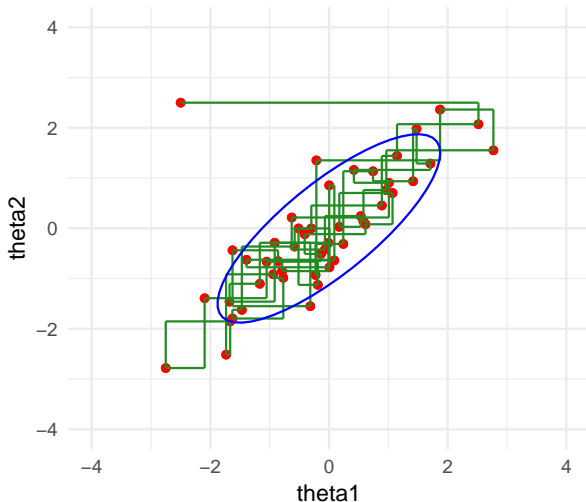
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- What to do in high dimensions?
  - Markov chain Monte Carlo (Ch 11-12)
  - Laplace, Variational\*, EP\* (Ch 4,13\*)



## Markov chain Monte Carlo (MCMC)

- Automatically focuses density evaluations where most of the posterior mass is



# Markov chain

- **Andrey Markov** proved weak law of large numbers and central limit theorem for certain dependent-random sequences, which were later named Markov chains
  - CLT saying the sum / mean converges towards normal if the variance is finite (we come back to this in the end of the course)

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- Markov's one example was the sequence of letters in Pushkin's novel "Yevgeniy Onegin"
  - Deep learning language models are super big Markov models

# Markov chain

- Example of a simple Markov chain

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  - + central limit theorem holds for expectations
    - draws are dependent
    - construction of efficient Markov chains is not always easy

# Markov chain

- Set of random variables  $\theta^1, \theta^2, \dots$ , so that with all values of  $t$ ,  $\theta^t$  depends only on the previous  $\theta^{(t-1)}$

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- Chain has to be initialized with some starting point  $\theta^0$
- Transition distribution  $T_t(\theta^t \mid \theta^{t-1})$  (may depend on  $t$ )
  - by choosing a suitable transition distribution, the stationary distribution of Markov chain is  $p(\theta \mid y)$

# Gibbs sampling

- Alternate sampling from 1D conditional distributions
  - e.g. normal distribution, sample alternating from  $p(\mu \mid \sigma^2, y)$  and  $p(\sigma^2 \mid \mu, y)$

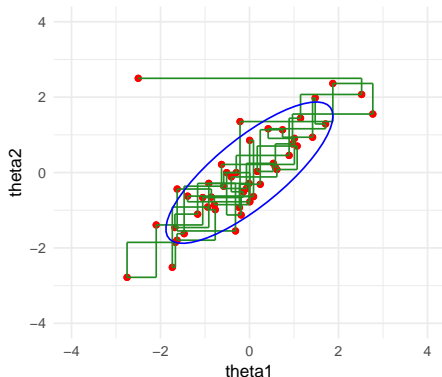
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  - 1D is easy even if no conjugate prior and analytic posterior



# Gibbs sampling

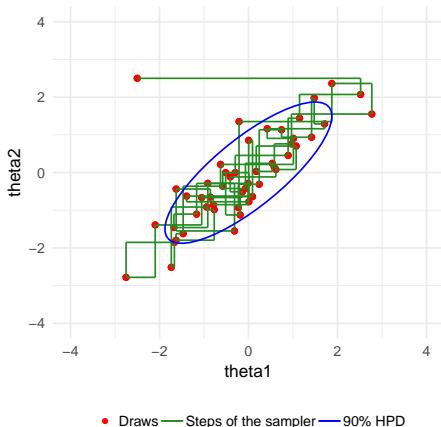
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- demo11\_1



• Draws — Steps of the sampler — 90% HPD

# Gibbs sampling

- Alternate sampling from 1D conditional distributions
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- Basic algorithm

sample  $\theta_j^t$  from  $p(\theta_j \mid \theta_{-j}^{t-1}, y)$ ,

where  $\theta_{-j}^{t-1} = (\theta_1^t, \dots, \theta_{j-1}^t, \theta_{j+1}^{t-1}, \dots, \theta_d^{t-1})$

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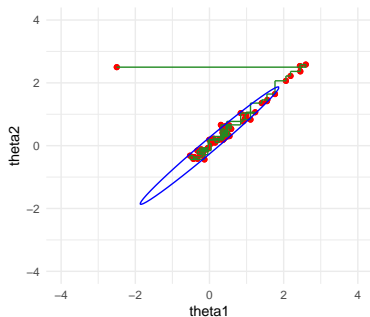
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- Slow if parameters are highly dependent in the posterior
  - demo11\_1 continues



## Conditional vs joint

- How about sampling  $\theta$  jointly?
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## Conditional vs joint

- How about sampling  $\theta$  jointly?
  - e.g. it is easy to sample from multivariate normal
- Can we use that to form a Markov chain?

# Metropolis algorithm

- Algorithm

1. starting point  $\theta^0$

2.  $t = 1, 2, \dots$

- (a) pick a proposal  $\theta^*$  from the proposal distribution  $J_t(\theta^* \mid \theta^{t-1})$ .

Proposal distribution has to be symmetric, i.e.

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ie, if  $p(\theta^* | y) > p(\theta^{t-1} | y)$  accept the proposal always  
and otherwise accept the proposal with probability  $r$

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ie, the new state is the same as previous
- step c is executed by generating a random number from  $U(0, 1)$
- $p(\theta^* | y)$  and  $p(\theta^{t-1} | y)$  have the same normalization terms, and thus instead of  $p(\cdot | y)$ , unnormalized  $q(\cdot | y)$  can be used, as the normalization terms cancel out!



# Metropolis algorithm

- Example: one bivariate observation  $(y_1, y_2)$ 
  - bivariate normal distribution with unknown mean and known covariance

$$\begin{pmatrix} \theta_1 \\ \theta_2 \end{pmatrix} \Big| y \sim \text{N} \left( \begin{pmatrix} y_1 \\ y_2 \end{pmatrix}, \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix} \right)$$

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- More examples <https://chi-feng.github.io/mcmc-demo/>

## Why Metropolis algorithm works

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- Intuitively more draws from the higher density areas as jumps to higher density are always accepted and only some of the jumps to the lower density are accepted
- Theoretically
  1. Prove that simulated series is a Markov chain which has unique stationary distribution
  2. Prove that this stationary distribution is the desired target distribution

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  - a) irreducible
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  - c) recurrent / not transient
    - = probability to return to a state  $i$  is 1
    - holds for a random walk on any proper distribution (except for trivial exceptions)



# Why Metropolis algorithm works

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$$\begin{aligned} p(\theta^t = \theta_a, \theta^{t-1} = \theta_b) &= p(\theta_b \mid y) J_t(\theta_a \mid \theta_b) \left( \frac{p(\theta_a \mid y)}{p(\theta_b \mid y)} \right) \\ &= p(\theta_a \mid y) J_t(\theta_a \mid \theta_b), \end{aligned}$$

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- consider any two such points  $\theta_a$  and  $\theta_b$  drawn from  $p(\theta \mid y)$  and labeled so that  $p(\theta_b \mid y) \geq p(\theta_a \mid y)$
- the unconditional probability density of a transition from  $\theta_a$  to  $\theta_b$  is

$$p(\theta^{t-1} = \theta_a, \theta^t = \theta_b) = p(\theta_a \mid y) J_t(\theta_b \mid \theta_a),$$

- the unconditional probability density of a transition from  $\theta_b$  to  $\theta_a$  is

$$\begin{aligned} p(\theta^t = \theta_a, \theta^{t-1} = \theta_b) &= p(\theta_b \mid y) J_t(\theta_a \mid \theta_b) \left( \frac{p(\theta_a \mid y)}{p(\theta_b \mid y)} \right) \\ &= p(\theta_a \mid y) J_t(\theta_a \mid \theta_b), \end{aligned}$$

which is the same as the probability of transition from  $\theta_a$  to  $\theta_b$ , since we have required that  $J_t(\cdot \mid \cdot)$  is symmetric

# Why Metropolis algorithm works

## 2. Prove that this stationary distribution is the desired target distribution $p(\theta \mid y)$

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- since their joint distribution is symmetric,  $\theta^t$  and  $\theta^{t-1}$  have the same marginal distributions, and so  $p(\theta \mid y)$  is the stationary distribution of the Markov chain of  $\theta$

# Metropolis-Hastings algorithm

- Generalization of Metropolis algorithm for non-symmetric proposal distributions
  - acceptance ratio includes ratio of proposal distributions

$$r = \frac{p(\theta^* | y) / J_t(\theta^* | \theta^{t-1})}{p(\theta^{t-1} | y) / J_t(\theta^{t-1} | \theta^*)}$$

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# Metropolis-Hastings algorithm

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    - long steps proposed, but many of those rejected and again chain moves slowly

# Metropolis-Hastings algorithm

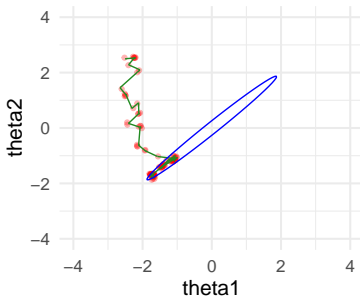
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  - big scale
    - long steps proposed, but many of those rejected and again chain moves slowly
- Generic rule for rejection rate is 60-90% (but depends on dimensionality and a specific algorithm variation)

# Gibbs sampling

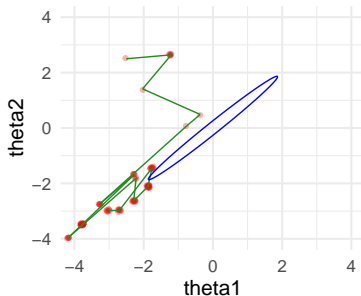
- Specific case of Metropolis-Hastings algorithm
  - single updated (or blocked)
  - proposal distribution is the conditional distribution
    - proposal and target distributions are same
    - acceptance probability is 1

# Metropolis

- Usually doesn't scale well to high dimensions
  - if the shape doesn't match the whole distribution, the efficiency drops
  - demo11\_2



• Draws — Steps of the sampler — 90% HPD



• Draws — Steps of the sampler — 90% HPD

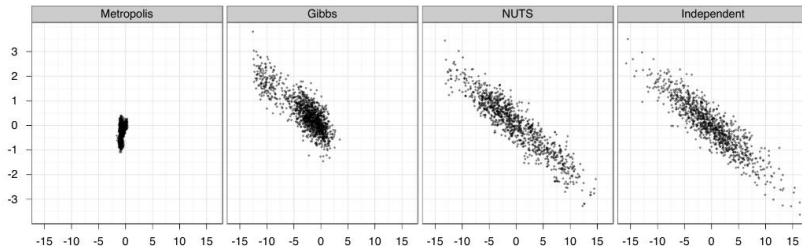
# Dynamic Hamiltonian Monte Carlo and NUTS

- Chapter 12 presents some more advanced methods
  - Chapter 12 includes Hamiltonian Monte Carlo and NUTS, which is one of the most efficient methods
    - uses gradient information
    - Hamiltonian dynamic simulation reduces random walk
    - state-of-the-art MCMC used by most modern probabilistic programming frameworks
- More next week

# HMC / NUTS

## Comparison of algorithms on **highly correlated** 250-dimensional Gaussian distribution

- Do **1,000,000** draws with both Random Walk Metropolis and Gibbs, thinning by 1000
- Do **1,000** draws using Stan's NUTS algorithm (no thinning)
- Do 1,000 independent draws (we can do this for multivariate normal)



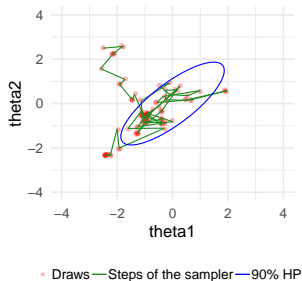


## Warm-up and convergence diagnostics

- Asymptotically chain spends the  $\alpha\%$  of time where  $\alpha\%$  posterior mass is

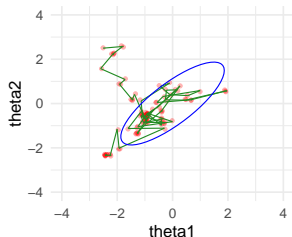
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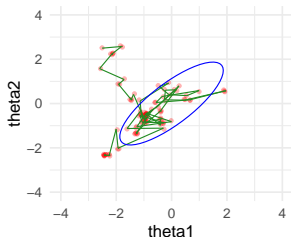


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  - warm-up may include also phase for adapting algorithm parameters

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• Draws — Steps of the sampler — 90% HPD

- Warm-up = remove draws from the beginning of the chain
  - warm-up may include also phase for adapting algorithm parameters
- Convergence diagnostics
  - Is the sample representative of the target distribution?

# MCMC draws are dependent

- Monte Carlo estimates still valid (central limit theorem holds)

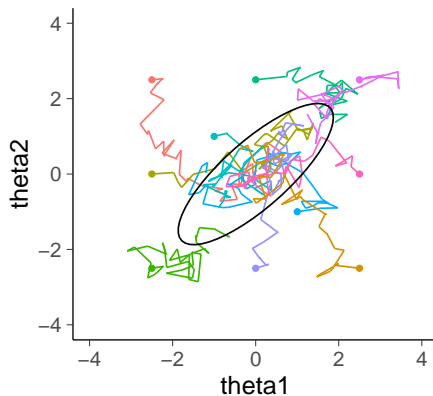
$$E_{p(\theta|y)}[f(\theta)] \approx \frac{1}{S} \sum_{s=1}^S f(\theta^{(s)})$$

- Estimation of Monte Carlo error is more difficult
  - evaluation of *effective* sample size

## Several chains

- Use of several chains make convergence diagnostics easier
- Start chains from different starting points – preferably overdispersed

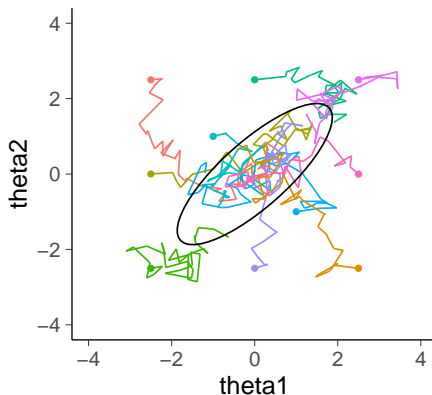
No convergence



## Several chains

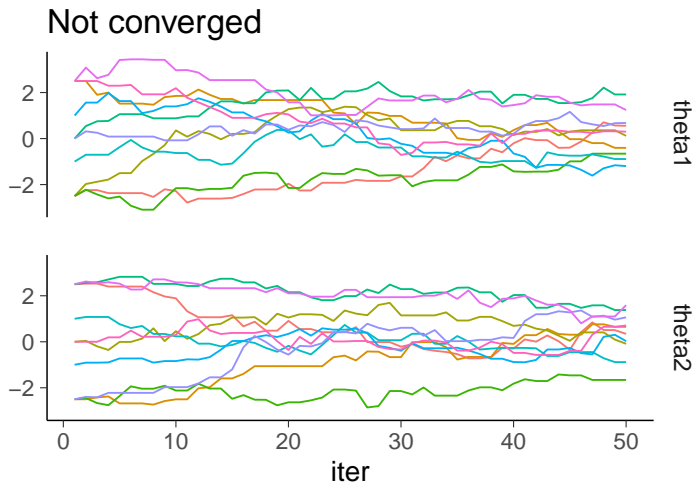
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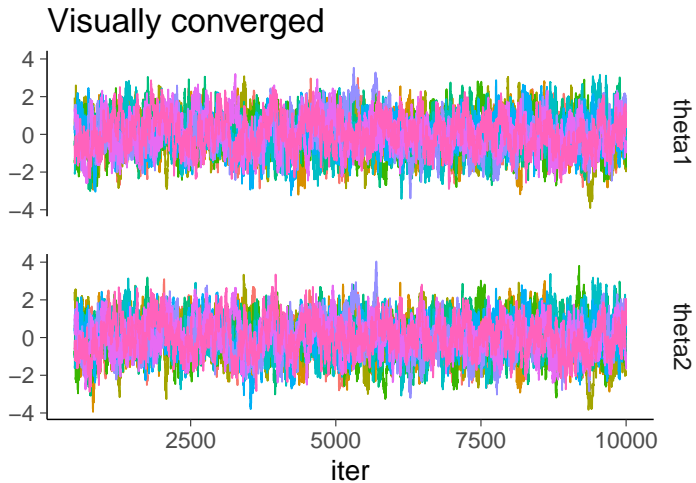
- Remove draws from the beginning of the chains and run chains long enough so that it is not possible to distinguish where each chain started and the chains are well mixed

## Several chains

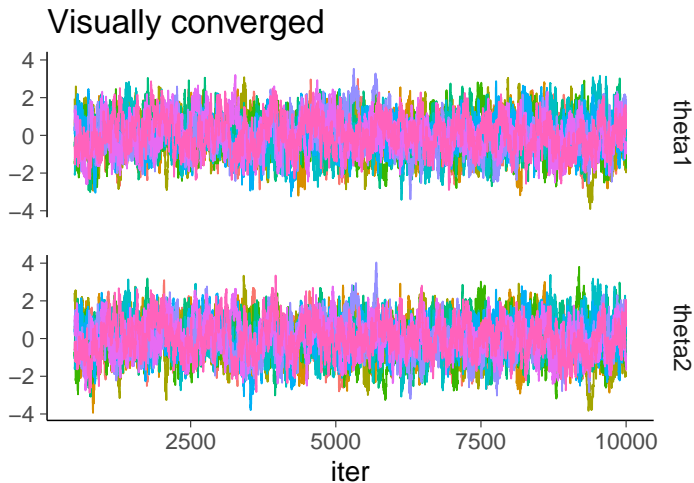




## Several chains



## Several chains



Visual convergence check is not sufficient

$\hat{R}$ : comparison of within and between variances of the chains

- BDA3:  $\hat{R}$  aka *potential scale reduction factor* (PSRF)
- Compare means and variances of the chains

# $\hat{R}$ : comparison of within and between variances of the chains

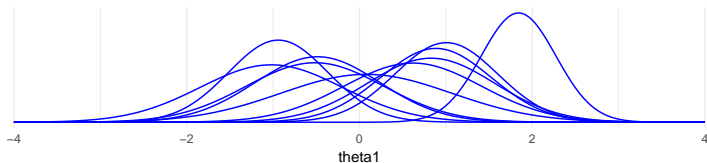
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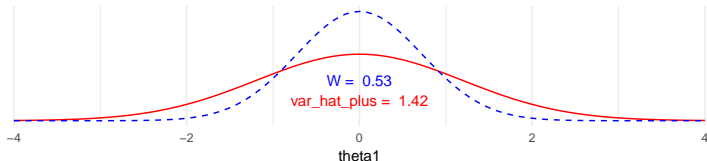
W = within chain variance estimate

var\_hat\_plus = total variance estimate

50 warmup, 50 post warmup iterations



Rhat = 1.64



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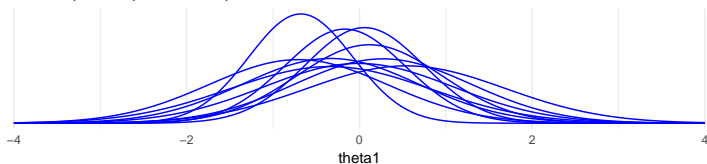
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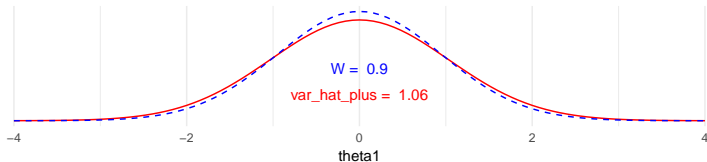
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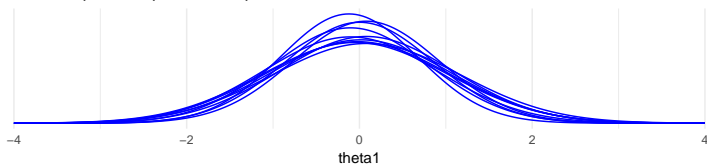
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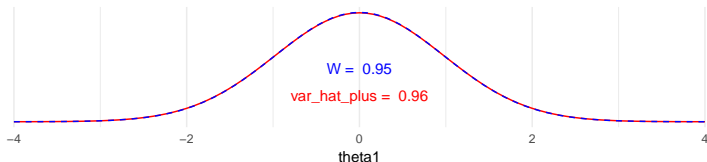
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$\hat{R}$

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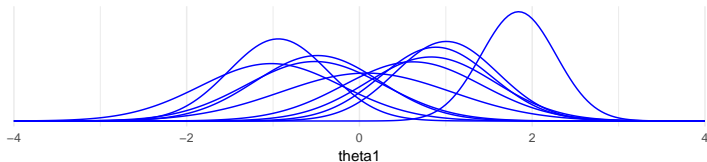
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- As  $\widehat{\text{var}}^+(\theta \mid y)$  overestimates and  $W$  underestimates, compute

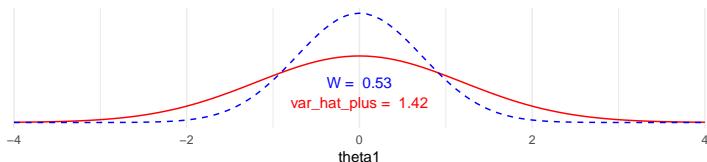
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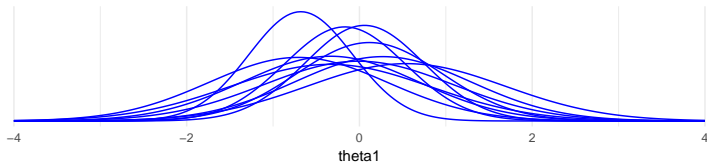
Rhat = 1.64



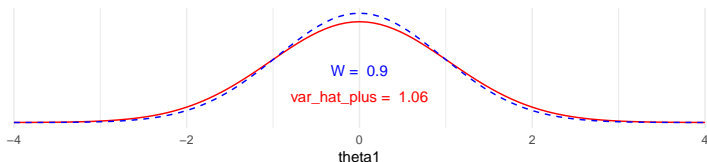
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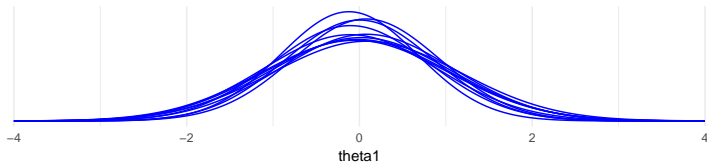




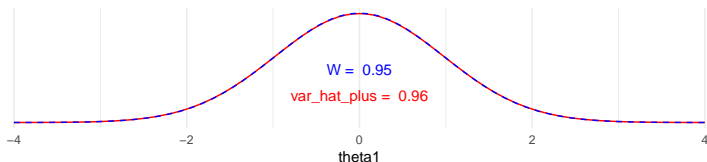
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$\widehat{R}$

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- If  $\widehat{R}$  close to 1, it is still possible that chains have not converged
  - if starting points were not overdispersed
  - distribution far from normal (especially if infinite variance)
  - just by chance when  $N$  is finite

## Split- $\hat{R}$

- BDA3: split- $\hat{R}$
- Examines *mixing* and *stationarity* of chains
- To examine stationarity chains are split to two parts
  - after splitting, we have  $M$  chains, each having  $N$  draws
  - scalar draws  $\theta_{nm}$  ( $n = 1, \dots, N; m = 1, \dots, M$ )
  - compare means and variances of the split chains

## Rank normalized $\hat{R}$

- Original  $\hat{R}$  requires that the target distribution has finite mean and variance

Vehtari, Gelman, Simpson, Carpenter, Bürkner (2020).  
Rank-normalization, folding, and localization: An improved  $\hat{R}$  for  
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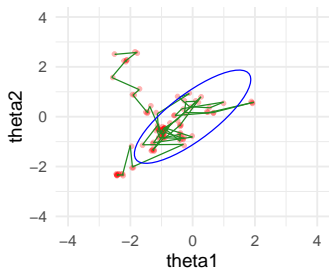
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# Time series analysis

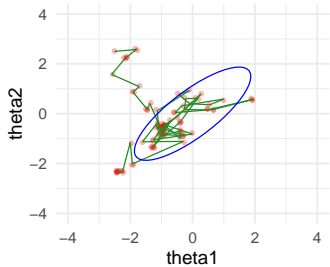
- Autocorrelation function
  - describes the correlation given a certain lag
  - can be used to compare efficiency of MCMC algorithms and parameterizations

# Autocorrelation



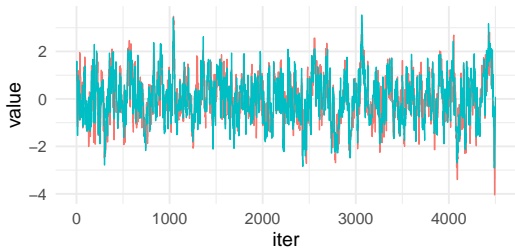
• Draws — Steps of the sampler — 90% HPI

# Autocorrelation



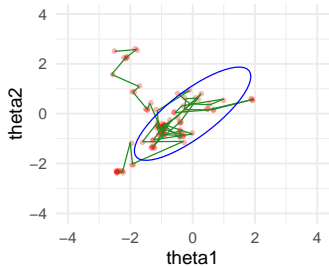
• Draws — Steps of the sampler — 90% HPD

## Trends



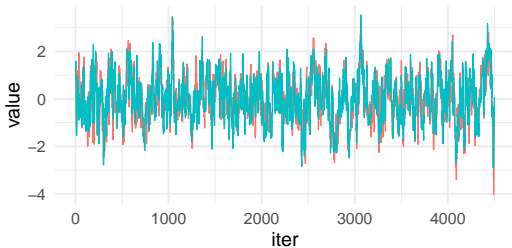
—  $\theta_1$  —  $\theta_2$

# Autocorrelation



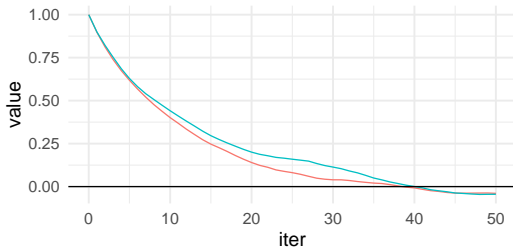
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## Trends

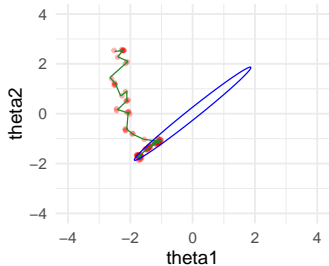


—  $\theta_1$  —  $\theta_2$

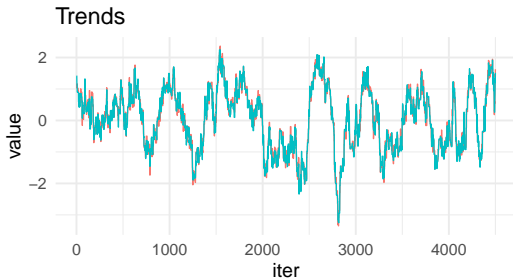
## Autocorrelation function



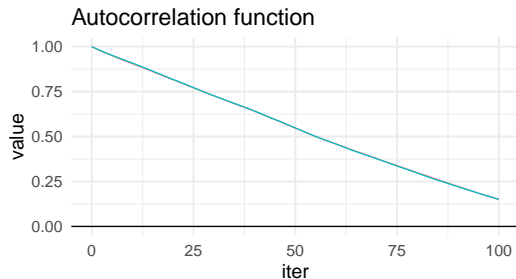
# Autocorrelation (slow mixing due to small step size)



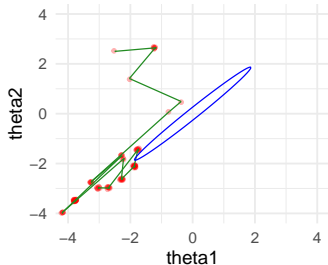
• Draws — Steps of the sampler — 90% HPI



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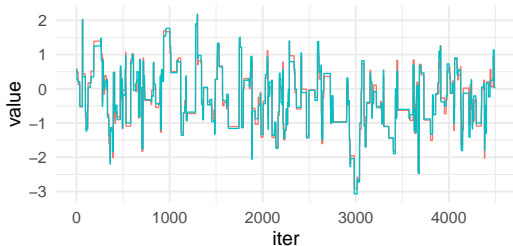


# Autocorrelation (slow mixing due to many rejections)



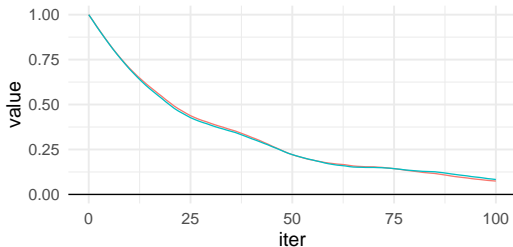
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## Trends



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## Autocorrelation function



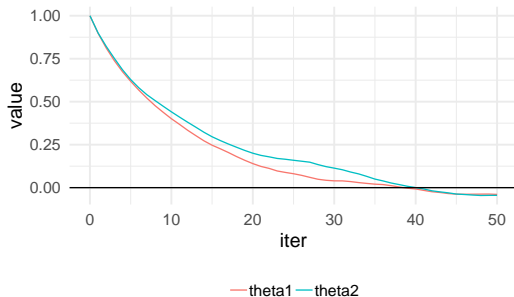
# Time series analysis

- Time series analysis can be used to estimate Monte Carlo error in case of MCMC
- For expectation  $\bar{\theta}$

$$\text{Var}[\bar{\theta}] = \frac{\sigma_{\theta}^2}{S_{\text{eff}}}$$

where  $S_{\text{eff}} = S/\tau$  (=ESS),  
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- BDA3 focuses on  $S_{\text{eff}}$  and not the Monte Carlo error directly  
new  $\hat{R}$  paper discusses more about MCSEs for different quantities

# Time series analysis

- Estimation of the autocorrelation using several chains

$$\hat{\rho}_n = 1 - \frac{W - \frac{1}{M} \sum_{m=1}^M \hat{\rho}_{n,m}}{2\widehat{\text{var}}^+}$$

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- BDA3 has slightly different and less accurate equation. The above equation is used in Stan 2.18+
- Compared to a method which computes the autocorrelation from a single chain, the multi-chain estimate has smaller variance

## Time series analysis

- Estimation of  $\tau$

$$\tau = 1 + 2 \sum_{t=1}^{\infty} \hat{\rho}_t$$

where  $\hat{\rho}_t$  is empirical autocorrelation

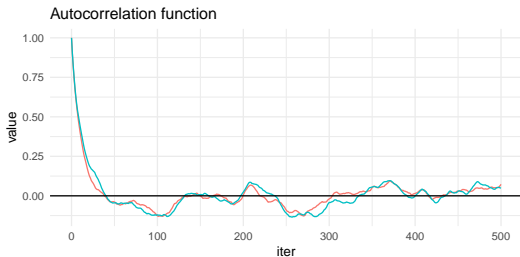


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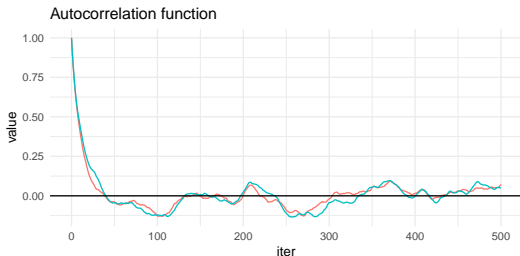


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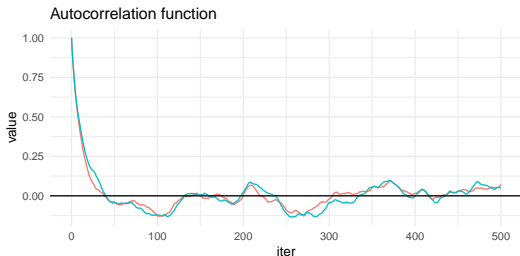
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- noise is larger for longer lags (less observations)
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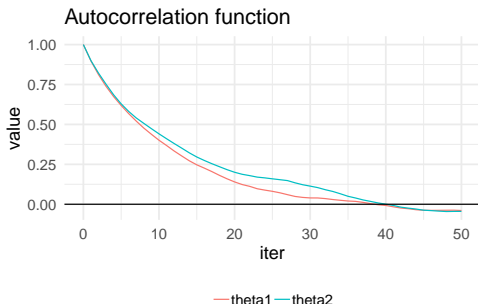
$$\hat{\tau} = 1 + 2 \sum_{t=1}^T \hat{\rho}_t$$

# Geyer's adaptive window estimator

- Truncation can be decided adaptively
  - for stationary, irreducible, recurrent Markov chain
  - let  $\Gamma_m = \rho_{2m} + \rho_{2m+1}$ , which is sum of two consequent autocorrelations
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- Initial positive sequence estimator (Geyer's IPSE)
  - Choose the largest  $m$  so, that all values of the sequence  $\hat{\Gamma}_1, \dots, \hat{\Gamma}_m$  are positive



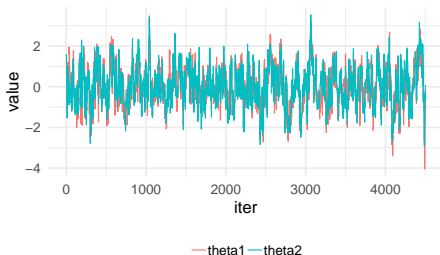
## Effective sample size

Effective sample size  $ESS = S_{\text{eff}} \approx S/\hat{\tau}$

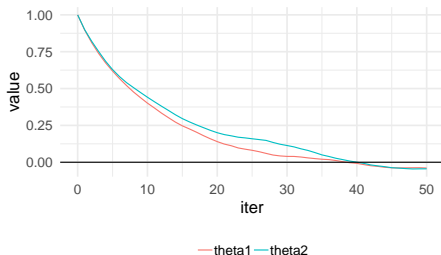
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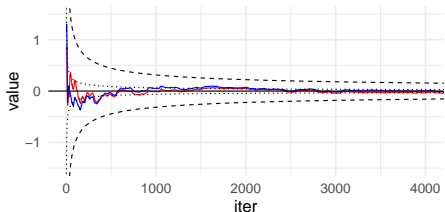
Trends



Autocorrelation function



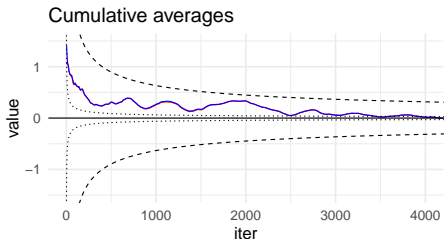
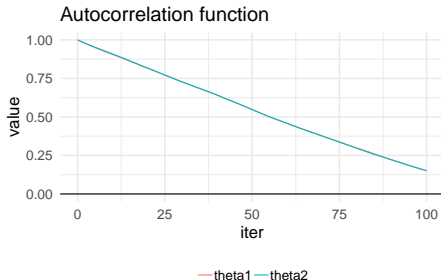
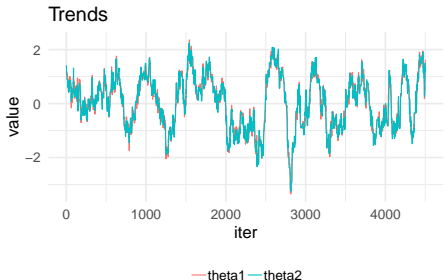
Cumulative averages



$$\hat{\tau} = 1 + 2 \sum_{t=1}^T \hat{\rho}_t$$
$$\approx 24$$

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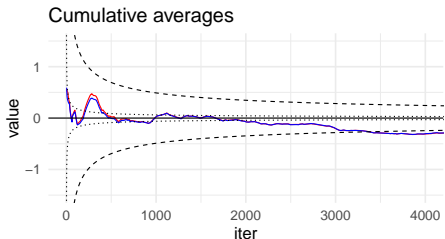
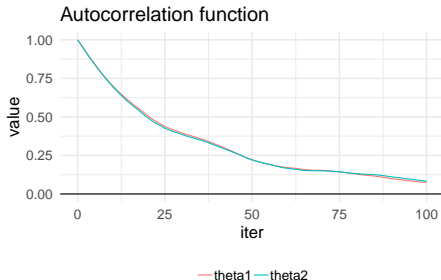
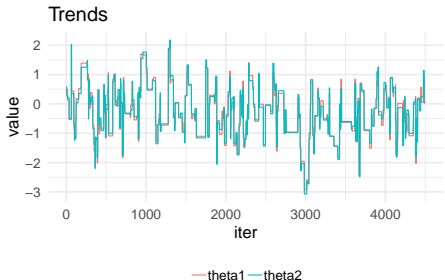
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# Diagnostic tools

For this week's assignment:

- $\hat{R}$ , ESS, mean, MCSE of mean in R
  - `library(posterior)`
  - `summarise_draws(th, basic_rhat, basic_ess)`
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  - see ArviZ package

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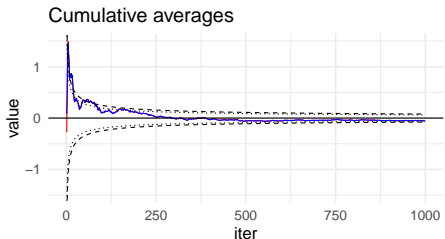
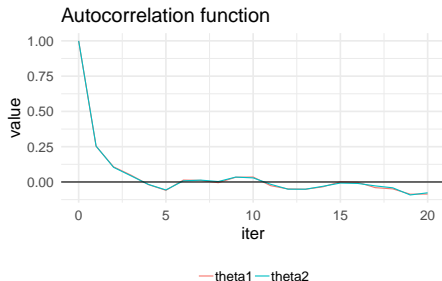
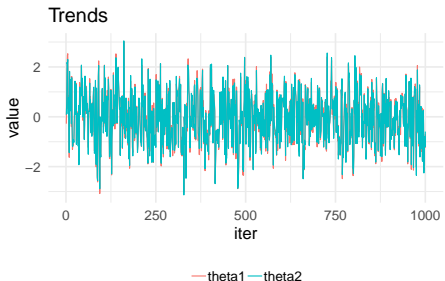
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- Nonlinear dependencies
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- Funnels
  - optimal proposal depends on location
- Multimodal
  - difficult to move from one mode to another
- Long-tailed with non-finite variance and mean
  - central limit theorem for expectations does not hold



# Next week: HMC, NUTS, and dynamic HMC

Effective sample size  $ESS = S_{\text{eff}} \approx S/\hat{\tau}$



$$\hat{\tau} = 1 + 2 \sum_{t=1}^T \hat{\rho}_t$$
$$\approx 1.6$$

## Further diagnostics

- Dynamic HMC/NUTS has additional diagnostics
  - divergences
  - tree depth exceedences
  - fraction of missing information

## MCMC summary

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- Probabilistic programming frameworks
  - provide efficient MCMC algorithms that work well without manual tuning for many posterior distributions (more next week)