Chapter 12

- 12.1 Efficient Gibbs samplers (not part of the course)
- 12.2 Efficient Metropolis jump rules (not part of the course)
- 12.3 Further extensions to Gibbs and Metropolis (not part of the course)
- 12.4 Hamiltonian Monte Carlo (important)
- 12.5 Hamiltonian dynamics for a simple hierarchical model (useful example)
- 12.6 Stan: developing a computing environment (useful intro)

Extra material for HMC / NUTS

- An introduction for applied users with good visualizations:
  Monnahan, Thorson, and Branch (2016) Faster estimation of Bayesian models in ecology using Hamiltonian Monte Carlo. https://dx.doi.org/10.1111/2041-210X.12681
- A review of why HMC works:
  Neal (2012). MCMC using Hamiltonian dynamics. https://arxiv.org/abs/1206.1901
- The No-U-Turn Sampler:
  Hoffman and Gelman (2014). The No-U-Turn Sampler: Adaptively Setting Path Lengths in Hamiltonian Monte Carlo. https://jmlr.csail.mit.edu/papers/v15/hoffman14a.html
- Multinomial variant of NUTS:
  Betancourt (2018). A Conceptual Introduction to Hamiltonian Monte Carlo. https://arxiv.org/abs/1701.02434

Extra material for Stan

- Gelman, Lee, and Guo (2015) Stan: A probabilistic programming language for Bayesian inference and optimization. http://www.stat.columbia.edu/~gelman/research/published/stan_jebs_2.pdf
- Carpenter et al (2017). Stan: A probabilistic programming language. Journal of Statistical Software 76(1). https://dox.doi.org/10.18637/jss.v076.i01
- Stan User's Guide, Language Reference Manual, and Language Function Reference (in html and pdf) https://mc-stan.org/users/documentation/
  - easiest to start from Example Models in User's guide
- Basics of Bayesian inference and Stan, part 1 Jonah Gabry & Lauren Kennedy (StanCon 2019 Helsinki tutorial)
  - https://www.youtube.com/watch?v=ZRpo41l02KQ&index=6&list=PLuwyh42iHquU4hUBQs20hkBsKSMrp6H0J
  - https://www.youtube.com/watch?v=6cc4N1vT8pk&index=7&list=PLuwyh42iHquU4hUBQs20hkBsKSMrp6H0J

Chapter 12 demos

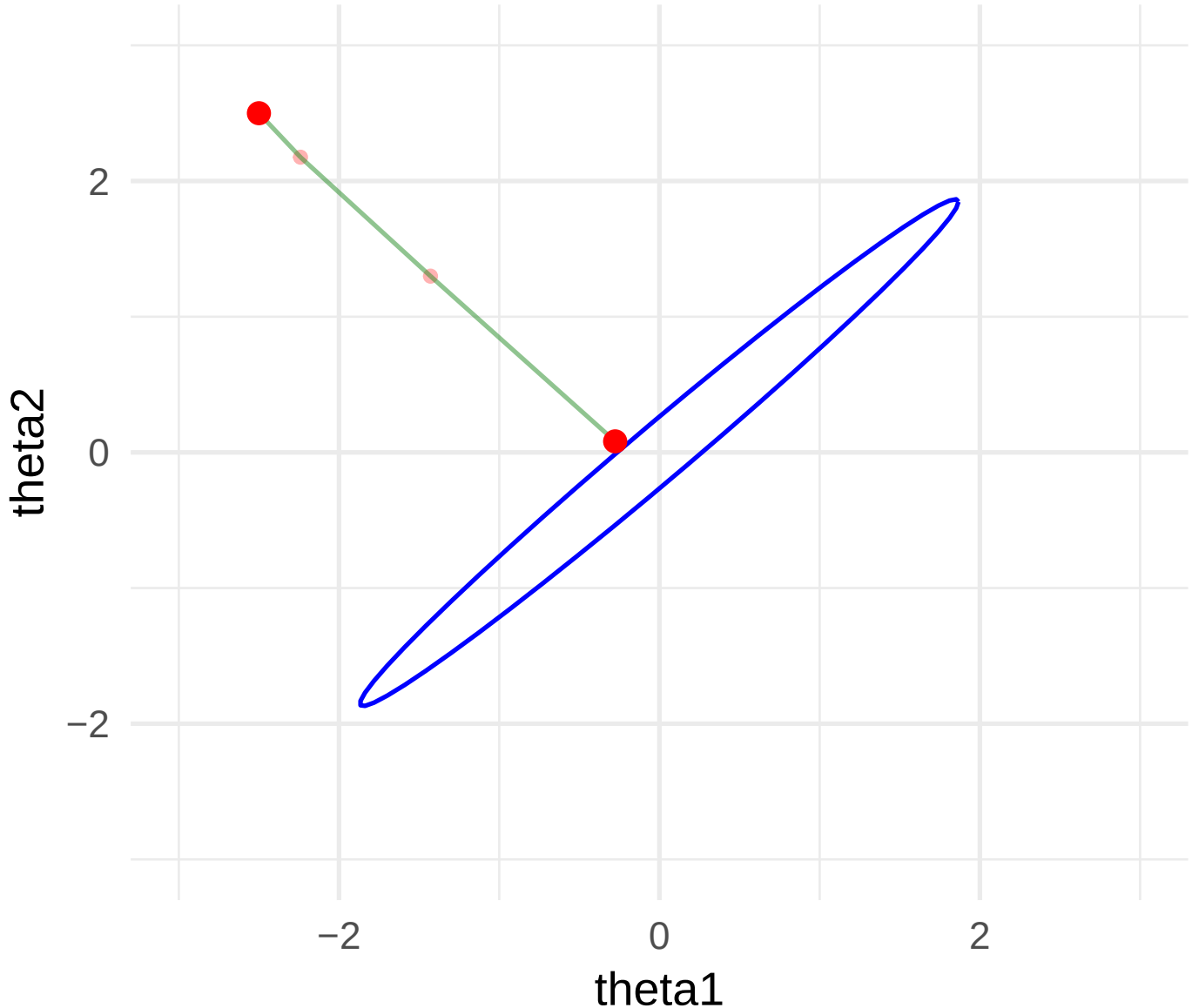
- demo12_1: HMC
- https://chi-feng.github.io/mcmc-demo/
- http://elevanth.org/blog/2017/11/28/build-a-better-markov-chain/
- cmdstanr_demo, rstan_demo
- http://sumsar.net/blog/2017/01/bayesian-computation-with-stan-and-farmer-jons/
- http://mc-stan.org/documentation/case-studies.html
- https://mc-stan.org/cmdstanr/
- https://mc-stan.org/rstan/

Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling

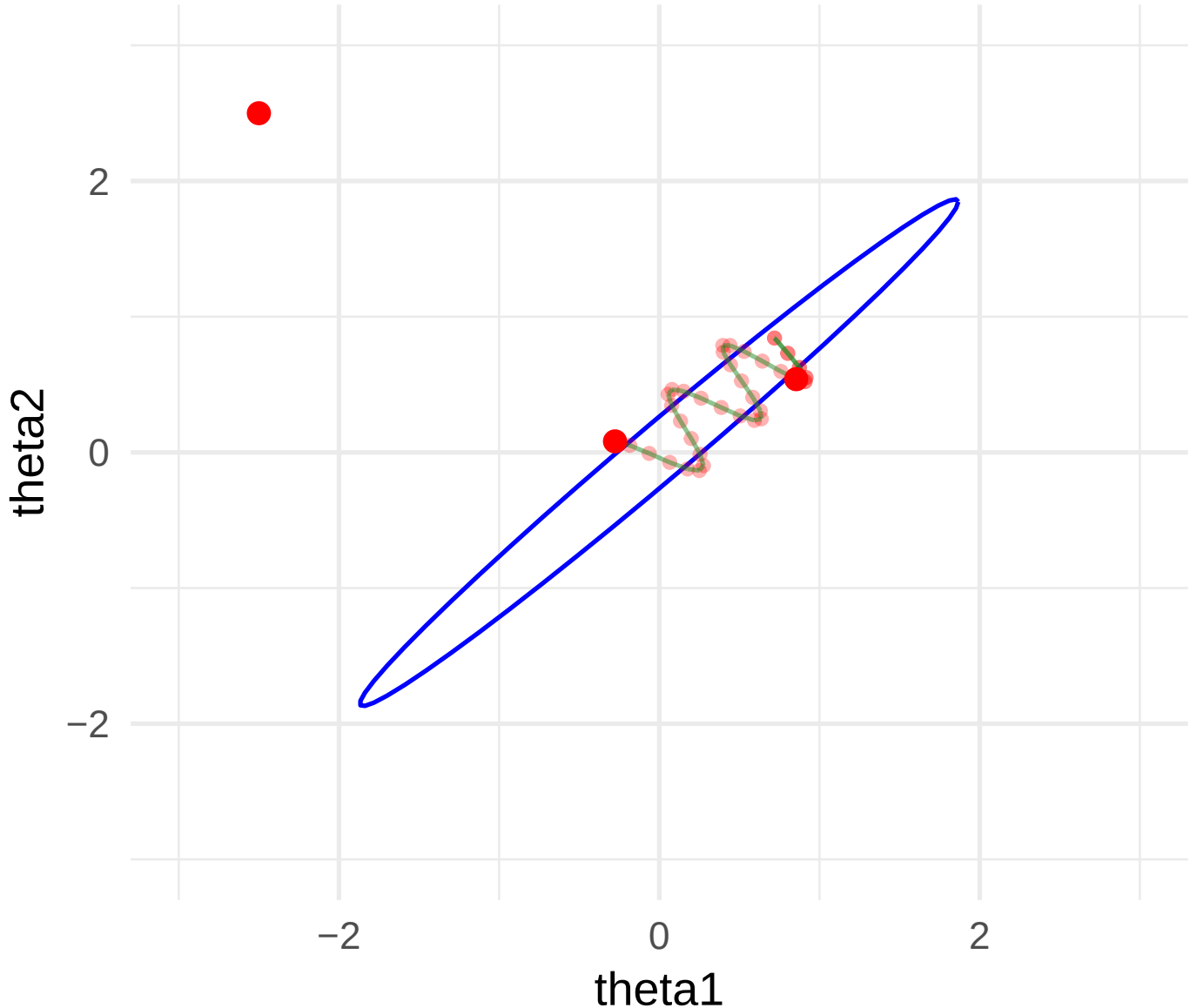
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



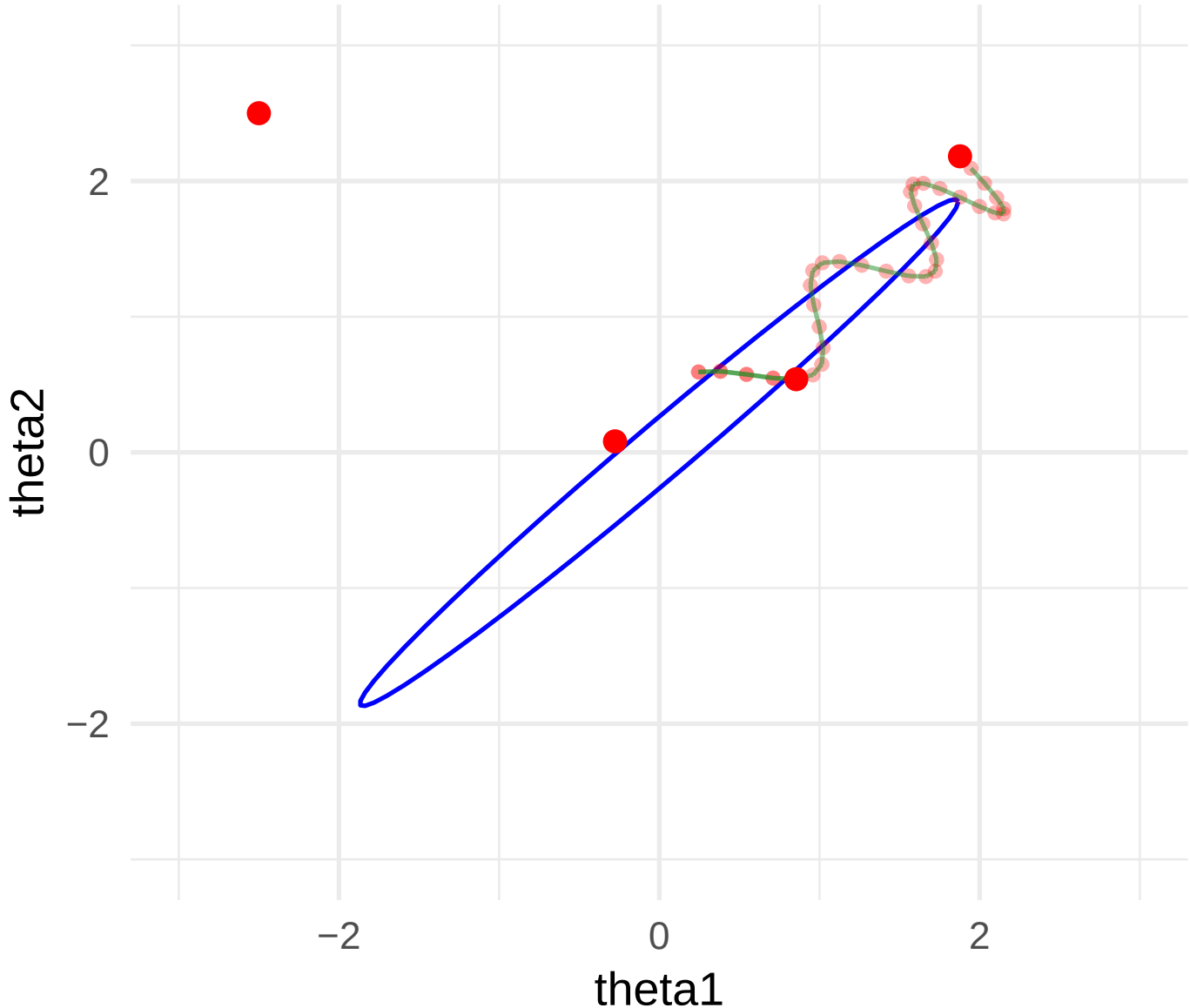
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



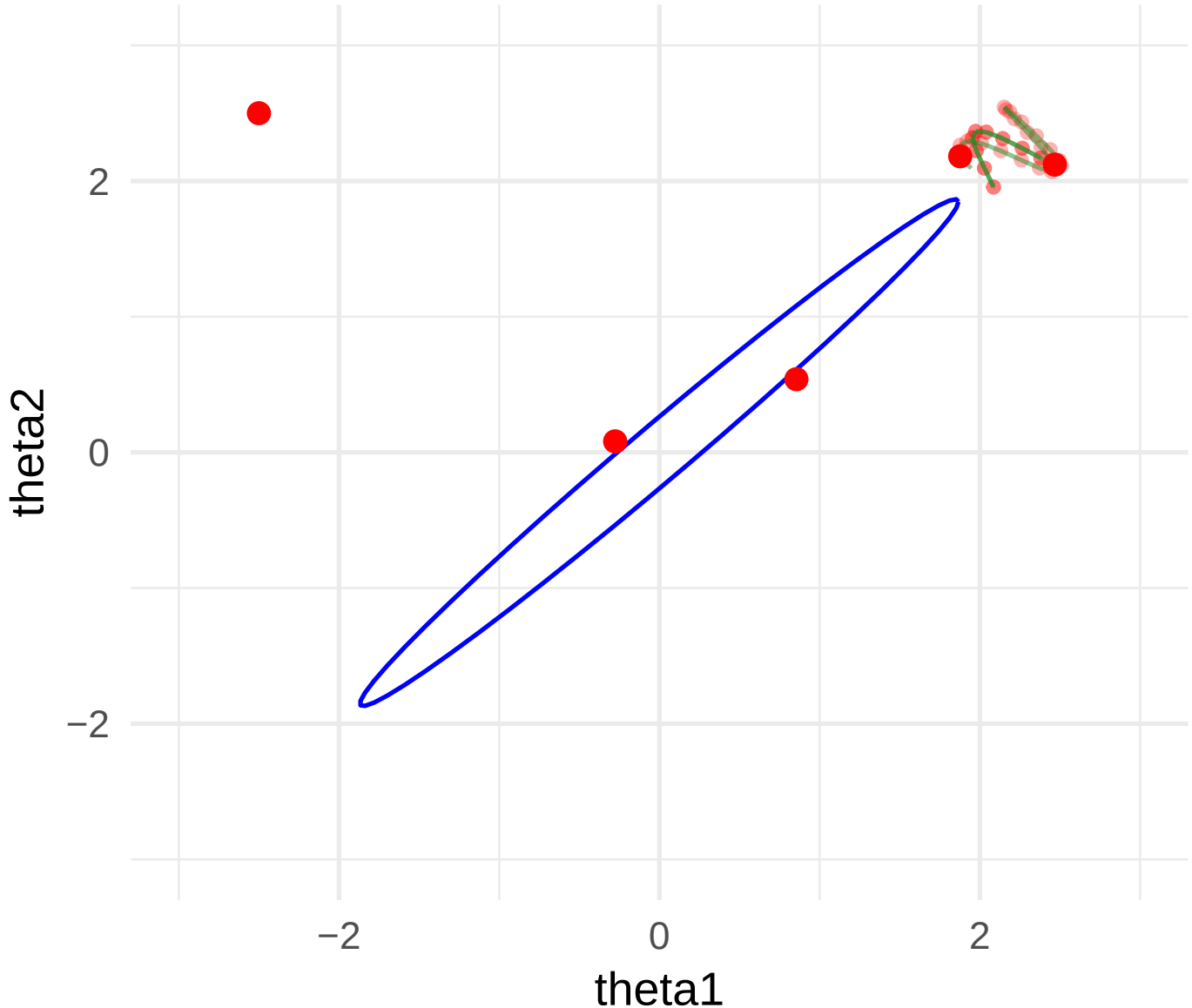
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



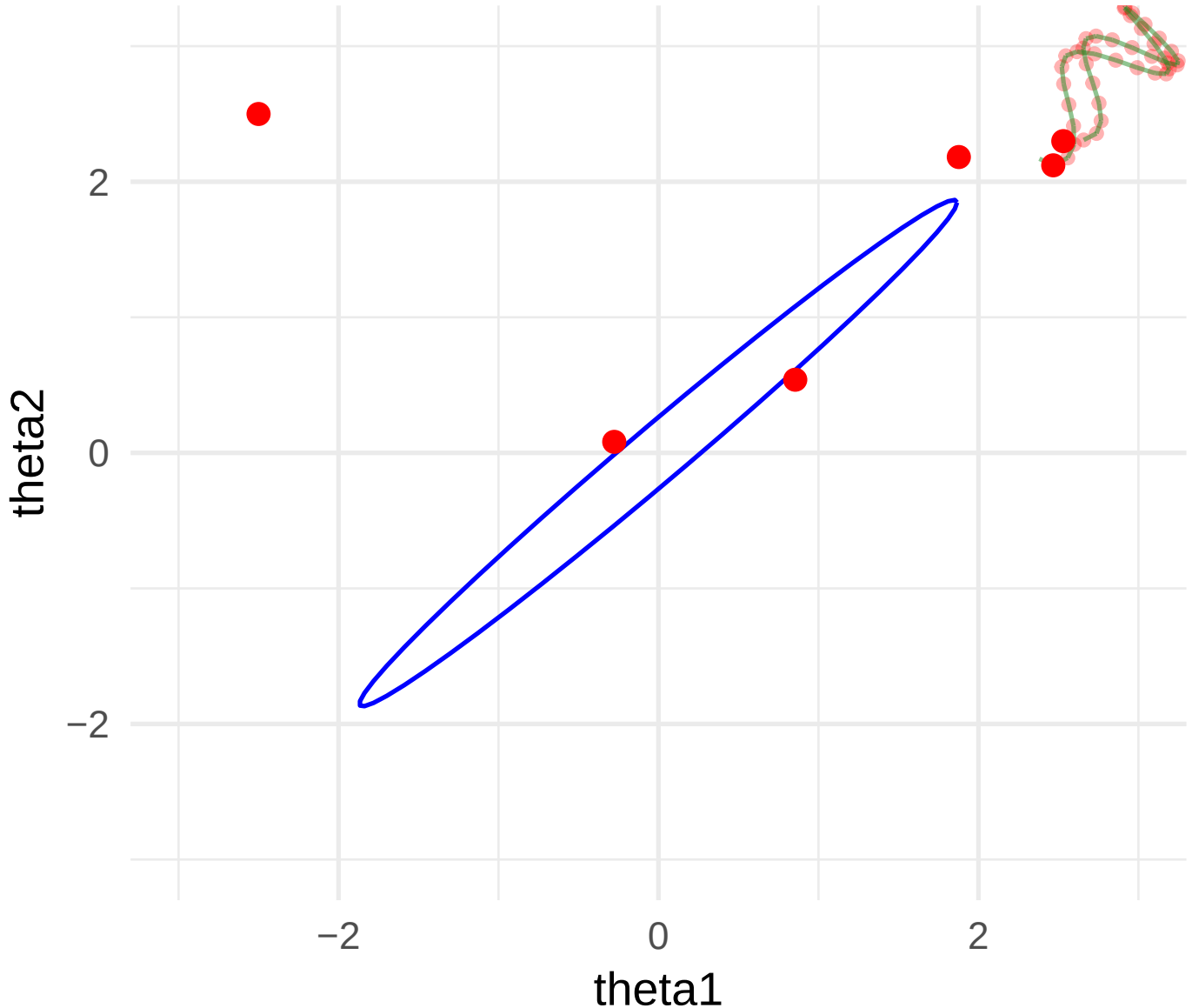
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



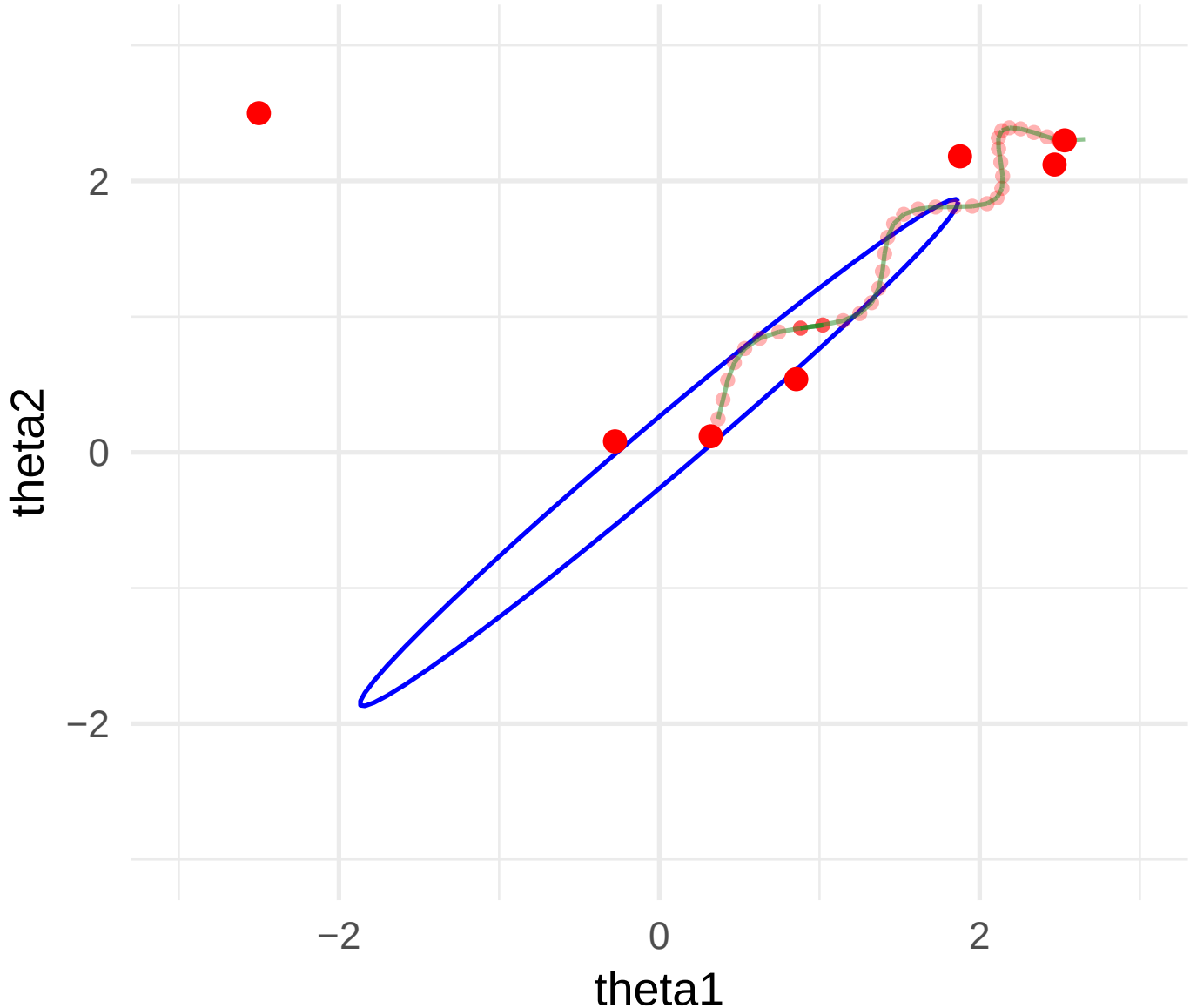
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



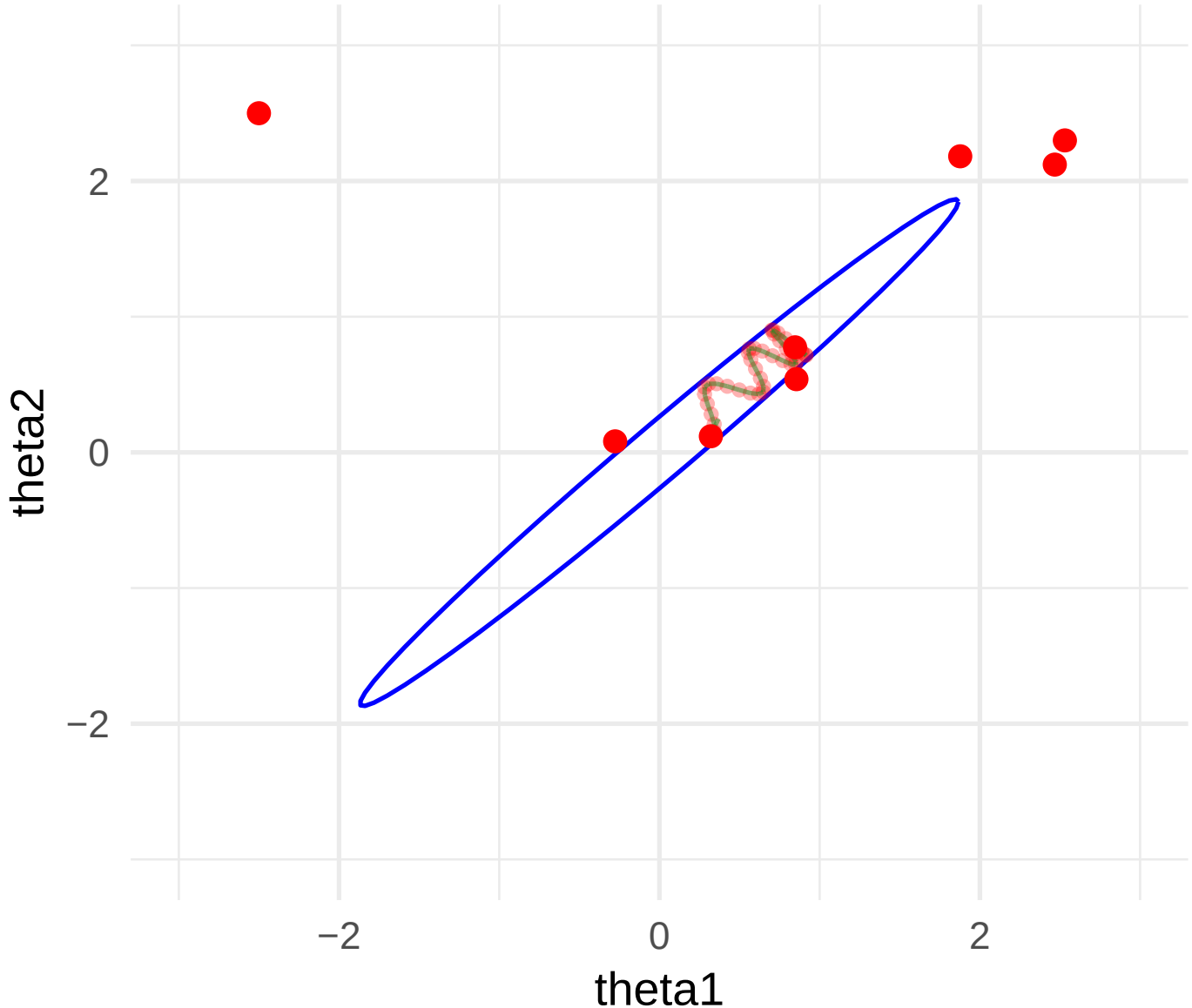
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



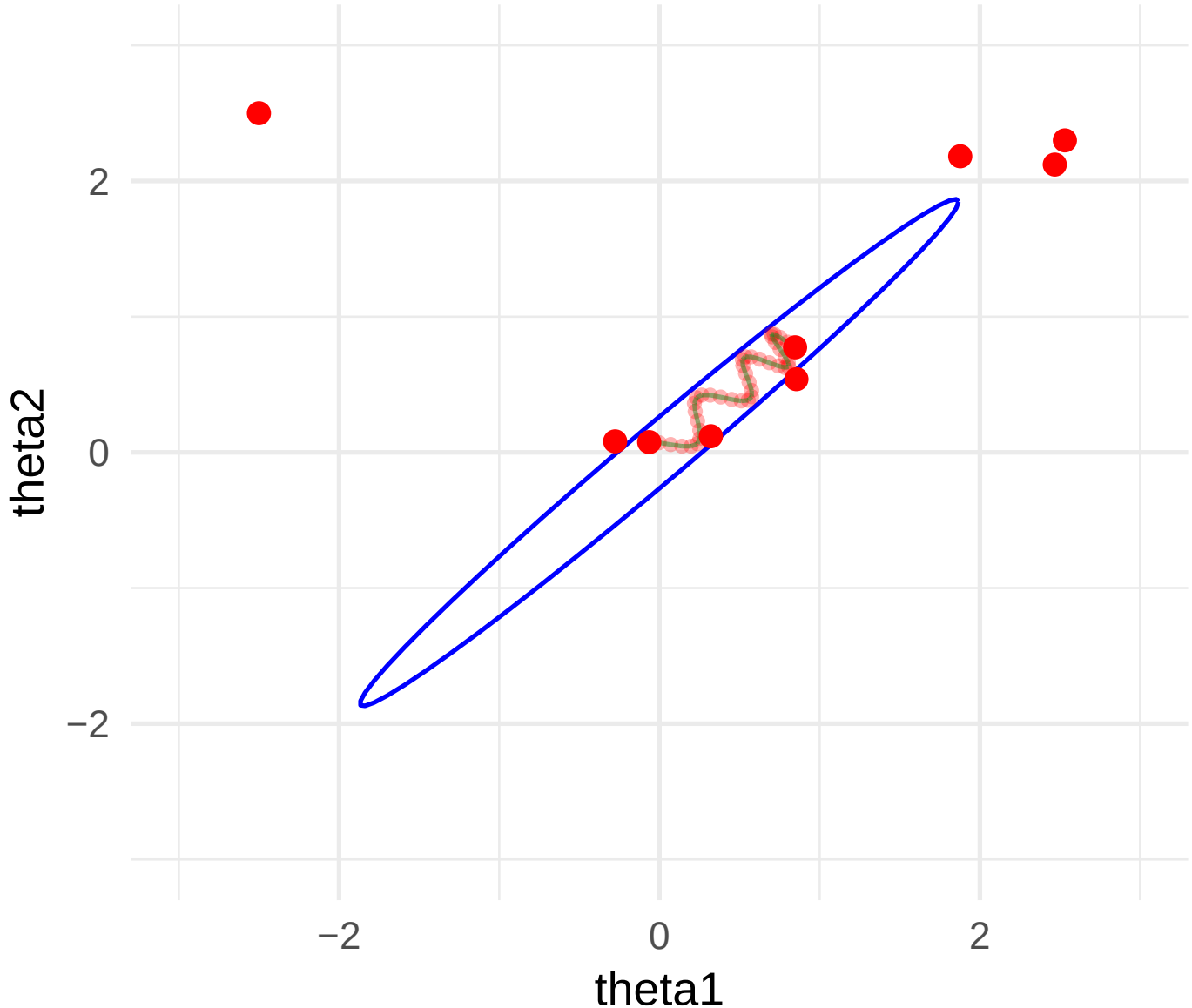
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



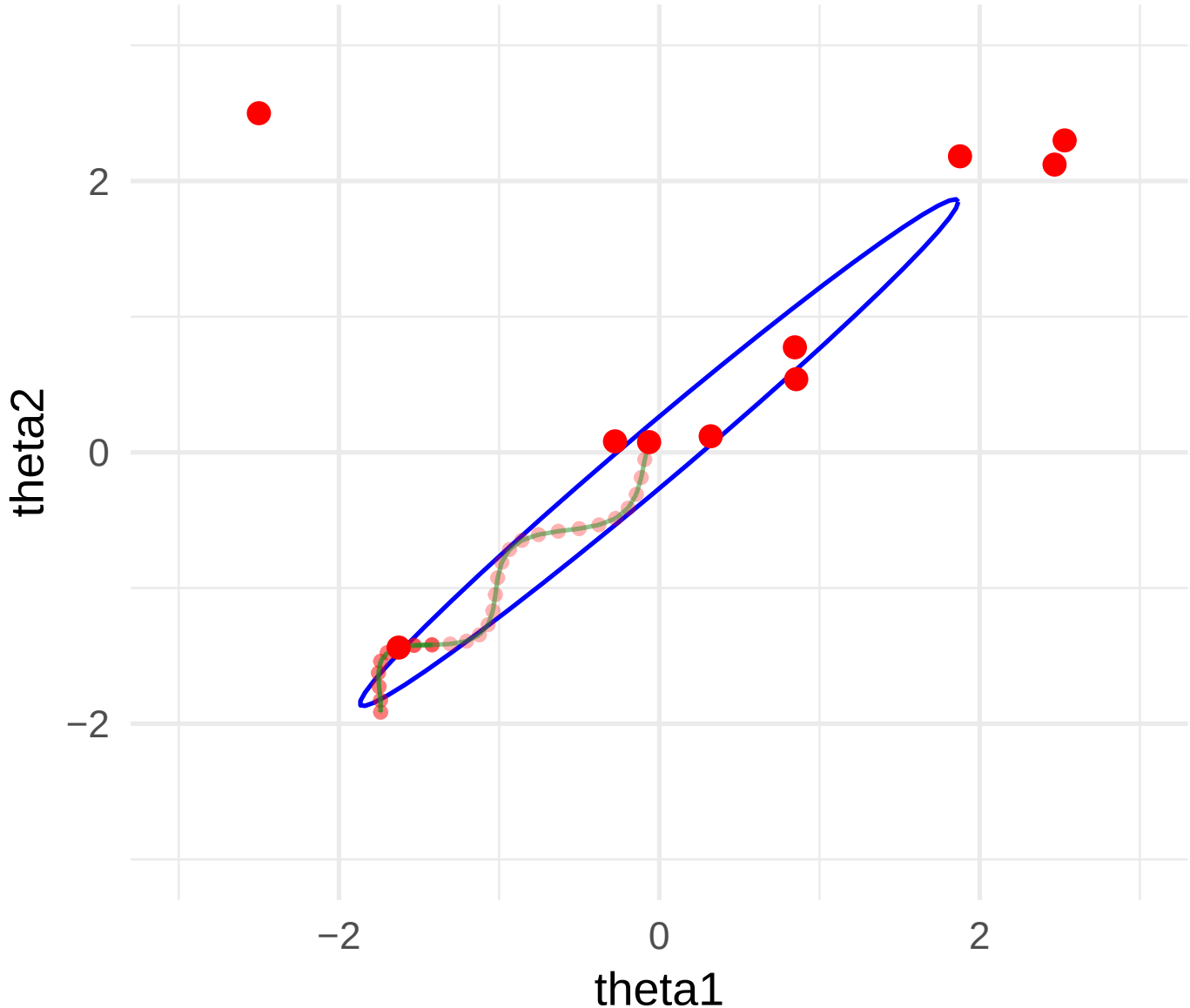
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



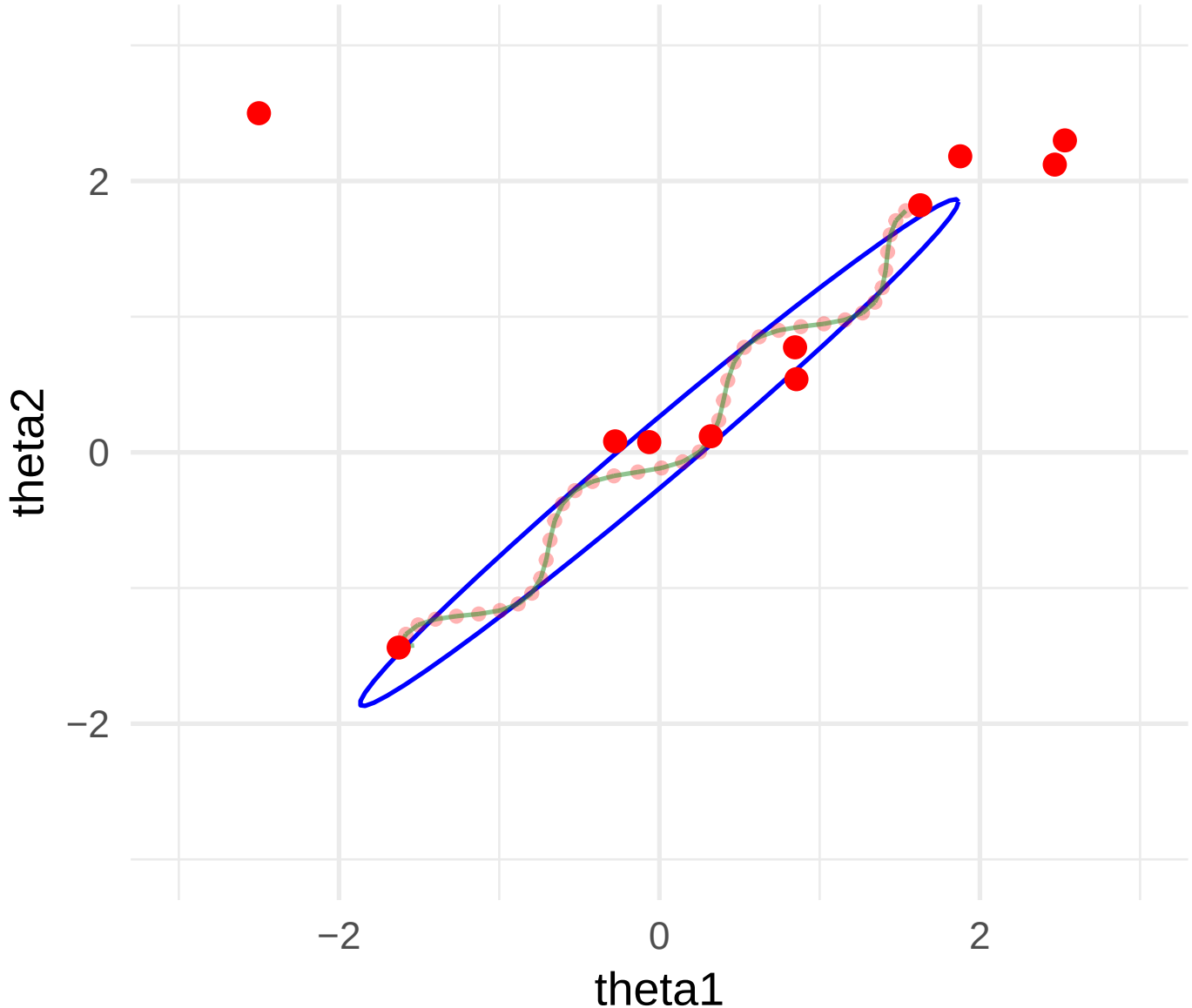
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



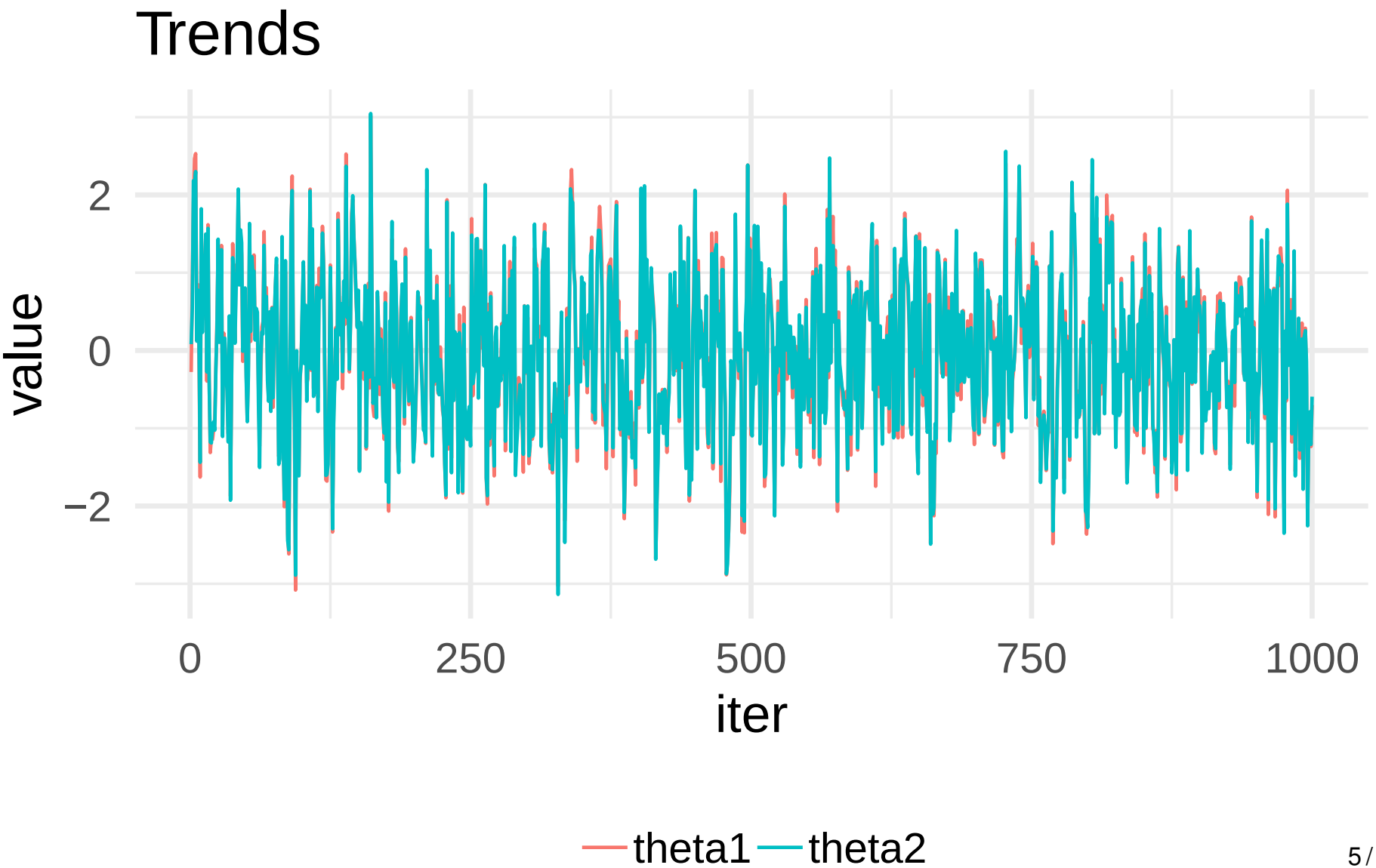
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



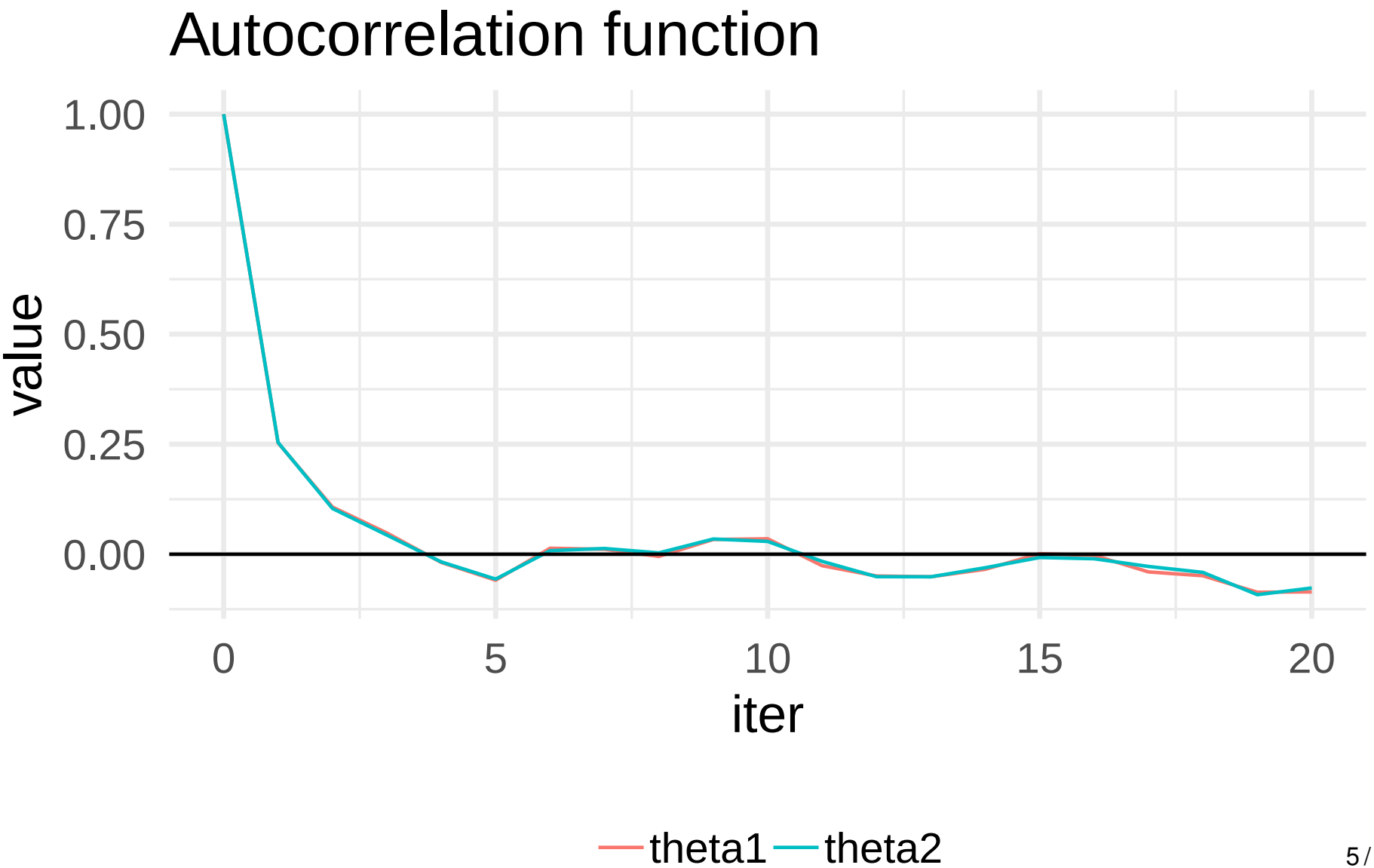
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



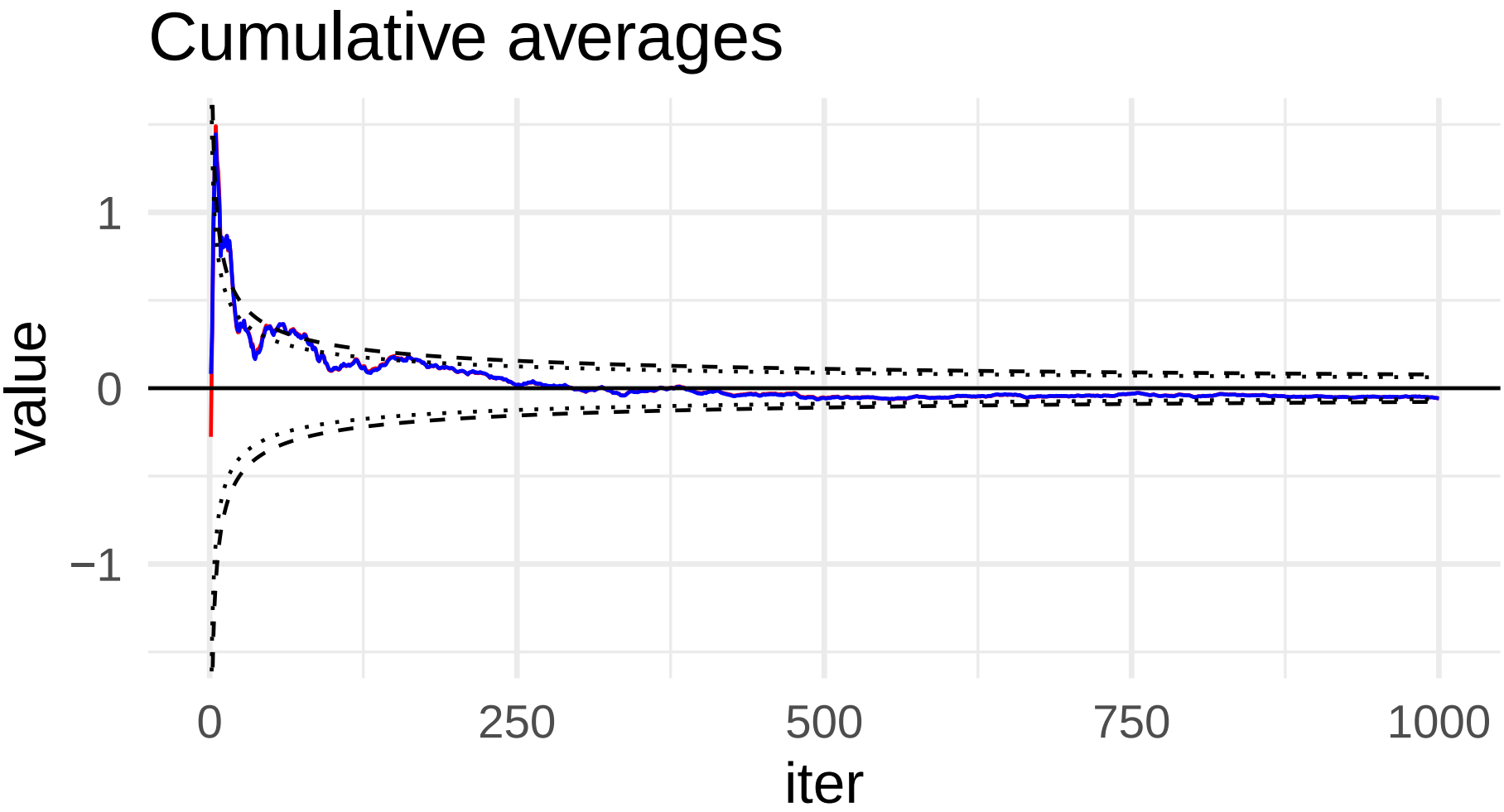
Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



Hamiltonian Monte Carlo

- Uses log density (negative log density is called energy)
- Uses gradient of log density for more efficient sampling



Hamiltonian Monte Carlo / No-U-Turn sampling

1. HMC basics (static HMC)
2. HMC + leapfrog discretization + Metropolis (static HMC)
3. NUTS + slice sampling + Metropolis (dynamic HMC)
4. NUTS + multinomial (dynamic HMC)

Hamiltonian Monte Carlo

- Previously
  - Factorizing: sample from
    1) $p(\sigma^2)$,
    2) $p(\mu \mid \sigma^2)$

Hamiltonian Monte Carlo

- Previously
  - Factorizing: sample from
    1) $p(\sigma^2)$,
    2) $p(\mu \mid \sigma^2)$
  - Gibbs: sample from
    1) $p(\sigma^2 \mid \mu)$,
    2) $p(\mu \mid \sigma^2)$

Hamiltonian Monte Carlo

- Previously
  - Factorizing: sample from
    1) $p(\sigma^2)$,
    2) $p(\mu \mid \sigma^2)$
  - Gibbs: sample from
    1) $p(\sigma^2 \mid \mu)$,
    2) $p(\mu \mid \sigma^2)$
  - Metropolis: jointly $p(\mu, \sigma)$
    jump distribution is a combination of proposal distribution and point mass at the previous value

Hamiltonian Monte Carlo

- Previously
  - Factorizing: sample from
    1) $p(\sigma^2)$,
    2) $p(\mu \mid \sigma^2)$
  - Gibbs: sample from
    1) $p(\sigma^2 \mid \mu)$,
    2) $p(\mu \mid \sigma^2)$
  - Metropolis: jointly $p(\mu, \sigma)$
    jump distribution is a combination of proposal distribution and point mass at the previous value
- HMC
  - Augment with ϕ (the same dimensionality as θ)
  - 1) sample directly from $p(\phi)$,
    2) make a special joint Metropolis step for $p(\theta, \phi) = p(\theta)p(\phi)$

Hamiltonian Monte Carlo

1) Sample from $p(\phi)$
   - define $p(\phi) = \text{normal}(0, 1)$
2) Metropolis update for $p(\theta, \phi) = p(\theta)p(\phi)$
   - proposal from Hamiltonian dynamic simulation

Hamiltonian dynamic simulation

- Statistical mechanics and canonical distribution

$$
\begin{aligned}
p(\theta, \phi) &= p(\theta)p(\phi) \\
&= \frac{1}{Z} \exp(-(U(\theta) + K(\phi))) \\
&= \frac{1}{Z} \exp(-H(\theta, \phi))
\end{aligned}
$$

where

- U is potential energy function
- K is kinetic energy function
- H is Hamiltonian energy function
- ϕ is called a momentum variable

Hamiltonian dynamic simulation

- Statistical mechanics and canonical distribution

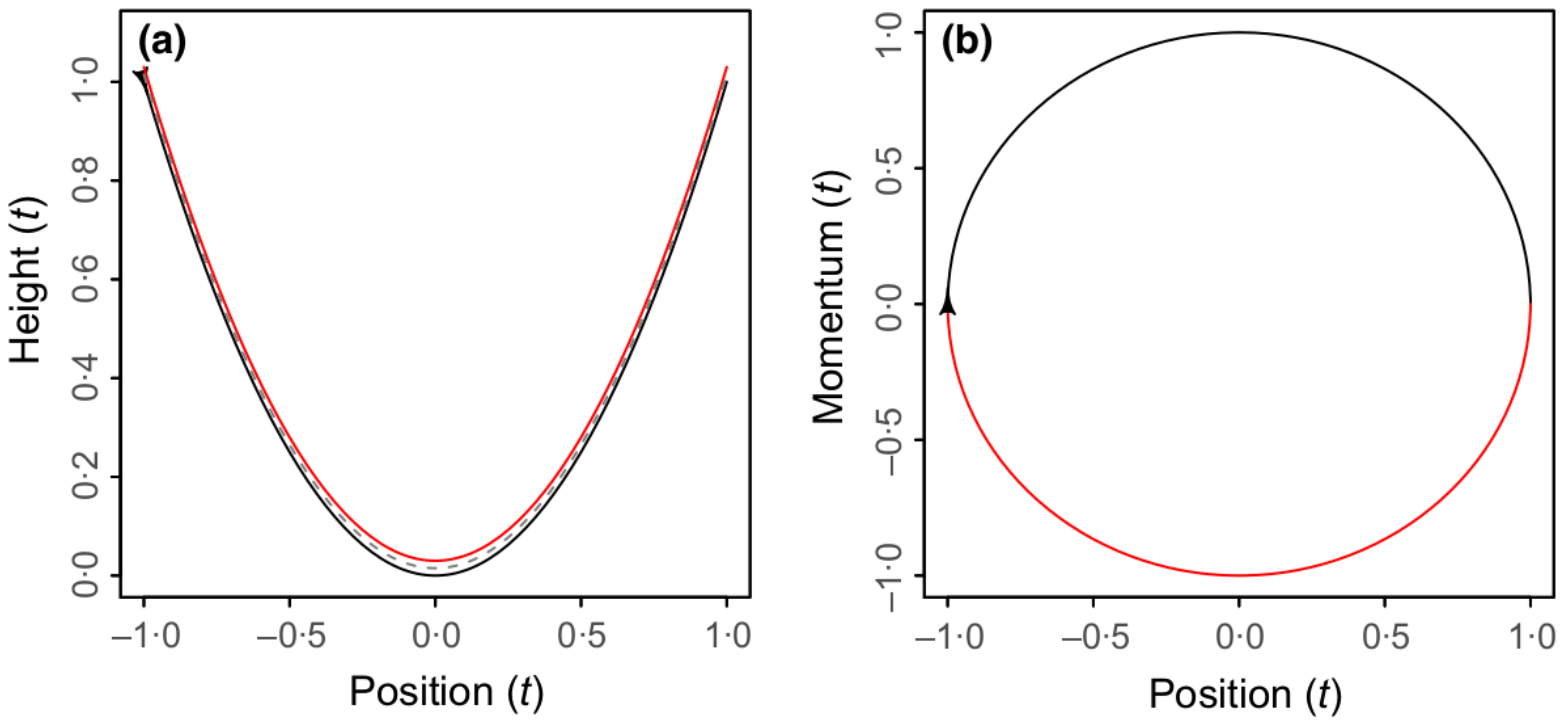
$$\begin{aligned} p(\theta, \phi) &= p(\theta)p(\phi) \\ &= \frac{1}{Z} \exp(-(U(\theta) + K(\phi))) \\ &= \frac{1}{Z} \exp(-H(\theta, \phi)) \end{aligned}$$

  where
  - U is potential energy function
  - K is kinetic energy function
  - H is Hamiltonian energy function
  - ϕ is called a momentum variable
- The potential energy is the negative log density $U(\theta) = -\log(p(\theta)) + C$

Hamiltonian dynamic simulation

Equations of motion, use also the gradient

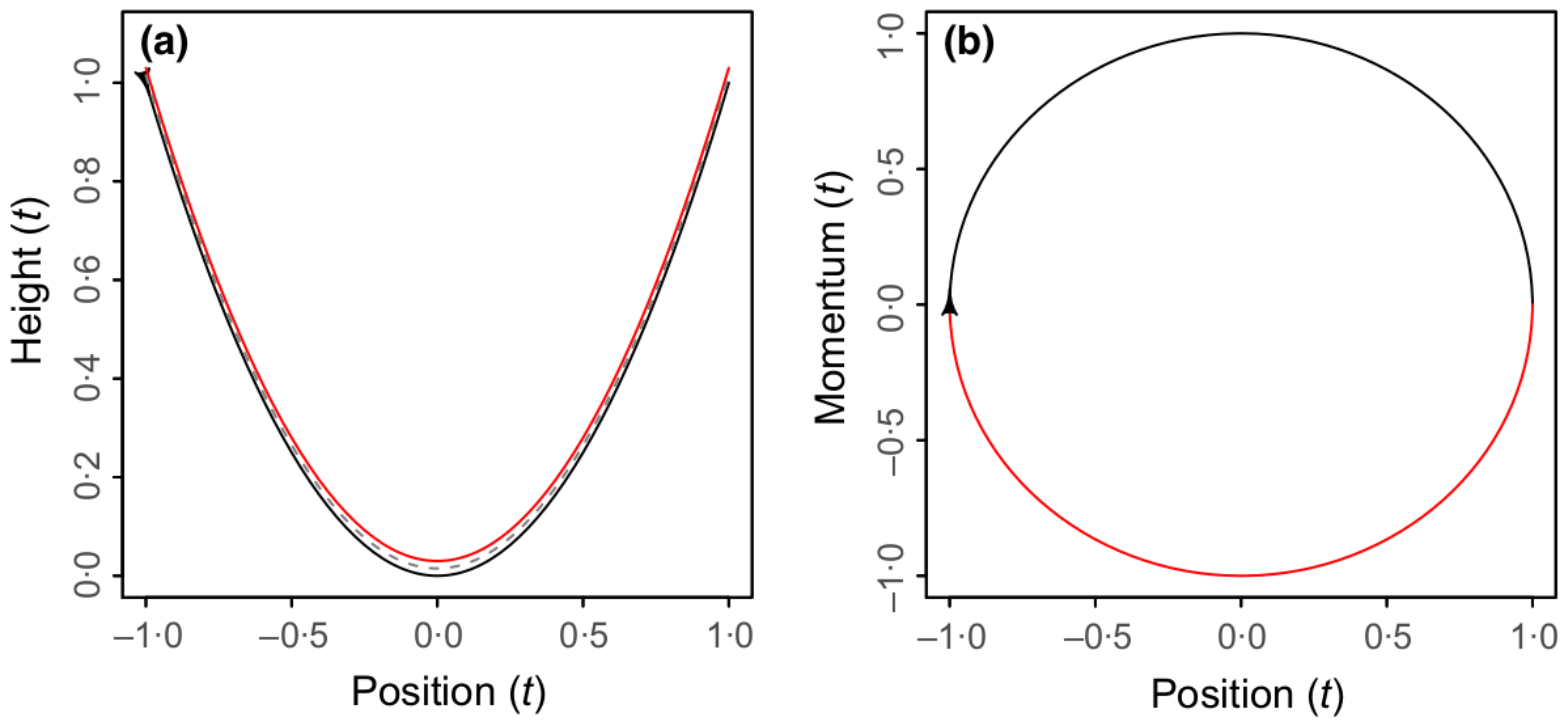
$$\frac{d\theta_i}{dt} = \frac{\partial H}{\partial \phi_i}$$
$$\frac{d\phi_i}{dt} = -\frac{\partial H}{\partial \theta_i}$$



From Monnahan et al (2017)

Hamiltonian Monte Carlo

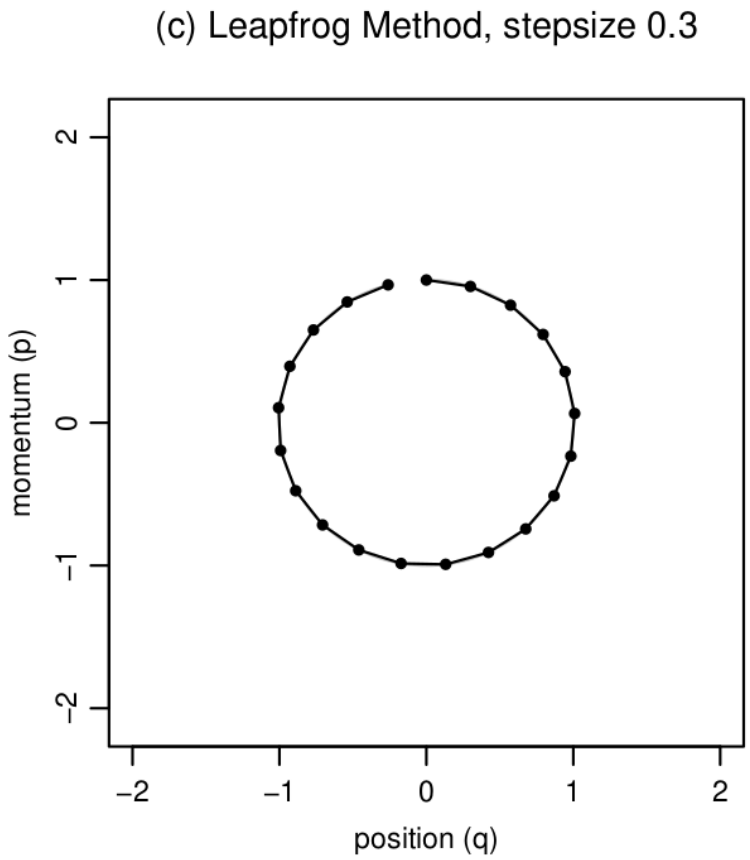
1) Sample from $p(\phi)$
   - define $p(\phi) = \text{normal}(0, 1)$
2) Metropolis update for $p(\theta, \phi) = p(\theta)p(\phi)$
   - proposal from Hamiltonian dynamic simulation $p(\theta, \phi) \propto \exp(-H(\theta, \phi))$



From Monnahan et al (2017)

Leapfrog discretization

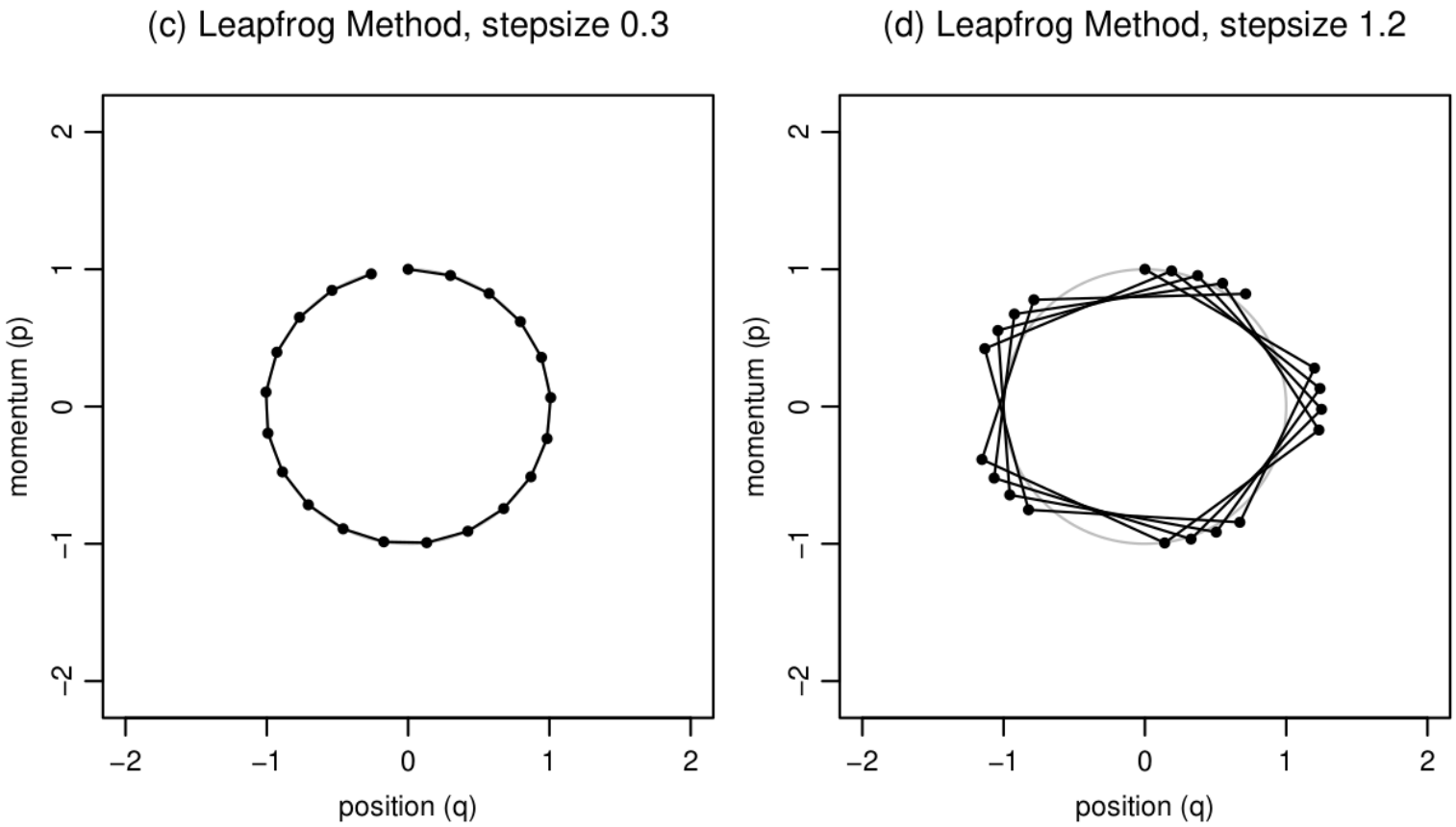
- Leapfrog discretization
  - preserves volume
  - reversible
  - discretization error does not usually grow in time



From Neal (2012)

Leapfrog discretization

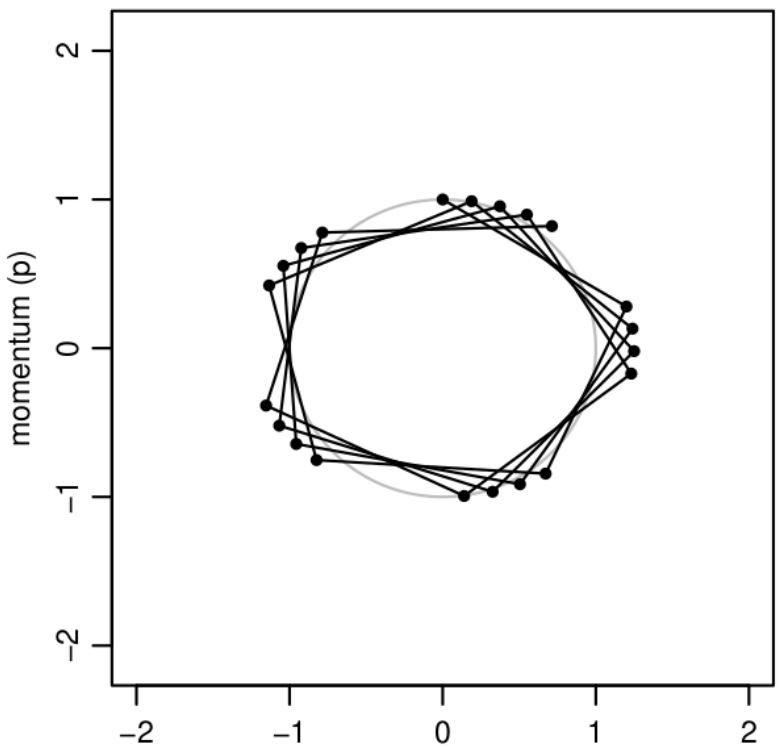
- Leapfrog discretization
  - preserves volume
  - reversible
  - discretization error does not usually grow in time



From Neal (2012)

Leapfrog discretization + Metropolis

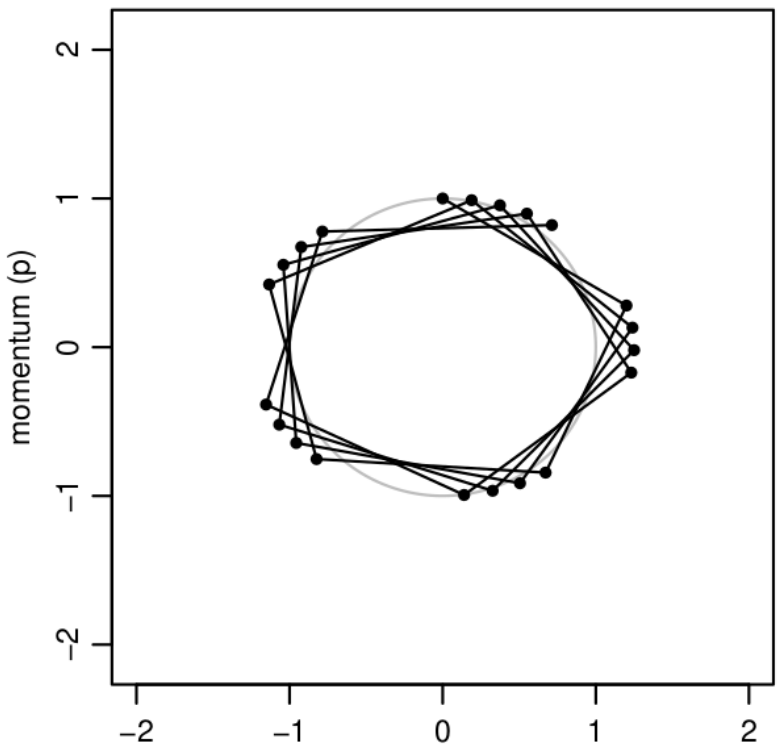
- Leapfrog discretization
  - due to the dicretization error the simulation steps away from the constant contour



Leapfrog discretization + Metropolis

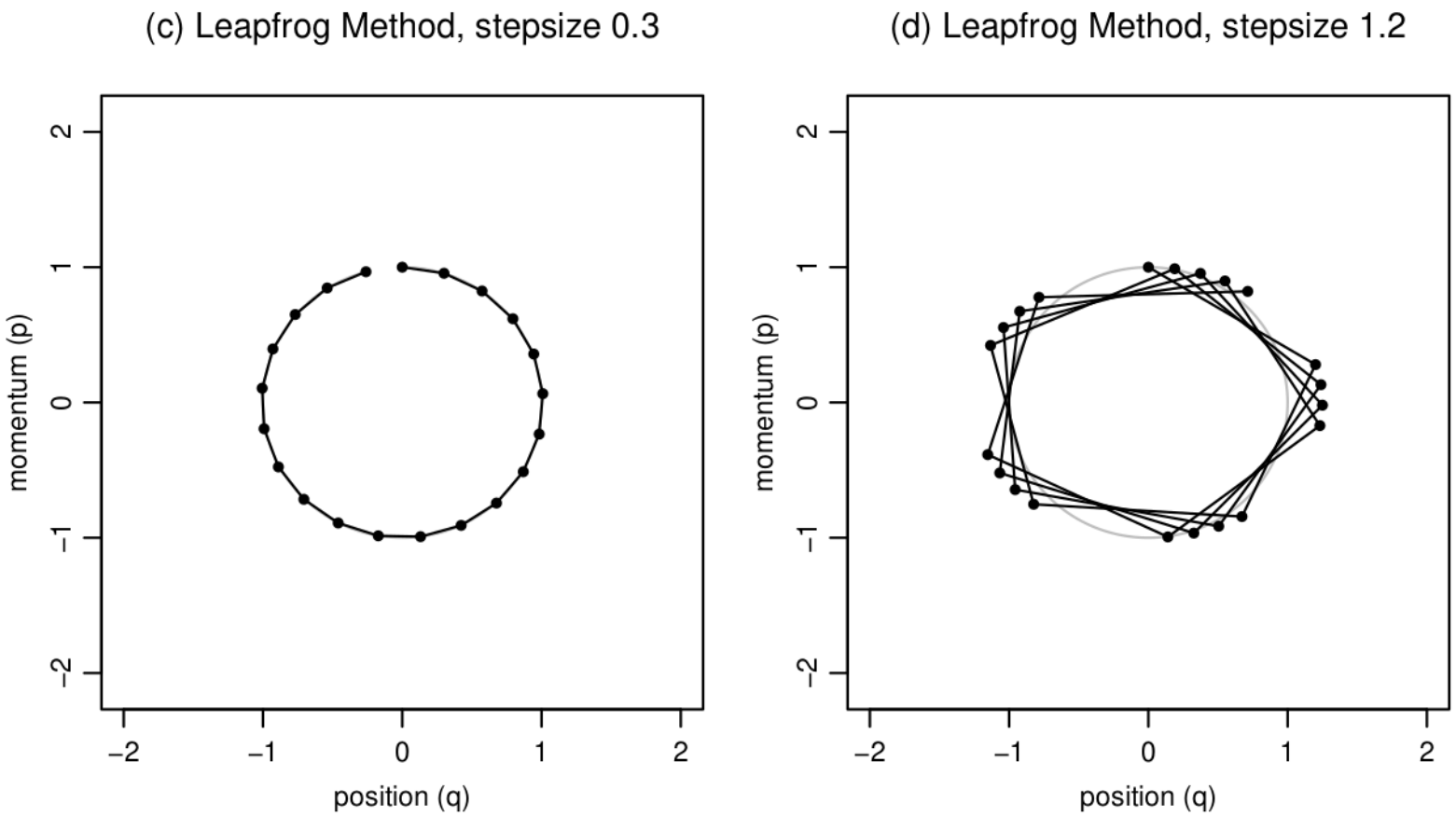
- Leapfrog discretization
  - due to the dicretization error the simulation steps away from the constant contour
- Metropolis step with

  $r = \exp\left(-H(\theta^*, \phi^*) + H(\theta^{(t-1)}, \phi^{(t-1)})\right)$
  - accept if the Hamiltonian energy in the end is higher
  - accept with some probability if the Hamiltonian energy in the end is lower



Two steps of Hamiltonian Monte Carlo

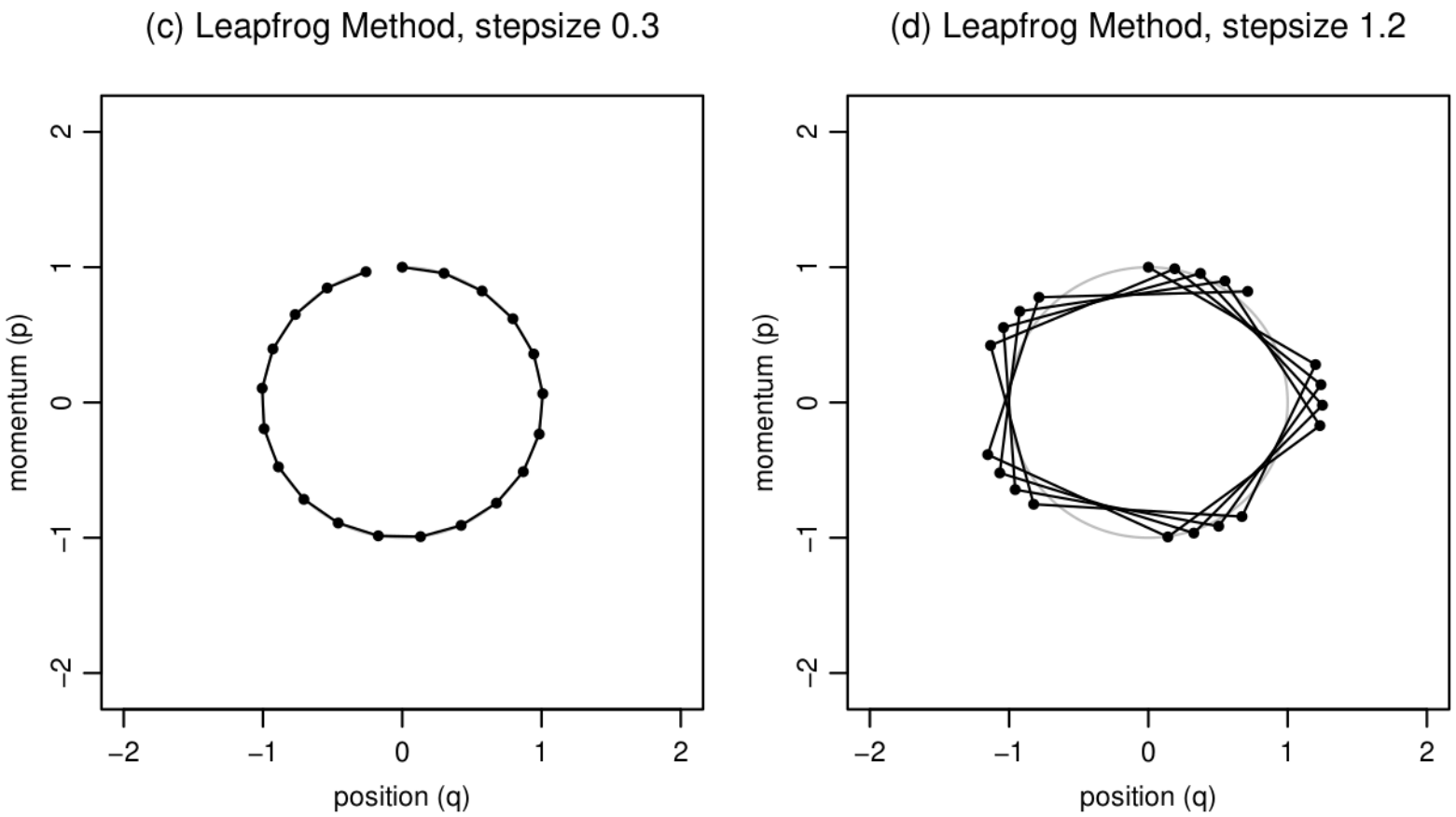
- Perfect simulation keeps $p(\theta, \phi)$ constant



From Neal (2012)

Two steps of Hamiltonian Monte Carlo

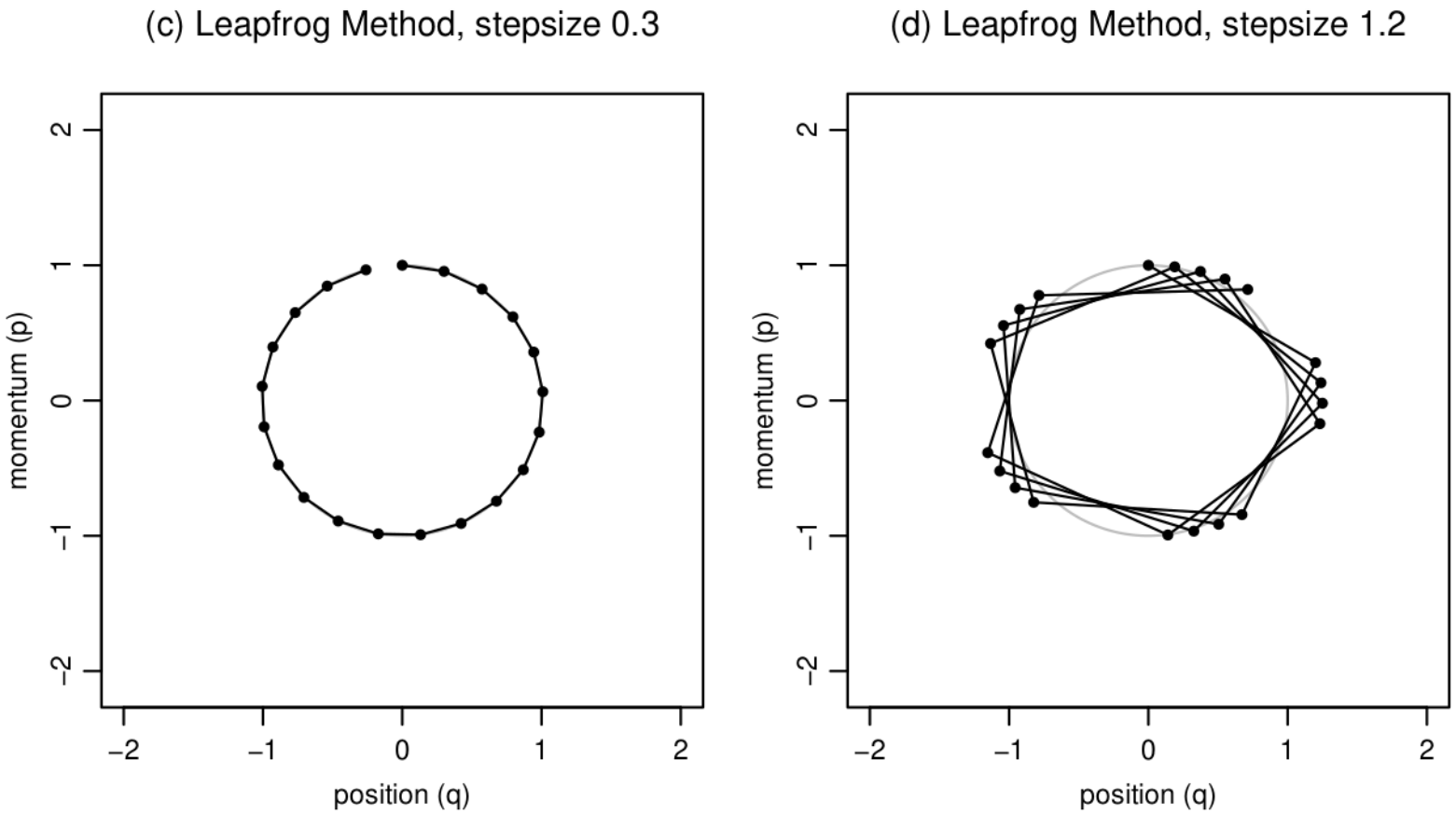
- Perfect simulation keeps $p(\theta, \phi)$ constant
- Discretized simulation keeps changes in $p(\theta, \phi)$ small



From Neal (2012)

Two steps of Hamiltonian Monte Carlo

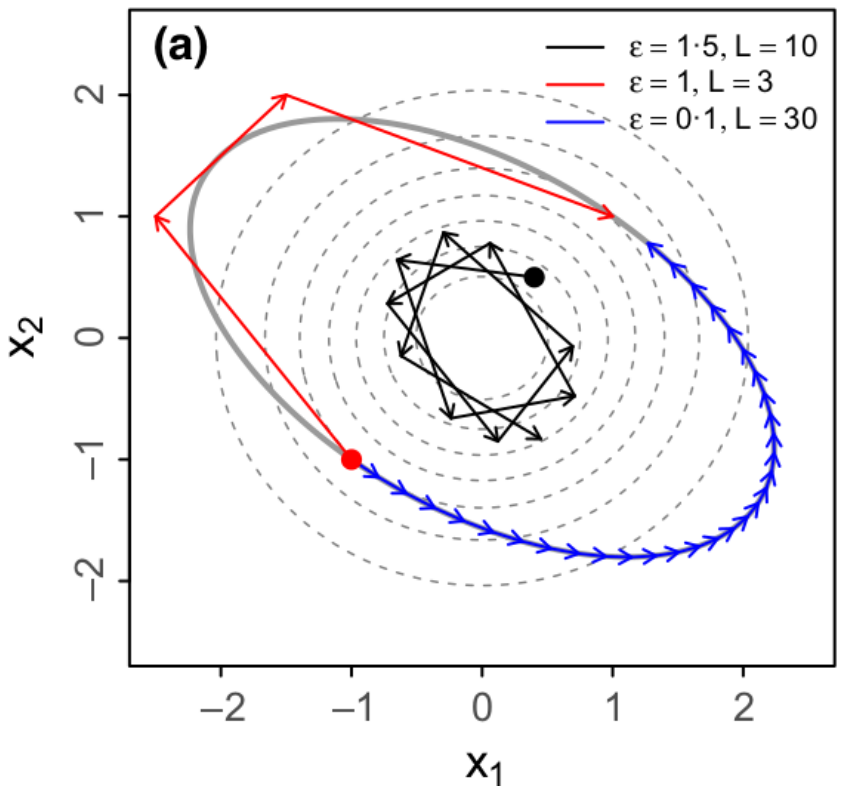
- Perfect simulation keeps $p(\theta, \phi)$ constant
- Discretized simulation keeps changes in $p(\theta, \phi)$ small
- Alternating sampling from $p(\phi)$ is crucial for moving to (θ, ϕ) points with different joint density



From Neal (2012)

Leapfrog discretization, step size

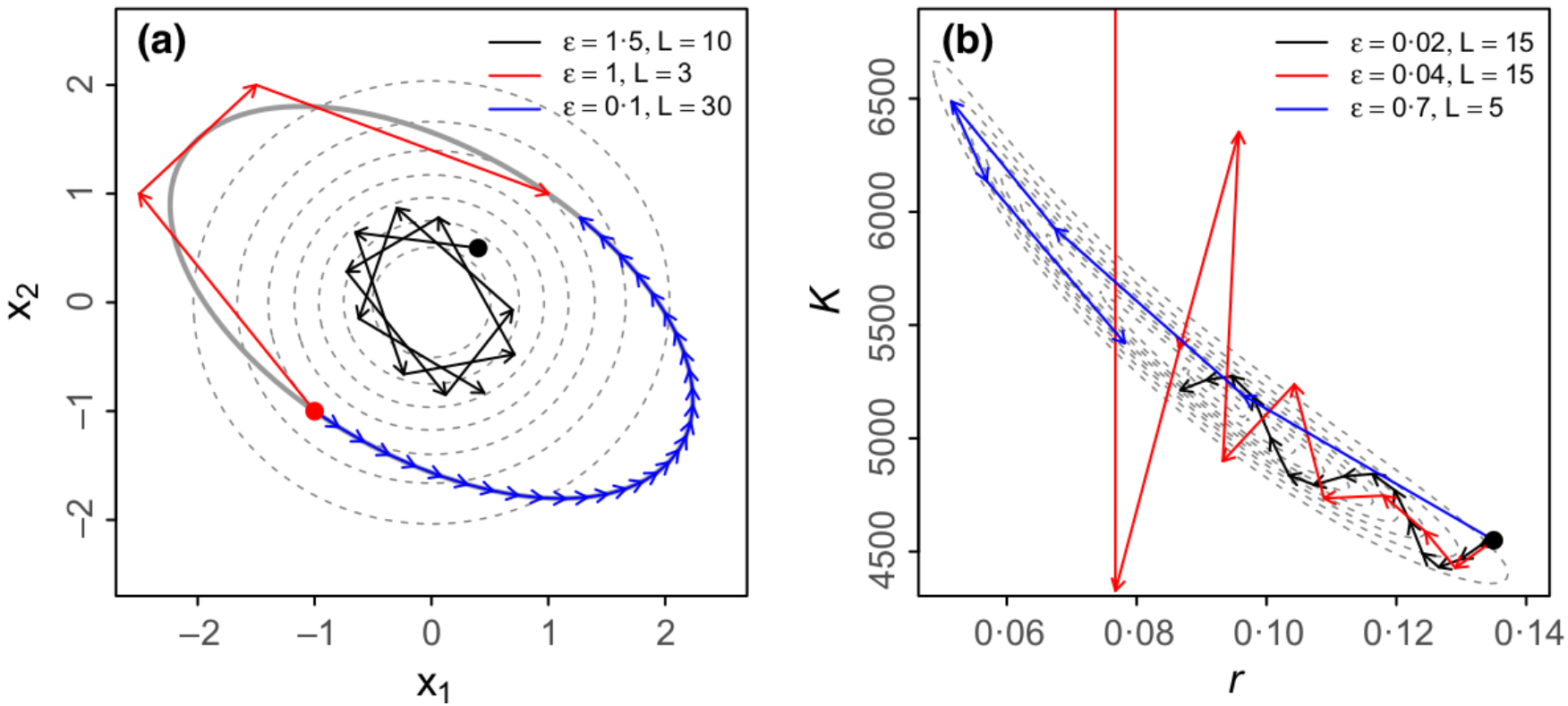
- Small step size $\rightarrow$ high acceptance rate, but many log density and gradient evaluations
- Big step size $\rightarrow$ less log density and gradient evaluations, but lower acceptance rate



From Monnahan et al (2017)

Leapfrog discretization, step size

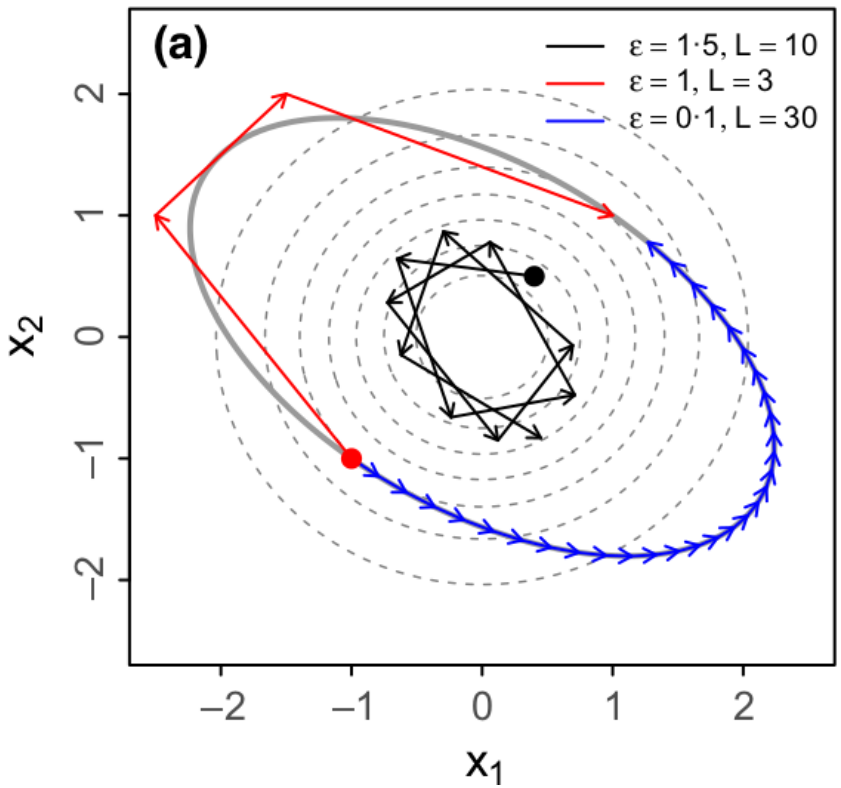
- Small step size $\rightarrow$ high acceptance rate, but many log density and gradient evaluations
- Big step size $\rightarrow$ less log density and gradient evaluations, but lower acceptance rate and the simulation may diverge



From Monnahan et al (2017)

Leapfrog discretization, the number of steps

- Many steps can reduce random walk
- Many steps require many log density and gradient evaluations



From Monnahan et al (2017)

Static Hamiltonian Monte Carlo

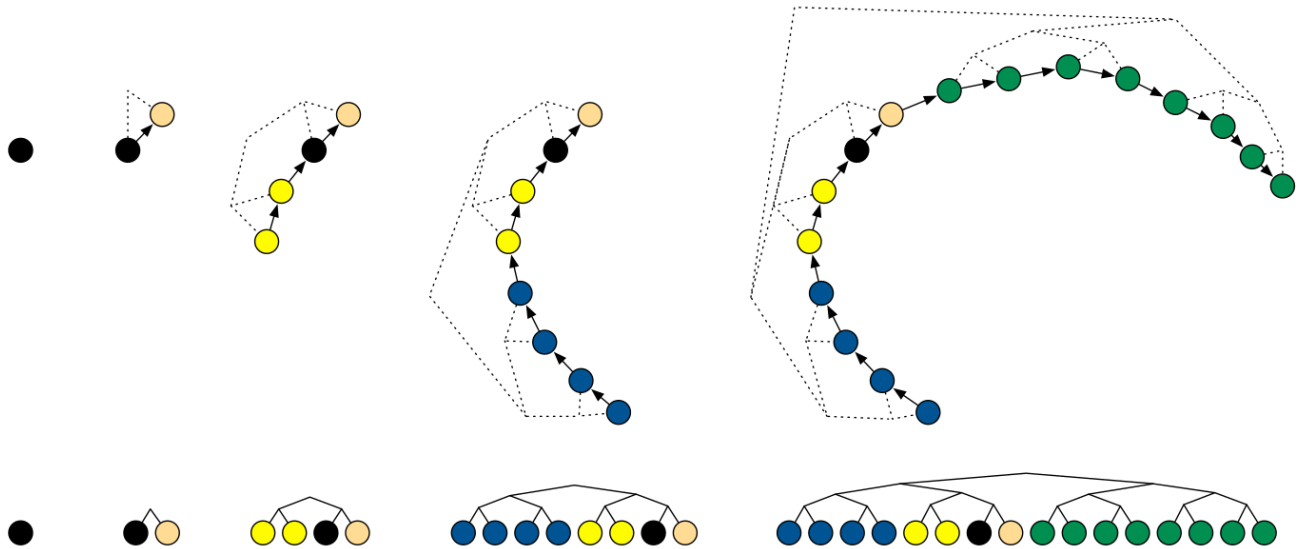
- Fixed number of steps
- Demo https://chi-feng.github.io/mcmc-demo/

No-U-Turn sampler

- Adaptively selects number of steps
  - NUTS is a dynamic HMC algorithm, where dynamic refers to the dynamic trajectory length

No-U-Turn sampler

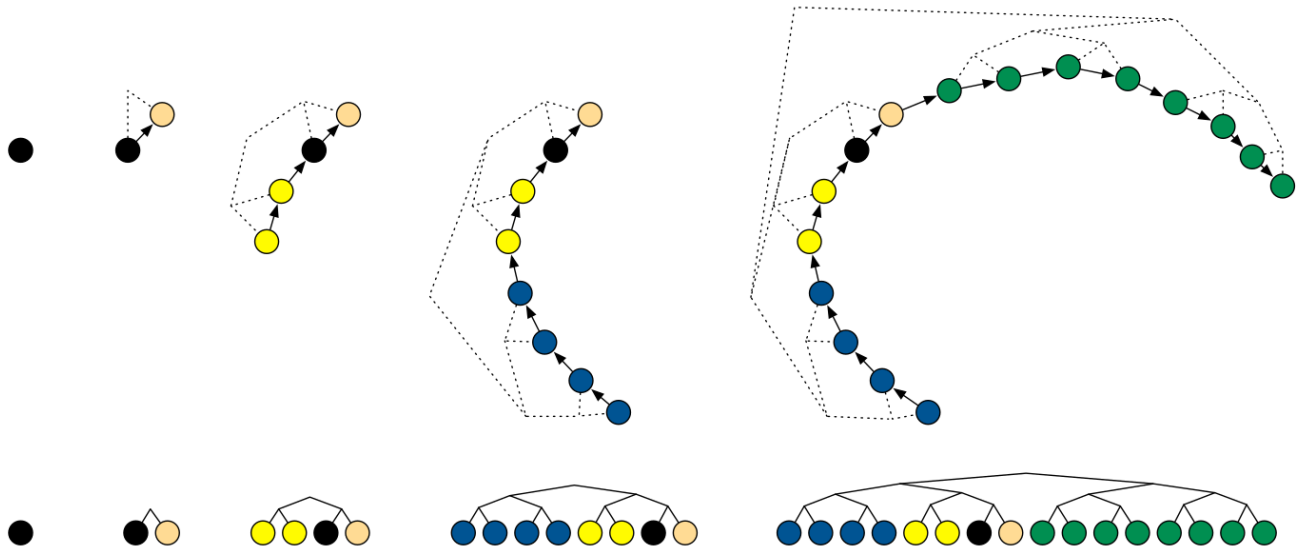
- Adaptively selects number of steps
  - NUTS is a dynamic HMC algorithm, where dynamic refers to the dynamic trajectory length
  - simulate until a U-turn is detected
  - the number of simulation steps doubled if no U-turn yet



from Hoffman & Gelman (2014)

No-U-Turn sampler

- Adaptively selects number of steps
  - NUTS is a dynamic HMC algorithm, where dynamic refers to the dynamic trajectory length
  - simulate until a U-turn is detected
  - the number of simulation steps doubled if no U-turn yet



from Hoffman & Gelman (2014)

- To keep reversibility of Markov chain
  - need to simulate in two directions
  - choose a point along the simulation path with slice sampling
  - Metropolis acceptance step for the selected point

No-U-Turn sampler

- Adaptively selects number of steps
  - NUTS is a dynamic HMC algorithm, where dynamic refers to the dynamic trajectory length
  - simulate until a U-turn is detected
  - the number of simulation steps doubled if no U-turn yet
- To keep reversibility of Markov chain
  - need to simulate in two directions
  - choose a point along the simulation path with slice sampling
  - Metropolis acceptance step for the selected point
- For further efficiency
  - simulation path parts further away from the starting point can have higher probability
  - max treedepth to keep computation in control

No-U-Turn sampler

- Adaptively selects number of steps
  - NUTS is a dynamic HMC algorithm, where dynamic refers to the dynamic trajectory length
  - simulate until a U-turn is detected
  - the number of simulation steps doubled if no U-turn yet
- To keep reversibility of Markov chain
  - need to simulate in two directions
  - choose a point along the simulation path with slice sampling
  - Metropolis acceptance step for the selected point
- For further efficiency
  - simulation path parts further away from the starting point can have higher probability
  - max treedepth to keep computation in control
- Demo https://chi-feng.github.io/mcmc-demo/

No-U-Turn sampler with multinomial sampling

- Original NUTS
  - choose a point along the simulation path with slice sampling
  - possibly with bigger weighting for further points
  - Metropolis acceptance step for the selected point
  - if the proposal is rejected the previous state is also the new state

No-U-Turn sampler with multinomial sampling

- Original NUTS
  - choose a point along the simulation path with slice sampling
  - possibly with bigger weighting for further points
  - Metropolis acceptance step for the selected point
  - if the proposal is rejected the previous state is also the new state
- NUTS with multinomial sampling
  - compute the probability of selecting a point and accepting it for all points
  - select the point with multinomial sampling
  - more likely to accept a point that is not the previous one

No-U-Turn sampler with multinomial sampling

- Original NUTS
  - choose a point along the simulation path with slice sampling
  - possibly with bigger weighting for further points
  - Metropolis acceptance step for the selected point
  - if the proposal is rejected the previous state is also the new state
- NUTS with multinomial sampling
  - compute the probability of selecting a point and accepting it for all points
  - select the point with multinomial sampling
  - more likely to accept a point that is not the previous one
- Demo https://chi-feng.github.io/mcmc-demo/

Mass matrix and the step size adaptation

- Mass matrix refers to having different scaling for different parameters and optionally also rotation to reduce correlations
  - mass matrix is estimated during the adaptation phase of the warm-up
  - mass matrix is estimated using the draws so far

Mass matrix and the step size adaptation

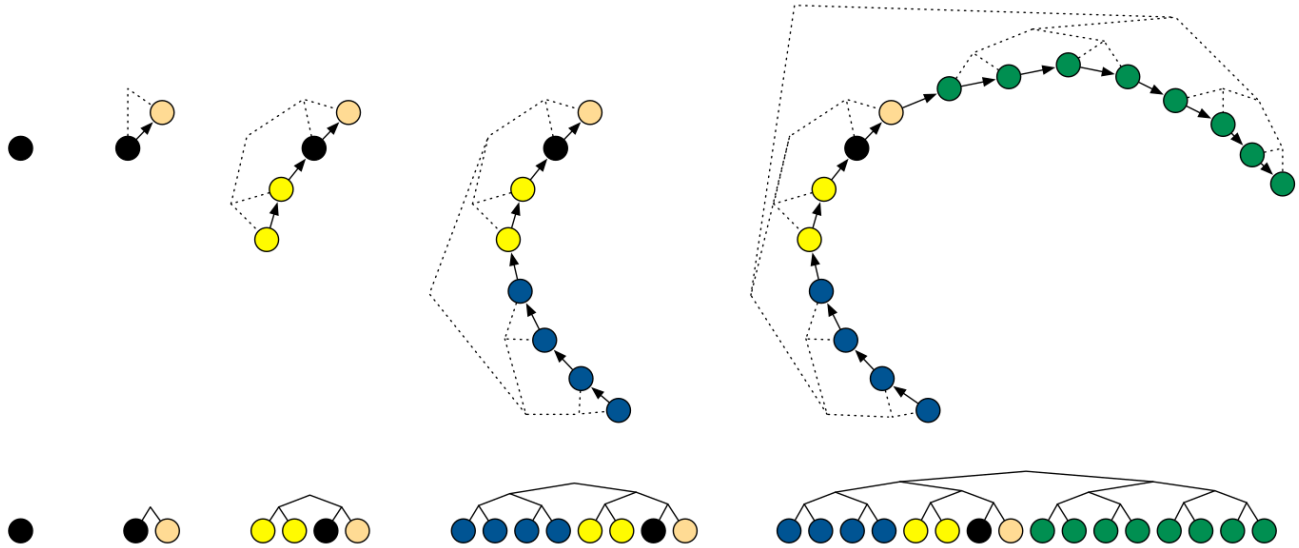
- Mass matrix refers to having different scaling for different parameters and optionally also rotation to reduce correlations
  - mass matrix is estimated during the adaptation phase of the warm-up
  - mass matrix is estimated using the draws so far
- Step size
  - adjusted to be as big as possible while keeping discretization error in control (adapt_delta)
  - “Dual averaging” demo https://chi-feng.github.io/mcmc-demo/

Mass matrix and the step size adaptation

- Mass matrix refers to having different scaling for different parameters and optionally also rotation to reduce correlations
  - mass matrix is estimated during the adaptation phase of the warm-up
  - mass matrix is estimated using the draws so far
- Step size
  - adjusted to be as big as possible while keeping discretization error in control (adapt_delta)
  - “Dual averaging” demo https://chi-feng.github.io/mcmc-demo/
- After adaptation the algorithm parameters are fixed and some more iterations run to finish the warmup

Max tree depth diagnostic

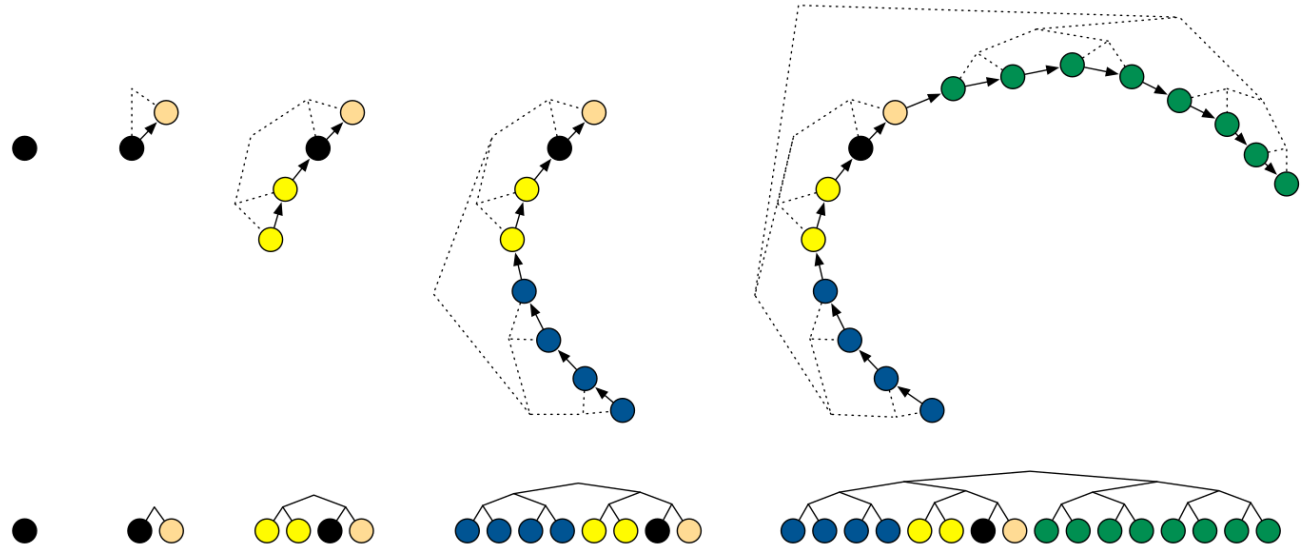
- NUTS specific diagnostic
  - the dynamic simulation is build as a binary tree



from Hoffman & Gelman (2014)

Max tree depth diagnostic

- NUTS specific diagnostic
  - the dynamic simulation is build as a binary tree

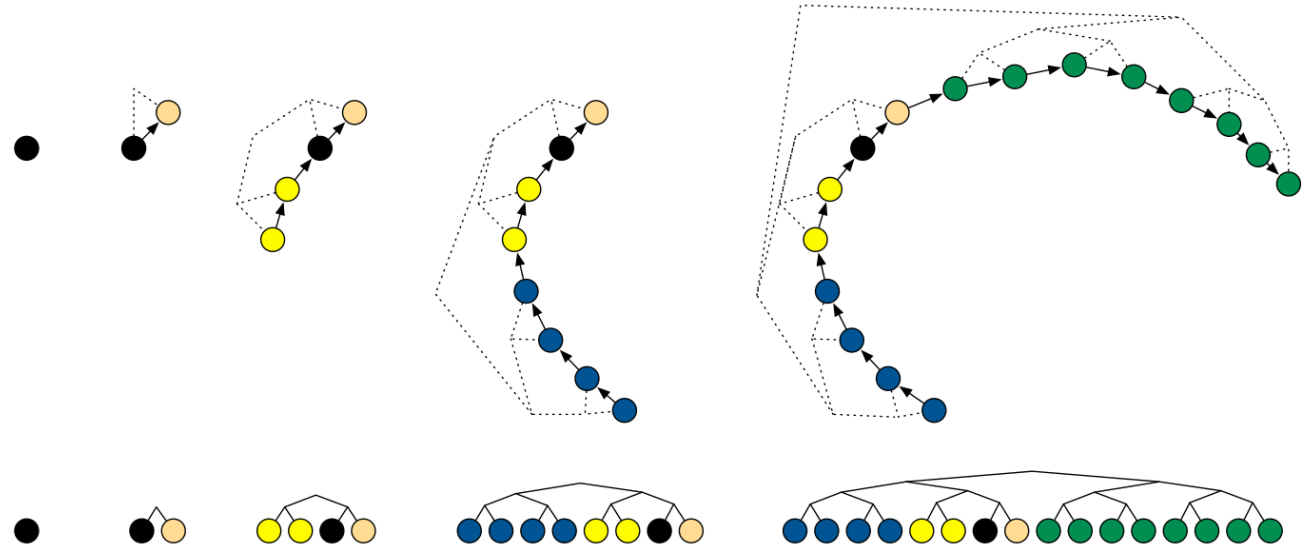


from Hoffman & Gelman (2014)

  - maximum simulation length is capped to avoid very long waiting times in case of bad behavior

Max tree depth diagnostic

- NUTS specific diagnostic
  - the dynamic simulation is build as a binary tree

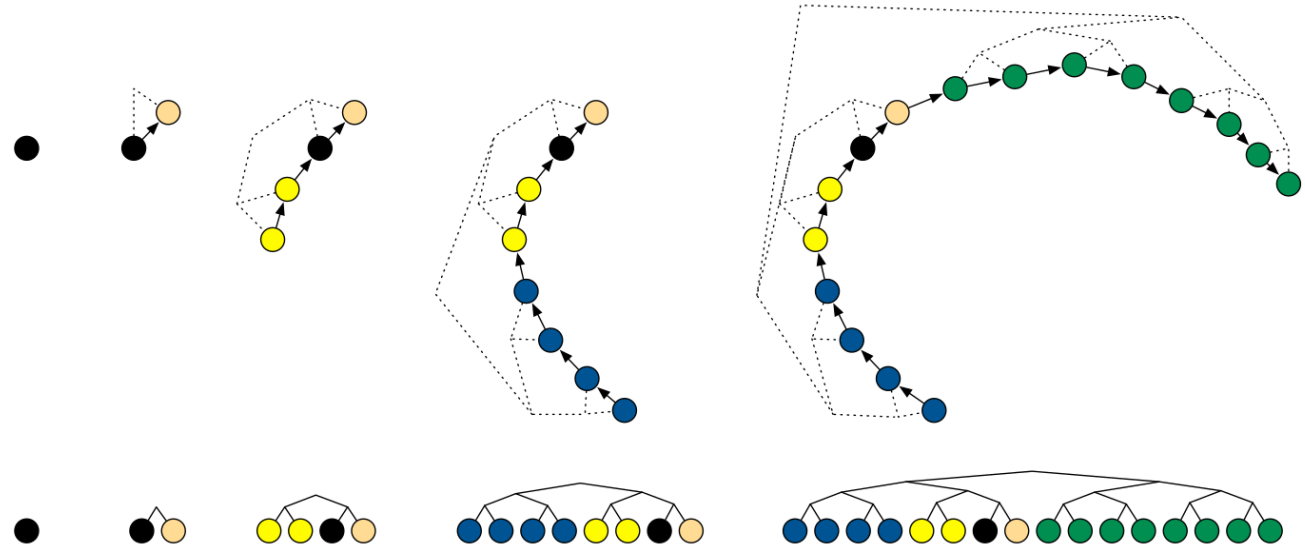


from Hoffman & Gelman (2014)

  - maximum simulation length is capped to avoid very long waiting times in case of bad behavior
- Indicates inefficiency in sampling leading to higher autocorrelations and lower ESS (S_{eff})
  - very low inefficiency can indicate problems that need to be inverse-distance
  - moderate inefficiency doesn't invalidate the result

Max tree depth diagnostic

- NUTS specific diagnostic
  - the dynamic simulation is build as a binary tree

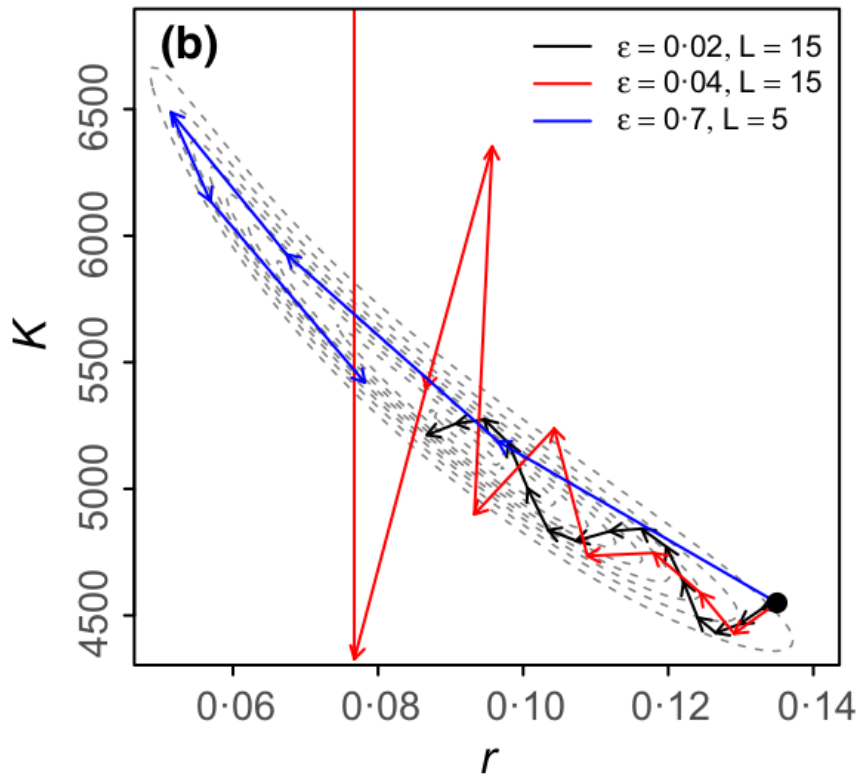


from Hoffman & Gelman (2014)

  - maximum simulation length is capped to avoid very long waiting times in case of bad behavior
- Indicates inefficiency in sampling leading to higher autocorrelations and lower ESS (S_{eff})
  - very low inefficiency can indicate problems that need to be inverse-distance
  - moderate inefficiency doesn't invalidate the result
- Different parameterizations matter

Divergences

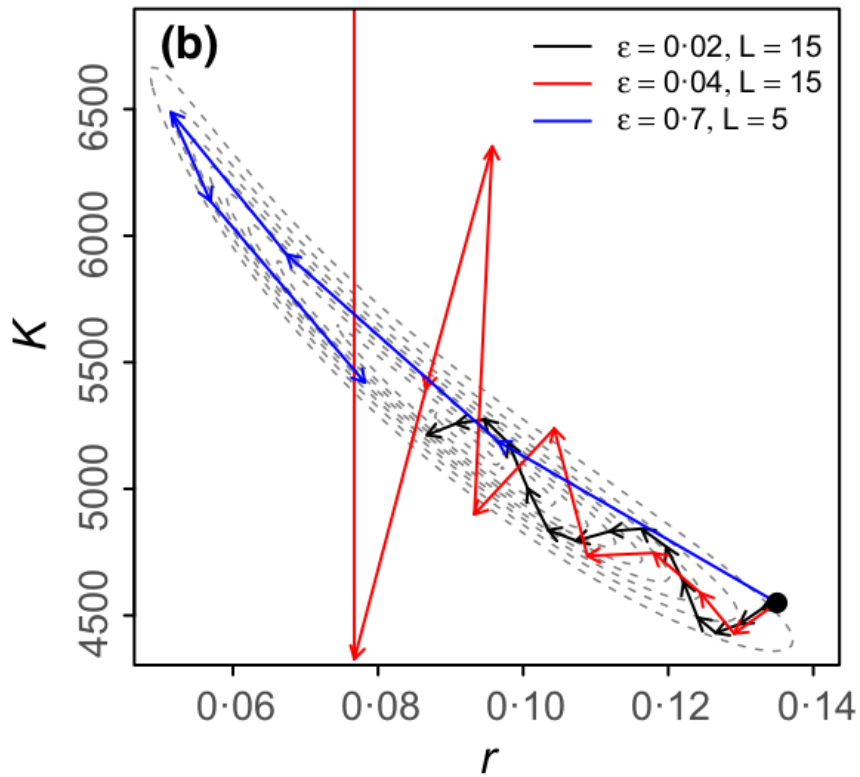
- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density (compared to the used step size)
  - indicates possibility of biased estimates



From Monnahan et al (2017)

Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density (compared to the used step size)
  - indicates possibility of biased estimates



From Monnahan et al (2017)

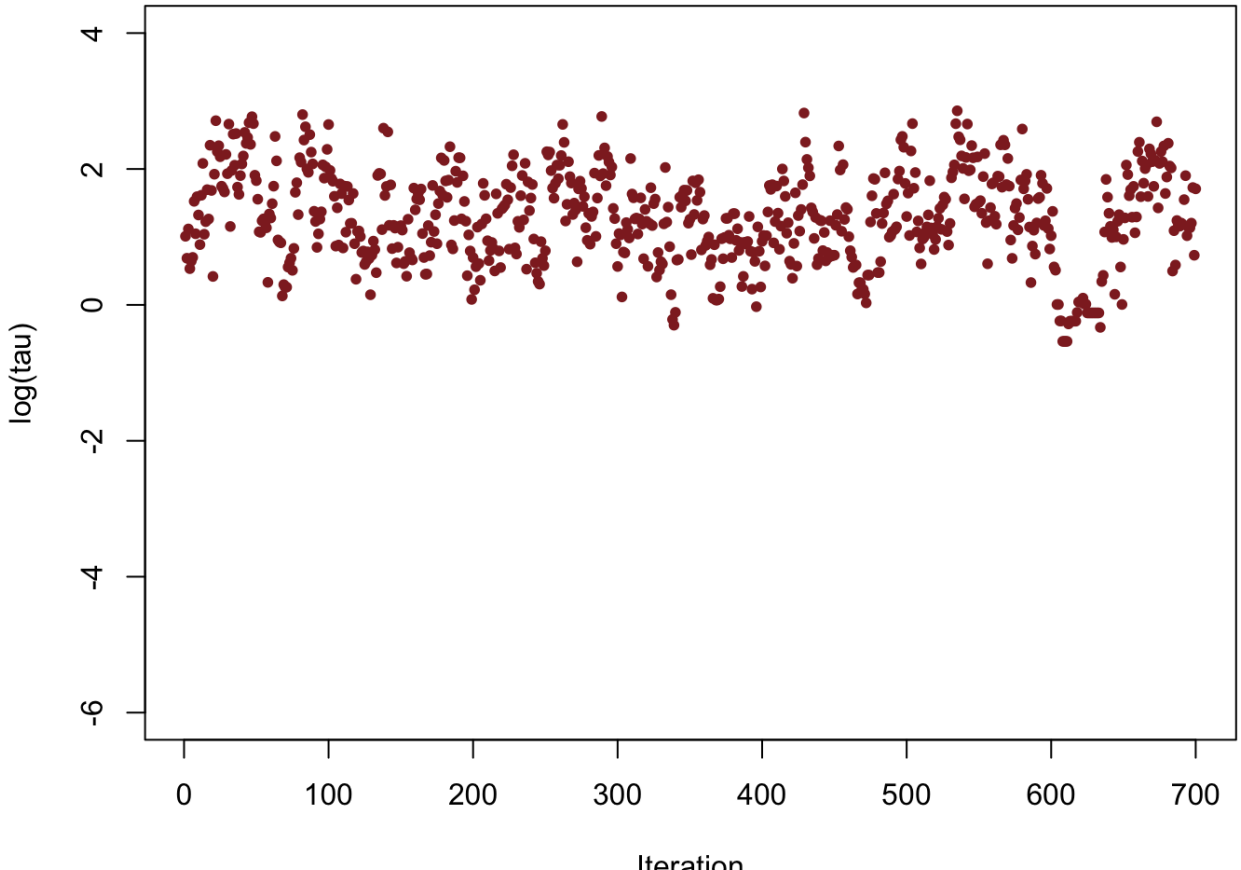
- Demo https://chi-feng.github.io/mcmc-demo/

Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html

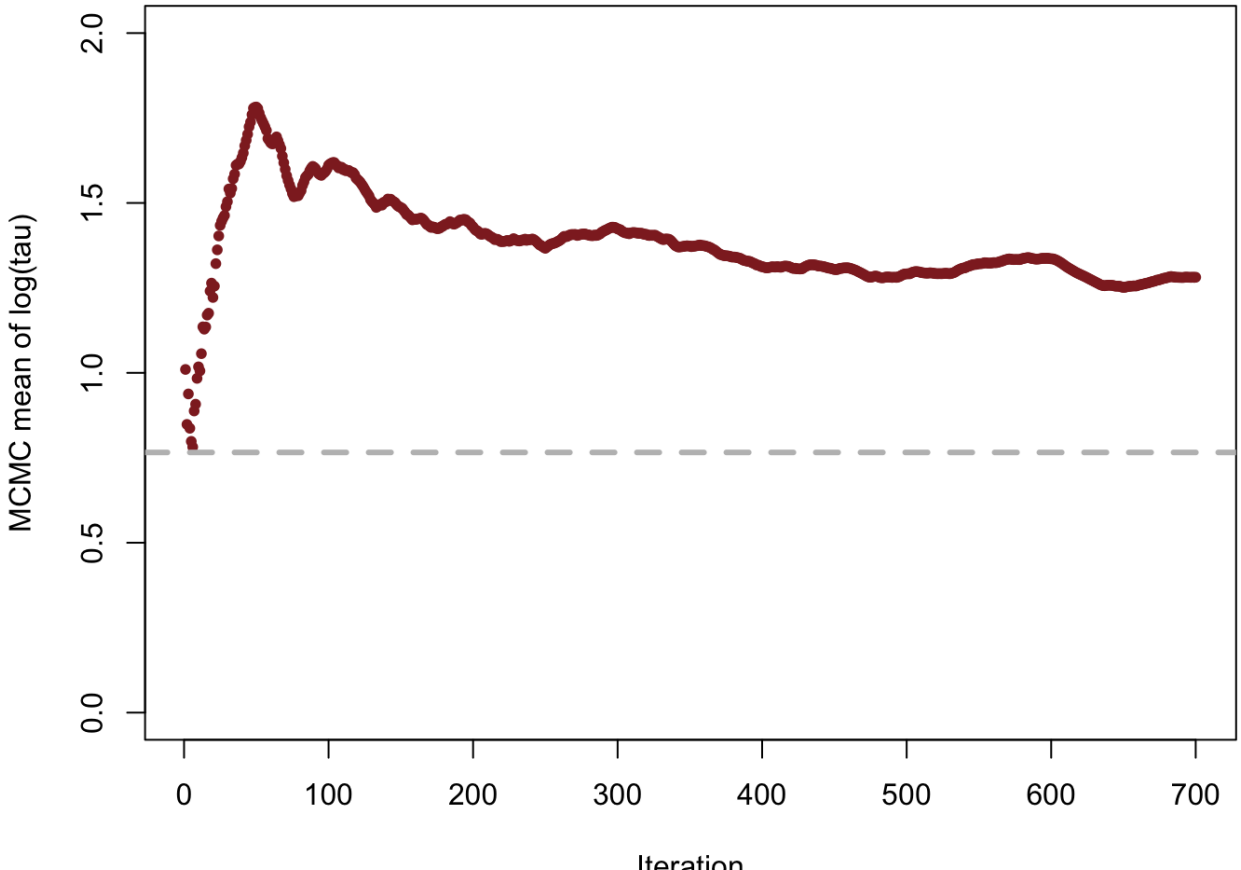
Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



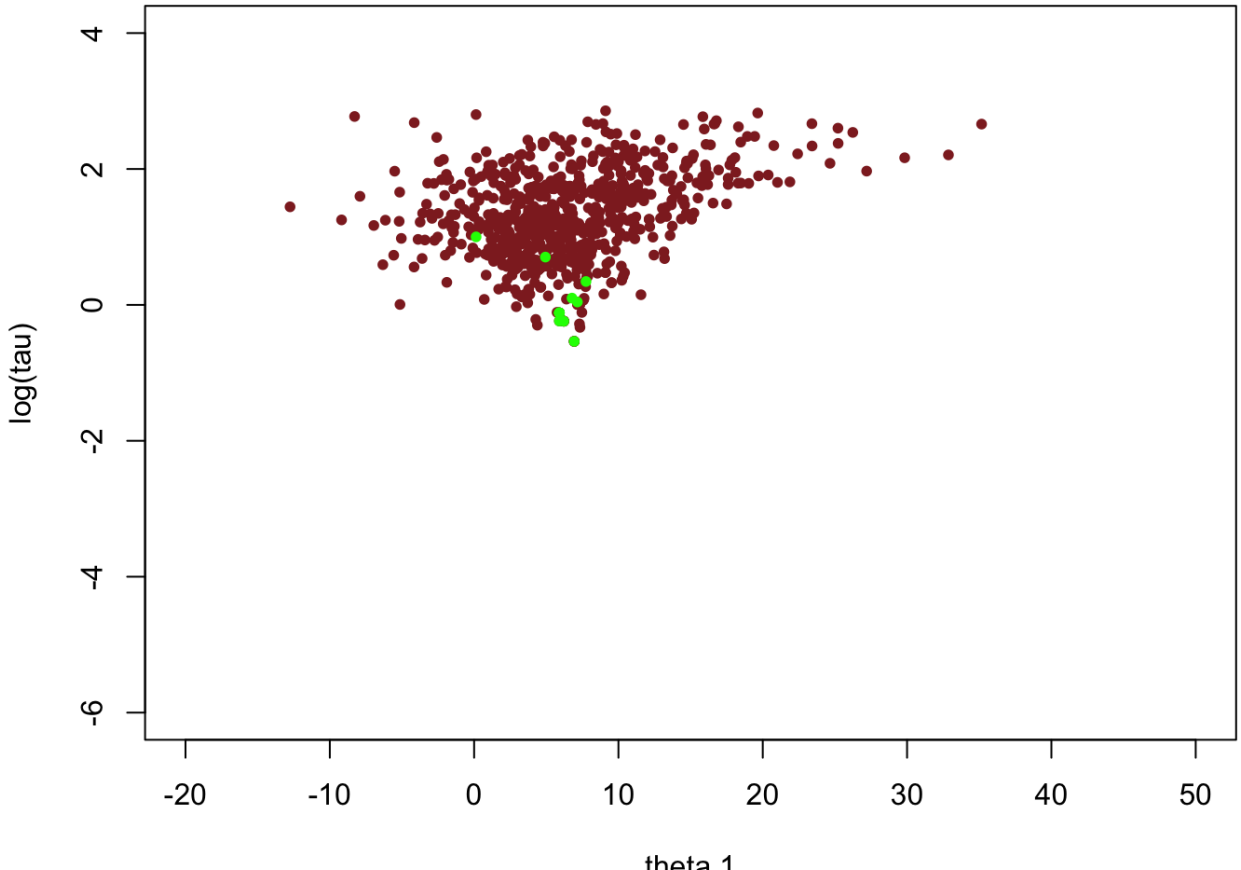
Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



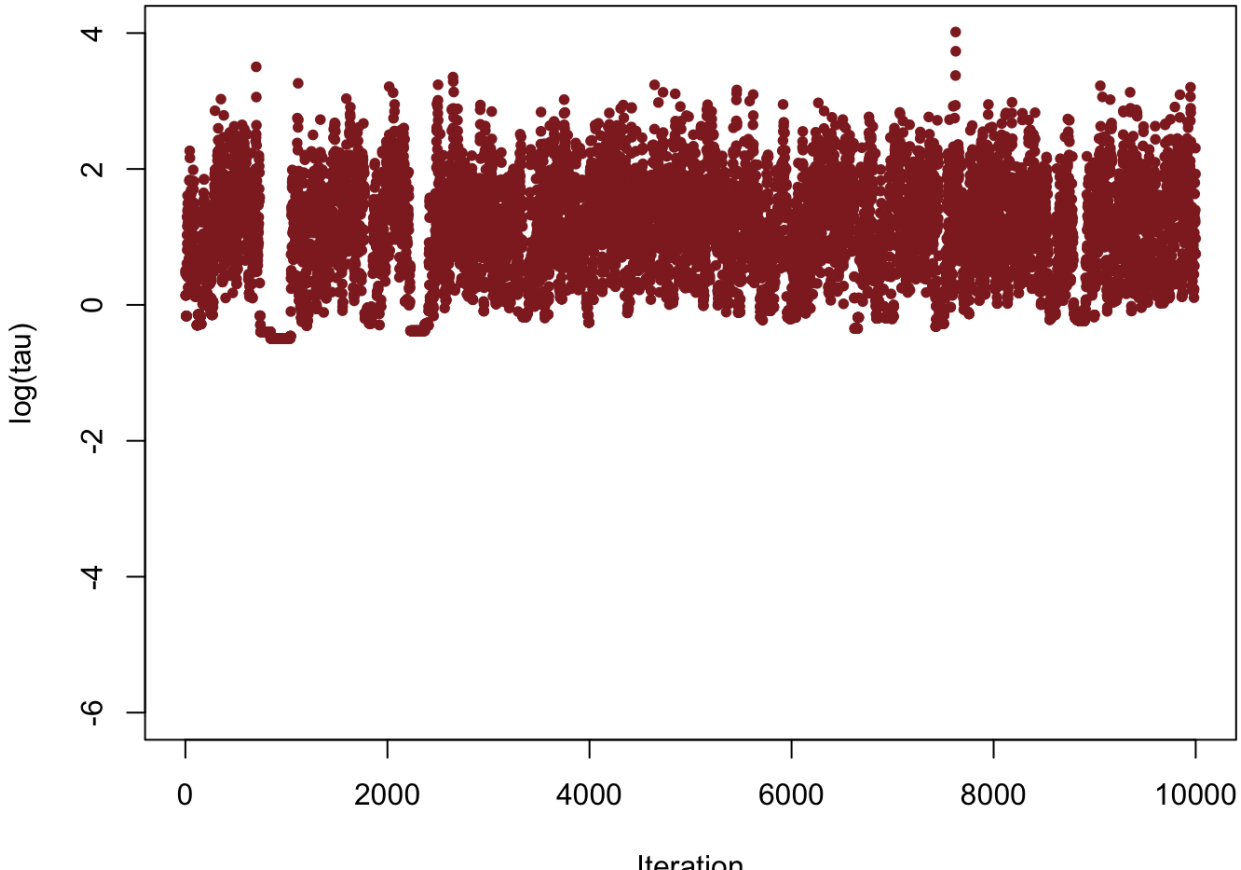
Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



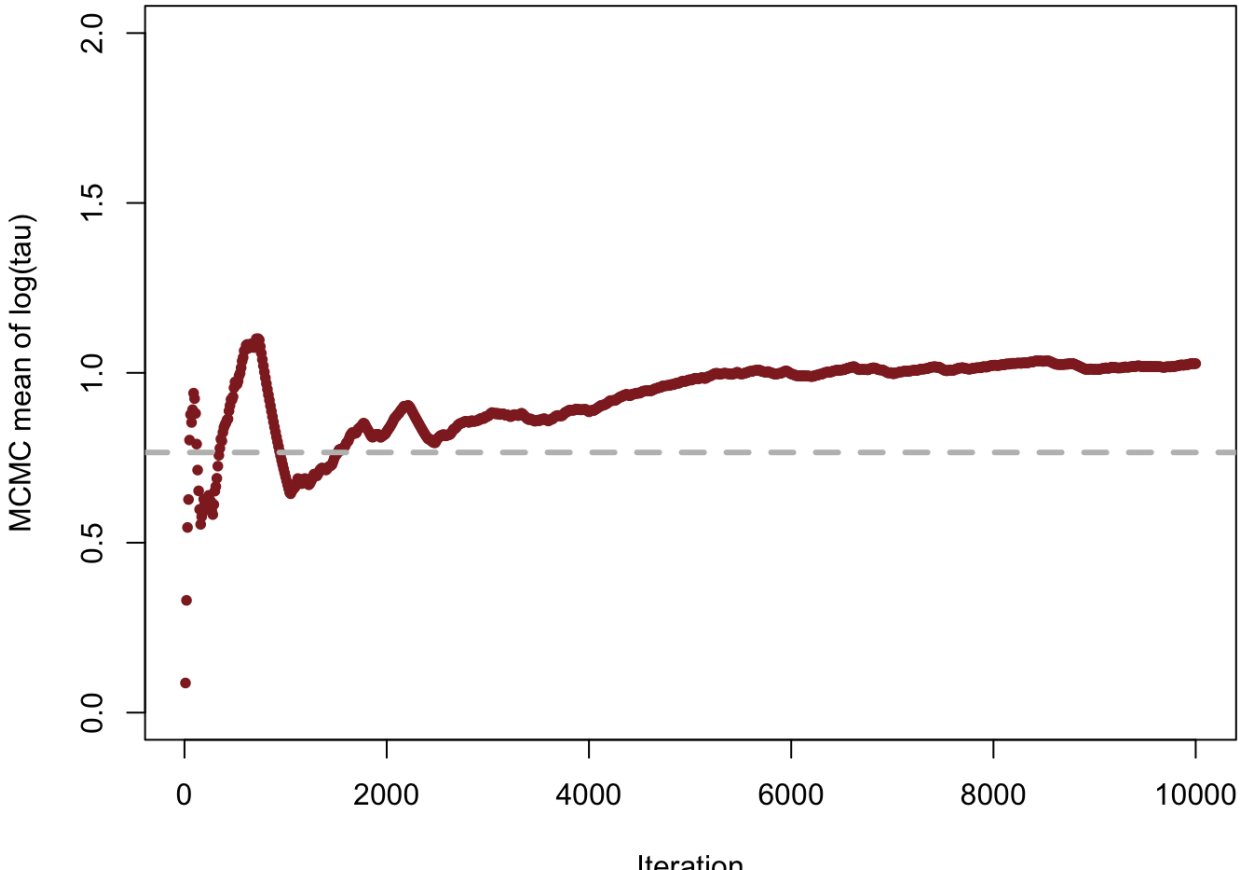
Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



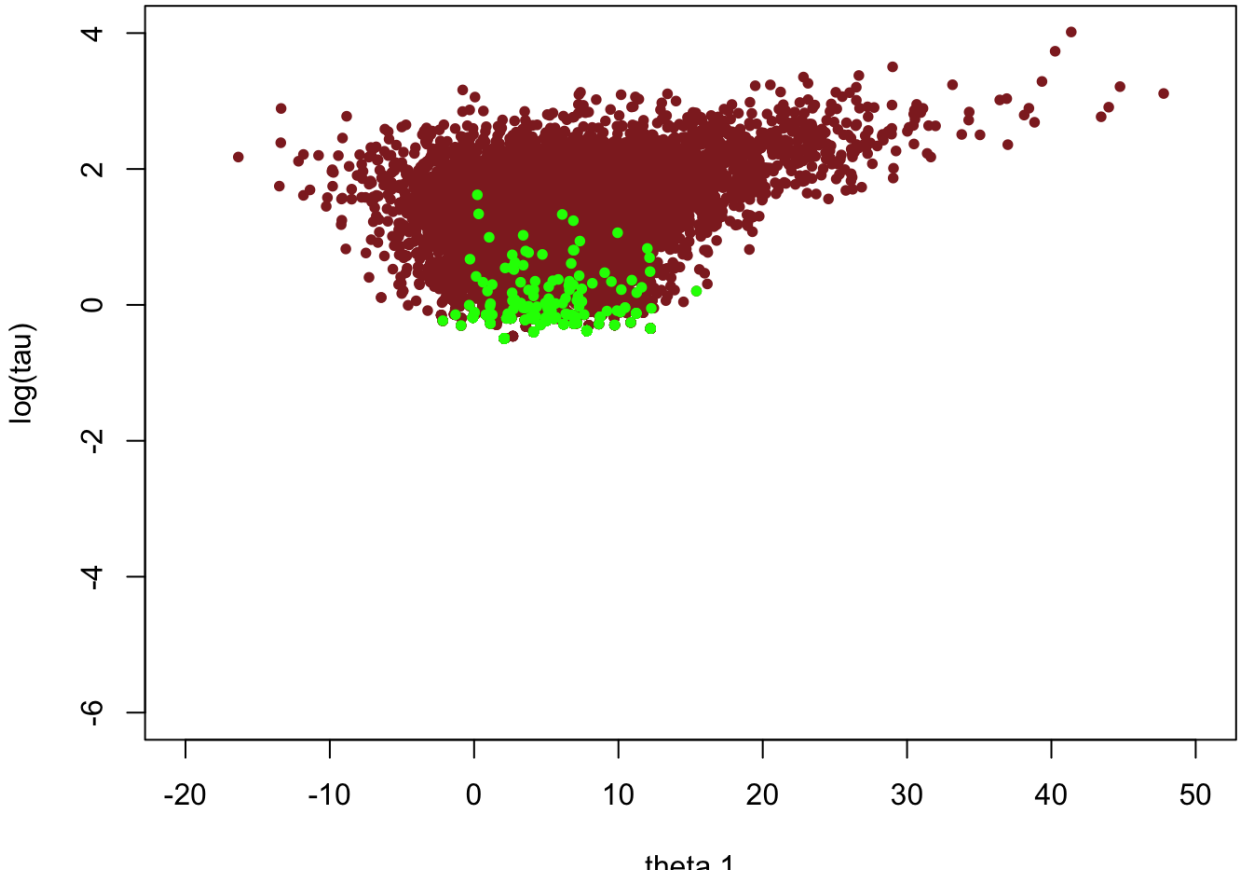
Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



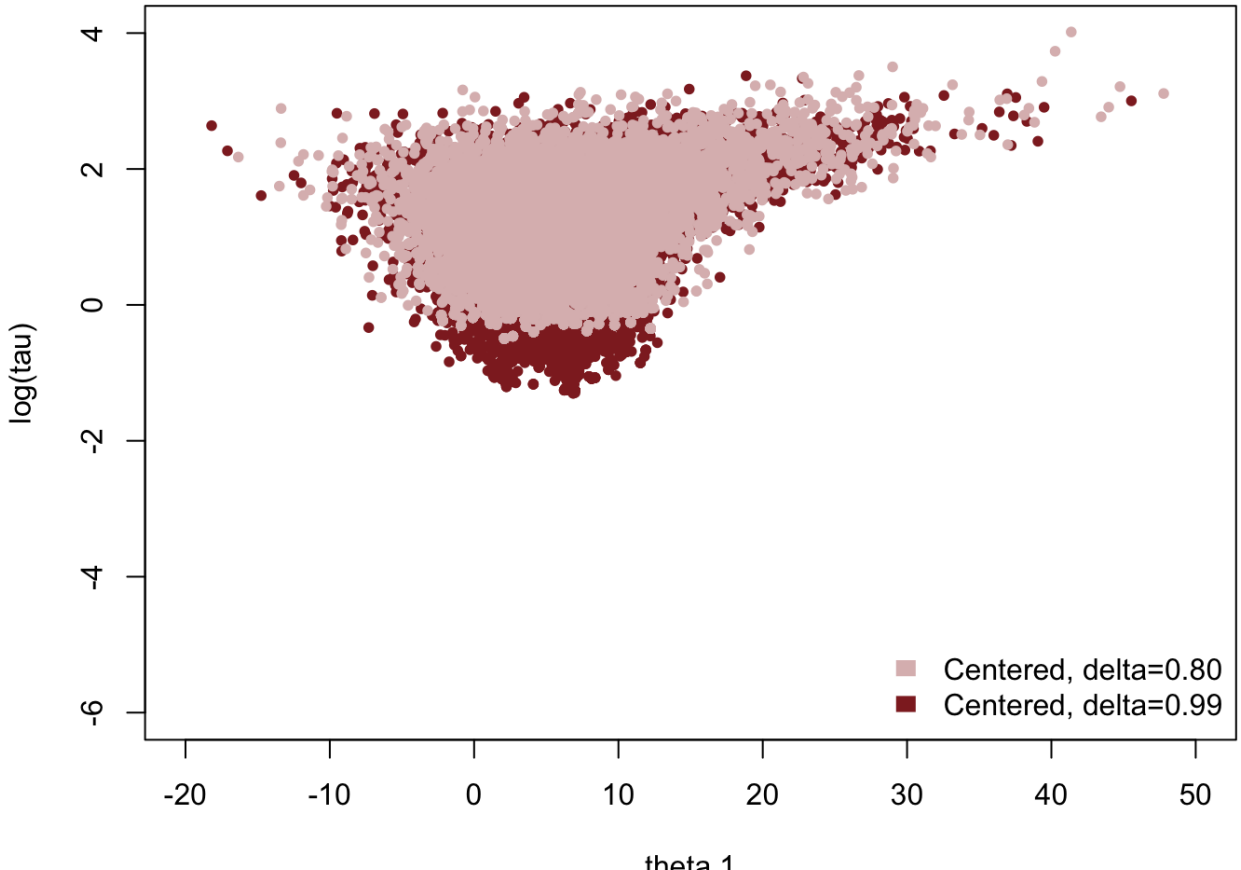
Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



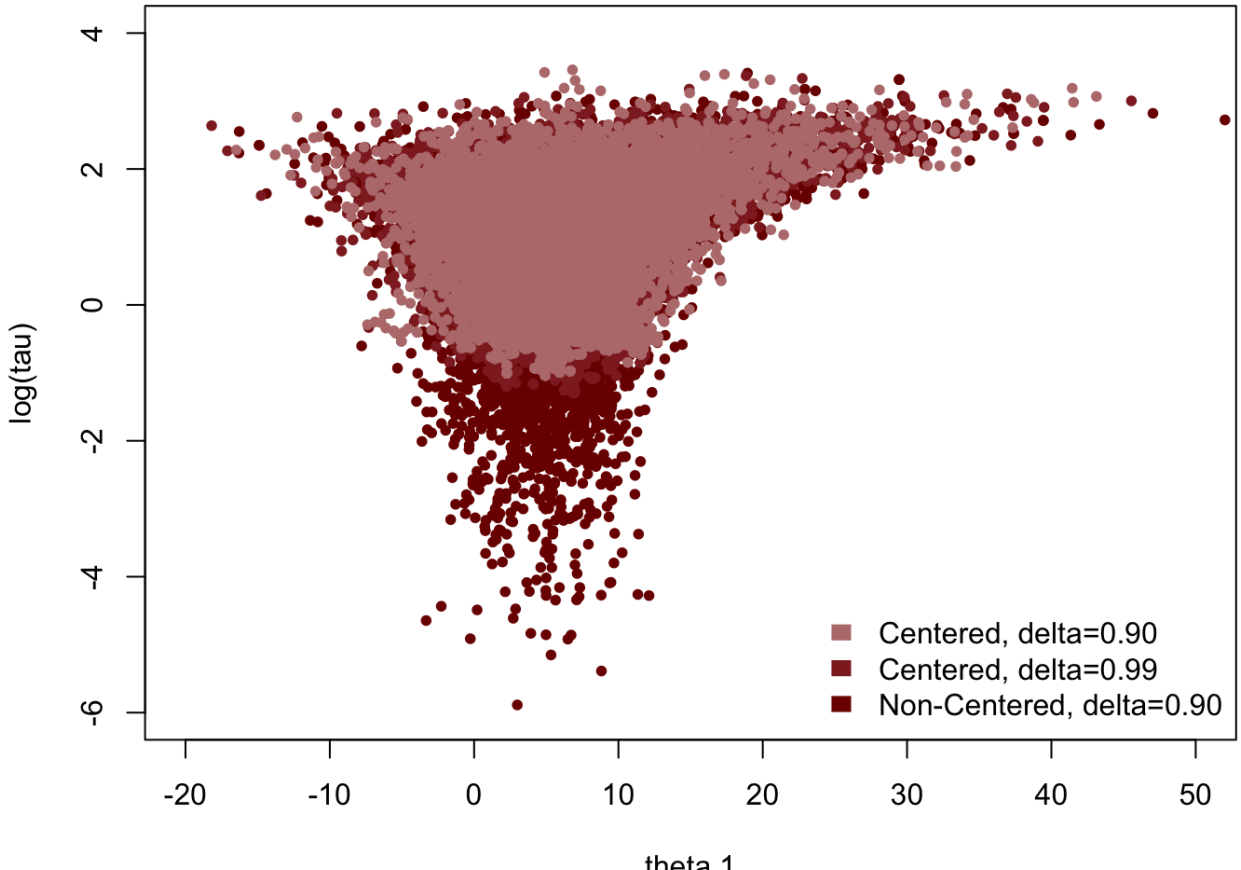
Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



Divergences

- HMC specific: indicates that Hamiltonian dynamic simulation has problems with unexpected fast changes in log-density
  - indicates possibility of biased estimates
- http://mc-stan.org/users/documentation/case-studies/divergences_and_bias.html



Problematic distributions

- Nonlinear dependencies
  - simple mass matrix scaling doesn't help

Problematic distributions

- Nonlinear dependencies
  - simple mass matrix scaling doesn't help
- Funnels
  - optimal step size depends on location

Problematic distributions

- Nonlinear dependencies
  - simple mass matrix scaling doesn't help
- Funnels
  - optimal step size depends on location
- Multimodal
  - difficult to move from one mode to another

Problematic distributions

- Nonlinear dependencies
  - simple mass matrix scaling doesn't help
- Funnels
  - optimal step size depends on location
- Multimodal
  - difficult to move from one mode to another
- Long-tailed with non-finite variance and mean
  - efficiency of exploration is reduced
  - central limit theorem doesn't hold for mean and variance

Probabilistic programming language

- Wikipedia “A probabilistic programming language (PPL) is a programming language designed to describe probabilistic models and then perform inference in those models”

Probabilistic programming language

- Wikipedia “A probabilistic programming language (PPL) is a programming language designed to describe probabilistic models and then perform inference in those models”
- To make probabilistic programming useful
  - inference has to be as automatic as possible
  - diagnostics for telling if the automatic inference doesn’t work
  - easy workflow (to reduce manual work)
  - fast enough (manual work replaced with automation)

Probabilistic programming

- Enables agile workflow for developing probabilistic models
  - language
  - automated inference
  - diagnostics
- Many frameworks Stan, PyMC, Pyro (Uber), TFP (Google), Turing.jl, JAGS, ELFI, ...

Stan - probabilistic programming framework

- Language, inference engine, user interfaces, documentation, case studies, diagnostics, packages, ...
  - autodiff to compute gradients of the log density

mc-stan.org

Stan - probabilistic programming framework

- Language, inference engine, user interfaces, documentation, case studies, diagnostics, packages, ...
  - autodiff to compute gradients of the log density
- More than 100K users in social, biological, and physical sciences, medicine, engineering, and business

mc-stan.org

Stan - probabilistic programming framework

- Language, inference engine, user interfaces, documentation, case studies, diagnostics, packages, ...
  - autodiff to compute gradients of the log density
- More than 100K users in social, biological, and physical sciences, medicine, engineering, and business
- Several full time developers, 40+ developers, more than 100 contributors

mc-stan.org

Stan - probabilistic programming framework

- Language, inference engine, user interfaces, documentation, case studies, diagnostics, packages, ...
  - autodiff to compute gradients of the log density
- More than 100K users in social, biological, and physical sciences, medicine, engineering, and business
- Several full time developers, 40+ developers, more than 100 contributors
- R, Python, Julia, Scala, Stata, Matlab, command line interfaces
- More than 140 R packages using Stan

mc-stan.org

Stan

- Stanislaw Ulam (1909-1984)
  - Monte Carlo method
  - H-Bomb

Binomial model - Stan code

```
data {
  int<lower=0> N;        // number of experiments
  int<lower=0,upper=N> y; // number of successes
}

parameters {
  real<lower=0,upper=1> theta; // parameter of the binom
}

model {
  theta ~ beta(1,1);      //prior
  y ~ binomial(N,theta); // observation model
}
```

Binomial model - Stan code

```
data {
  int<lower=0> N;      // number of experiments
  int<lower=0,upper=N> y; // number of successes
}

parameters {
  real<lower=0,upper=1> theta; // parameter of the binom
}

model {
  theta ~ beta(1,1);      //prior
  y ~ binomial(N,theta); // observation model
}
```

Binomial model - Stan code

```
data {
  int<lower=0> N;      // number of experiments
  int<lower=0,upper=N> y; // number of successes
}

parameters {
  real<lower=0,upper=1> theta; // parameter of the binom
}

model {
  theta ~ beta(1,1);      //prior
  y ~ binomial(N,theta); // observation model
}
```

Binomial model - Stan code

```
data {
  int<lower=0> N;        // number of experiments
  int<lower=0,upper=N> y; // number of successes
}
```

- Data type and size are declared
- Stan checks that given data matches type and constraints

Binomial model - Stan code

```
data {
  int<lower=0> N;       // number of experiments
  int<lower=0,upper=N> y; // number of successes
}
```

- Data type and size are declared
- Stan checks that given data matches type and constraints
  - If you are not used to strong typing, this may feel annoying, but it will reduce the probability of coding errors, which will reduce probability of data analysis errors

Binomial model - Stan code

```
parameters {
  real<lower=0,upper=1> theta;
}
```

- Parameters may have constraints
- Stan makes transformation to unconstrained space and samples in unconstrained space
  - e.g. log transformation for <lower=a>
  - e.g. logit transformation for <lower=a,upper=b>

Binomial model - Stan code

```
parameters {
  real<lower=0,upper=1> theta;
}
```

- Parameters may have constraints
- Stan makes transformation to unconstrained space and samples in unconstrained space
  - e.g. log transformation for <lower=a>
  - e.g. logit transformation for <lower=a,upper=b>
- For these declared transformation Stan automatically takes into account the Jacobian of the transformation (see BDA3 p. 21)

Binomial model - Stan code

```
model {
  theta ~ beta(1,1);       // prior
  y ~ binomial(N,theta);   // likelihood
}
```

Binomial model - Stan code

```
model {
  theta ~ beta(1,1);        // prior
  y ~ binomial(N,theta);    // likelihood
}
```

$\sim$ is syntactic sugar and this is equivalent to

```
model {
  target += beta_lpdf(theta | 1, 1);
  target += binomial_lpmf(y | N, theta);
}
```

Binomial model - Stan code

```
model {
  theta ~ beta(1,1);       // prior
  y ~ binomial(N,theta); // likelihood
}
```

$\sim$ is syntactic sugar and this is equivalent to

```
model {
  target += beta_lpdf(theta | 1, 1);
  target += binomial_lpmf(y | N, theta);
}
```

- `target` is the log posterior density

Binomial model - Stan code

```
model {
  theta ~ beta(1,1);       // prior
  y ~ binomial(N,theta); // likelihood
}
```

$\sim$ is syntactic sugar and this is equivalent to

```
model {
  target += beta_lpdf(theta | 1, 1);
  target += binomial_lpmf(y | N, theta);
}
```

- `target` is the log posterior density
- `_lpdf` for continuous, `_lpmf` for discrete distributions (discrete for the left hand side of `|`)

Binomial model - Stan code

```
model {
  theta ~ beta(1,1);       // prior
  y ~ binomial(N,theta); // likelihood
}
```

$\sim$ is syntactic sugar and this is equivalent to

```
model {
  target += beta_lpdf(theta | 1, 1);
  target += binomial_lpmf(y | N, theta);
}
```

- `target` is the log posterior density
- `_lpdf` for continuous, `_lpmf` for discrete distributions (discrete for the left hand side of `|`)
- for Stan sampler there is no difference between prior and likelihood, all that matters is the final `target`

Binomial model - Stan code

```
model {
  theta ~ beta(1,1);       // prior
  y ~ binomial(N,theta); // likelihood
}
```

$\sim$ is syntactic sugar and this is equivalent to

```
model {
  target += beta_lpdf(theta | 1, 1);
  target += binomial_lpmf(y | N, theta);
}
```

- `target` is the log posterior density
- `_lpdf` for continuous, `_lpmf` for discrete distributions (discrete for the left hand side of `|`)
- for Stan sampler there is no difference between prior and likelihood, all that matters is the final `target`
- you can write in Stan language any program to compute the log density (Stan language is Turing complete)

Stan

- Stan compiles (transplies) the model written in Stan language to C++
  - this makes the sampling for complex models and bigger data faster
  - also makes Stan models easily portable, you can use your own favorite interface

CmdStanR

RStan

```
library(cmdstanr)
options(mc.cores = 1)

d_bin <- list(N = 10, y = 7)
mod_bin <- cmdstan_model(stan_file = 'binom.stan')
fit_bin <- mod_bin$sample(data = d_bin)
```

CmdStanR

RStan

```
library(cmdstanr)
options(mc.cores = 1)

d_bin <- list(N = 10, y = 7)
mod_bin <- cmdstan_model(stan_file = 'binom.stan')
fit_bin <- mod_bin$sample(data = d_bin)
```

PyStan

PyStan

```
import pystan
import stan_utility

data = dict(N=10, y=8)
model = stan_utility.compile_model('binom.stan')
fit = model.sampling(data=data)
```

PyStan

PyStan

```
import pystan
import stan_utility

data = dict(N=10, y=8)
model = stan_utility.compile_model('binom.stan')
fit = model.sampling(data=data)
```

Stan

- Compilation (unless previously compiled model available)
- Warm-up including adaptation
- Sampling
- Generated quantities
- Save posterior draws
- Report divergences, n_{eff}, $\widehat{R}$

Difference between proportions

- An experiment was performed to estimate the effect of beta-blockers on mortality of cardiac patients
- A group of patients were randomly assigned to treatment and control groups:
  - out of 674 patients receiving the control, 39 died
  - out of 680 receiving the treatment, 22 died

Difference between proportions

```
data {
  int<lower=0> N1;
  int<lower=0> y1;
  int<lower=0> N2;
  int<lower=0> y2;
}
parameters {
  real<lower=0,upper=1> theta1;
  real<lower=0,upper=1> theta2;
}
model {
  theta1 ~ beta(1,1);
  theta2 ~ beta(1,1);
  y1 ~ binomial(N1,theta1);
  y2 ~ binomial(N2,theta2);
}

generated quantities {
  real oddsratio;
  oddsratio = (theta2/(1-theta2))/(theta1/(1-theta1));
}
```

Difference between proportions

```
data {
  int<lower=0> N1;
  int<lower=0> y1;
  int<lower=0> N2;
  int<lower=0> y2;
}
parameters {
  real<lower=0,upper=1> theta1;
  real<lower=0,upper=1> theta2;
}
model {
  theta1 ~ beta(1,1);
  theta2 ~ beta(1,1);
  y1 ~ binomial(N1,theta1);
  y2 ~ binomial(N2,theta2);
}

generated quantities {
  real oddsratio;
  oddsratio = (theta2/(1-theta2))/(theta1/(1-theta1));
}
```

Difference between proportions

```
generated quantities {
  real oddsratio;
  oddsratio = (theta2/(1-theta2))/(theta1/(1-theta1));
}
```

- generated quantities is run after the sampling

Difference between proportions

```
d_bin2 <- list(N1 = 674, y1 = 39, N2 = 680, y2 = 22)
mod_bin2 <- cmdstan_model(stan_file = 'binom2.stan')
fit_bin2 <- mod_bin2$sample(data = d_bin2, refresh=1000)
```

```
> Running MCMC with 4 parallel chains...

Chain 1 Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 1 Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 1 Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 1 Iteration: 2000 / 2000 [100%]  (Sampling)
...
All 4 chains finished successfully.
Mean chain execution time: 0.0 seconds.
Total execution time: 0.2 seconds.
```

Difference between proportions

```
fit_bin2$summary()
```

	variable	mean	median	sd	mad	q5	q95	rhat	ess_bulk	ess_tail
1	lp__	−253.	−253.	1.0	0.74	−255.	−253.	1.0	1751.	2231.
2	theta1	0.059	0.059	0.0093	0.0093	0.045	0.075	1.0	3189.	2657.
3	theta2	0.034	0.033	0.0069	0.0067	0.023	0.046	1.0	3229.	2163.
4	oddsratio	0.57	0.55	0.16	0.15	0.35	0.87	1.0	2998.	2685.

Difference between proportions

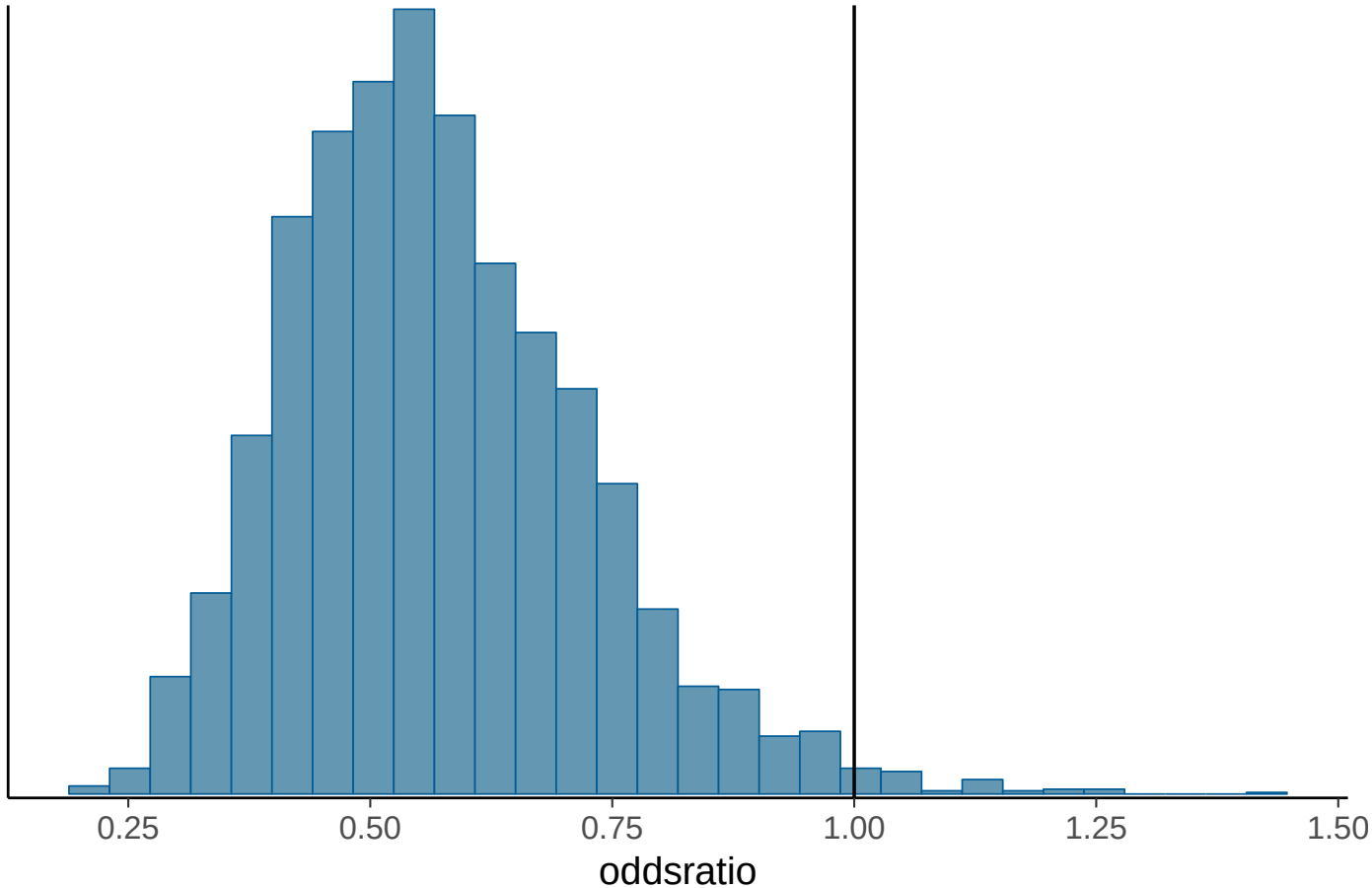
```
fit_bin2$summary()
```

	variable	mean	median	sd	mad	q5	q95	rhat	ess_bulk	ess_tail
1	lp__	−253.	−253.	1.0	0.74	−255.	−253.	1.0	1751.	2231.
2	theta1	0.059	0.059	0.0093	0.0093	0.045	0.075	1.0	3189.	2657.
3	theta2	0.034	0.033	0.0069	0.0067	0.023	0.046	1.0	3229.	2163.
4	oddsratio	0.57	0.55	0.16	0.15	0.35	0.87	1.0	2998.	2685.

- `lp__` is the log density, ie, same as `target`

Difference between proportions

```
draws <- fit_bin2$draws()
mcmc_hist(draws, pars = 'oddsratio') +
  geom_vline(xintercept = 1) +
  scale_x_continuous(breaks = c(seq(0.25,1.5,by=0.25)))
```

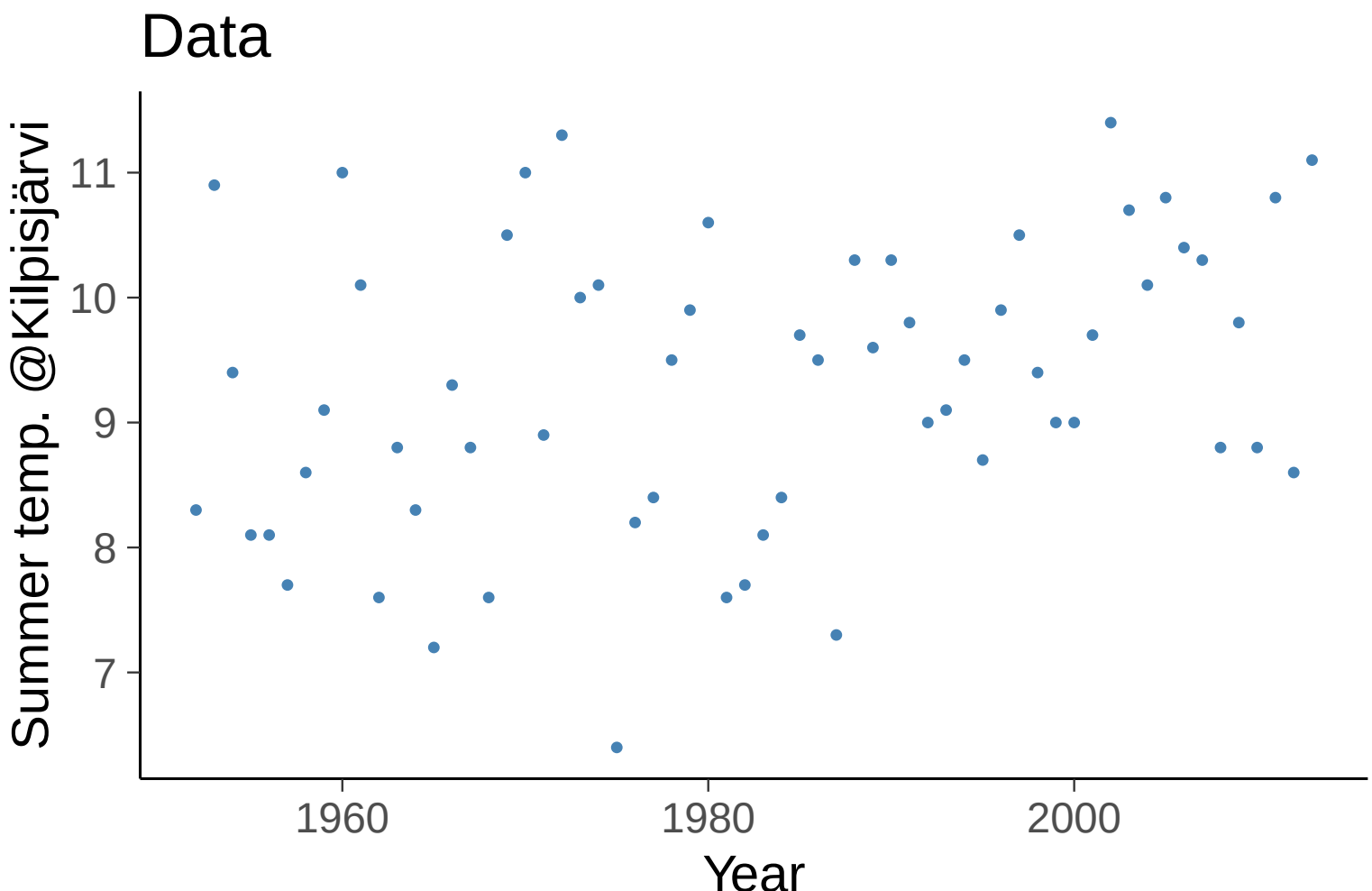


Shinystan

- Graphical user interface for analysing MCMC results

Kilpisjärvi summer temperature

- Temperature at Kilpisjärvi in June, July and August from 1952 to 2013
- Is there change in the temperature?



Gaussian linear model

```
data {
    int<lower=0> N; // number of data points
    vector[N] x; //
    vector[N] y; //
}
parameters {
    real alpha;
    real beta;
    real<lower=0> sigma;
}
transformed parameters {
    vector[N] mu;
    mu <- alpha + beta*x;
}
model {
    y ~ normal(mu, sigma);
}
```

Gaussian linear model

```
data {
    int<lower=0> N; // number of data points
    vector[N] x; //
    vector[N] y; //
}
```

- difference between `vector[N] x` and `array[N] real x`

Gaussian linear model

```
data {
    int<lower=0> N; // number of data points
    vector[N] x; //
    vector[N] y; //
}
```

- difference between `vector[N] x` and `array[N] real x`
- no integer vectors: `array[N] int x`

Gaussian linear model

```
parameters {
      real alpha;
      real beta;
      real<lower=0> sigma;
}
transformed parameters {
      vector[N] mu;
      mu <- alpha + beta*x;
}
```

- transformed parameters are deterministic transformations of parameters and data

Priors for Gaussian linear model

```
data {
    int<lower=0> N; // number of data points
    vector[N] x; //
    vector[N] y; //
    real pmualpha; // prior mean for alpha
    real psalpha;  // prior std for alpha
    real pmubeta;  // prior mean for beta
    real psbeta;   // prior std for beta
}
...
transformed parameters {
    vector[N] mu;
    mu <- alpha + beta*x;
}
model {
    alpha ~ normal(pmualpha,psalpha);
    beta ~ normal(pmubeta,psbeta);
    y ~ normal(mu, sigma);
}
```

Student-t linear model

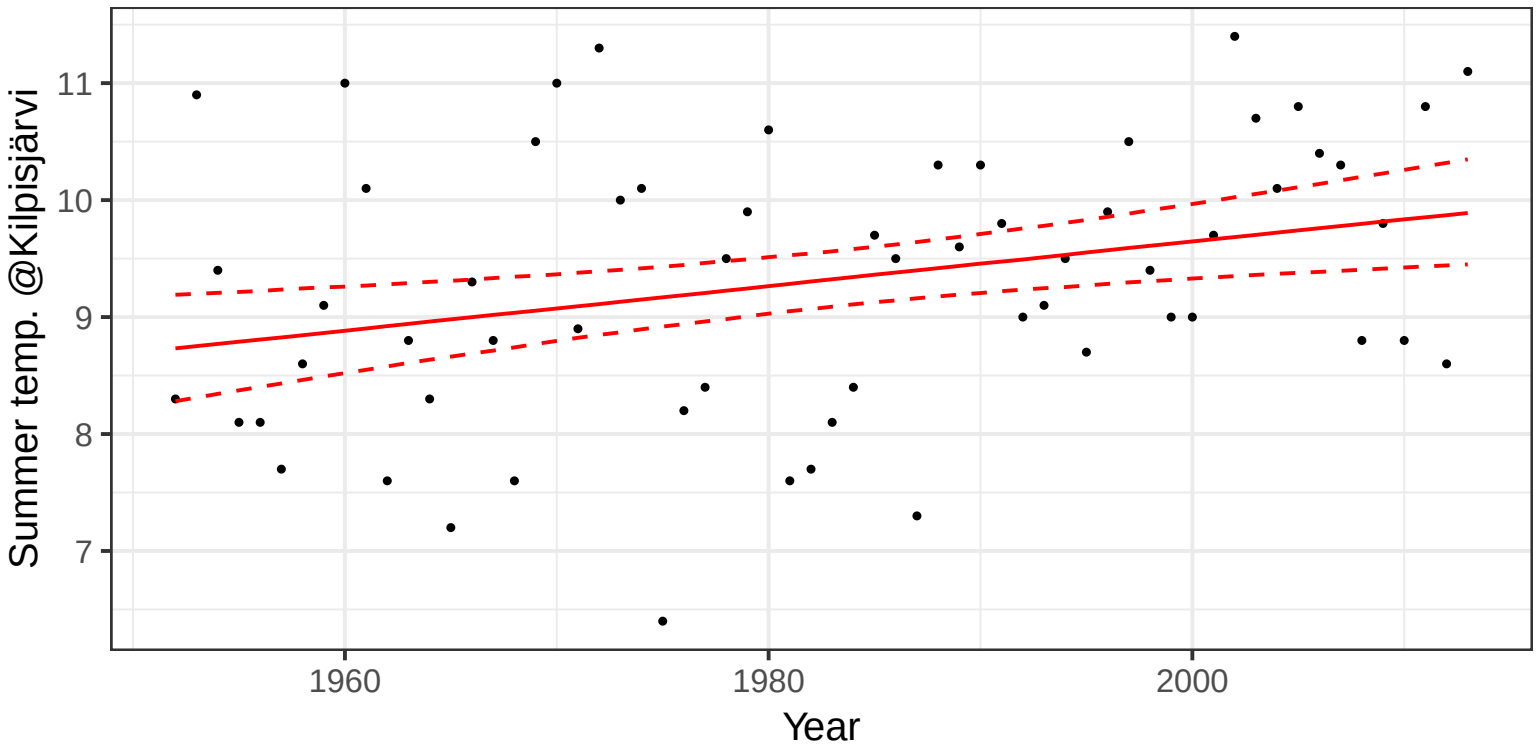
```
...
parameters {
  real alpha;
  real beta;
  real<lower=0> sigma;
  real<lower=1,upper=80> nu;
}
transformed parameters {
  vector[N] mu;
  mu <- alpha + beta*x;
}
model {
  nu ~ gamma(2,0.1);
  y ~ student_t(nu, mu, sigma);
}
```

Priors

- Prior for temperature increase?

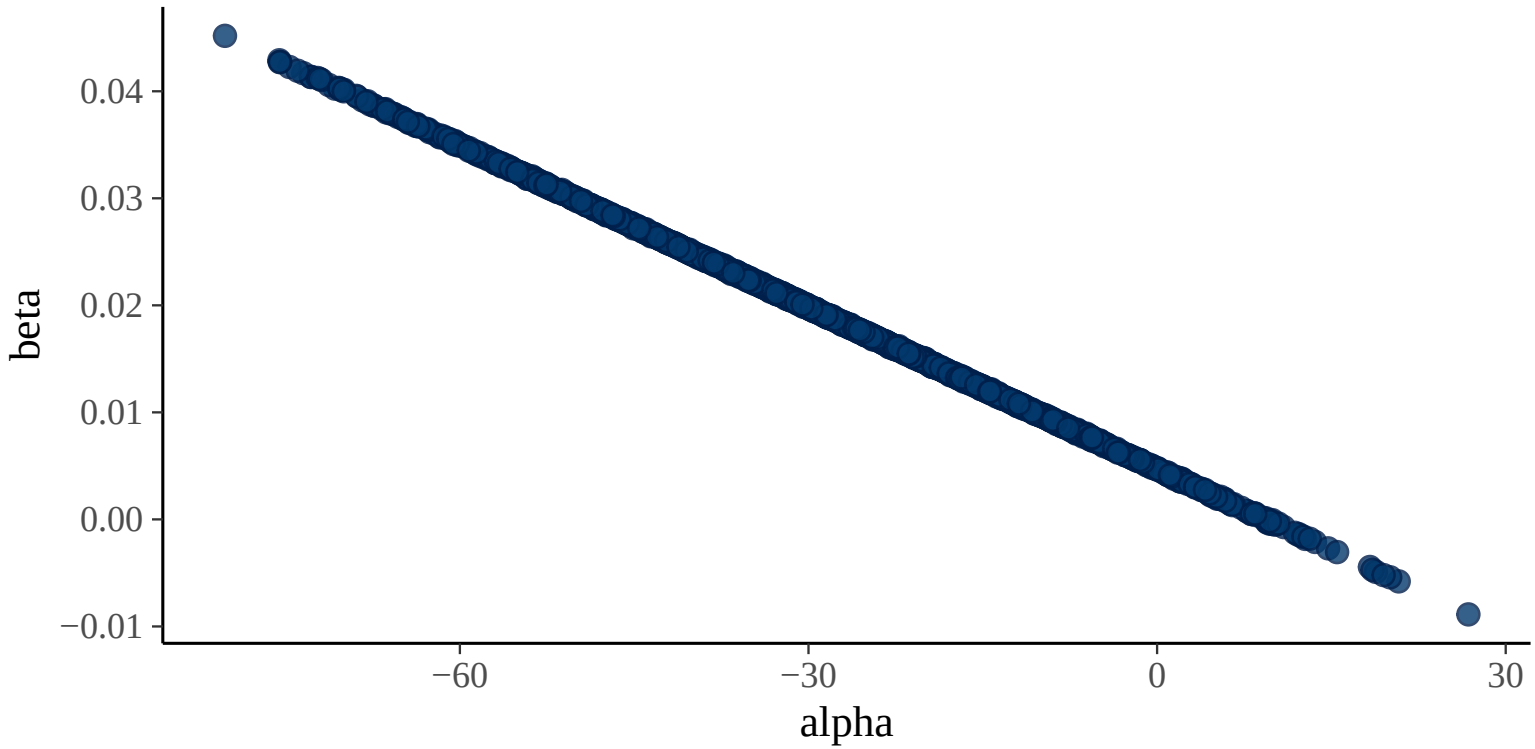
Kilpisjärvi summer temperature

Posterior fit



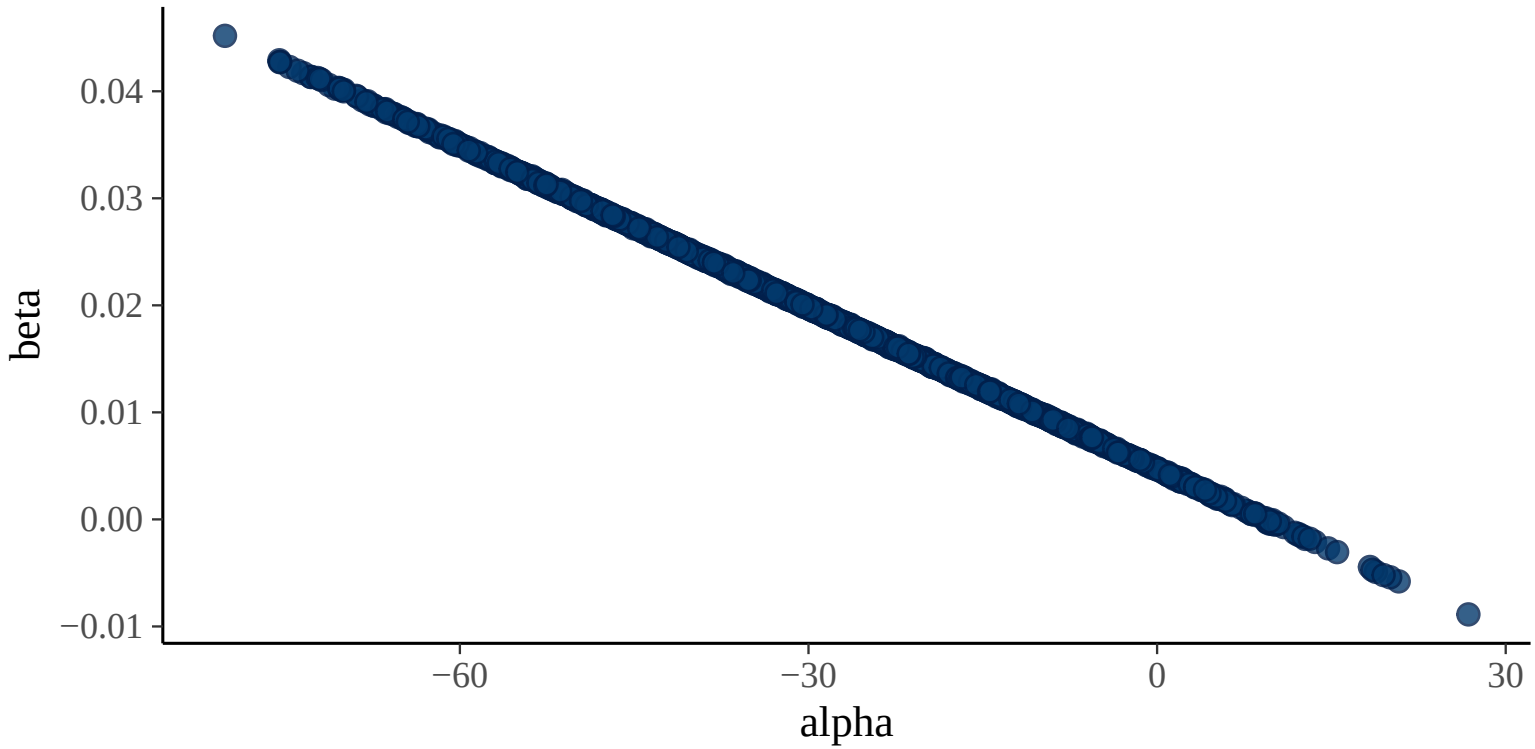
Kilpisjärvi summer temperature

Posterior draws of alpha and beta



Kilpisjärvi summer temperature

Posterior draws of alpha and beta




```
Warning: 1 of 4000 (0.0%) transitions hit the maximum treedepth limit
See https://mc-stan.org/misc/warnings for details.
```

Linear regression model in Stan

```
data {
  int<lower=0> N; // number of data points
  vector[N] x; //
  vector[N] y; //
  real xpred; // input location for prediction
}
transformed data {
  vector[N] x_std;
  vector[N] y_std;
  real xpred_std;
  x_std = (x - mean(x)) / sd(x);
  y_std = (y - mean(y)) / sd(y);
  xpred_std = (xpred - mean(x)) / sd(x);
}
```

RStanARM

- RStanARM provides simplified model description with pre-compiled models
  - no need to wait for compilation
  - a restricted set of models

Two group Binomial model:

```
d_bin2 <- data.frame(N = c(674, 680), y = c(39,22), grp2 = c(0,1))
fit_bin2 <- stan_glm(y/N ~ grp2, family = binomial(), data = d_bin2,
                     weights = N)
```

RStanARM

- RStanARM provides simplified model description with pre-compiled models
  - no need to wait for compilation
  - a restricted set of models

Two group Binomial model:

```
d_bin2 <- data.frame(N = c(674, 680), y = c(39,22), grp2 = c(0,1))
fit_bin2 <- stan_glm(y/N ~ grp2, family = binomial(), data = d_bin2,
                     weights = N)
```

Gaussian linear model

```
fit_lin <- stan_glm(temp ~ year, data = d_lin)
```

BRMS

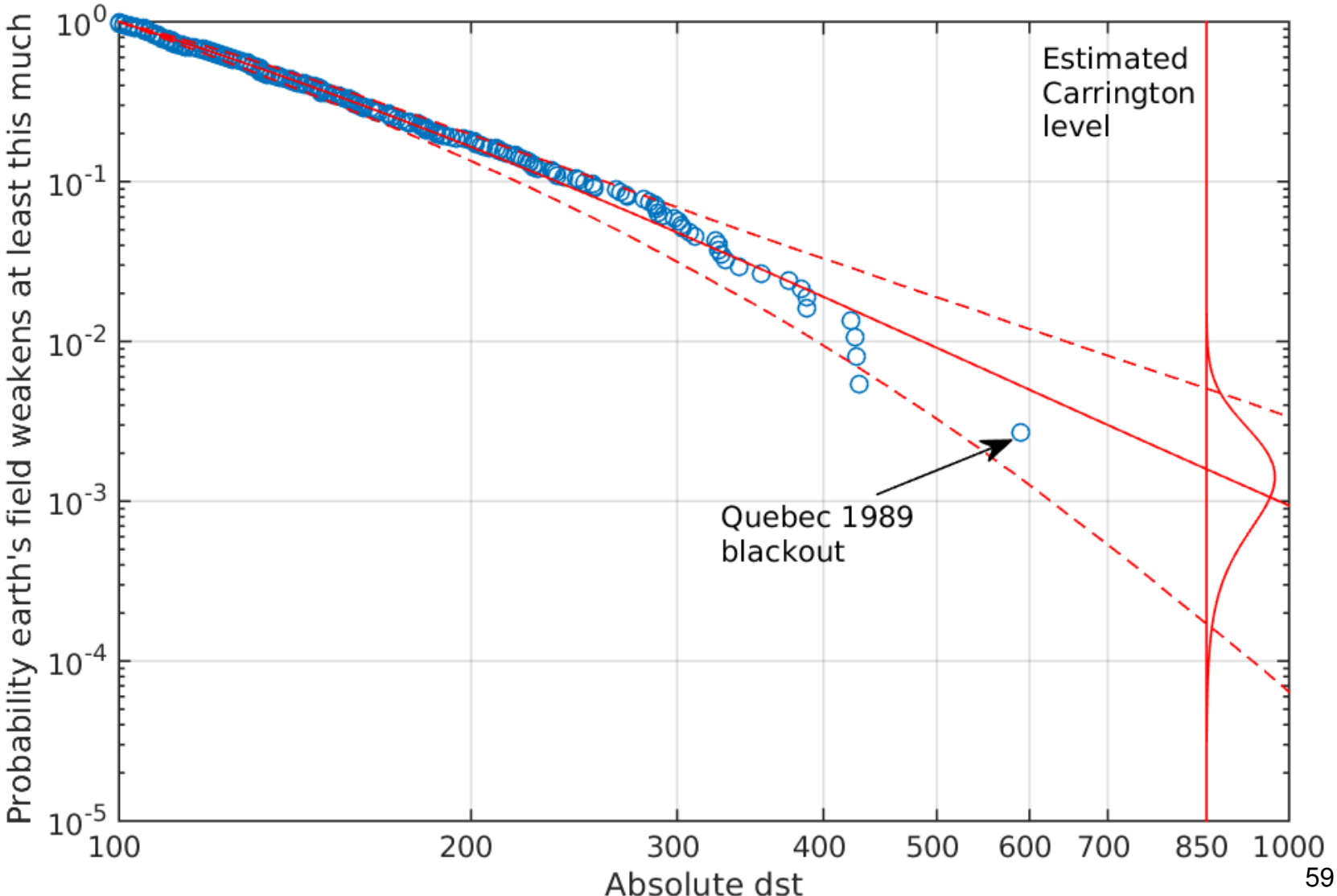
- BRMS provides simplified model description
  - a larger set of models than RStanARM, but still restricted
  - need to wait for the compilation

```
fit_bin2 <- brm(y/N ~ grp2, family = binomial(), data = d_bin2,
                weights = N)
```

```
fit_lin_t <- brm(temp ~ year, data = d_lin, family = student())
```

Extreme value analysis

Geomagnetic storms



Extreme value analysis

```
data {
  int<lower=0> N;
  vector<lower=0>[N] y;
  int<lower=0> Nt;
  vector<lower=0>[Nt] yt;
}
transformed data {
  real ymax;
  ymax <- max(y);
}
parameters {
  real<lower=0> sigma;
  real<lower=-sigma/ymax> k;
}
model {
  y ~ gpareto(k, sigma);
}
generated quantities {
  vector[Nt] predccdf;
  predccdf<-gpareto_ccdf(yt,k,sigma);
}
```

Functions

```
functions {
  real gpareto_lpdf(vector y, real k, real sigma) {
    // generalised Pareto log pdf with mu=0
    // should check and give error if k<0
    // and max(y)/sigma > -1/k
    int N;
    N <- dims(y)[1];
    if (fabs(k) > 1e-15)
      return -(1+1/k)*sum(log1pv(y*k/sigma)) -N*log(sigma);
    else
      return -sum(y/sigma) -N*log(sigma); // limit k->0
  }
  vector gpareto_ccdf(vector y, real k, real sigma) {
    // generalised Pareto log ccdf with mu=0
    // should check and give error if k<0
    // and max(y)/sigma < -1/k
    if (fabs(k) > 1e-15)
      return exp((-1/k)*log1pv(y/sigma*k));
    else
      return exp(-y/sigma); // limit k->0
  }
}
```

Other packages

- R
  - posterior — posterior handling and diagnostics
  - shinystan — interactive diagnostics
  - bayesplot — visualization and model checking (see model checking in Ch 6)
  - tideybayes and ggdist – more visualization
  - loo — cross-validation model assessment and comparison (see Ch 7)
  - projpred — projection predictive variable selection
  - priorsense — prior and likelihood sensitivity diagnostics

- Python
  - ArviZ — visualization, and model checking and assessment (see Ch 6 and 7)

Different interfaces

- CmdStanR / CmdStanPy
  - Lightweight interface on top of commandline program CmdStan
  - Lacks some features that are not needed in this course, but is usually easier to install
- RStan / PyStan
  - C++ functions of Stan are called directly from R / Python
  - Higher integration between R/Python and Stan, but maybe more difficult to install due to more requirements of compatible C++ compilers and libraries
- More recent useful R packages
  - posterior: for handling posterior draws, convergence diagnostics, and summaries
  - tidybayes + ggdist: pretty plots