

Chapter 10

- 10.1 Numerical integration (overview)
- 10.2 Distributional approximations (overview, more in Chapter 4 and 13)
- 10.3 Direct simulation and rejection sampling (overview)
- 10.4 **Importance sampling** (used in PSIS-LOO, Lecture 9)
- 10.5 **How many simulation draws are needed?**
 - see chapter notes for how many significant digits to report
 - this week focus on independent draws and importance sampling, next week necessary adjustments needed for **Markov chain Monte Carlo**
- 10.6 Software (can be skipped)
- 10.7 Debugging (can be skipped)

Notation

- In this chapter, generic $p(\theta)$ is used instead of $p(\theta|y)$
- Unnormalized distribution is denoted by $q(\cdot)$
 - $\int q(\theta)d\theta \neq 1$, but finite
 - $q(\cdot) \propto p(\cdot)$
- Proposal distribution is denoted by $g(\cdot)$

Numerical accuracy – floating point

- Floating point presentation of numbers. e.g. with 64bits
 - closest value to zero is $\approx 2.2 \cdot 10^{-308}$
 - generate sample of 600 from normal distribution:
`qr=rnorm(600)`
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 - `pbeta(0.5, 241945, 251527)` → 1 (rounding)
 - `pbeta(0.5, 241945, 251527, lower.tail=FALSE)` $\approx -1.2 \cdot 10^{-42}$
there is more accuracy near 0

Numerical accuracy – log scale

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 - use log densities to avoid over- and underflows in floating point presentation
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e.g. $\log(\exp(800) + \exp(800)) \rightarrow \text{Inf}$ but $800 + \log(1 + \exp(800 - 800)) \approx 800.69$
 - e.g. in Metropolis-algorithm (Assignment 5) compute the log of ratio of densities using the identity
$$\log(a/b) = \log(a) - \log(b)$$

It's all about expectations

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

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 (lecture 3)

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

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- Monte Carlo methods which can sample from $p(\theta^{(s)}|y)$ using only $q(\theta^{(s)}|y)$ (each draw has weight 1/S)

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

It's all about expectations

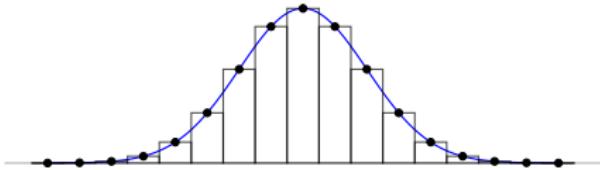
$$E_{\theta}[h(\theta)] = \int h(\theta)p(\theta|y)d\theta$$

- Conjugate priors and analytic solutions (Ch 1-5, Lec 2–3)
- Grid integration and other quadrature rules (Ch 3, 10, Lec 3–4)
- Independent Monte Carlo, rejection and importance sampling (Ch 10, Lec 4)
- Markov Chain Monte Carlo (Ch 11-12, Lec 5–6)
- Distributional approximations (Laplace, VB, EP) (Ch 4, 13)

Quadrature integration

- The simplest quadrature integration is grid integration

$$E[\theta] \approx \sum_{t=1}^T \theta^{(t)} w^{(t)},$$

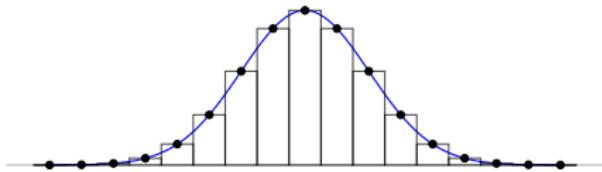


where $w^{(t)}$ is the normalized probability of a grid cell t , and $\alpha^{(t)}$ and $\beta^{(t)}$ are center locations of grid cells

Quadrature integration

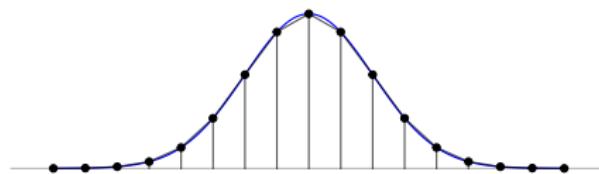
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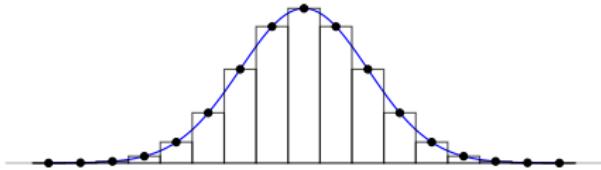
- In 1D further variations with better accuracy, e.g. trapezoid



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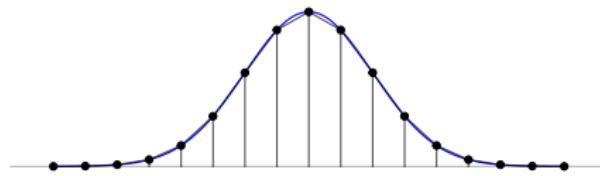
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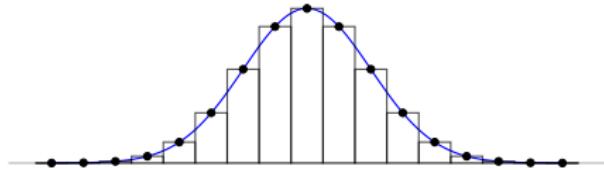


- Adaptive quadrature methods add evaluation points where needed, e.g., R function `integrate()`

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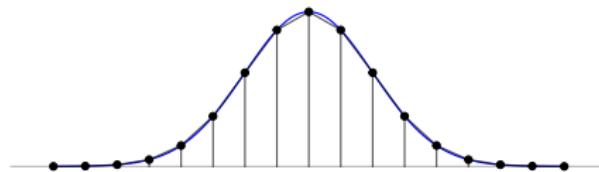
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- Adaptive quadrature methods add evaluation points where needed, e.g., R function `integrate()`
- In 2D and higher
 - nested quadrature
 - product rules

Monte Carlo - history

- Used already before computers
 - Buffon (18th century; needles)
 - De Forest, Darwin, Galton (19th century)
 - Pearson (19th century; roulette)
 - Gosset (Student, 1908; hat)

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- Bayesians started to have enough cheap computation time in 1990s
 - BUGS project started 1989 (last OpenBUGS release 2014)
 - Gelfand & Smith, 1990
 - Stan initial release 2012

Monte Carlo

- Simulate draws from the target distribution
 - these draws can be treated as any observations
 - a collection of draws is sample
- Use these draws, for example,
 - to compute means, deviations, quantiles
 - to draw histograms
 - to marginalize
 - etc.

Monte Carlo vs. deterministic

- Monte Carlo = simulation methods
 - evaluation points are selected stochastically (randomly)
- Deterministic methods (e.g. grid)
 - evaluation points are selected by some deterministic rule
 - good deterministic methods converge faster (need less function evaluations)

How many simulation draws are needed?

- How many draws or how big sample size?
- If draws are independent
 - usual methods to estimate the uncertainty due to a finite number of observations (finite sample size)
- Markov chain Monte Carlo produces dependent draws
 - requires additional work to estimate the effective sample size
 - next week

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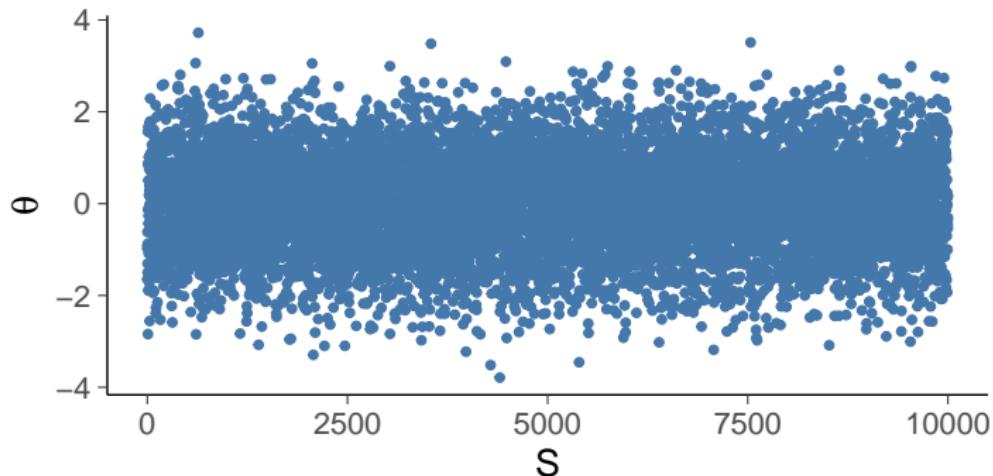
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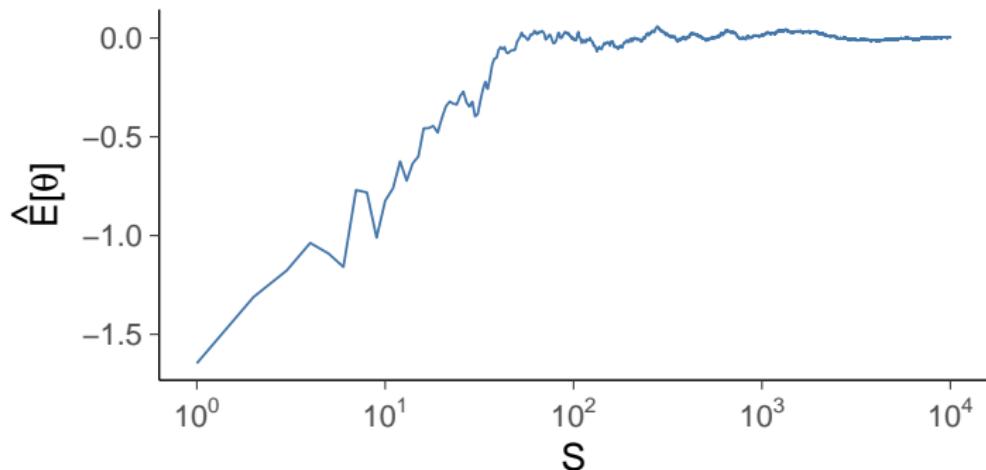


`rnorm(n=10000, mean=0, sd=1)`

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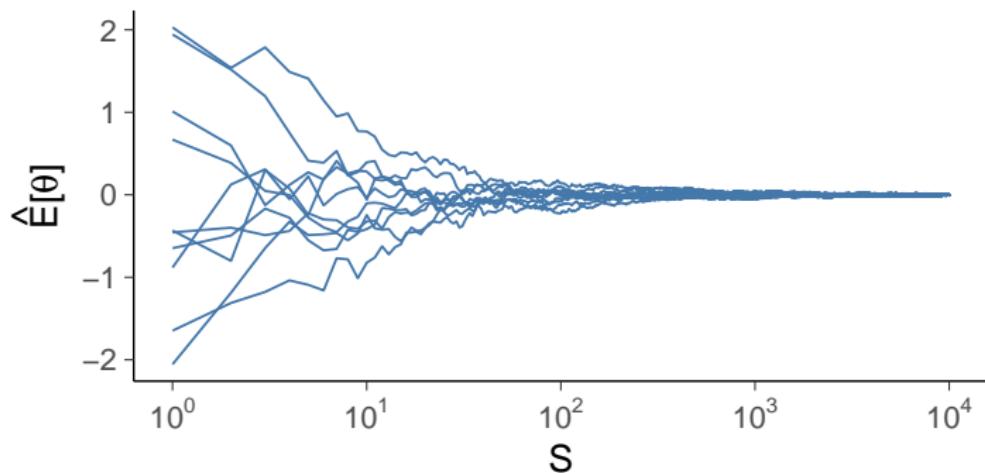


`cummean(rnorm(n=10000, mean=0, sd=1))`

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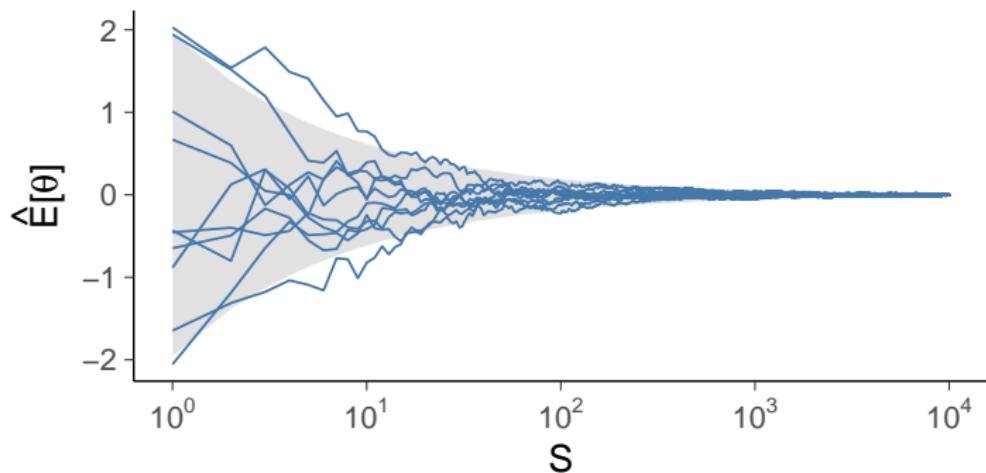
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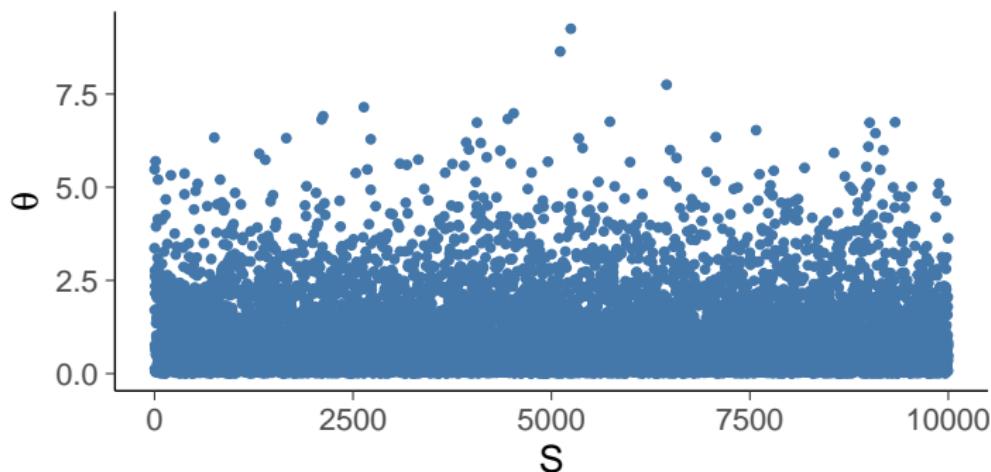
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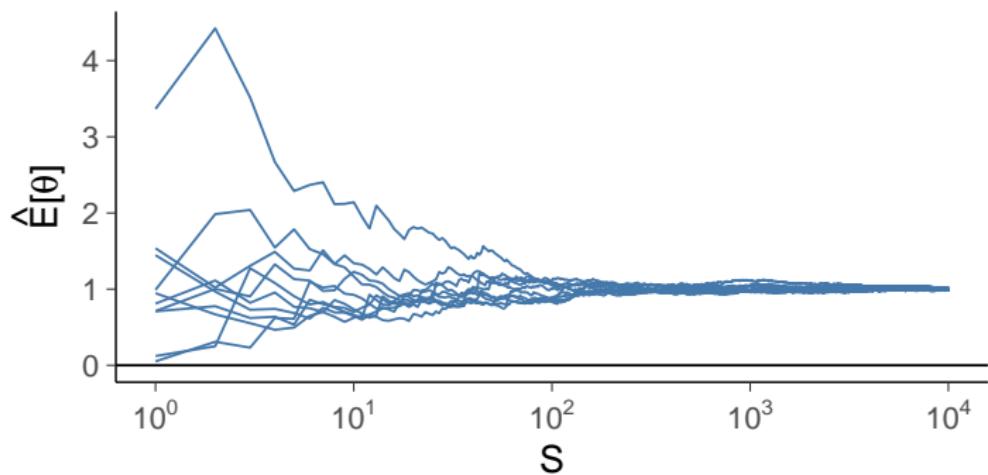


`rexp(n=10000, rate=1)`

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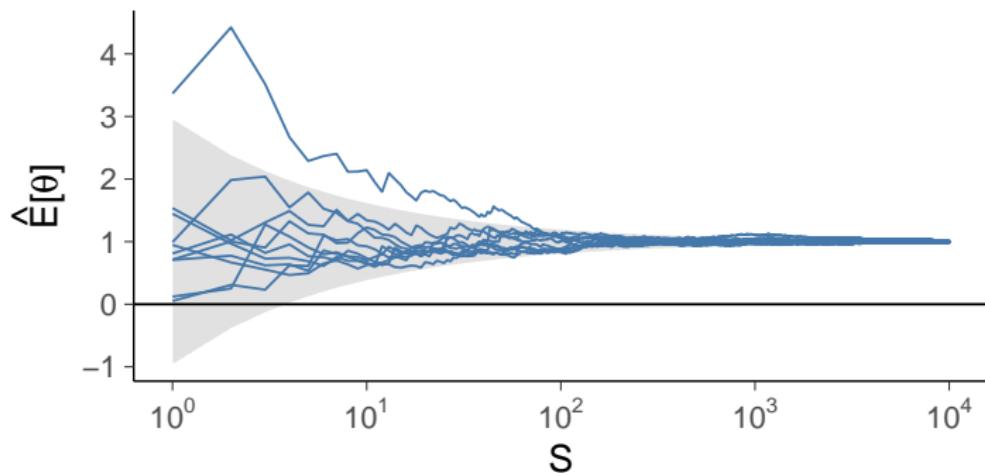


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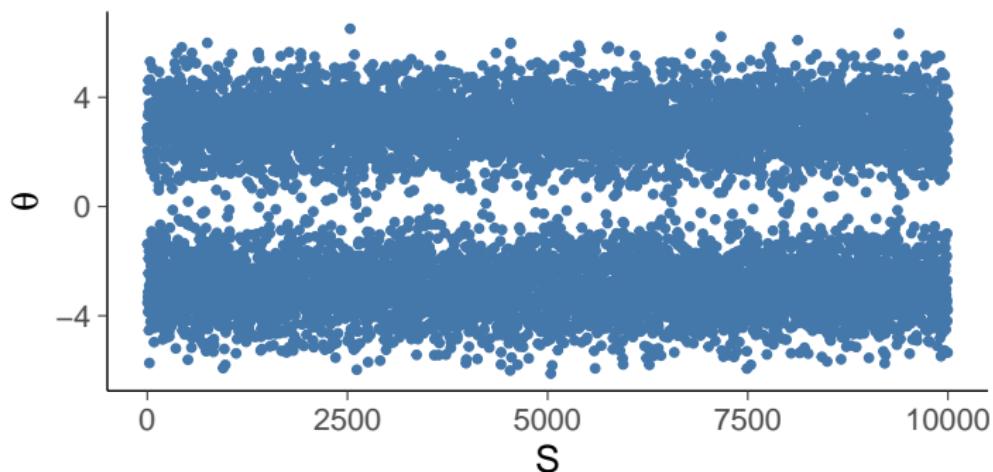
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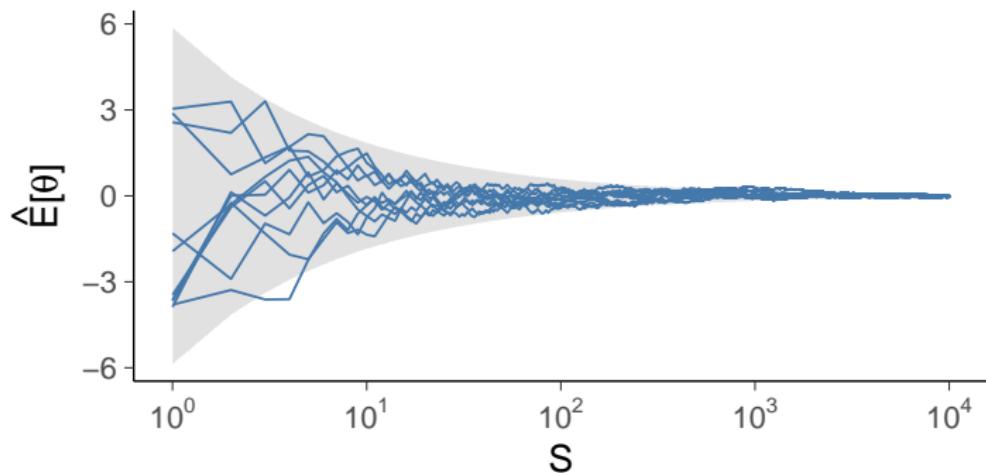


```
rnorm(n=10000, mean=sample(c(-3,3), 10000, replace=TRUE))
```

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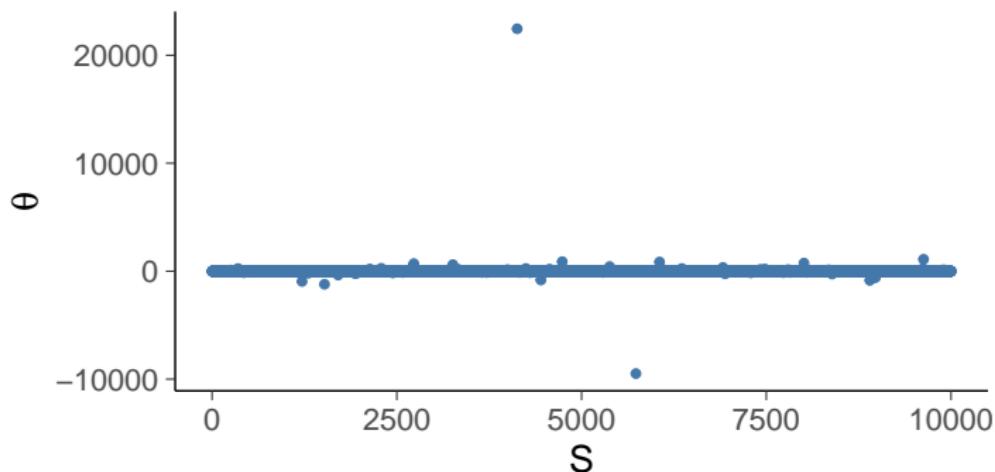
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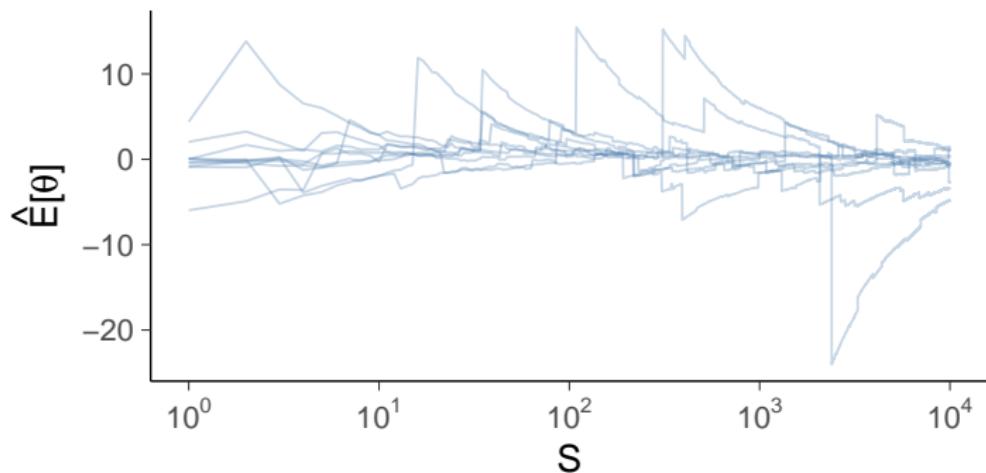


`rt(n=10000, df=1)`

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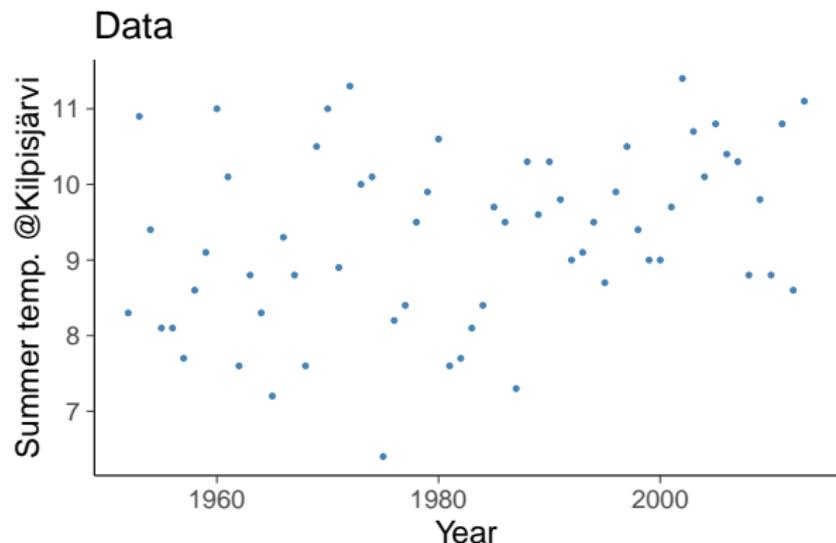
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- σ_θ/\sqrt{S} is called Monte Carlo standard error (MCSE)
- In practice, σ_θ will be estimated by

$$\sqrt{1/(S-1) \sum_{s=1}^S (\theta^{(s)} - E(\theta))^2}$$

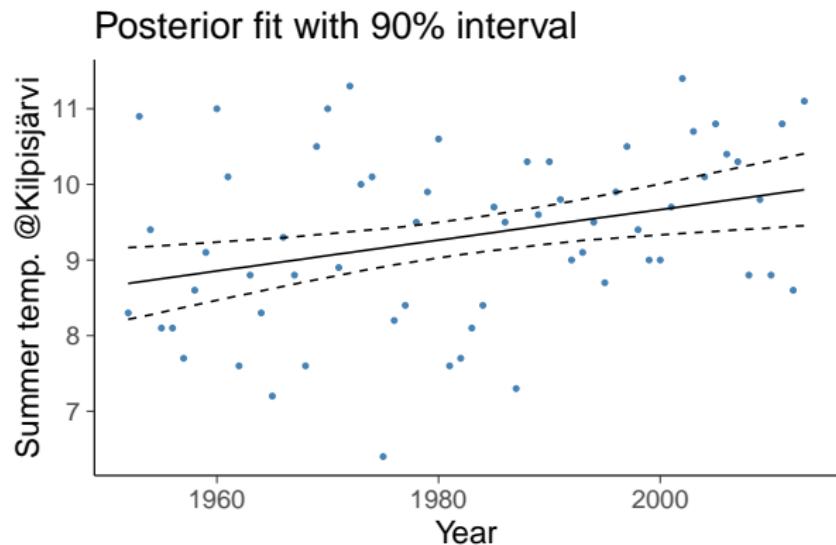
Example: Kilpisjärvi summer temperature

Average temperature in June, July, and August at Kilpisjärvi, Finland
in 1952–2013



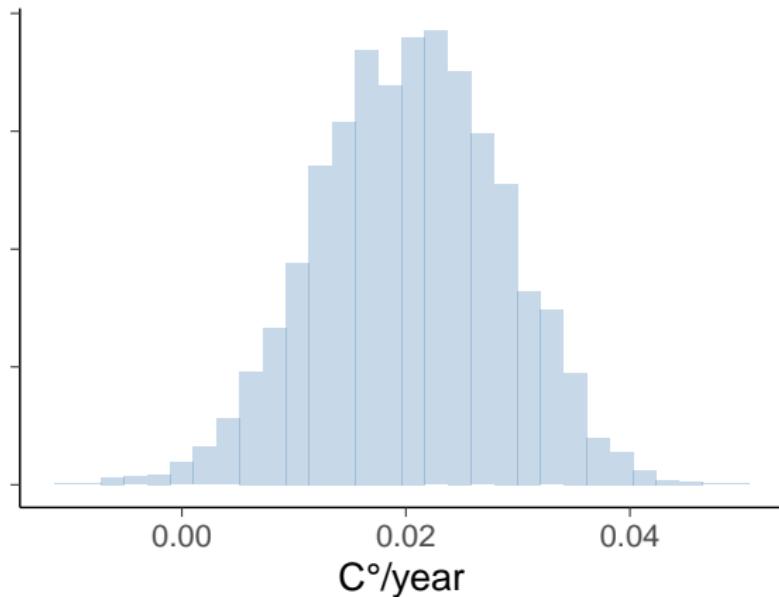
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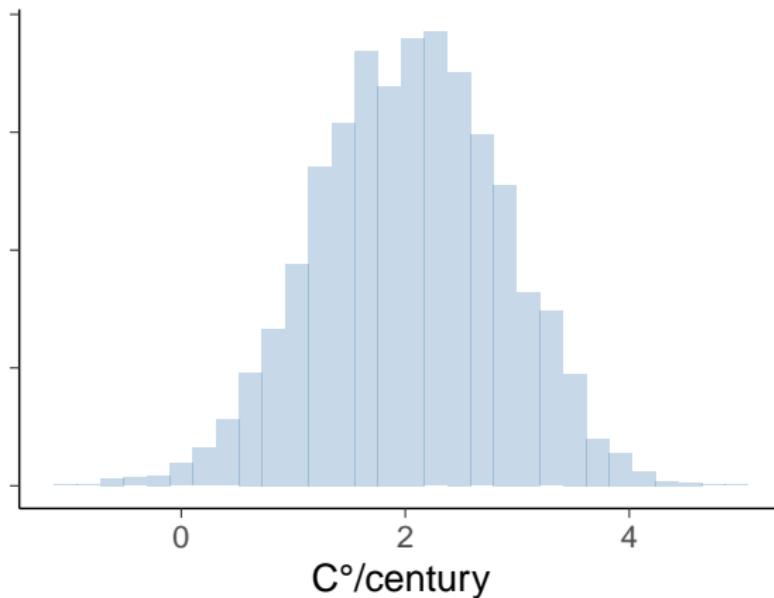
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Posterior of temperature change

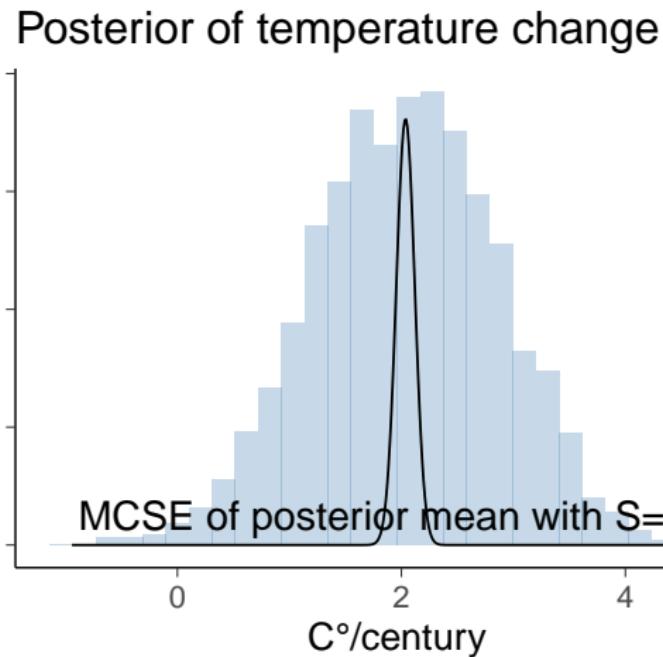


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Posterior of temperature change



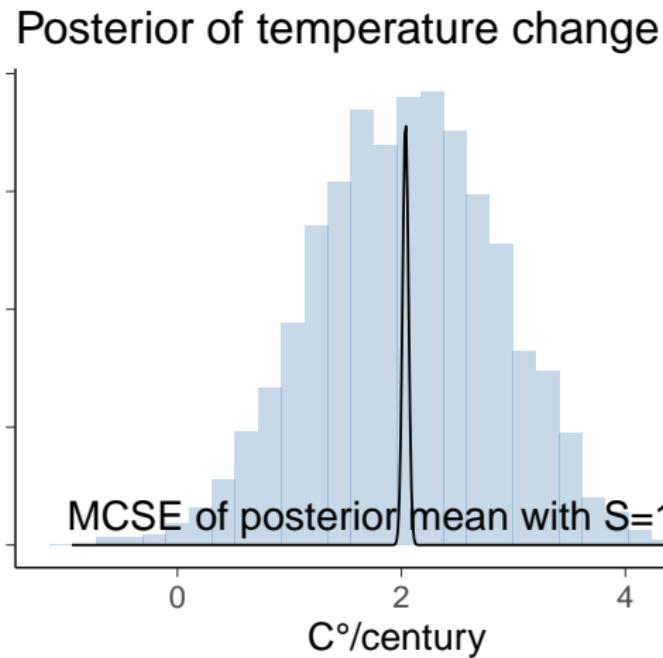
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$$\sigma_\theta \approx 0.83, \text{ MCSE} = \sigma_\theta / \sqrt{S} \approx 0.083,$$

in repeated sampling we may expect mean estimate to vary within
(1.8, 2.1) (90% interval)

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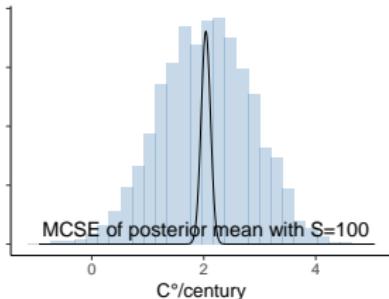


$$\sigma_\theta \approx 0.83, \text{MCSE} \approx 0.026,$$

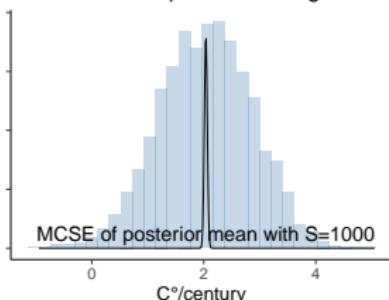
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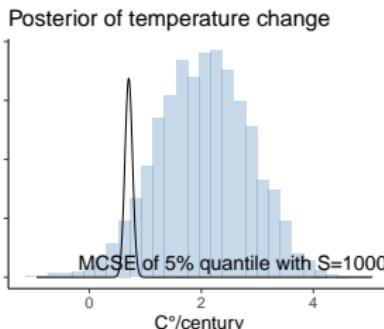
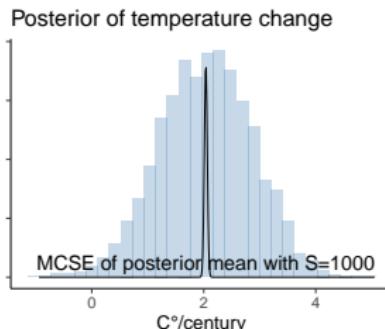
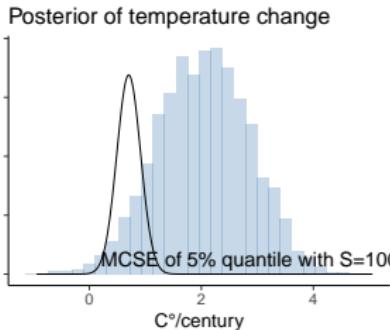
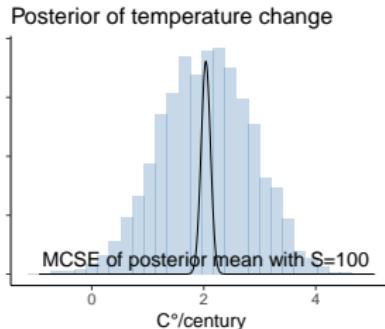
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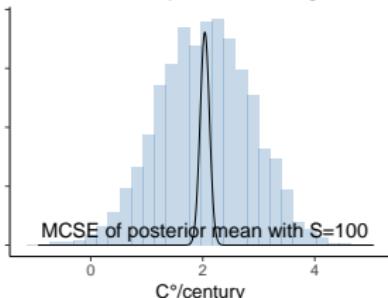


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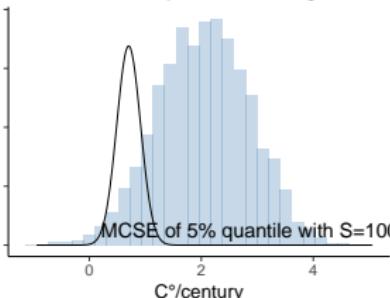


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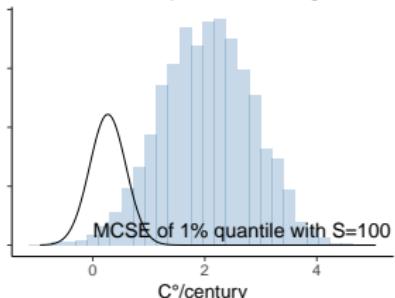
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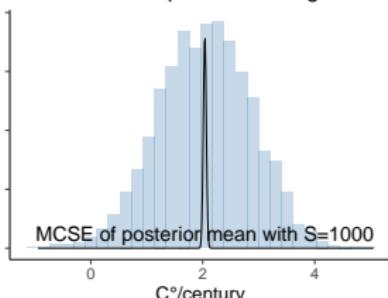
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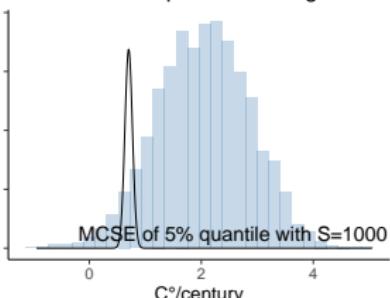
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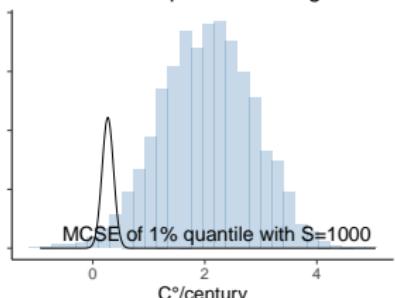
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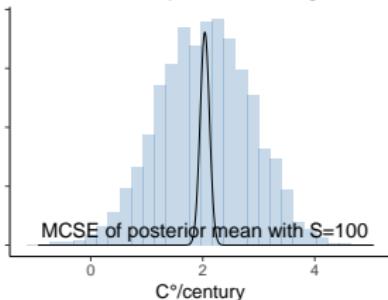


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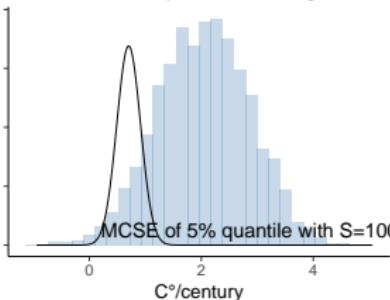


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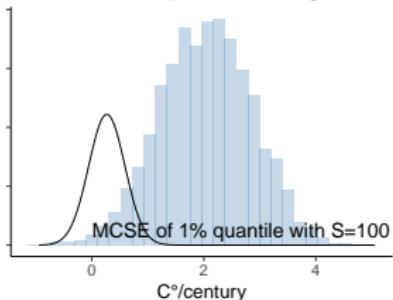
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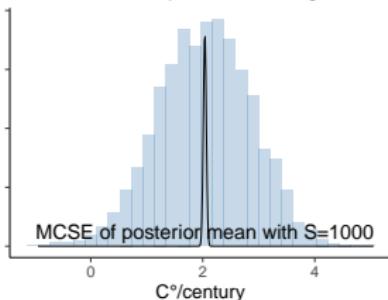
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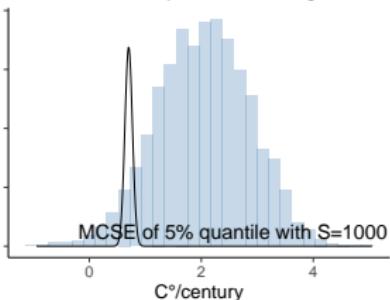
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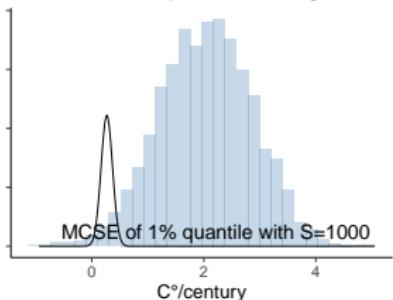
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Tail quantiles are more difficult to estimate

See Vehtari, Gelman, Simpson, Carpenter, & Bürkner (2021) for quantile MCSE computation.

How many simulation draws are needed?

- Posterior probability

$$p(\theta \in A) \approx \frac{1}{S} \sum_l I(\theta^{(s)} \in A)$$

where $I(\theta^{(s)} \in A) = 1$ if $\theta^{(s)} \in A$

- $I(\cdot)$ is binomially distributed as $p(\theta \in A)$
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 - $\text{var}(I(\cdot)) = p(1-p)S$ (Appendix A, p. 579)
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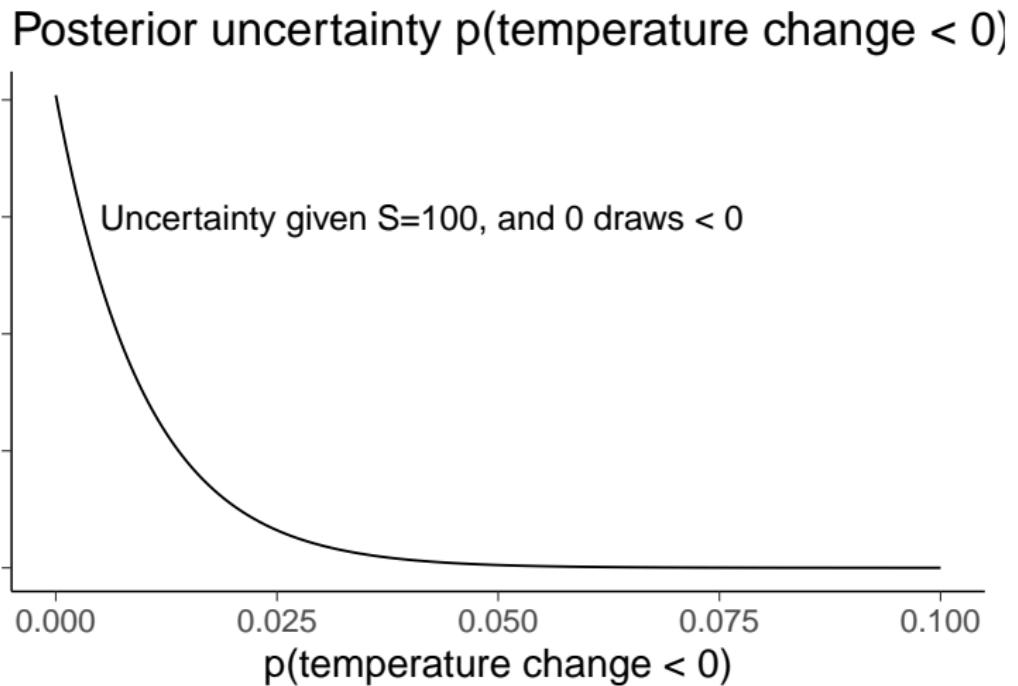
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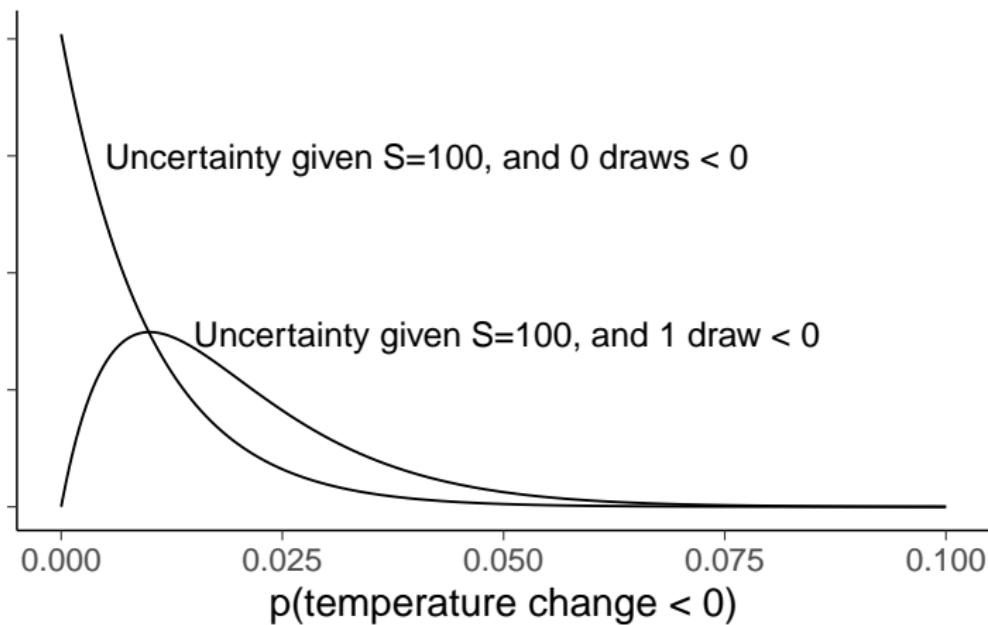
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- $S = 2000$ draws needed for 1% unit accuracy
- To estimate small probabilities, a large number of draws is needed
 - to be able to estimate small p , need to get draws with $\theta^{(l)} \in A$, which in expectation requires $S \gg 1/p$

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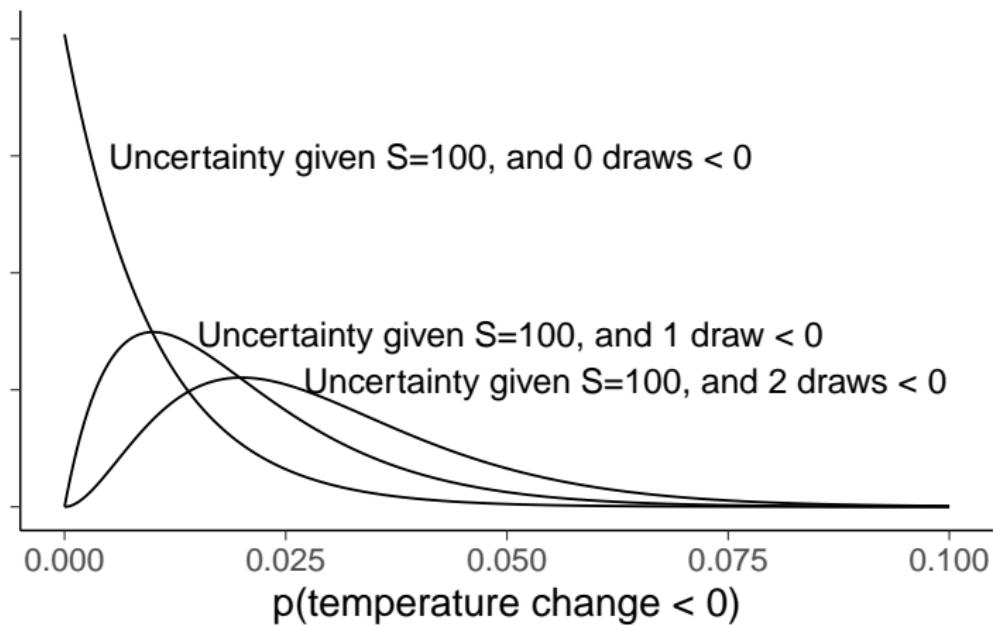
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Posterior uncertainty $p(\text{temperature change} < 0)$



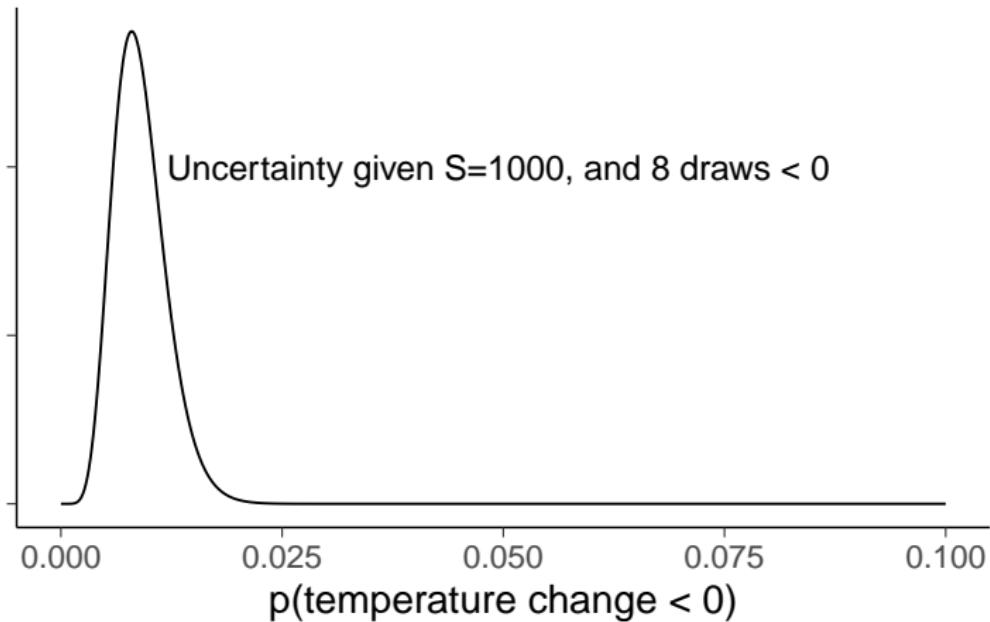
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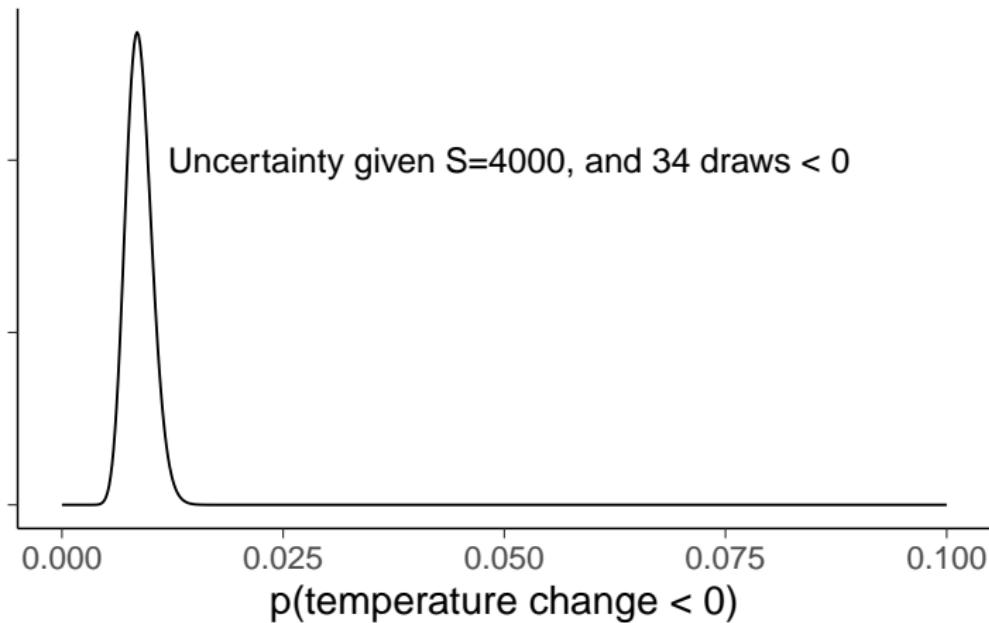
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From probabilities to quantiles

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- If $S = 1000$ and uncertainty interval for 5% probability is $(0.04, 0.06)$ (see earlier slide), we can find uncertainty interval (A^-, A^+) , so that $p(\theta < A^-) = 0.04$, and $p(\theta < A^+) = 0.06$

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 - we can summarise this interval by transforming it to MCSE
 - see examples in
<https://avehtari.github.io/casestudies/Digits/digits.html>
 - if interested, see algorithm details in Vehtari, Gelman, Simpson, Carpenter, & Bürkner (2021), doi.org/10.1214/20-BA1221.

posterior package

Posterior mean and 5% and 95% quantiles:

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draws %>%  
  subset_draws("beta100") %>%  
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These _mcse functions are for MCMC draws, but if the number of draws is big (≥ 1000), then these are accurate enough for independent MC draws, too

posterior package

Posterior probability and the corresponding MCSE estimate:

```
draws %>%  
  mutate_variables(beta0p = beta100>0) %>%  
  subset_draws("beta0p") %>%  
  summarize_draws(mean,  
                  mcse = mcse_mean)
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See also <https://users.aalto.fi/~ave/casestudies/Digits/digits.html>

More data

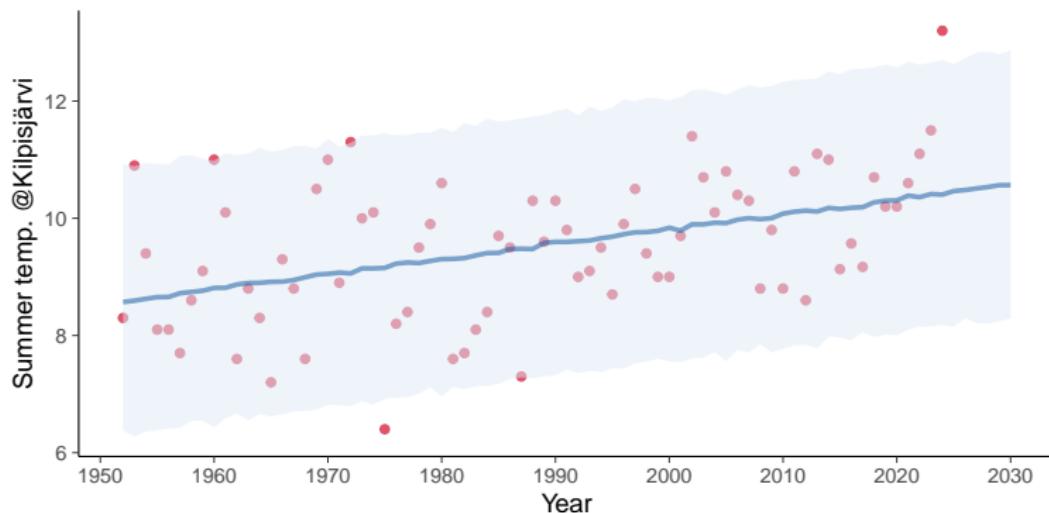
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- With data from 1952–2024
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 - With data from other locations we would be even more certain
- Summer 2023 was the second hottest in the recorded history
- Summer 2024 was the hottest in the recorded history



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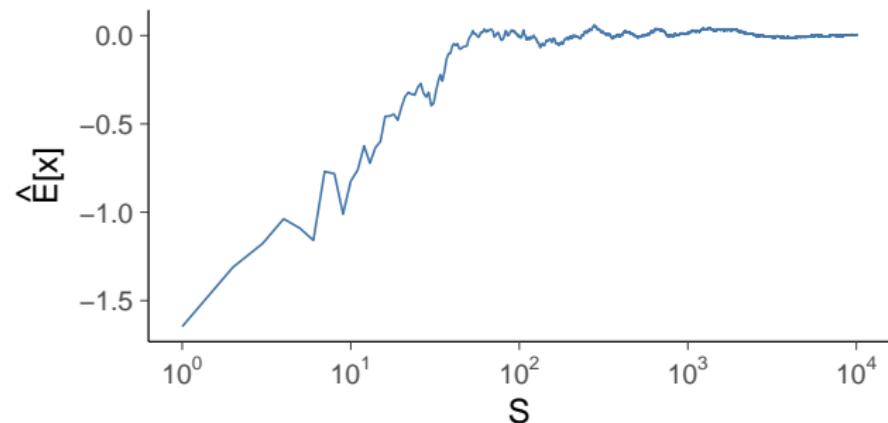
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- How to check if a distribution has finite mean and variance?
 - Pareto- \hat{k} diagnostic

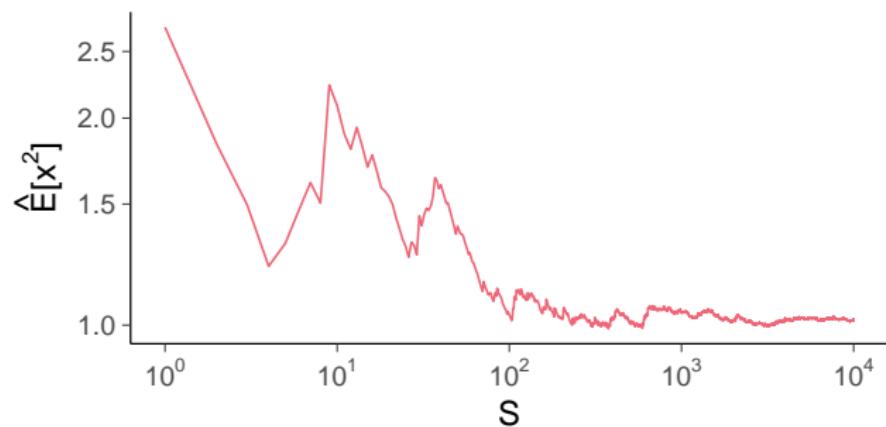
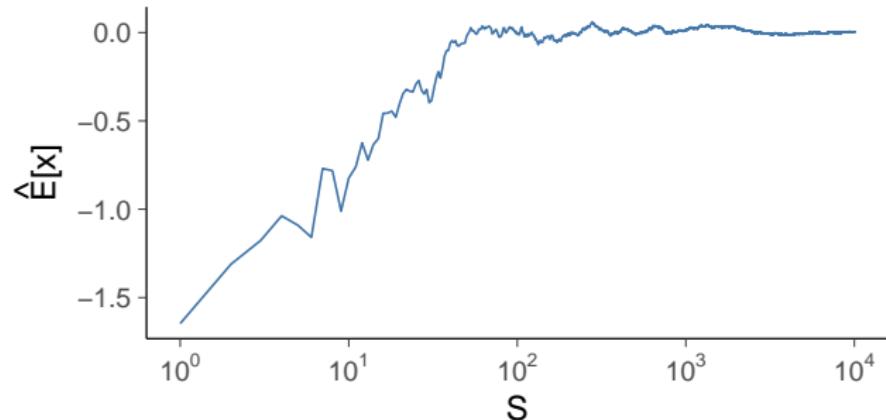
Simple example: $x \sim N$, t_4 , t_2 , t_1 , $t_{1/2}$

- N has all moments finite
- t_ν has less than ν fractional moments

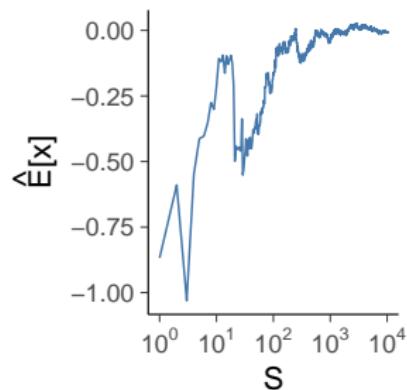
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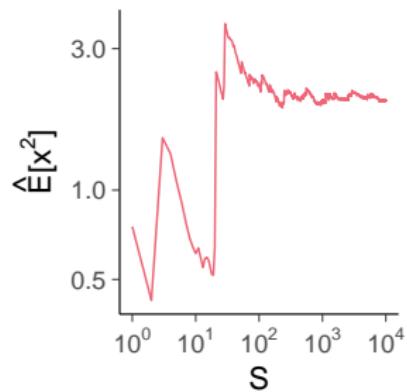
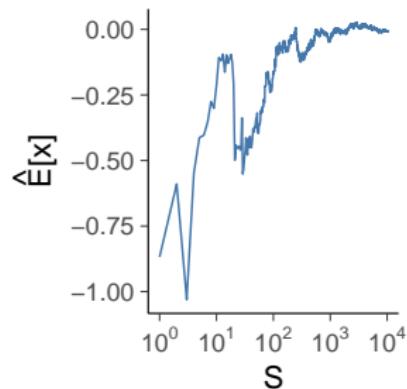
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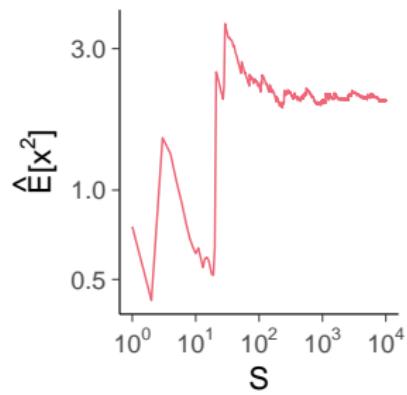
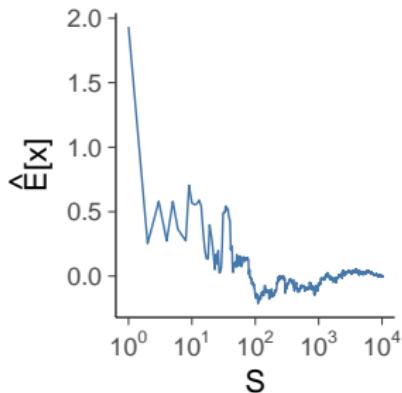
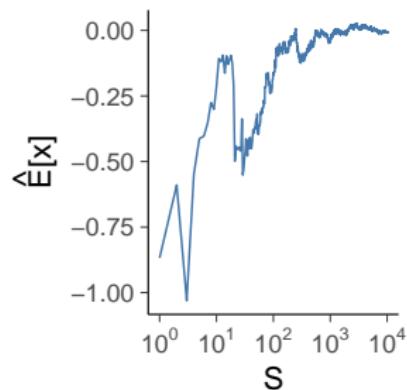
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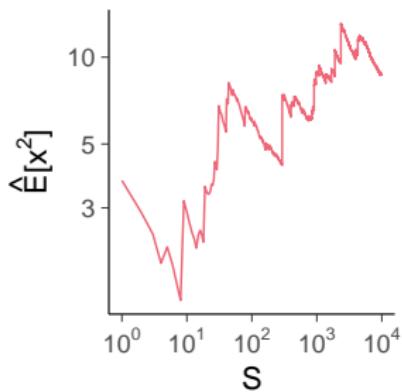
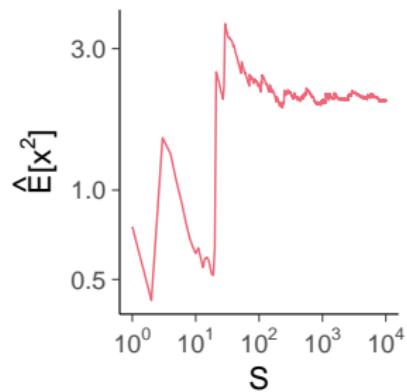
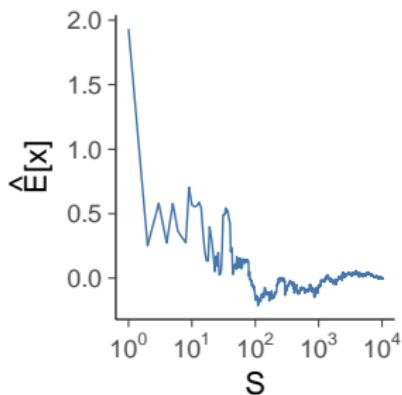
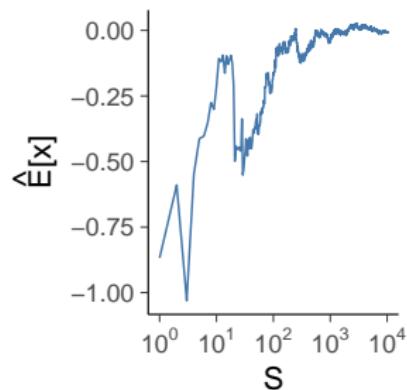
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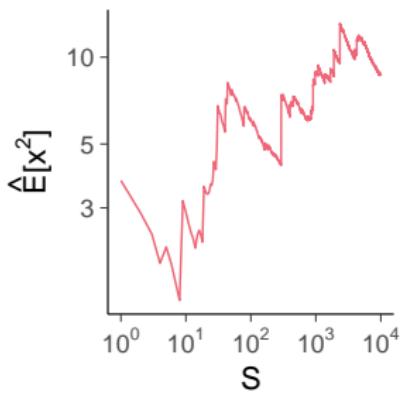
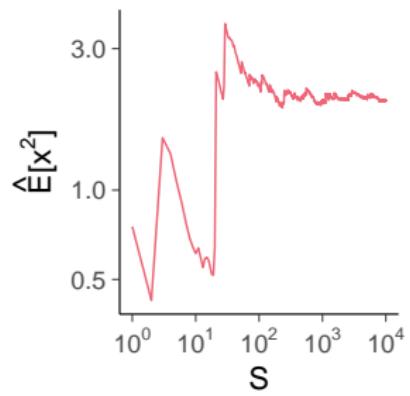
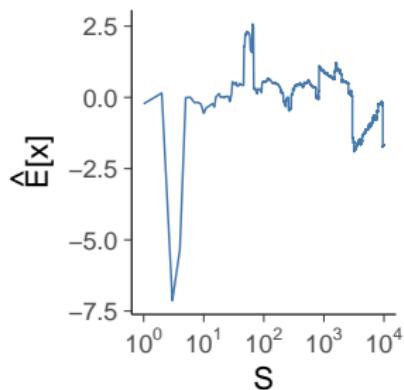
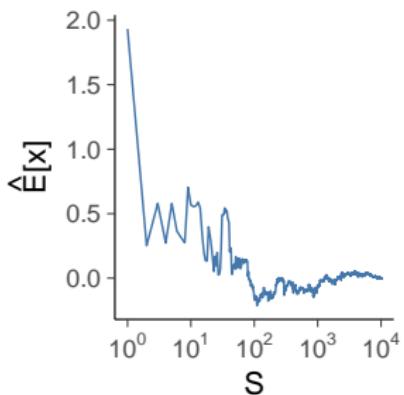
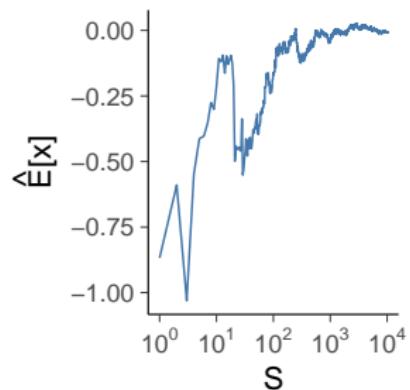
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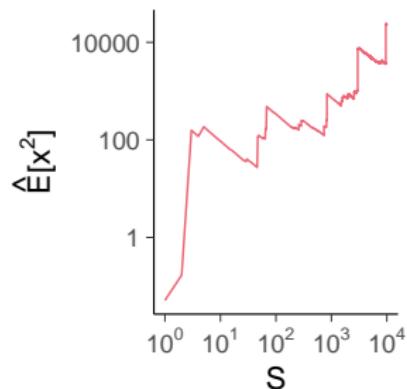
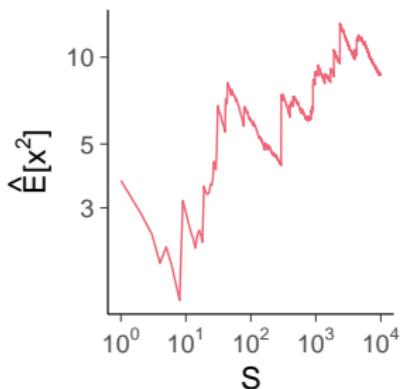
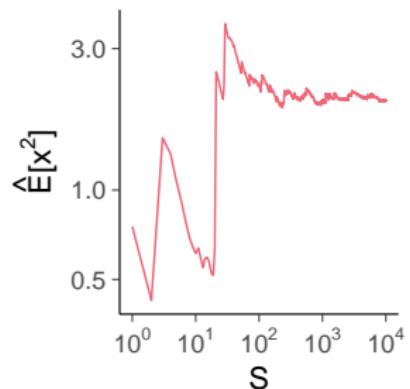
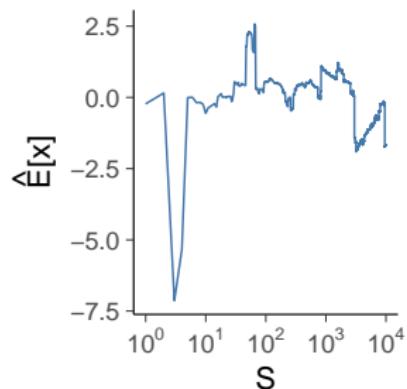
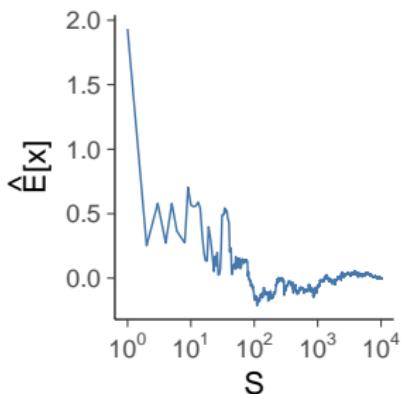
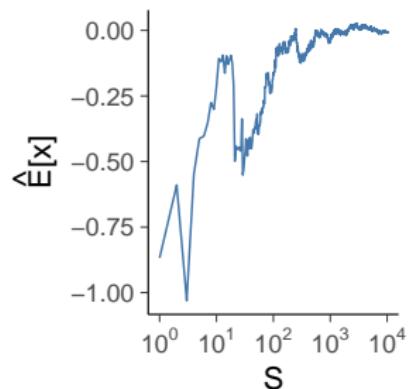
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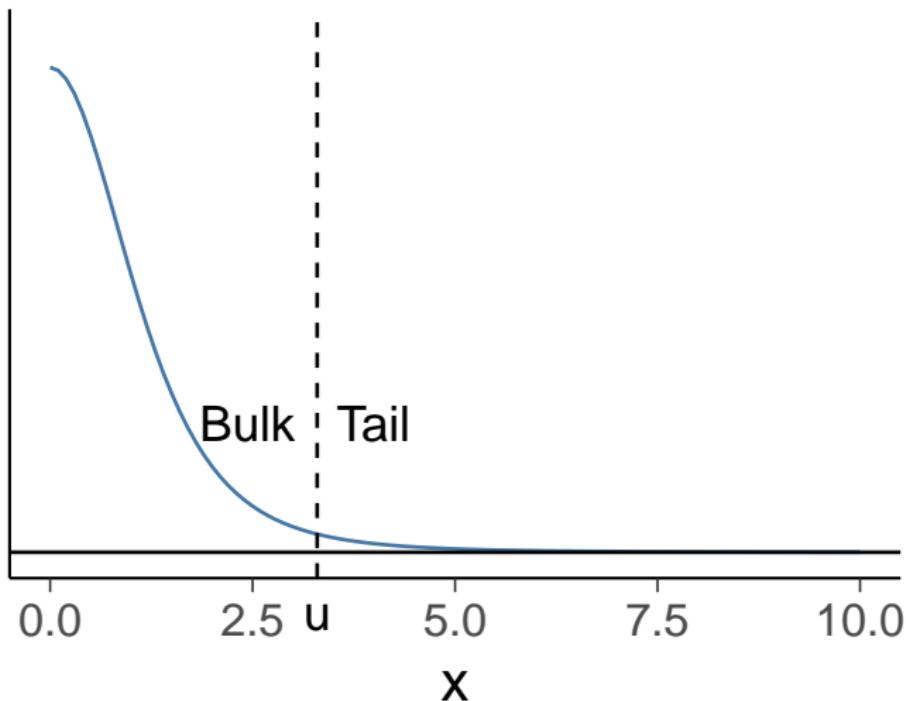


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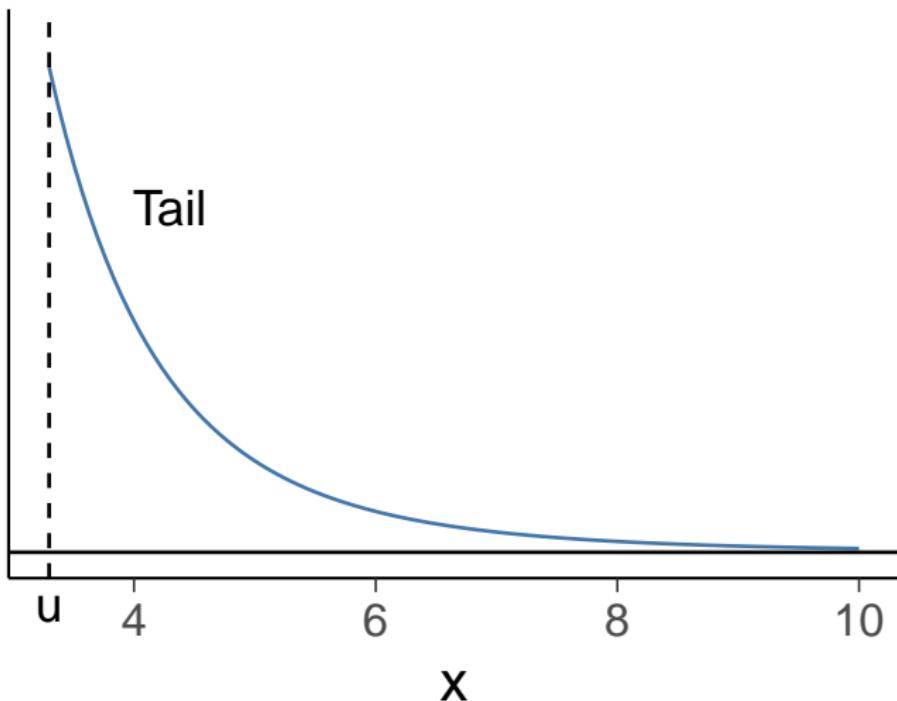
Pareto- \hat{k} diagnostic

Pickands (1975): many distributions have tail ($x > u$) that is well approximated with Generalized Pareto distribution (GPD)



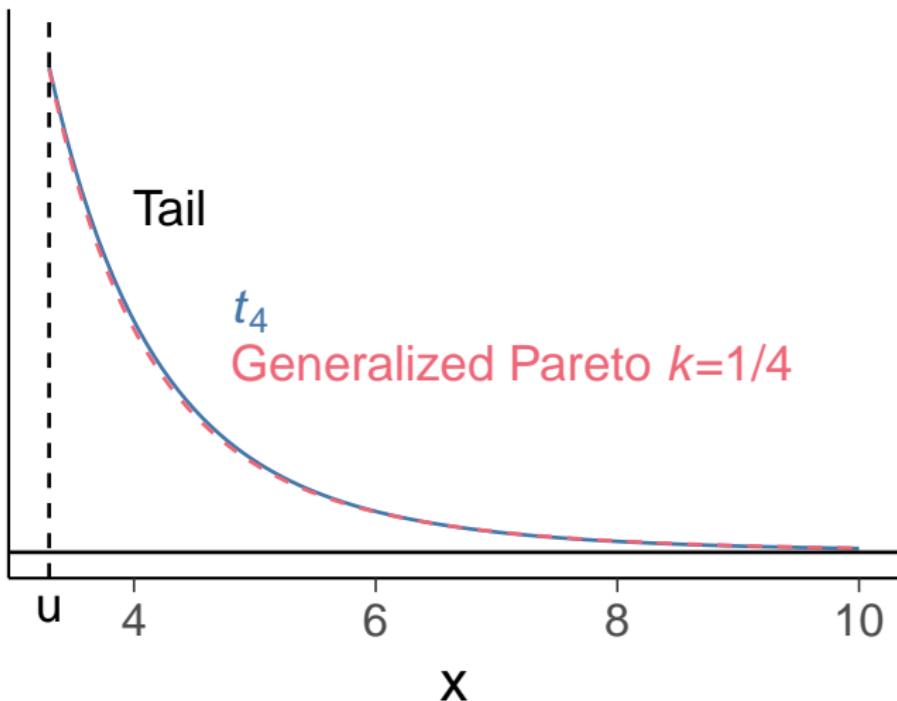
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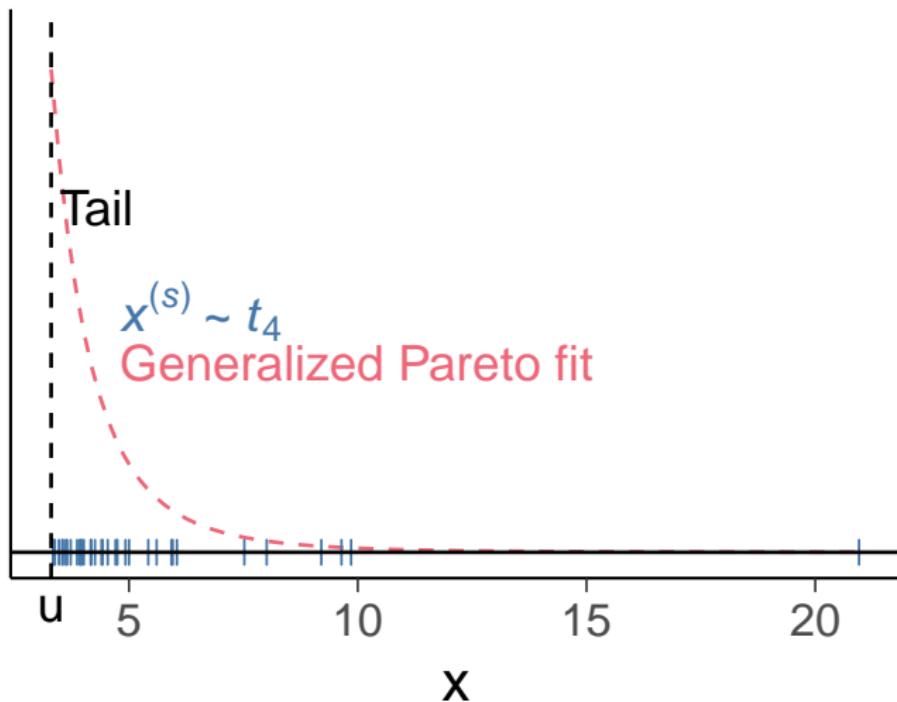
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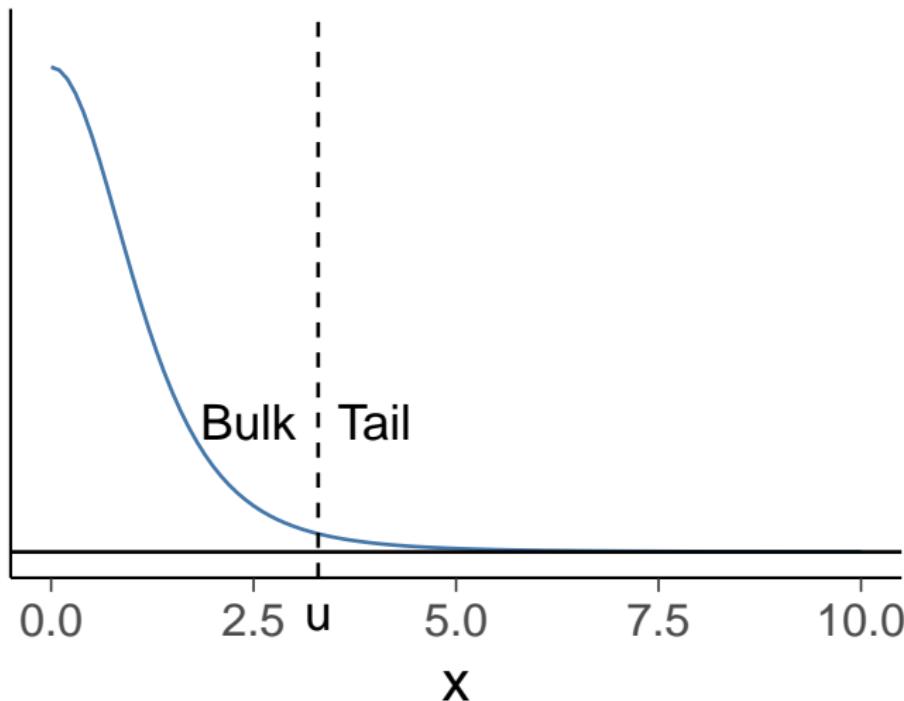
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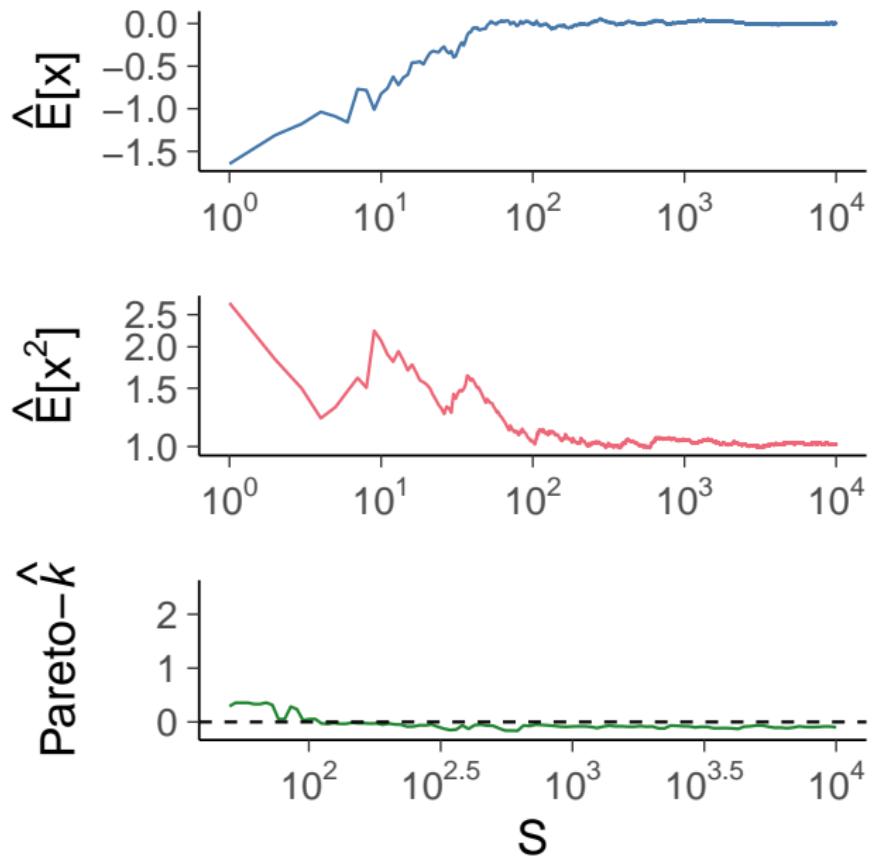


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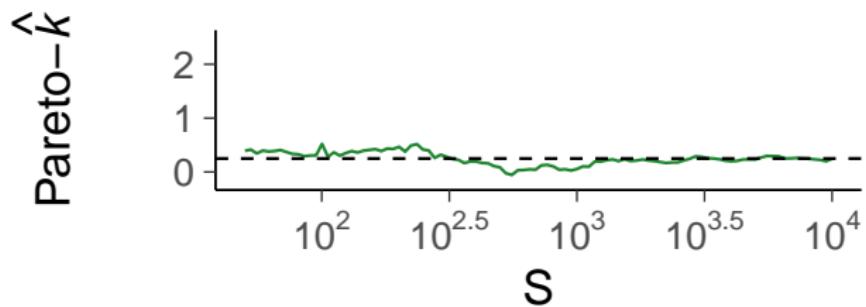
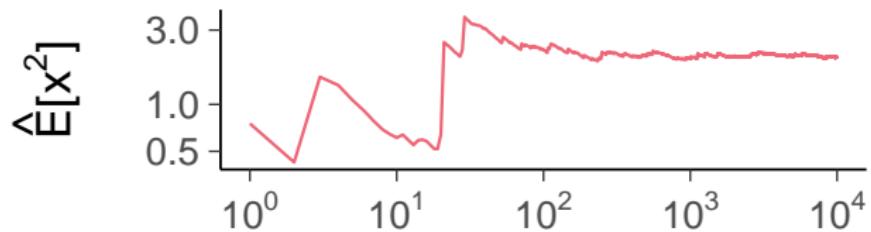
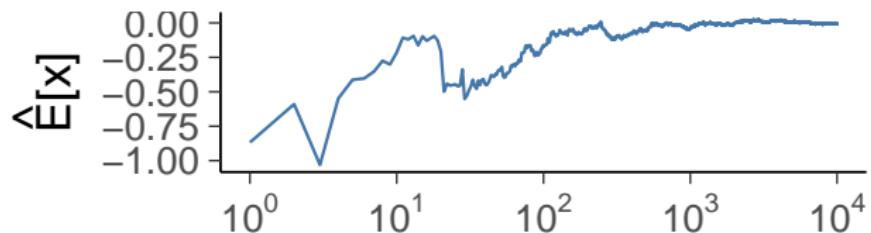
GPD has a shape parameter k ,
and $1/k$ finite fractional moments



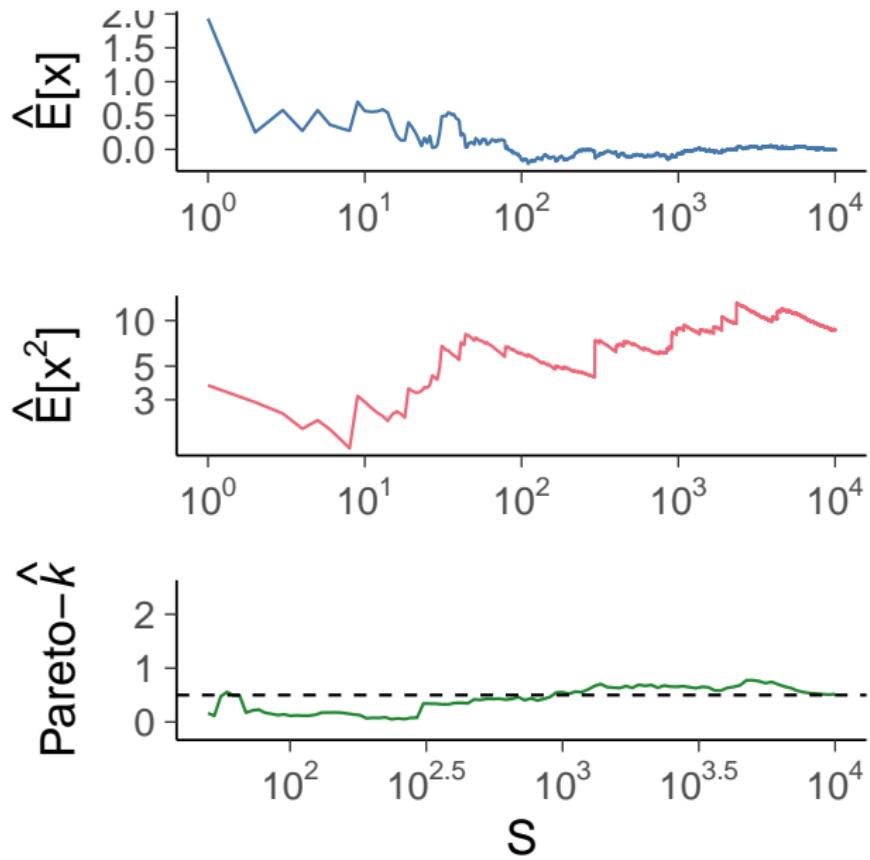
Pareto- \hat{k} diagnostic: $x \sim N$



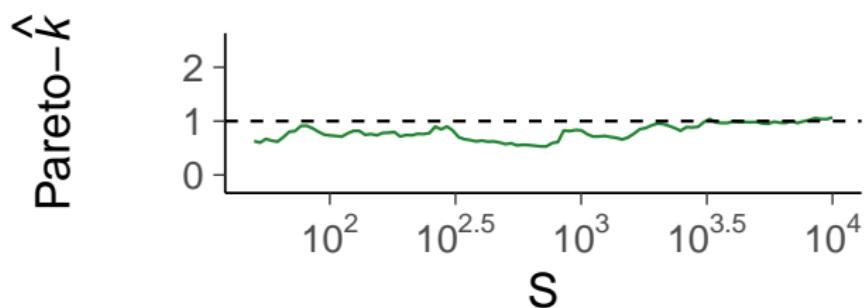
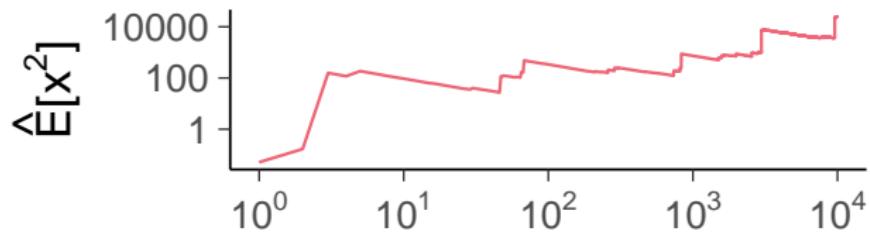
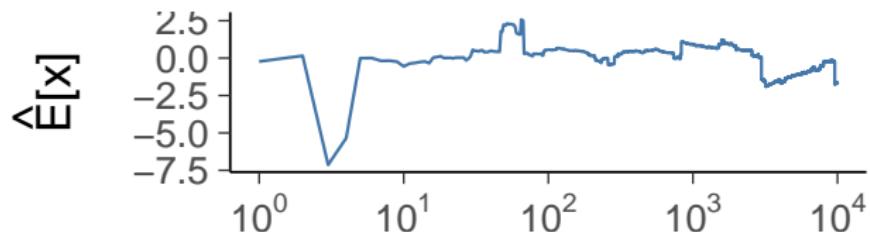
Pareto- \hat{k} diagnostic: $x \sim t_4$



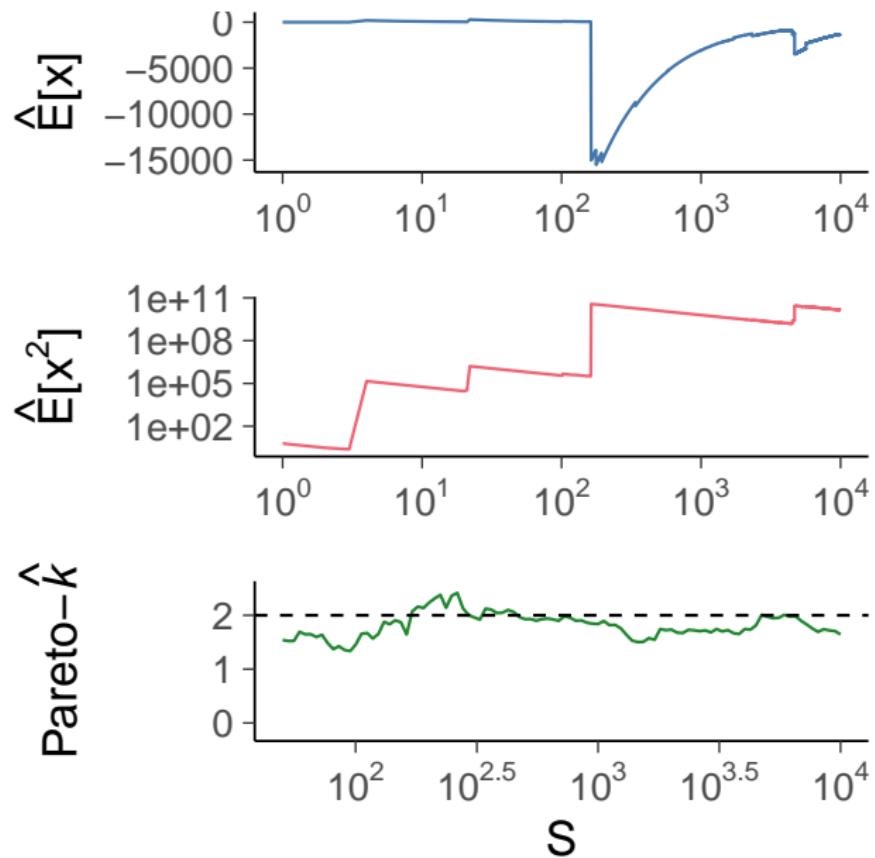
Pareto- \hat{k} diagnostic: $x \sim t_2$



Pareto- \hat{k} diagnostic: $x \sim t_1$



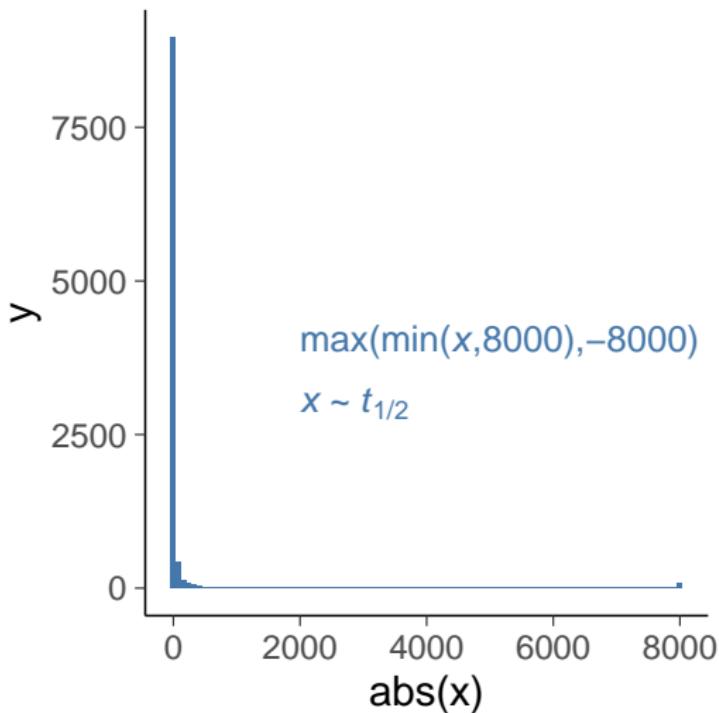
Pareto- \hat{k} diagnostic: $x \sim t_{1/2}$



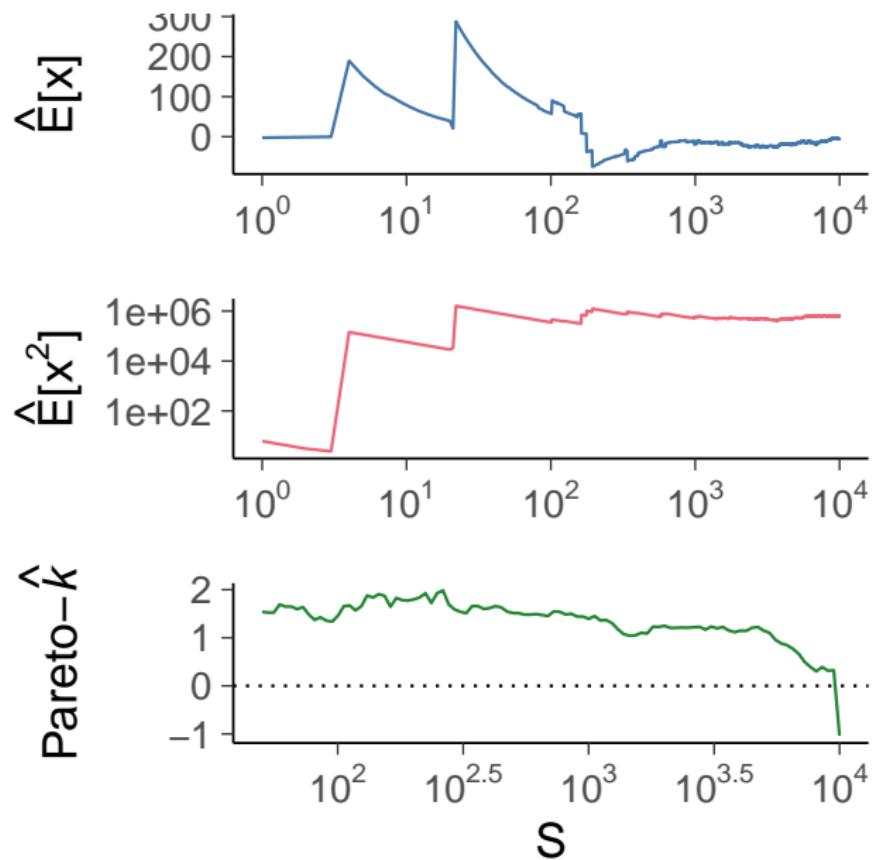
Pareto- \hat{k} diagnostic is pre-asymptotic diagnostic

Thick tailed but truncated distribution

We can make estimates only based on what we have observed.



Pareto- \hat{k} diagnostic: thick-tailed bounded distribution



Thick-tailed bounded distributions in practice

- Thick-tailed distributions are common in importance sampling and variational divergence estimation

Pareto- \hat{k} in posterior package

```
> drt |> summarise_draws(mean, mcse_mean)
```

variable	mean	mcse_mean
xn	0.010	0.021
xt3	0.025	0.033
xt2_5	0.031	0.039
xt2	0.046	0.054
xt1_5	0.092	0.13
xt1	0.33	1.5

Pareto- \hat{k} in posterior package

```
> drt |> summarise_draws(mean, mcse_mean, pareto_khat)
```

variable	mean	mcse_mean	khat
xn	0.010	0.021	-0.072
xt3	0.025	0.033	0.33
xt2_5	0.031	0.039	0.41
xt2	0.046	0.054	0.52
xt1_5	0.092	0.13	0.69
xt1	0.33	1.5	1.0

How to use Pareto- \hat{k} diagnostic

- To check posterior of any quantity of interest
 - if high \hat{k} , maybe use some other summary than mean, e.g., quantiles

See more in Vehtari, Simpson, Gelman, Yao, and Gabry (2024). Pareto smoothed importance sampling. *JMLR*, 25(72):1-58.

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 - e.g. if close to 0.5 more draws help to improve to decide whether $k < 0.5$
- Pareto-smoothing improves the mean estimate
 - reliable mean and MCSE estimates when Pareto- $k < 0.7$
 - required minimum sample size and convergence rate estimates for different values of k
 - more on lecture 9

See more in Vehtari, Simpson, Gelman, Yao, and Gabry (2024). Pareto smoothed importance sampling. *JMLR*, 25(72):1-58.

Direct simulation

- Produces independent draws
 - Using analytic transformations of uniform random numbers (e.g. appendix A)
 - factorization
 - numerical inverse-CDF
- Problem: restricted to limited set of models

Random number generators

- Good pseudo random number generators are sufficient for Bayesian inference
 - pseudo random generator uses deterministic algorithm to produce a sequence which is difficult to make difference from truly random sequence
 - modern software used for statistical analysis have good pseudo RNGs

Direct simulation: Example

- Box-Muller -method:

If U_1 and U_2 are independent draws from distribution $U(0, 1)$, and

$$X_1 = \sqrt{-2 \log(U_1)} \cos(2\pi U_2)$$
$$X_2 = \sqrt{-2 \log(U_1)} \sin(2\pi U_2)$$

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then X_1 and X_2 are independent draws from the distribution $N(0, 1)$

- not the fastest method due to trigonometric computations
- for normal distribution more than ten different methods
- e.g. R uses inverse-CDF

Grid sampling and curse of dimensionality

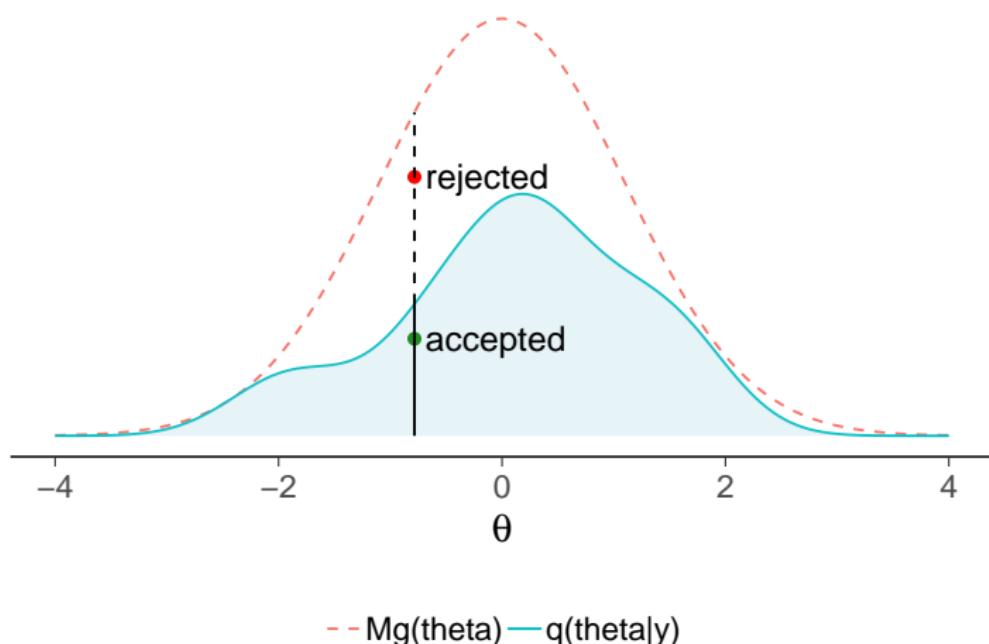
- 10 parameters
- if we don't know beforehand where the posterior mass is
 - need to choose wide box for the grid
 - need to have enough grid points to get some of them where essential mass is
- e.g. 50 or 1000 grid points per dimension
 - $50^{10} \approx 1e17$ grid points
 - $1000^{10} \approx 1e30$ grid points
- R and my current laptop can compute density of normal distribution about 50 million times per second
 - evaluation in $1e17$ grid points would take 60 years
 - evaluation in $1e30$ grid points would take 600 billion years

Indirect sampling

- Rejection sampling
- Importance sampling
- Markov chain Monte Carlo (next week)

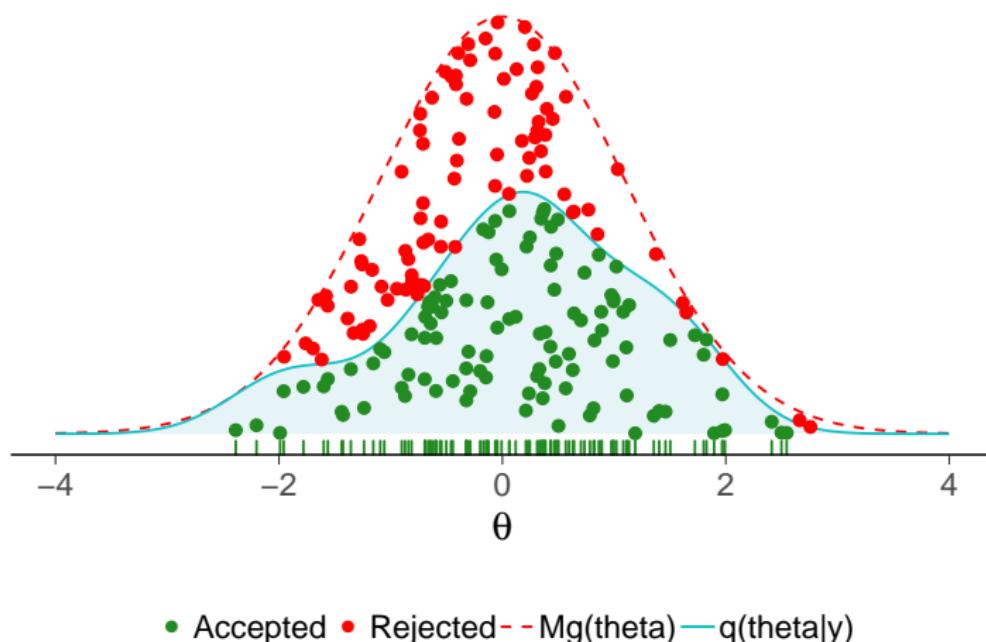
Rejection sampling

- Proposal forms envelope over the target distribution
 $q(\theta|y)/Mg(\theta) \leq 1$
- Draw from the proposal and accept with probability
 $q(\theta|y)/Mg(\theta)$



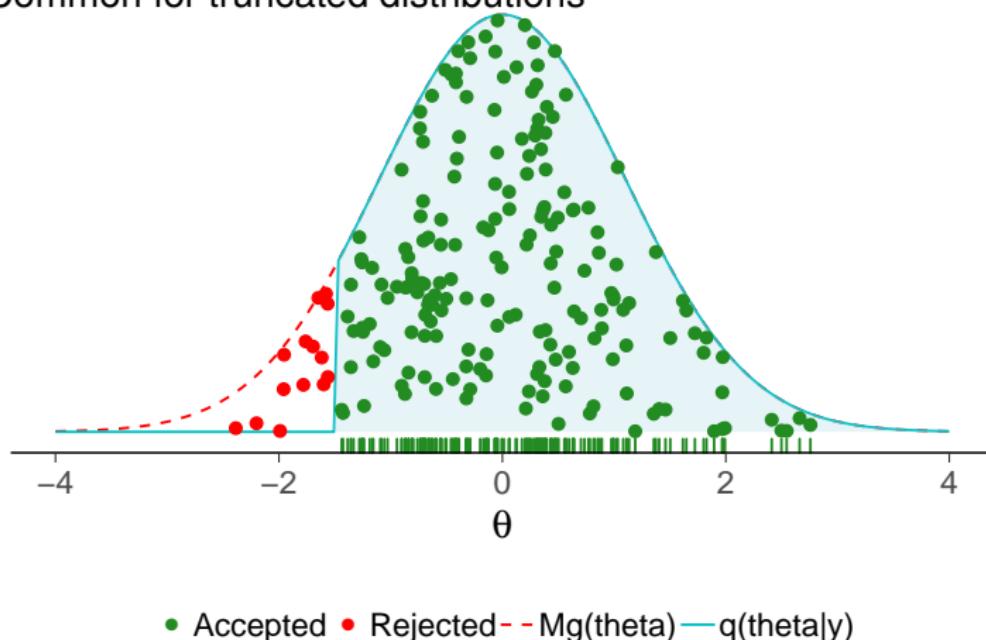
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Rejection sampling

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- Common for truncated distributions



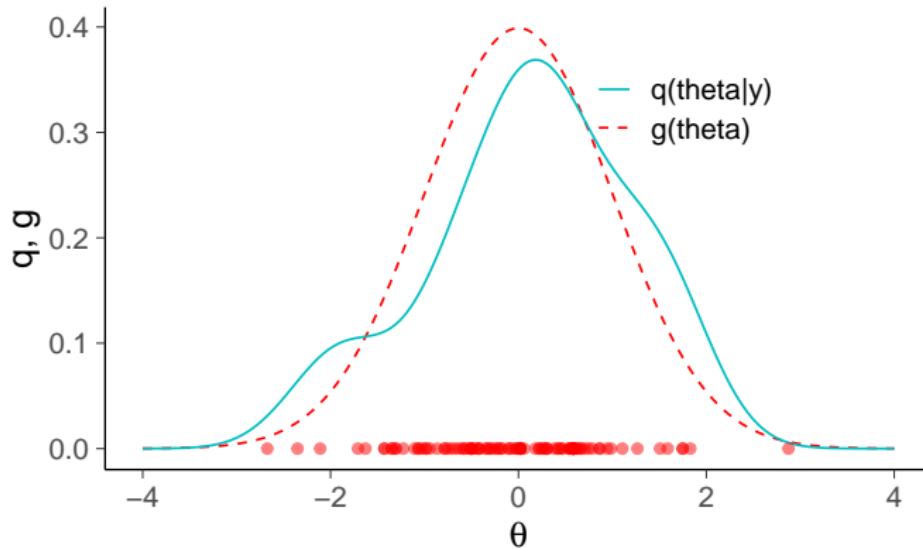
Rejection sampling

- The effective sample size (ESS) is the number of accepted draws
 - with bad proposal distribution may require a lot of trials
 - selection of good proposal gets very difficult when the number of dimensions increase
 - reliable diagnostics and thus can be a useful part

Importance sampling

- Proposal does not need to have a higher value everywhere

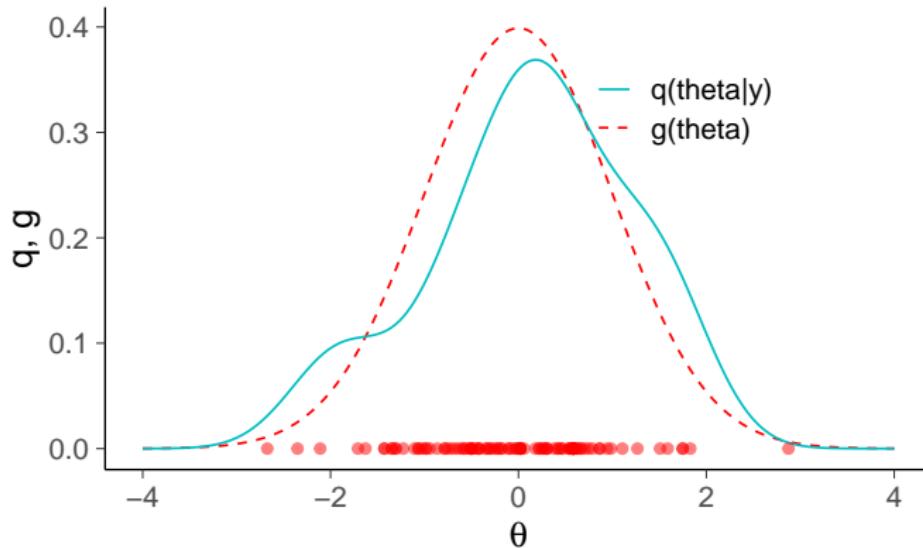
Target, proposal, and draws



Importance sampling

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Target, proposal, and draws

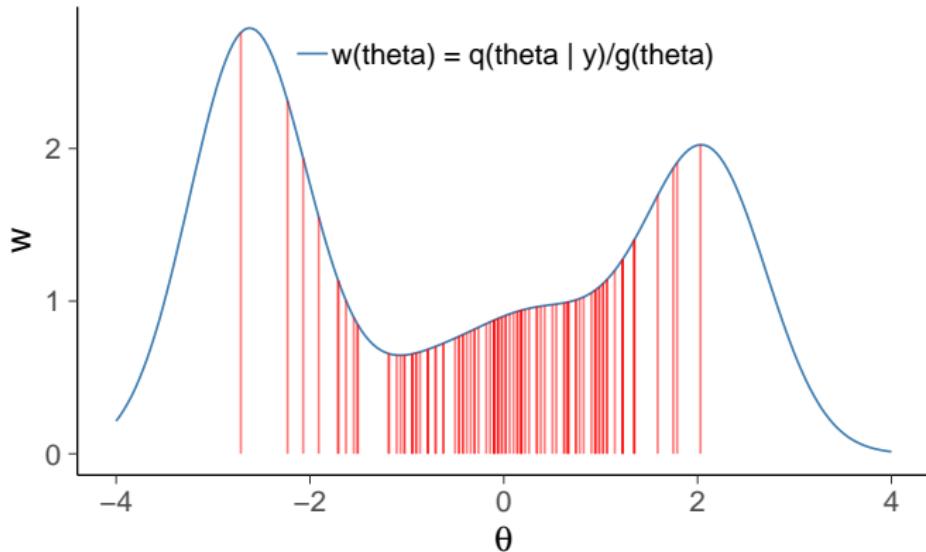


$$E[h(\theta)] \approx \frac{\sum_s w_s h(\theta^{(s)})}{\sum_s w_s}, \quad \text{where} \quad w_s = \frac{q(\theta^{(s)})}{g(\theta^{(s)})}$$

Importance sampling

- Proposal does not need to have a higher value everywhere

Draws and importance weights



$$E[h(\theta)] \approx \frac{\sum_s w_s h(\theta^{(s)})}{\sum_s w_s}, \quad \text{where} \quad w_s = \frac{q(\theta^{(s)})}{g(\theta^{(s)})}$$

Some uses of importance sampling

In general selection of good proposal gets more difficult when the number of dimensions increase, but there are many special use case which scale well (e.g. I've used IS up to 10k dimensions)

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In general selection of good proposal gets more difficult when the number of dimensions increase, but there are many special use case which scale well (e.g. I've used IS up to 10k dimensions)

- Fast leave-one-out cross-validation
- Fast bootstrapping
- Fast prior and likelihood sensitivity analysis
- Conformal Bayesian computation
- Particle filtering
- Improving distributional approximations (e.g Laplace, VI)

IS finite variance and central limit theorem

- If $h(\theta)w$ and w have finite variance \rightarrow CLT
 - variance goes down as $1/S$
 - Effective sample size (ESS) takes into account the variability in the weights

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 - generally not trivial
- Pre-asymptotic and asymptotic behavior can be really different!

Importance re-sampling

- Using the weighted draws is good

$$\text{E}[h(\theta)] \approx \frac{\sum_s w_s h(\theta^{(s)})}{\sum_s w_s}$$

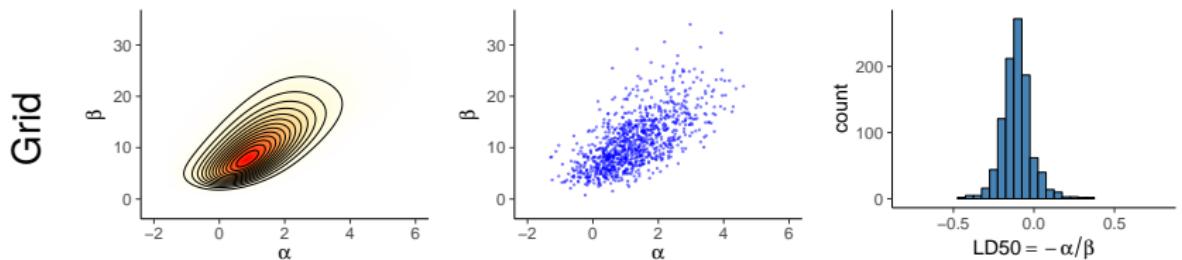
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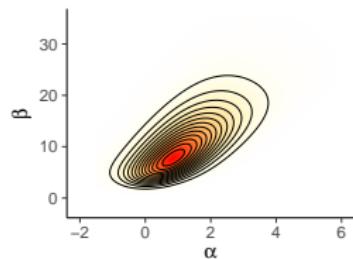
- But it can be convenient to obtain draws with equal weights
 - resample the draws according to the weights
 - some original draws may be included more than once
 - loses some information, but now the weights are equal

Example: Importance sampling in Bioassay

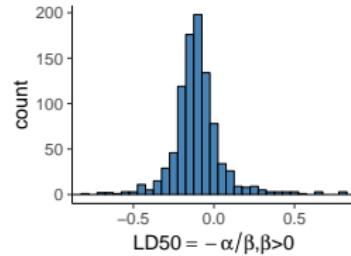
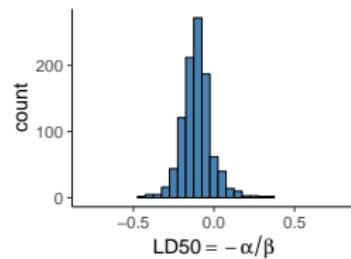
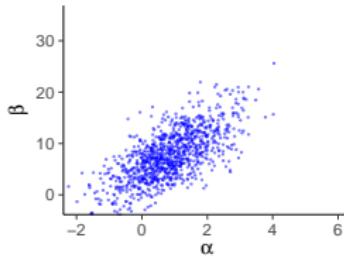
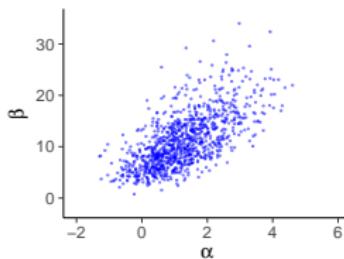
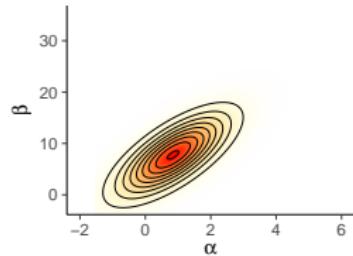


Example: Importance sampling in Bioassay

Grid

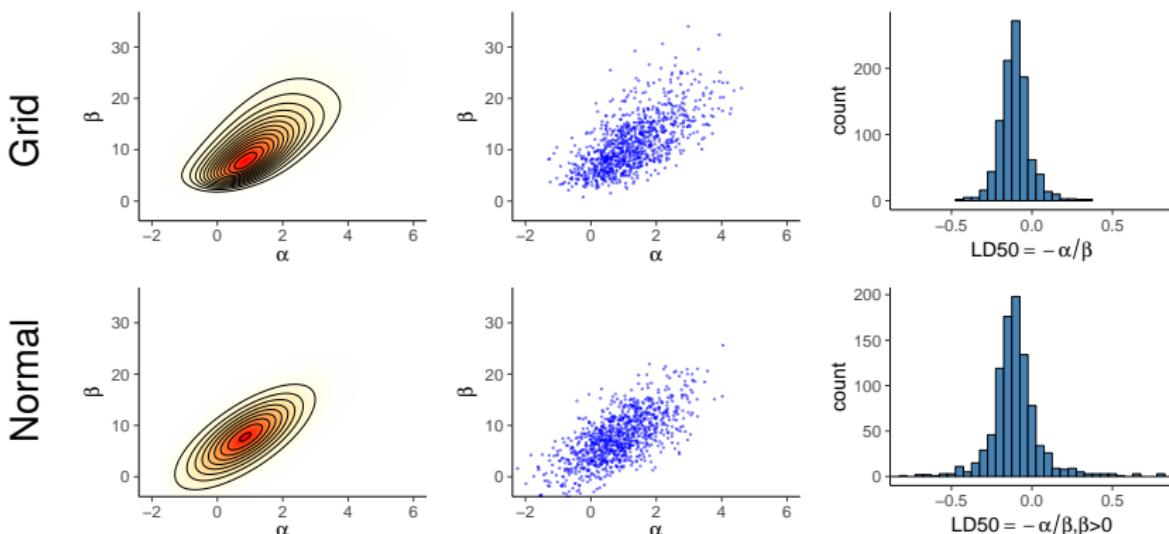


Normal



Normal approximation is discussed more in BDA3 Ch 4

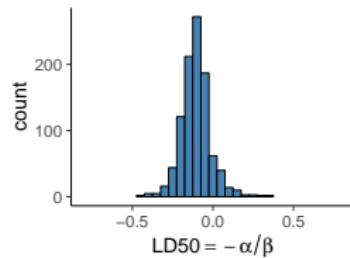
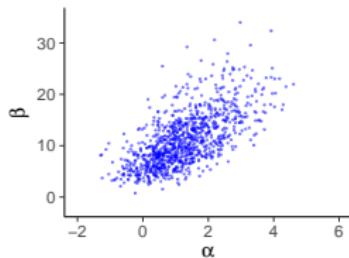
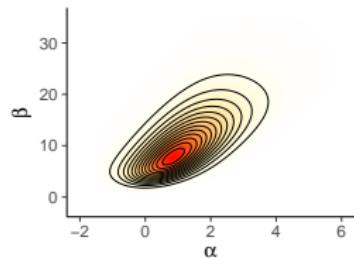
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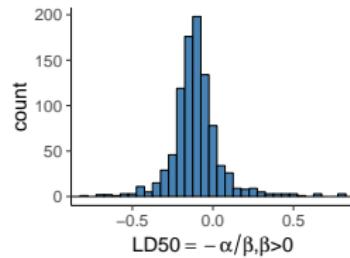
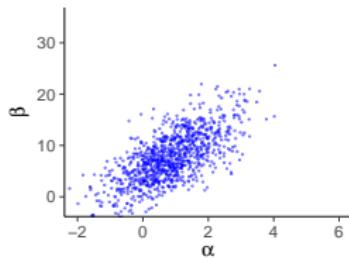
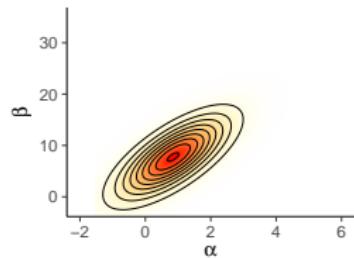
Normal approximation is discussed more in BDA3 Ch 4
But the normal approximation is not that good here:
Grid $\text{sd}(\text{LD50}) \approx 0.1$, Normal $\text{sd}(\text{LD50}) \approx .75!$

Example: Importance sampling in Bioassay

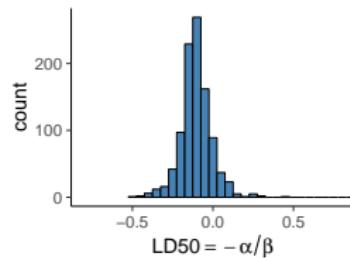
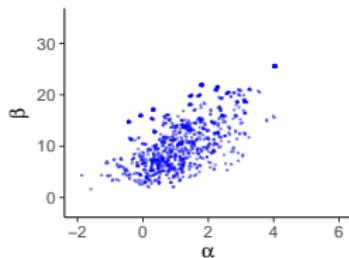
Grid



Normal

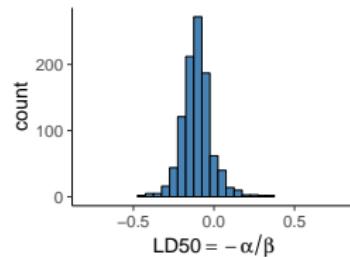
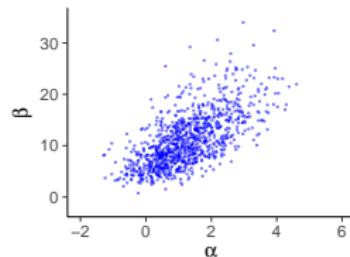
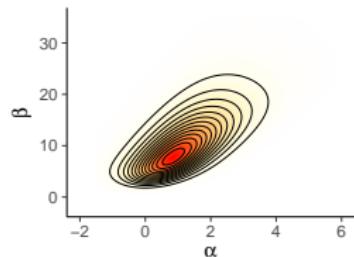


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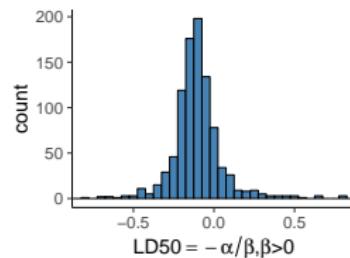
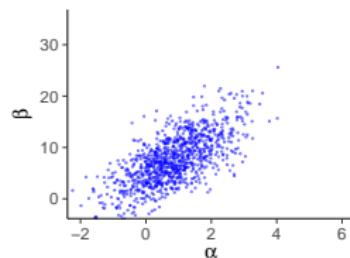
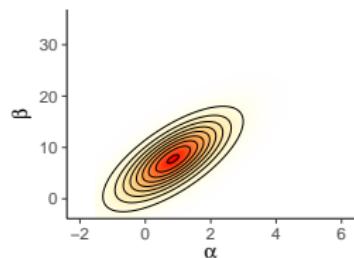


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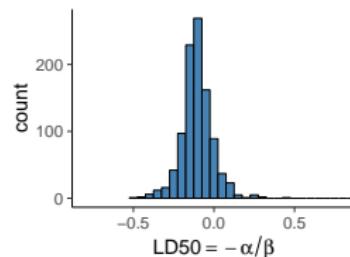
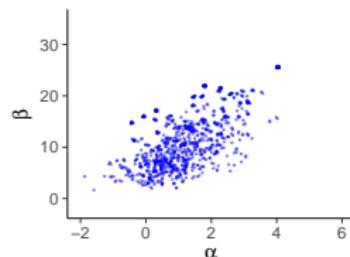
Grid



Normal



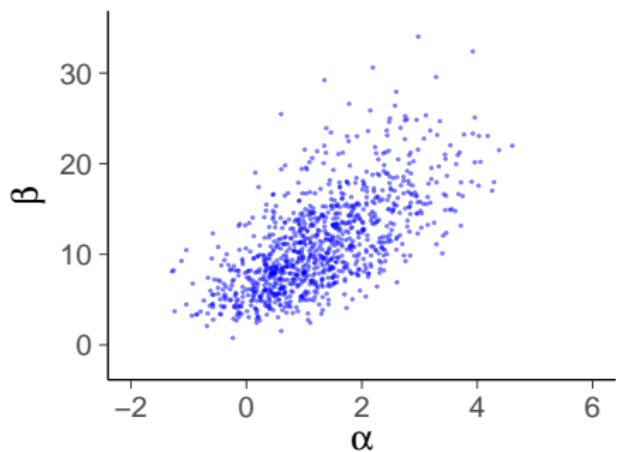
IR



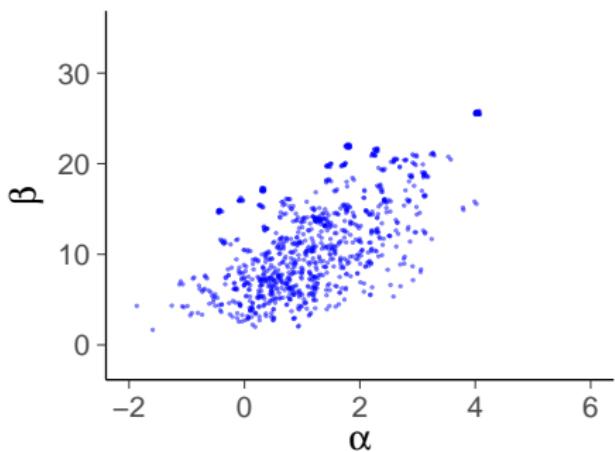
Grid $sd(LD50) \approx 0.1$, IR $sd(LD50) \approx 0.1$

Example: Importance sampling in Bioassay

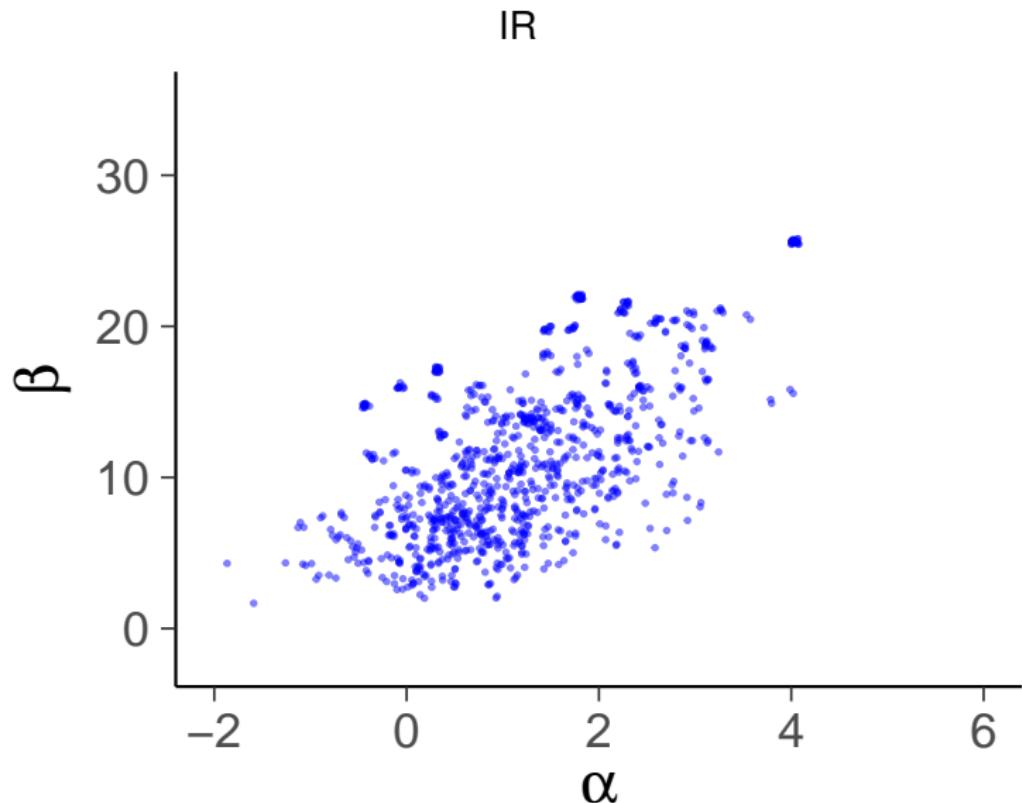
Grid



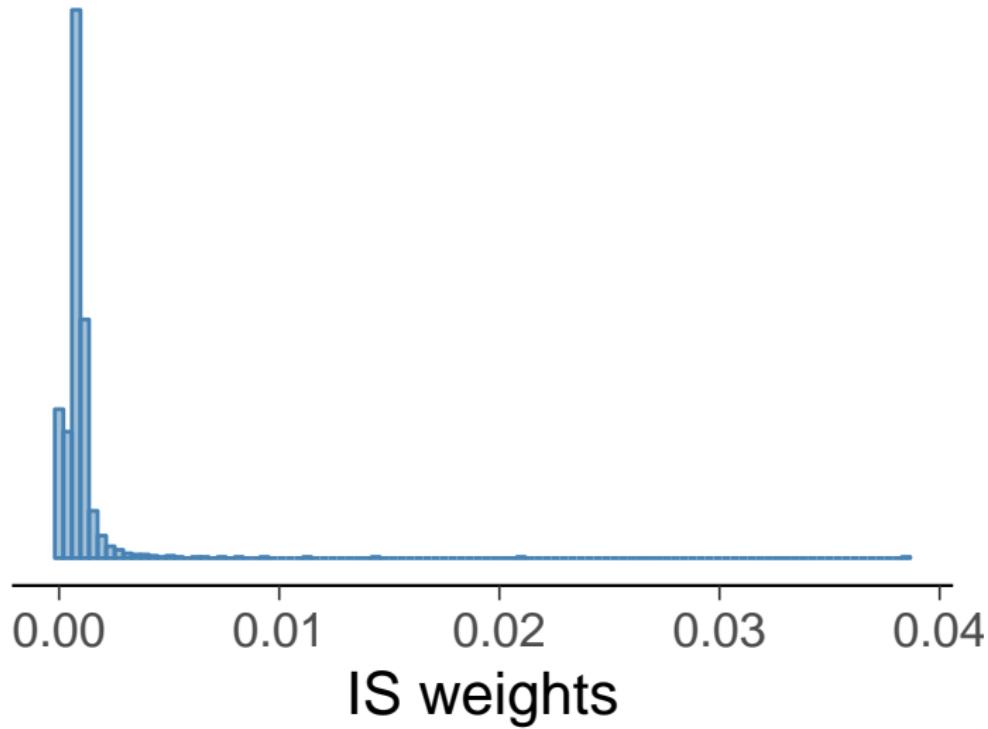
IR



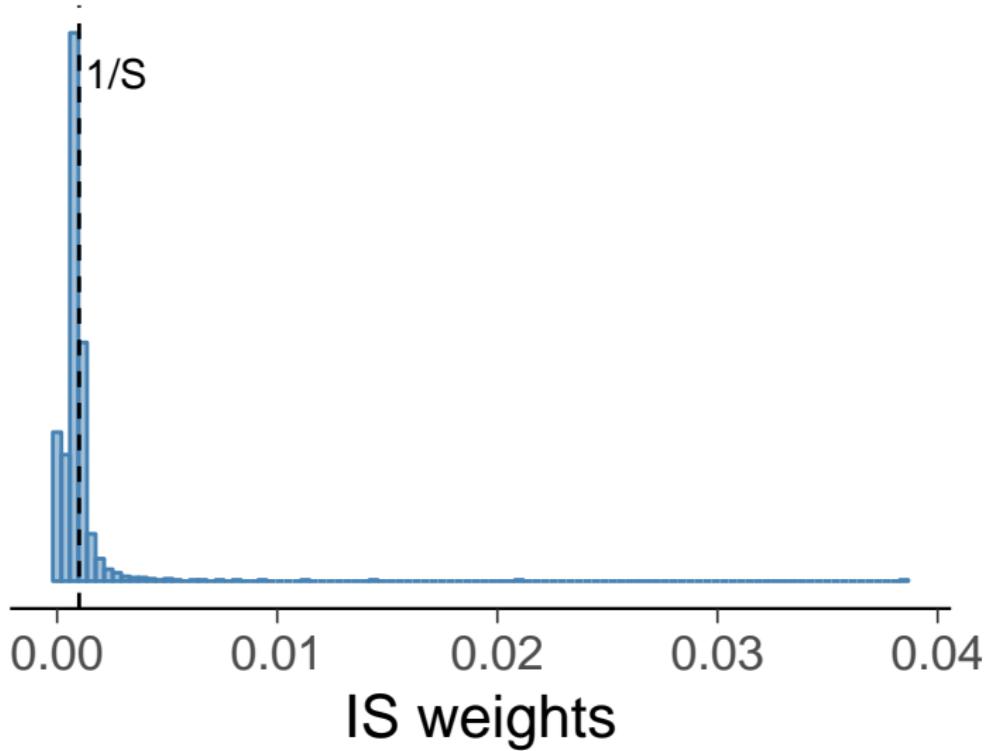
Example: Importance sampling in Bioassay



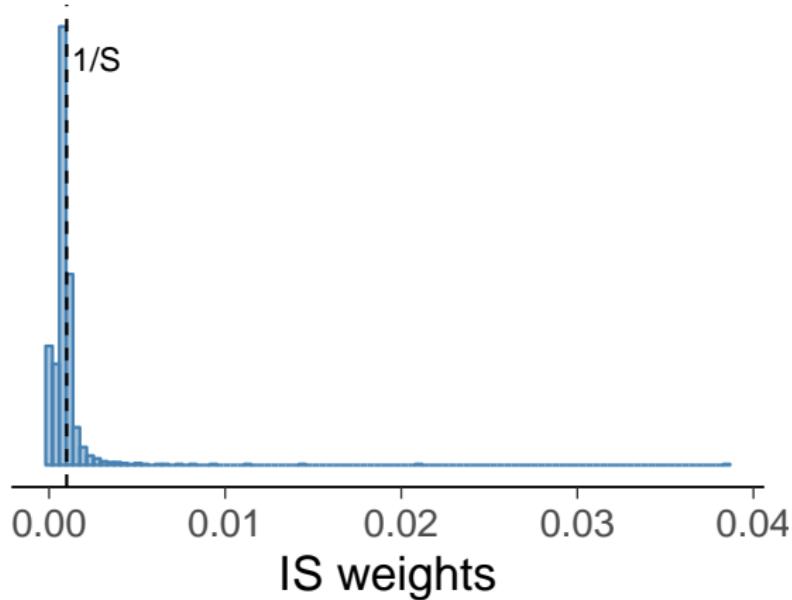
Example: Importance sampling in Bioassay



Example: Importance sampling in Bioassay

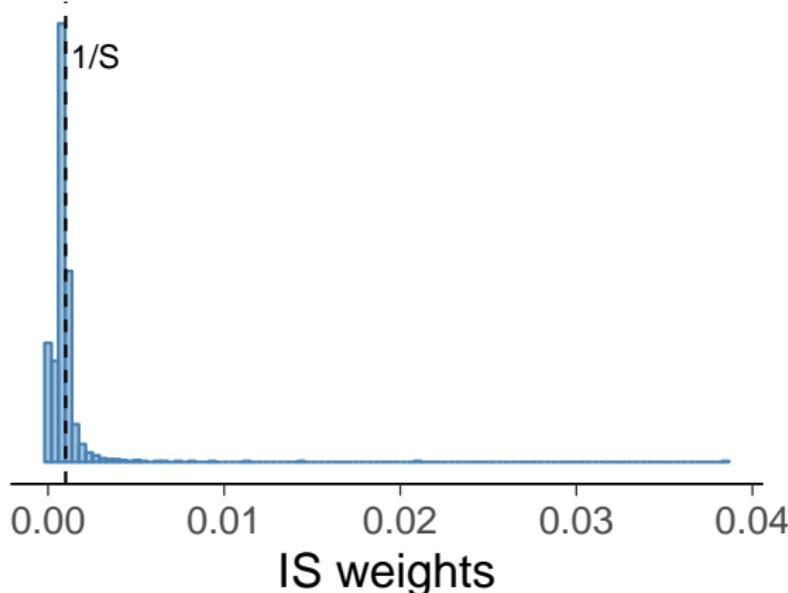


Example: Importance sampling in Bioassay



$$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}, \quad \text{where } \tilde{w}(\theta^s) = w(\theta^s) / \sum_{s'=1}^S w(\theta^{s'})$$

Example: Importance sampling in Bioassay

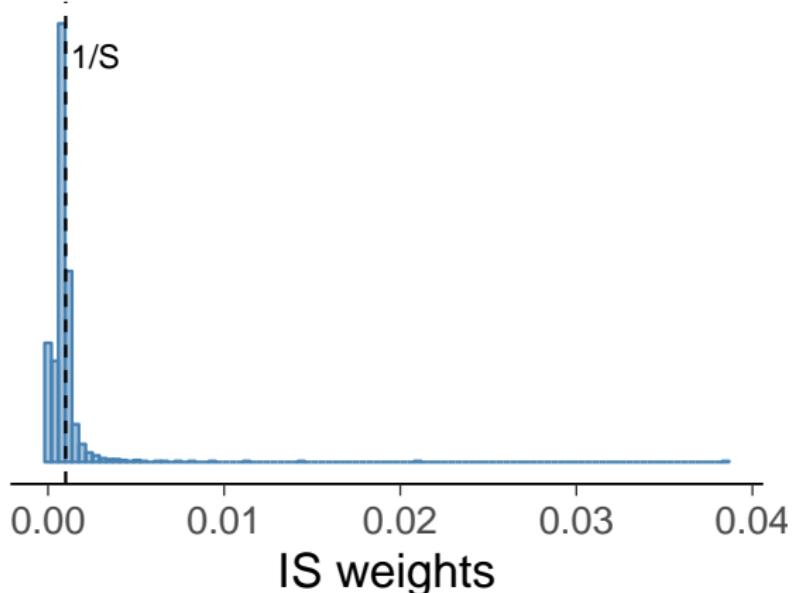


$$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}, \quad \text{where } \tilde{w}(\theta^s) = w(\theta^s) / \sum_{s'=1}^S w(\theta^{s'})$$

BDA3 1st (2013) and 2nd (2014) printing have an error for $\tilde{w}(\theta^s)$. The equation should not have the multiplier S (the normalized weights should sum to one). Online version is correct. Errata for the book

http://www.stat.columbia.edu/~gelman/book/errata_bda3.txt

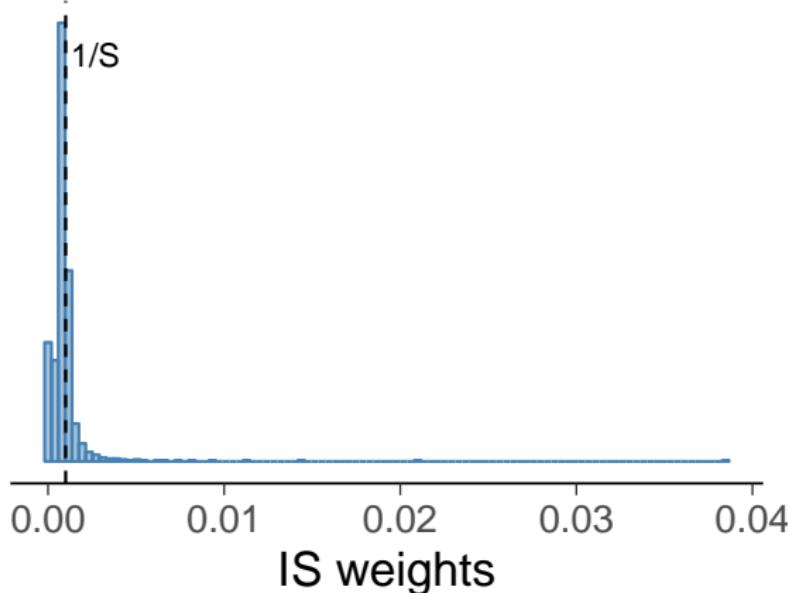
Example: Importance sampling in Bioassay



$$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}, \quad \text{where } \tilde{w}(\theta^s) = w(\theta^s) / \sum_{s'=1}^S w(\theta^{s'})$$

$$\text{ESS} \approx 396, \quad (\text{ESS} < S = 1000)$$

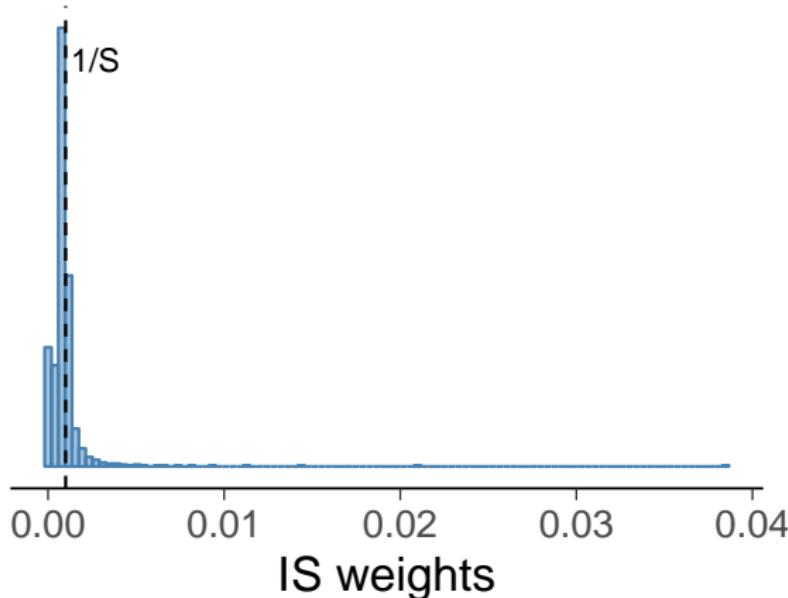
Example: Importance sampling in Bioassay



$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}$, is based on variance of $\tilde{w}(\theta^s)$

$$\text{ESS} \approx 396$$

Example: Importance sampling in Bioassay

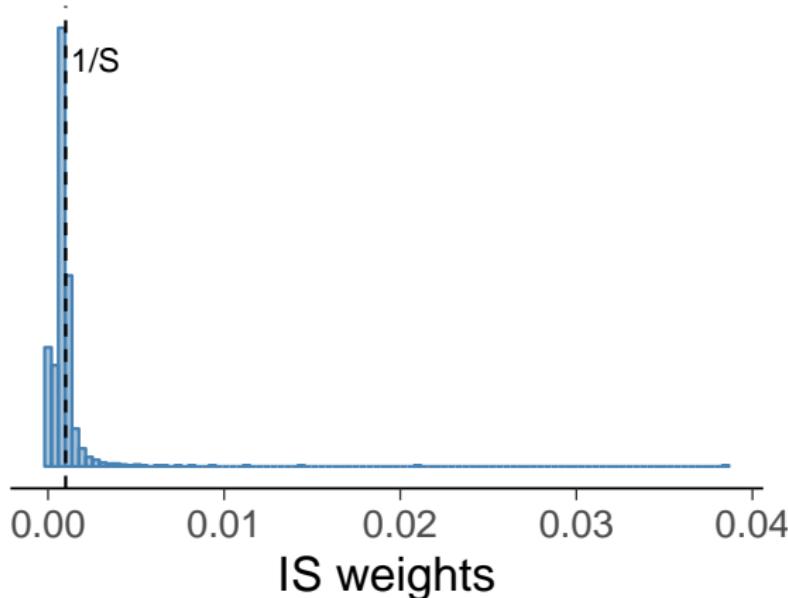


$$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}, \quad \text{is based on variance of } \tilde{w}(\theta^s)$$

$$\text{ESS} \approx 396$$

If all $\tilde{w}(\theta^s) = 1/S$, then $\text{ESS} = 1/(SS^{-2}) = S$

Example: Importance sampling in Bioassay



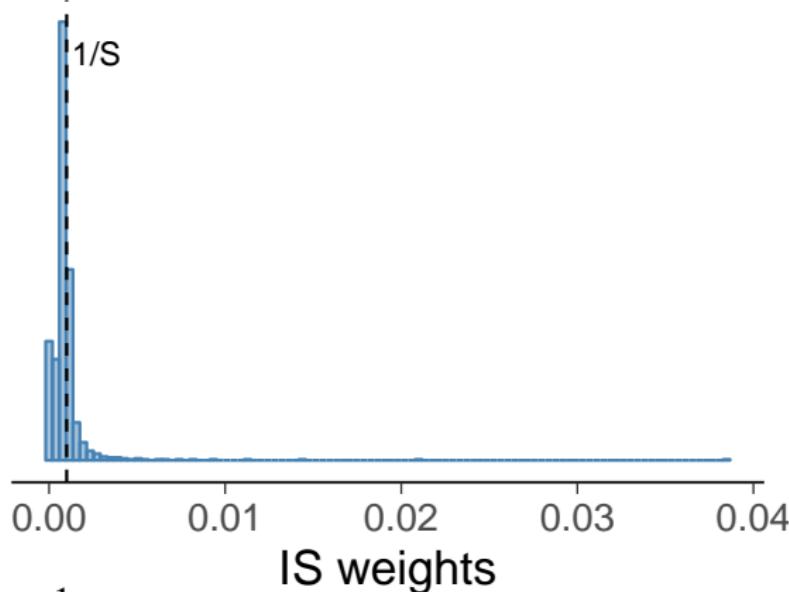
$$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}, \quad \text{is based on variance of } \tilde{w}(\theta^s)$$

$$\text{ESS} \approx 396$$

If all $\tilde{w}(\theta^s) = 1/S$, then $\text{ESS} = 1/(SS^{-2}) = S$

If one $\tilde{w}(\theta^s) = 1$, and others 0, then $\text{ESS} = 1/1 = 1$

Example: Importance sampling in Bioassay

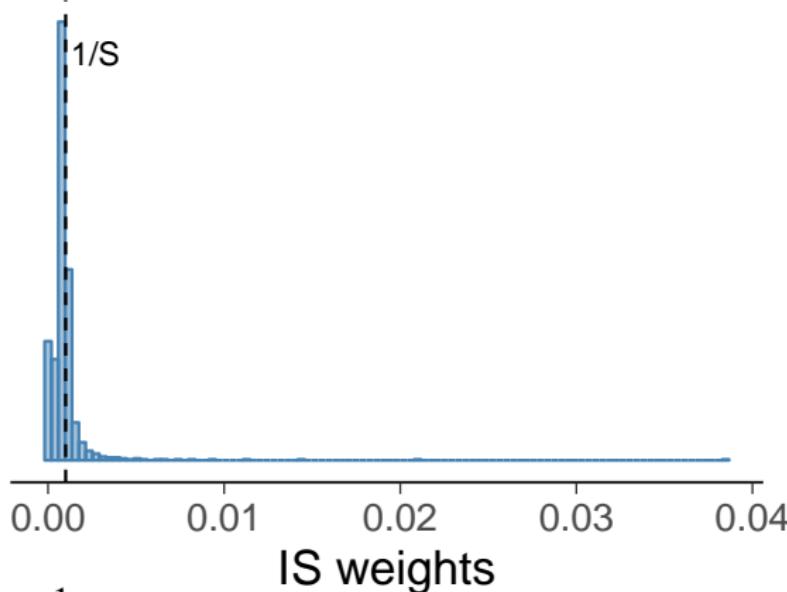


$$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}, \quad \text{is based on variance of } \tilde{w}(\theta^s)$$

$$\text{ESS} \approx 396$$

Pareto- \hat{k} ≈ 0.65 , CLT does not hold

Example: Importance sampling in Bioassay



$$\text{ESS} = \frac{1}{\sum_{s=1}^S (\tilde{w}(\theta^s))^2}, \quad \text{is based on variance of } \tilde{w}(\theta^s)$$

$\text{ESS} \approx 396$

Pareto- \hat{k} ≈ 0.65 , CLT does not hold

with Pareto-smoothing the estimate would be fine if $\hat{k} < 0.7$

Importance sampling leave-one-out cross-validation

- Later in the course you will learn how $p(\theta|y)$ can be used as a proposal distribution for $p(\theta|y_{-i})$
 - which allows fast computation of leave-one-out cross-validation

$$p(y_i|y_{-i}) = \int p(y_i|\theta)p(\theta|y_{-i})d\theta$$

Pareto- \hat{k} diagnostic use cases

- Importance sampling
 - leave-one-out cross-validation (Vehtari et al., 2016, 2017; Bürkner et al, 2020)
 - Bayesian stacking (Yao et al., 2018, 2021, 2022)
 - leave-future-out cross-validation (Bürkner et al., 2020)
 - Bayesian bootstrap (Paananen et al, 2021, online appendix)
 - prior and likelihood sensitivity analysis (Kallioinen et al., 2021)
 - improving distributional approximations (Yao et al., 2018; Zhang et al., 2021; Dhaka et al., 2021)
 - implicitly adaptive importance sampling (Paananen et al., 2021)
- Stochastic optimization (Dhaka et al., 2020)
- Divergences and gradients in VI (Dhaka et al., 2021)
- MCMC (Paananen et al., 2021)

Curse of dimensionality

- Number of grid points increases exponentially
- Concentration of the measure, that is, where is the most of the mass?

Markov chain Monte Carlo (MCMC)

- Pros
 - Markov chain goes where most of the posterior mass is
 - Certain MCMC methods scale well to high dimensions
- Cons
 - Draws are dependent (affects how many draws are needed)
 - Convergence in practical time is not guaranteed
- MCMC methods in this course
 - Gibbs: “iterative conditional sampling”
 - Metropolis: “random walk in joint distribution”
 - Dynamic Hamiltonian Monte Carlo: “state-of-the-art” used in Stan