Monte Carlo methods

Nordic Probabilistic AI School

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Statistical physics

$$\pi(\theta) \propto \exp\left(-E(\theta)\right)$$

• Bayesian inference

$$\pi(\theta) = p(\theta \mid y) \propto p(\theta)p(y \mid \theta)$$

• Variational inference

$$\pi(\theta) = q(\theta)$$

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What might we want to learn about these distributions?

- Expectation, variance, and quantiles of $f(\theta)$ with respect to π .
- Monte Carlo: draw samples and construct sample estimators,

$$\theta^{(1)}, \theta^{(2)}, \cdots, \theta^{(N)} \sim \pi(\theta).$$

• When no exact simulation is possible, use Markov chains.



Markov chain Monte Carlo

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Can get a sample estimator for mean, variance and quantiles.

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$$= \left[\left(\hat{\Xi}_{1,2}(x), -\Xi_{1,2}(x) \right)^{2} \right] = 2 \quad \text{for } [\hat{\Xi}_{1,2}(x), -\Xi_{1,2}(x)]^{2}$$

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We also have a central limit theorem, i.e. for large N

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 $\widehat{\mathbb{E}}[f(\theta)] \stackrel{\text{approx}}{\sim} \text{normal}\left(\mathbb{E}f(\theta), \sqrt{\frac{\text{Var}[f(\theta)]}{N}}\right).$

Markov chain Monte Carlo:

- Start with an initial draw $\theta^{(0)} \sim p_0(\theta)$. Apply a transition kernel, $\theta^{(i+1)} \sim \Gamma(\theta^{(i+1)} \mid \theta^{(i)})$.

Markov chain Monte Carlo:

- Start with an initial draw θ⁽⁰⁾ ~ p₀(θ).
 Apply a transition kernel, θ⁽ⁱ⁺¹⁾ ~ Γ(θ⁽ⁱ⁺¹⁾ | θ⁽ⁱ⁾).

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- The first samples suffer from a large bias.
- Discard these samples during a burn-in or warmup phase.

• Start at an initial point, $\theta^{(0)} \sim p_0$.

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- - Propose a new sample

$$\theta^{(i+1)} \sim \text{normal}\left(\theta^{(i)}, \sigma^2 I\right)$$

Accept the proposal with probability

$$\Pr = \min \left(\frac{p(\theta^{(i+1)} \mid z)}{p(\theta^{(i)} \mid z)}, 1 \right).$$

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3 Return the chain $(\theta^{(1)}, \theta^{(2)}, ..., \theta^{(N)})$.

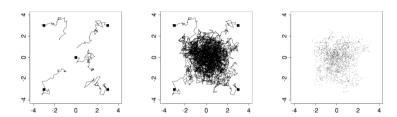


Figure from [Gelman et al., 2013].

Benefits:

- Only requires evaluating $p(\theta, y) = p(\theta)p(y \mid \theta)$.
- Asymptotically, the algorithm samples from $p(\theta \mid y)$.

Drawbacks:

- In the finite regime, the samples are biased.
- The samples are <u>not</u> independent; there are correlated, which <u>increases</u> the <u>variance</u> of our Monte Carlo estimators.

Example: Continuous diffusion process

In the limit where we take infinitesimally small steps, many MCMC algorithms can be approximated by a random diffusion process [Gelman et al., 1997, Roberts and Rosenthal, 1998].

- Initial distribution: $p_0 = \text{normal}(\mu_0, \sigma_0^2)$.
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- Target distribution: $p = \text{normal}(\mu, \sigma^2)$.

Then after time T,

$$\theta^{(T)} \sim \text{normal} \left[(\mu_0 - \mu) e^{-T} + \mu, (\sigma_0^2 - \sigma^2) e^{-2T} + \sigma^2 \right].$$

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For T large enough, the bias becomes negligible.

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$$\frac{1}{N} \sum_{i} f(\theta^{(n)}) \stackrel{\text{approx}}{\sim} \text{Normal}\left(\mathbb{E}[f(\theta)], \frac{\text{Var}f(\theta)}{N_{\text{eff}}}\right)$$

where N_{eff} is the effective sample size (ESS).

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$$N_{\text{eff}} = \frac{N}{1 + 2\sum_{i=1}^{\infty} \rho_i}.$$

 ρ_t is the chain's autocorrelation between $\theta^{(i)}$ and $\theta^{(i+t)}$.

Handling the error of MCMC



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Warmup phase: We run the process for several steps for the <u>bias</u> to become negligible but don't use any of those samples in our Monte Carlo estimator.

Sampling phase: Collect enough samples to have a large ESS and reduce the variance of the Monte Carlo estimator.

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Metropolis, Gibbs, Hamiltonian Monte Carlo, Metropolis-adjusted Langevin approximation, \dots

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- Gradient based, requires evaluating $\nabla_{\theta} \log p(\theta \mid y)$.
- Difficult to tune!

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- Difficult to tune!
- Stan provides automated calculations of gradients and a self-tuning HMC.

II Warmup example

How Stan works

• The Stan file specifies the joint distribution

$$p(\theta, y) = p(y|\theta)p(\theta) \propto p(\theta \mid y)$$

- The input includes:
 - the data, y
 - tuning parameters for the algorithm
- The output can include:
 - an approximate sample from the posterior distribution
 - summaries of the run which can help us diagnose problems.

Inference algorithms in Stan

- Hamiltonian Monte Carlo (HMC)
- No-U Turn Sampler (NUTS)
- Automatic differentiation variational inference (ADVI)
- Pathfinder Variational Inference
- ...

We can manage the **Stan** file, the input, and the output using a scripting language, such as:

- R
- Python
- Julia
- The command line
- . . .

Example: Bayesian linear regression

The data generating process is:

$$p(\beta) = \text{Normal}(2, 1)$$
$$p(\sigma) = \text{Normal}^{+}(1, 1)$$
$$p(y \mid \beta, \sigma) = \text{Normal}(\beta x, \sigma)$$

Our goal is to estimate $\theta = (\beta, \sigma)$, based on the observation z = (x, y) and prior knowledge we have of β and σ .

Writing the Stan file

```
data {
 Declare the data that will be given as an input.
parameters {
 Declare the parameters we want to sample.
model {
 Compute the log joint distribution.
```

code demo

Convergence diagnostic

Are the chains still biased by their initializations?

Proposition: Start multiple chains at a different locations and check that they all converge to the same distribution.

Examine:

- the trace plots
- the density plots
- \bullet the \widehat{R} statistic

$$\widehat{R} := \frac{\text{Standard deviation across all chains}}{\text{Standard deviation within chain}}$$

- If the chains sample from the same target, expect $\widehat{R} \approx 1$.
- If the chains are disagreement, $\hat{R} \gg 1$.

code demo

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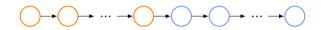
- \widehat{B} is the sample variance of $\overline{f}(\theta^{(\cdot m)})$.
- \widehat{W} is the (average) within-chain variance.

$$\widehat{R} \le 1 + \epsilon \iff \widehat{B} \lessapprox 2\epsilon \widehat{W} + \mathcal{O}(\epsilon^2).$$

Want to make sure $\operatorname{Var}\left[f\left(\bar{\theta}^{(\cdot m)}\right)\right]$ is small.



Question. What can $\operatorname{Var}\left[f\left(\bar{\theta}^{(\cdot m)}\right)\right]$ teach us about convergence and bias decay?



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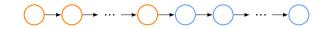
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As we warm up the chains, both the nonstationary variance and squared bias decay to 0, and so \widehat{R} acts as a "proxy clock" for bias.

- What quantity does \widehat{R} measure and how close to 1 should it be?
 - [Vehtari et al., 2021] propose checking that $\hat{R} \leq 1.01$.
 - [Margossian et al., 2024] examine \widehat{R} for nonstationary chains and propose a more direct measure of the nonstationary variance.



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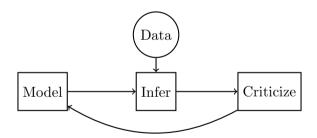
- ESS_{tail} quantifies information for tail estimates [Vehtari et al., 2021].
- Median, $M(\theta)$ and Median Absolute Deviation (MAD),

$$M(|\theta^{(i)} - M(\theta)|)$$

can be helpful when the first moments are not finite.

Posterior predictive checks

- Recall Box's loop (from Bayesian Workflow)!
- Does our model accurately describe the data?



Posterior predictive checks ("check trained model")

Proposition:

Each time we draw a sample, $\theta^{(i)} = (\beta^{(i)}, \sigma^{(i)})$, we will also simulate data, according to:

$$y_{\text{pred}}^{(i)} \sim \text{Normal}\left(x\beta^{(i)}, \sigma^{(i)}\right)$$

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Want to study the posterior predictive distribution,

$$p(y_{\text{pred}} \mid y) = \int_{\Theta} p(y_{\text{pred}} \mid \theta) p(\theta \mid y) d\theta.$$

code demo

Improving the model

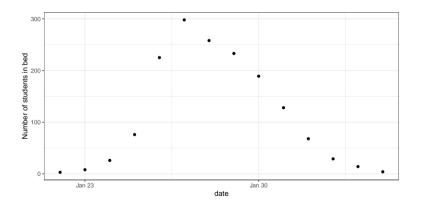
- The ppc suggest our model can improve with an intercept parameter.
- Exercise: repeat the above procedure, but this time add an intercept parameter β_0 . Check that the inference is reliable and perform new posterior predictive checks.

III

Disease transmission model

1978 influenza outbreak in a British boarding school.

Data: daily number of students in bed.



Susceptible-Infected-Recovered (SIR) model

N: total number of individuals, N = S + I + R.

Susceptible-Infected-Recovered (SIR) model

$$\begin{array}{rcl} \dot{S} & = & -\beta SI/N \\ \dot{I} & = & \beta SI/N - \gamma I \\ \dot{R} & = & \gamma I \end{array}$$

N: total number of individuals, N = S + I + R.

 β : transmission rate.

 γ : rate of recovery of infected individuals.

Susceptible-Infected-Recovered (SIR) model

$$N$$
: total number of individuals,
 $N = S + I + R$.
 β : transmission rate.
 γ : rate of recovery of infected

individuals.

- I/N: the proportion of infectious individuals.
- $\beta(I/N)$: the probability that a single susceptible individual becomes infected in one day.

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- Poisson likelihood parameterized by $\lambda(t) = I(t)$.
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 - Negative-Binomial parameterized by $\mu = I(t)$ and ϕ .
 - Then $\mathbb{E}(y(t)) = I(t)$ and $\operatorname{Var}(y(t)) = I(t) + \frac{I(t)^2}{2}$.

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 - Then $\mathbb{E}(y(t)) = I(t)$ and $\operatorname{Var}(y(t)) = I(t) + \frac{I(t)^2}{4}$.
 - In Stan use neg_binomial_2.
 - Define in parameters block ϕ^{-1} .

Which prior should we use?

- $p(\beta) = \text{normal}^+(2, 1)$: restricts β to be positive and $p(\beta < 4) = 0.975$.
- $p(\gamma) = \text{normal}^+(0.4, 0.5)$: restricts γ to be positive and $p(\gamma < 1) = 0.9$, i.e. 90% of the time, we expect the average time spent in bed to be less than 1 day).
- $p(\phi^{-1}) = \text{exponential}(5)$, see [Grinsztajn et al., 2021].

code demo

Additional controls for the MCMC sampler.

- Number of (parallel) chains
- Number of warmup iterations
- Number of sampling iterations

Exercise: Write and fit an SIR model for the 1978 influenza outbreak.

- Check the standard diagnostics (\hat{R} and ESS) and examine the density and trace plots. Is the inference reliable?
- Do posterior predictive checks: does the model accurately describe the data?
- Report β , γ , $R_0 = \beta/\gamma$ and the recovery time $T = 1/\gamma$.
- How precise are your estimates of T? Should you run longer Markov chains? Shorter ones?
- Compare the two proposed measurement models: Poisson and negative binomial.

For more discussion about this model (e.g. choice of priors, sensitivity tests), see [Grinsztajn et al., 2021].

For more discussion about the length of Markov chains, see [?].

IV Model Comparison

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• Validation set: The data y_{val} we use to "test" the model's predictions.

Example: At t = 12, the model predicts $\tilde{y}(t = 12)$. Compute the prediction error,

$$\text{Err} = (\tilde{y}(t=12) - y_{\text{val}}(t=12))^2$$
.

Testing uncertainty calibration in (point) predictions

Suppose we have a normal likelihood, with point estimates for the learned parameters,

Normal $(\hat{\mu}(t), \hat{\sigma})$.

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and $\hat{\sigma}$ is unaccounted for!

Instead, let's evaluate the point-estimate log predictive density,

p-lpd =
$$\log p(y_{\text{val}}(t) \mid \hat{\mu}, \hat{\sigma})$$

 = $\text{const.} - \log \hat{\sigma} - \frac{1}{2\hat{\sigma}^2} (y_{\text{val}}(t) - \hat{\mu}(t))^2$.

Suppose we have a Bernoulli likelihood, with point estimates for the learned parameters,

Bernoulli(
$$\hat{\pi}(t)$$
).

Our "best" prediction is $\tilde{y}(t) = \mathbb{I}[\hat{\pi}(t) > 0.5]$.

Then the prediction error is

$$\operatorname{Err} = \mathbb{I}[\tilde{y}(t) = y_{\operatorname{val}}(t)].$$

Instead, let's evaluate the point-estimate log predictive density,

p-lpd =
$$\log p(y_{\text{val}}(t) | \hat{\pi}(t))$$

= $y_{\text{val}}(t) \log \hat{\pi}(t) + (1 - y_{\text{val}}(t)) \log(1 - \hat{\pi}(t))$.

Testing uncertainty calibration in Bayesian predictions

We have a general strategy which accounts for uncertainty in the likelihood for a fixed θ ,

$$p$$
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Testing uncertainty calibration in Bayesian predictions

We have a general strategy which accounts for uncertainty in the likelihood for a fixed θ , $\text{p-lpd} = \log p(y_{\text{val}}(t) \mid \theta).$

In a Bayesian framework, we integrate with respect to the posterior and obtain the *expected log predictive density*,

elpd =
$$\log p(y_{\text{val}}(t) \mid y_{\text{train}})$$

 = $\log \int_{\Theta} p(y_{\text{val}}(t) \mid \theta) p(\theta \mid y_{\text{train}}) d\theta$.

$$elpd_{loo} = \sum_{i=1}^{N} log p(y_i \mid y_{-i}),$$

 $p(y_i \mid y_{-i}) = \int_{\Omega} p(y_i \mid \theta) p(\theta \mid y_{-i}) d\theta.$

Proposition: Do leave-one-out cross validation and compute

where

How do we split the data (t, y) into a training and a test set?

Recap.

Prediction error based on "best" prediction, $(y_{\text{val}} - \tilde{y})^2$

 \rightarrow point-wise log predictive score, p-lpd = log $p(y_{\text{val}} \mid \hat{\theta})$

 \rightarrow expected log predictive score, elpd = log $p(y_{\text{val}} \mid y_{\text{train}})$

 \rightarrow loo CV, elpd_{loo} = $\sum_{i=1}^{N} \log p(y_i \mid y_{-i})$

How do we estimate elpd_{loo} efficiently?

• Idea: Suppose we need to estimate an expectation with respect to $\ell(\theta)$,

$$\int_{\Theta} f(\theta) \ell(\theta) d\theta,$$

but using samples from $q(\theta)$.

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• The IS Monte Carlo estimator is

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Proposition

When the y_j 's are independent conditioned on θ , the importance sampling Monte Carlo estimator is

$$\widehat{p}(y_i \mid y_{-i}) = \frac{1}{\sum_{s=1}^{S} \frac{1}{p(y_i \mid \theta^{(s)})}},$$

where $\theta^{(s)} \sim p(\theta \mid y)$.

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- PSIS comes equipped with a \hat{k} diagnostic:
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 - if $\hat{k} < 0.5$, PSIS estimators is reliable.
 - if $\hat{k} > 0.7$, importance weights have non-finite variance.
- The R package loo computes PSIS.
- In Stan 's generated quantities, need to compute log_lik, where

```
log_lik[i] = log p(cases[i] | theta);
```

Exercise: Compare the predictive scores of the SIR models.

- Evaluate in generated quantities the log probability mass functions using poisson_lpmf and neg_binomial_2_lpmf.
- In R, use the loo package to compute the PSIS estimates of the $elpd_{loo}$.
- Check \hat{k} to see if the IS estimators are reliable.
- Which likelihood achieves the best predictive score?

V Concluding Remarks

Where does Stan fit in the Bayesian modeler's toolkit?

Historical contribution:

- Stan was born around 2012.
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Several algorithms were developed as part of Stan 's development:

- Adaptive Hamiltonian Monte Carlo [?, ?]
- ADVI: a black box variational inference [?]
- PathFinder: an improved variational inference [?].
- Delayed rejection HMC [?]
- Adjoint-differentiated Laplace approximation [?]

Markov chain Monte Carlo Variational inference

Markov chain Monte Carlo

• use general transition kernel

Variational inference

• requires an approximating model

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Where does MCMC fit in the probabilistic modeling toolkit?

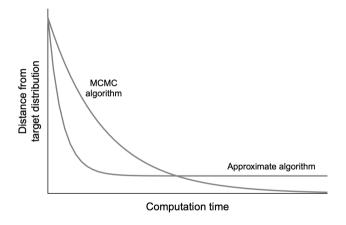


Figure from [Gelman et al., 2020].

Stan by the people, for the people

- Stan is open source: https://github.com/stan-dev
- So is Torsten: https://github.com/metrumresearchgroup/Torsten
- Contributing new functions to Stan: https://github.com/stan-dev/stan/wiki/Contributing-New-Functions-to-Stan

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