An Introduction to MCMC

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July 24, 2019







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Outline

1 Monte Carlo Sampling

- A Bit of History
- Monte Carlo Sampling
- 2 Sampling: Acceptance-Rejection Method
 - Motivation: Bayesian inference
 - 3 Markov chains
 - Definition
 - Stationary Equilibrium

4 MCMC

- Numerical posterior sampling with MCMC
- MCMC Convergence
- MCMC Burn-In
- MCMC Tuning

Homework (Data Collection)

• What do you belief is the share of winnable deals?

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Homework (Data Collection)

- What do you belief is the share of winnable deals?
- How many deals have you played? How many won?

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Homework (Analysis)

• Our estimated ratio of winnable games is $f_{\text{winnable}} = W/N = \dots$

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Homework (Analysis)

- Our estimated ratio of winnable games is $f_{\text{winnable}} = W/N = \dots$
- Win-Lose scenario with fixed probability follows a **binomial distribution**. Hence, there is a 68% (95%) chance that the true probability lies within 1 (2) σ of our estimate with:

$$\sigma^2 = f_{\mathrm{winnable}}(1 - f_{\mathrm{winnable}})/N = \dots$$

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From cards to nukes



John von Neumann



• Ulam told his colleague John von Neumann, a pioneer in computer science (besides many other fields of expertise) about his idea.

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From cards to nukes



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- Ulam told his colleague John von Neumann, a pioneer in computer science (besides many other fields of expertise) about his idea.
- Von Neumann realized the potential of using it in combination with the new "electronic computing" and proposed a program to apply it to neutron scattering.
- Instead of solving the problem statistically for the whole assemble of neutrons, he proposed to follow a subset of neutrons and decide randomly the outcome of events those neutron face (e.g. either fission, scattering or absorbtion)

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Algorithm:

Define an domain for input



- Define an domain for input
- Generate random inputs from a probability distribution over the domain



- Define an domain for input
- Generate random inputs from a probability distribution over the domain
- Perform a deterministic computation on the inputs



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- Generate random inputs from a probability distribution over the domain
- Perform a deterministic computation on the inputs
- Aggregate results



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vit Der This	y = 0 on a set $y = 0$ of $y = 1$,	

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	which take para here a start h attention the para here a start h attention the para here a start h attention the parameters of f and attention at $f(f)$. It is the h attention the parameters h at f and h attention h at f and hh attention h at h at h at h and h at h at h at h at h at hh at h at hh at h at hh at h	 Choose a tractable density h(Θ) and a constant C so C ⋅ h ≥ q ∀Θ
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 Θ' from h

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- Ochoose a tractable density h(Θ) and a constant C so C ⋅ h ≥ q ∀Θ
- 3 Draw a candidate parameter value Θ' from h
- **③** Draw a random uniform number $u \in [0,1]$

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- constant C so $C \cdot h > q \forall \Theta$ 2 Draw a candidate parameter value Θ' from h
 - **O** Draw a random uniform number $u \in [0, 1]$
 - If $u < \frac{C \cdot h(\Theta')}{a(\Theta')}$ accept Θ' as a sample

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An Introduction to MCMC

Motivation: Bayesian inference

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- In case of Solitaire, we consider a deal as a binary random event with a given probability p to obtain one result (win) and (1 p) the other (lose).

Motivation: Bayesian inference

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- In case of Solitaire, we consider a deal as a binary random event with a given probability p to obtain one result (win) and (1 p) the other (lose).
- According to Bayes' theorem, this posterior belief is given by

$$\underbrace{P(\{\Theta_i\}|\text{Data})}_{\text{Posterior Prob.}} = \underbrace{P(\{\Theta_i\})}_{\text{Prior Prob.}} \cdot \underbrace{P(\text{Data}|\{\Theta_i\})}_{\text{Likelihood}} / \underbrace{P(\text{Data})}_{\text{Model evidence}}$$

Bayesian inference - Prior Belief/Probability

$$P(\{\Theta_i\}|\text{Data}) = \underbrace{P(\{\Theta_i\})}_{\text{Prior Prob.}} \cdot P(\text{Data}|\{\Theta_i\}) / P(\text{Data})$$

• mathematical expression (i.e. pdf) quantifying our belief about the model parameters

Bayesian inference - Prior Belief/Probability

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- mathematical expression (i.e. pdf) quantifying our belief about the model parameters
- two approaches: least-/uninformative vs informative prior



Bayesian inference - Data Likelihood

$$P(\{\Theta_i\}|\text{Data}) = P(\{\Theta_i\}) \cdot \underbrace{P(\text{Data}|\{\Theta_i\})}_{\text{Likelihood}} / P(\text{Data})$$

• probability of the data for a given parameter set for a specific model
Bayesian inference - Data Likelihood

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- probability of the data for a given parameter set for a specific model
- for Solitaire, the likelihood function is the binomial distribution, i.e. the likelihood that exactly *k* out of *n* random deals are winnable assuming an underlying propability to win *p* is given by

$$L(\lbrace k,n\rbrace | \lbrace p\rbrace) = Binom(k,n,p) = \binom{n}{k} p^k (1-p)^{n-k}$$

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 in general, more complicated (i.e. no analytical expression, can only be computed numerically) Bayesian inference - Probability of Evidence



 Obtained by marginalizing the Likelihood over all possible parameters of a model type, i.e. the probability to obain specific data independently of the choice of model parameters

$$P(\text{Data}) = \int P(\text{Data}|\{\Theta_i\})P(\{\Theta_i\})d\{\Theta_i\}$$

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- Usually very difficult/expensive to compute
- Fortunately as a constant proportionality factor Z, we do not need to know its value if we are only interested in ratios of posterior propabilities:

$$P(\{\Theta_i\}|\text{Data}) \simeq P(\{\Theta_i\}) \cdot P(\text{Data}|\{\Theta_i\})$$

Bayesian inference - Posterior Probability



• In some cases, posterior likelihood can be analytically calculated e.g. for our Solitaire model and an uninformative, flat prior or certain analytical prior probability (here e.g. beta-distribution)

Bayesian inference - Posterior Probability (uninformative prior)

In general, the posterior for a flat, uninformative prior is identical to the likelihood function (in the part of the parameter space of interest and vanishes elsewhere)

$$P(\{\Theta_i\}|\text{Data}) = P(\text{Data}|\{\Theta_i\})|_{\text{support}}$$

Thus, for our Solitaire example we get

$$P(\{p\}|\{n,k\}) = Binom(n,k,p)$$



Bayesian inference - Posterior Prob. (inform. prior)

• If we have an informative analytical prior, e.g. here a beta-distribution, we may still be able to calculate the posterior analytically. For our Solitaire example, we obtain

$$P(\{p\}|\{n,k\}) = Beta(p, x, y) \cdot Binom(n, k, p)$$

= Beta(p, x + k, y + (n - k))

Bayesian inference - Posterior Prob. (inform. prior)

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$$= Beta(p, x + k, y + (n - k))$$

• Here, posterior is again a beta-distr. i.e prior and posterior belong to the same distribution family. Hence, this is called a **conjugate prior** to this binomial likelihood.



Bayesian inference - Posterior Probability (cont.)

 In general, this is not possible as the prior or the likelihood may not be available as an analytical pdf (see e.g. your Solitaire prior beliefs)

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- In general, this is not possible as the prior or the likelihood may not be available as an analytical pdf (see e.g. your Solitaire prior beliefs)
- cannot simply use MC + Acceptance-Rejection method to sample/compute posterior as we don't know our maximum density. Even if we know it, for a high dimensional parameter space, rejection rate will be very high due to difficult choice of bounding probability density.

Bayesian inference - Posterior Probability (cont.)

- In general, this is not possible as the prior or the likelihood may not be available as an analytical pdf (see e.g. your Solitaire prior beliefs)
- cannot simply use MC + Acceptance-Rejection method to sample/compute posterior as we don't know our maximum density. Even if we know it, for a high dimensional parameter space, rejection rate will be very high due to difficult choice of bounding probability density.
- need to find an alternative more efficient way to sample such a posterior

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Markov Chains: Definition



• A Markov Chain is a sequence of events {*S*_t} in which the probability of each event depends only on the state attained in the previous event (Markov property):

$$P(S_t|\{S_{t-1}, S_{t-2}, \dots\}) = P(S_t|S_{t-1})$$

• (Time-homog.) Transition kernel

$$P(S_t = y | S_{t-1} = x) = T(y | x)$$

Markov Chains: Definition (cont.)

• Prob. to be in state y at time t:

$$P(S_t = y) = P(\text{stay at y}) + P(\text{move to y}) - P(\text{move from y})$$

in discrete case:

$$P(S_t = y) = P(S_{t-1} = y) + \sum_{x \neq y} P(S_{t-1} = x)T(y|x)$$
$$- \sum_{x \neq y} P(S_{t-1} = y)T(x|y))$$

can also be written as:

$$P(S_t = y) = P(S_{t-1} = y)T(y|y) + \sum_{x \neq y} P(S_{t-1} = x)T(y|x)$$

$$\Rightarrow \vec{P}(S_t) = \vec{P}(S_{t-1})T = \vec{P}(S_{t-2})T^2 = \dots$$

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Markov Chains: Stationary Equilibrium

• Let's consider

$$\vec{P}(S_0) = (P(S_0 = A) \ P(S_0 = E)) = (1 \ 0)$$

$$T = \begin{pmatrix} T(A|A) & T(A|E) \\ T(E|A) & T(E|E) \end{pmatrix} = \begin{pmatrix} 0.6 & 0.7 \\ 0.4 & 0.3 \end{pmatrix}$$

and calculate the first few transitions using $\vec{P}(S_t) = \vec{P}(S_{t-1})T$:



Markov Chains: Stationary Equilibrium

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:
 $\begin{pmatrix} 0\\1 \end{pmatrix} \rightarrow \begin{pmatrix} 0.7\\0.3 \end{pmatrix} \rightarrow \begin{pmatrix} 0.63\\0.37 \end{pmatrix} \rightarrow \begin{pmatrix} 0.637\\0.363 \end{pmatrix} \rightarrow \begin{pmatrix} 0.6363\\0.3637 \end{pmatrix} \rightarrow \dots$

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Markov Chains: Stationary Equilibrium

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• In general, for the Markov chain to have a stationary equilibrium distribution, we need

$$P_{\text{eq}}(S_t = y) = P_{\text{eq}}(\text{stay at y}) \ \forall y$$

Hence P_{eq} (move to y) – P_{eq} (move from y) has to vanish.

Markov Chains: Stationary Equilibrium (cont.)

• in discrete case, we get:

$$\sum_{x \neq y} \left[P_{eq}(S_{t-1} = x) T(y|x) - P_{eq}(S_{t-1} = y) T(x|y) \right] = 0$$

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• One sufficient (but not necessary) condition to satisfy this is:

$$P_{eq}(S_{t-1} = x)T(y|x) = P_{eq}(S_{t-1} = y)T(x|y))$$

which is called **detailed balance** condition.

Markov Chains: Stationary Equilibrium (cont.)

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• if we want to sample a (non-tracable) probability function q using a Markov chain, we simply have to pick a transistion kernel with q as its equilibrium distribution !

MARCOV CHAIN MONTE CARLO SAMPLING

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An Introduction to MCMC

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- Borrow from acceptance/rejection idea: Introduce acceptance criterion with acceptance prob. α(y|x) to lower probability on LHS and maximise it on RHS, i.e. construct transition kernel as follows:

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In case above, we maximise RHS by setting α(x|y) = 1, thus obtaining for x ≠ y for the detailed balance condition:

$$q(x)T = q(y)T \Leftrightarrow q(x)k(y|x)\alpha(x|y) = q(y)k(x|y)$$
$$\Leftrightarrow \alpha(y|x) = \frac{q(y)k(x|y)}{q(x)k(y|x)} \quad \text{and } y \in \mathbb{R}$$

MCMC to the rescue! (cont.)

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$$\alpha(y|x) = \begin{cases} \frac{q(y)k(x|y)}{q(x)k(y|x)} & \text{if } q(x)k(y|x) > q(y)k(x|y) \\ 1 & \text{otherwise} \end{cases}$$

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MCMC - Metropolis-Hastings algorithm

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• The art of MCMC is in specifying the proposal distribution k(y|x)

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• Popular choice: Multivariate Gaussian distribution

$$k(y|x) \simeq \exp(-\frac{1}{2}(y-x)^T \Sigma^{-1}(y-x))$$

MCMC - Random Walk Metropolis - Log densities

Switching to logarithms:

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- This is important when dealing with a wide dynamical range to avoid over-/underflows (but may cause some occurrences of $-\infty$ we have to deal with)
- The acceptance-rejection step then reads:
 - If $\ln u < \ln q(\Theta') \ln q(\Theta)$, set $S_t = \Theta'$; else $setS_t = \Theta$



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MCMC - Convergence



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- no simply/reliable answer to this key question; absolute convergence of pdf difficult to quantify/prove
- relying on heuristics e.g. to check whether your walker has traversed the high density reasons at least a couple of times. This implies e.g. any substantial subset of the chain shows the same post. morph.

MCMC - Convergence (cont.)



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MCMC - Convergence (cont.)



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- Most important tool is the so-called **autocorrelation time** τ_x . It tells us how many steps it takes for a chain to ensure that samples on both end of the interval are (virtually) independent; is 2-point statistic, thus requires significant amount of data to be estimated precisely.

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- Most important tool is the so-called **autocorrelation time** τ_x . It tells us how many steps it takes for a chain to ensure that samples on both end of the interval are (virtually) independent; is 2-point statistic, thus requires significant amount of data to be estimated precisely.
- For multiple chains, there is the **Gelman-Rubin diagnostic** which compares the variance with a chain with that across chains

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 Initial state is often randomly chosen, but not from the underlying posterior, thus may end up in a "non-typical" place and then over-samples the region around initial → not good sample of posterior

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- Initial state is often randomly chosen, but not from the underlying posterior, thus may end up in a "non-typical" place and then over-samples the region around initial → not good sample of posterior
- Ignore/discard initial steps aka burn-in before you do any inference on the chain(s)



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$$k(y|x) \simeq \exp(-\frac{1}{2}(y-x)^T \Sigma^{-1}(y-x))$$

there are D(D+1)/2 parameters in the $D \times D$ sym.,pos.def. covariance matrix to be set

• Question: How to find the optimal parameters ?

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MCMC - Tuning (Problem 1)



 if distribution is too wide, while steps cover parameter space easily, almost all proposals are rejected

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MCMC - Tuning (Problem 2)



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- As previously mentioned, τ_x can be difficult to measure without significantly huge amounts of data. Instead we can use proxy statistics:

Acceptance fraction With shrinking step size the acceptance ratio grows and vice versa. The Goldilock value is roughly between 0.5 and 0.25. Can be used during the Burn-in phase to update the parameters if observed acceptance differs significantly.

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> You can decompose the D-dim. tuning problem into D 1-dim. problems by updating each model parameter separately.

Accepted Squared Jump Distance This is the mean squared distance the walker moves and maximises when the acceptance rate is reasonable and the step size is large - easy to measure and well correlated with the autocorrelation

MCMC - Final Notes

We saw that MCMC is by construction a fair sampler for our posterior (or any other) probability, which allows us to integrate over the probability function (e.g. to calculate the mean or median), but we have to also point out, what it is not ...

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• It is **NOT** a **good search algorithm**. Chains are not guaranteed to find/sample every local maximum, let alone a global one in the whole parameter space.

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- It is **NOT** a **good search algorithm**. Chains are not guaranteed to find/sample every local maximum, let alone a global one in the whole parameter space.
- It is definitely also NOT a good optimizer i.e. generically samples will not lie close the maximum of the sampled pdf (gets worse with higher dimensionality) ⇒ "Best-Fit" value is meaningless.

Web-/Bibliography

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