

Markov-chain Monte Carlo


An (almost) maths-less introduction

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(with the help of many others!
Thanks: Sam Brand, Simon Spencer, Samik Datta...!)

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Outline

- Introduction
 - The main example – coin tossing
 - Explaining confusing concepts
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 - MCMC
- MCMC in practice – Metropolis-Hastings
 - MCMC for coin tossing (1 dim)
 - Diagnosing your MCMC
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 - MCMC in 2 dim
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Example – coin tosses

- You toss a coin $n = 10$ times. You get:

H	H	T	H	H	T	H	H	H	H
1	1	0	1	1	0	1	1	1	1

- Arbitrarily, call H a success (1) and T a failure (0):
- The number of heads is: $k = 8$
- Questions:
 - is the coin is fair?
 - how confident are you in your answer?
 - and what if you had 79 head out of 100 tosses?
- Key point:
 - Estimating a single number is usually not enough information!

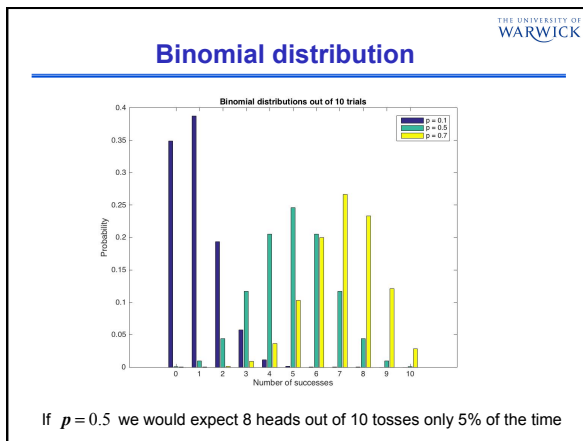


Binomial distribution

- If we believe that:
 - all tosses are independent of each other
 - output can only be head or tail (and nothing else)
 - head occurs with the same probability p each time
- Then the probability of getting k heads out of n trials, each with success probability p is:

$$\mathbb{P}(k | n, p) = \binom{n}{k} p^k (1-p)^{n-k}$$

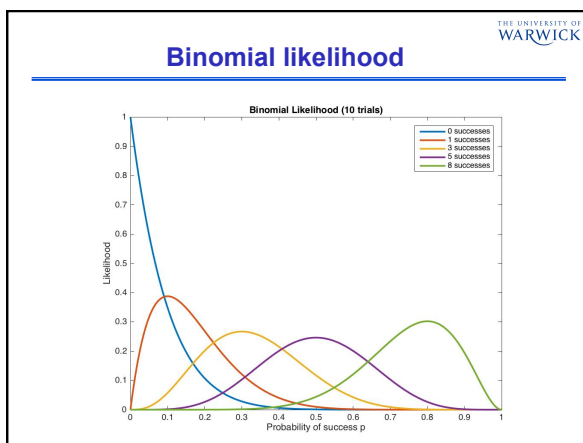
binomial coefficient
- Key point: we are **assuming** a model (often without realising it)



Likelihood function

- For parameters θ and data D , the likelihood function is defined as:

$$\mathcal{L}_D(\theta) = \mathbb{P}(D | \theta)$$
- Numerically same as the probability, but different interpretation.
- In $\mathbb{P}(D | \theta)$,
 - θ is thought as fixed, D varies; and
 - $\int_D \mathbb{P}(D | \theta) = 1$
- In $\mathcal{L}_D(\theta)$,
 - D is thought as fixed, θ varies; and
 - $\int_\theta \mathcal{L}_D(\theta) \neq 1$ in general



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Classical VS Bayesian

- This is mostly a philosophical question, but in summary:
- Frequentist (classical) perspective:
 - a parameter has a **true exact value**, which we don't know
- Bayesian perspective:
 - a parameter is a **random variable**, which we can describe using its distribution function

Classical statistics

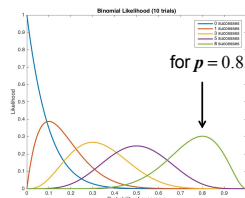
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graph TD
    Data[Data] --> Likelihood[Likelihood]
    Model[Model] --> Likelihood
  
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- The goal is to study the likelihood

Maximum likelihood estimator (MLE)

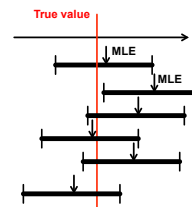
- Given there is only 1 true value of the parameter (classical stats), the interest is in finding the maximum likelihood (ML) estimate:
 - the parameter value at which the likelihood is maximal



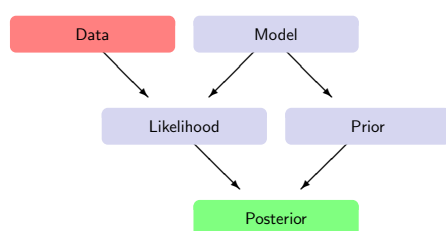
- This can be found analytically or using numerical methods that "climb" up the hill

Confidence interval

- How confident I am in my ML estimate?
- I can draw **confidence intervals** (CI)
 - assuming asymptotic normality
- Note that:
 - The parameter is fixed
 - The MLE is a random variable
 - The CI is an interval centred in the MLE
 - a 95% CI is a random interval that covers the true value 95% of the times



Bayesian statistics



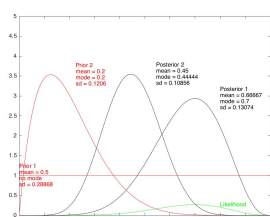
- The likelihood is still key, but the goal now is to study the posterior

Bayes' theorem

$$\mathbb{P}(\theta | D) = \frac{\mathbb{P}(D | \theta) \mathbb{P}(\theta)}{\int_{\theta} \mathbb{P}(D | \theta) d\theta}$$

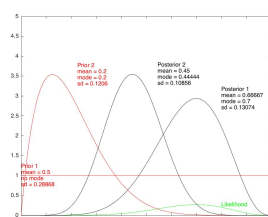
Bayes' theorem

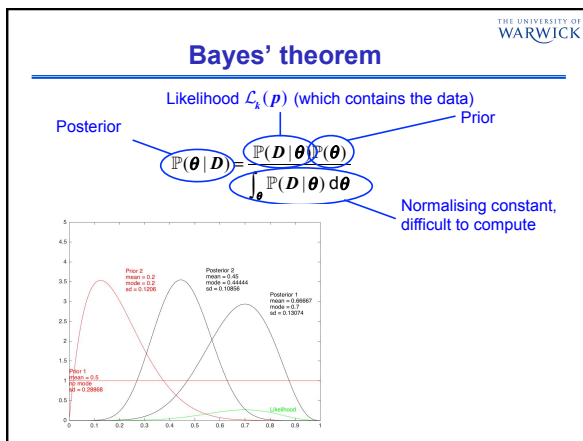
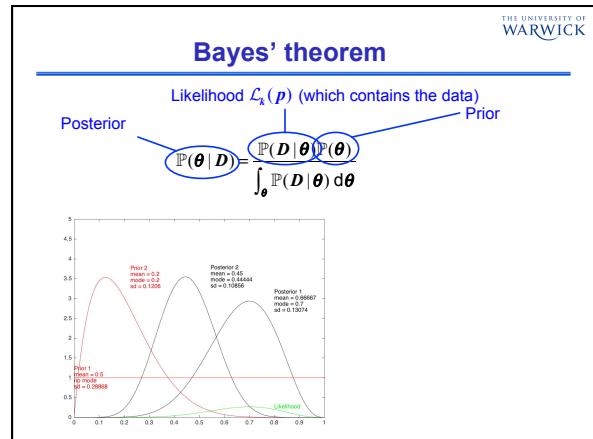
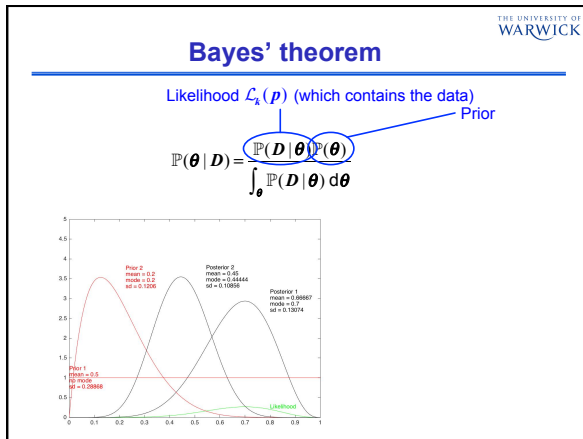
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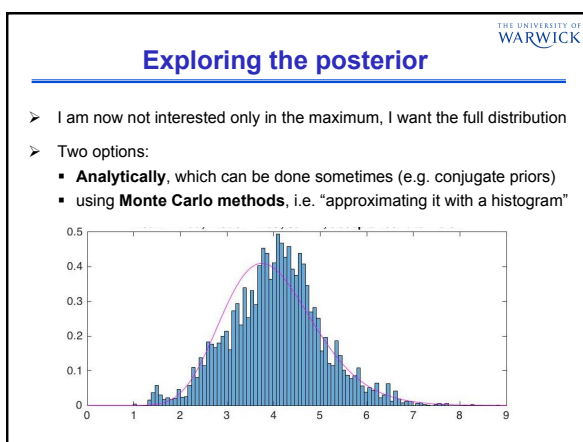
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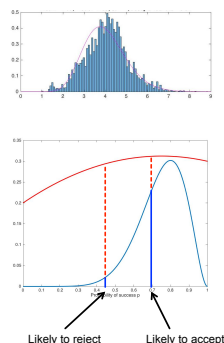
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Monte Carlo methods

- Monte Carlo means "by generating random numbers"
- By generating lots of random numbers from a distribution I can
 - explore it
 - compute functions of the random variable with that distribution
 - I might even explore a distribution that I can't even write, as long as it is the result of a simulation (often the case in biology)
- Monte Carlo methods are the only thing that works in high dimensions (often the case in practice)
- Biological applications (e.g. epidemiology, phylogenetics) always have high dimensions, because you need to impute a lot of unobserved events (infections, coalescence events)

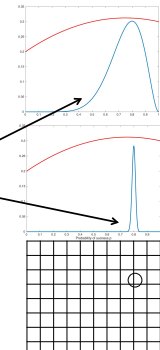
Monte Carlo Rejection Sampling

- Ordinary Monte Carlo methods explore a function by generating lots of **independent samples**
- If I can draw directly from the distribution of interest (blue line), then I simply do it
- If I can't I can use the **rejection sampling** method:
 - Sampling from another distribution I can sample from (red line) which "cover" the other distribution
 - accept/reject with some probability



Problems with rejection sampling

- Hard to find a good distribution (red line) to sample from
- Hard to find how much I need to "inflate" it to "cover the other curve"
- Can be very inefficient
 - Sampling this is easy (few rejections)
 - Sampling this is hard (lots of rejections)
- In general it is **really hard** to explore a distribution by independent samples in **many dimensions** (too many rejections – very inefficient)
- **MCMC is a way to explore more efficiently distributions in many dimensions**



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Markov chains

- A Markov chain is a stochastic process, i.e. a system that evolves in time according to a probabilistic rule, where
 - the time is discrete
 - the probabilistic rule at each step depends only on the current step (and nothing before then) – **Markov property**
- It is described by a family of random variables $X_0, X_1, X_2, \dots, X_n, \dots$ with values in a state space \mathcal{S} (discrete or continuous)
- where for each n , X_n depends only on X_{n-1} and not on X_{n-2}, X_{n-3}, \dots
- **Example:** snakes and ladders (it doesn't matter how you arrived where you are; it only matter where you are and the result of rolling the die)
- Under some assumptions, the chain has a **stationary distribution**: if you let it run long enough, no matter where you started from, you end up bouncing around this distribution

Markov chain Monte Carlo

- **Goal:** we need to explore the posterior distribution
- It might be difficult to sample from it, but it is **surprisingly easy** to construct a Markov chain that has as stationary distribution the posterior distribution. So,
 - run the Markov chain for long enough, until it has "converged"
 - from that moment onwards I am sampling from the posterior
- **Pros:** I explore the posterior efficiently, even in high dimensions (because I stay in the regions of high probability, if already there)
- **Cons:** I am not drawing independent samples anymore:
 - I need more samples to have the same "exploratory power"
 - I don't know many "more samples" are enough
- It's a "**dark art**": I know that if it has converged it's giving me the right answer, but there is no principled way of telling it has converged

Summary: why MCMC

- In a Bayesian framework, we pull together prior and likelihood (i.e. data) to obtain the posterior
- We want to explore the posterior, but it's difficult to do it analytically
- This is particularly the case for many applied problems
- Monte Carlo methods are ductile and can in principle work in high dimensions, but in practice are very inefficient
- MCMC methods improve the efficiency, at the price of having dependent samples (rather than "more powerful" independent ones)
- We need to make sure that this "dependency" is not ruining our job

MCMC for coin tossing (1 dim)
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Tricks
MCMC in 2 dim

MCMC IN PRACTICE

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MCMC IN PRACTICE

MCMC structure

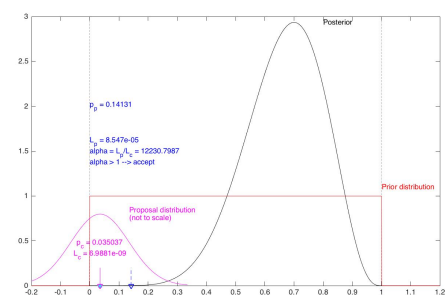
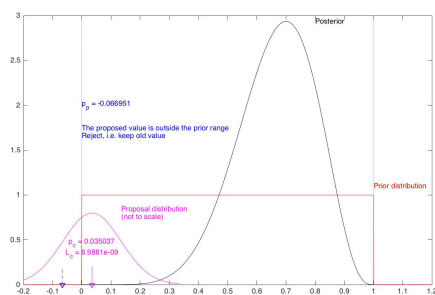
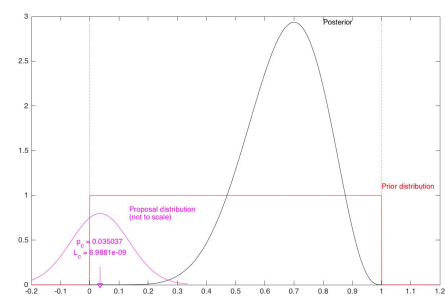
3 main steps:

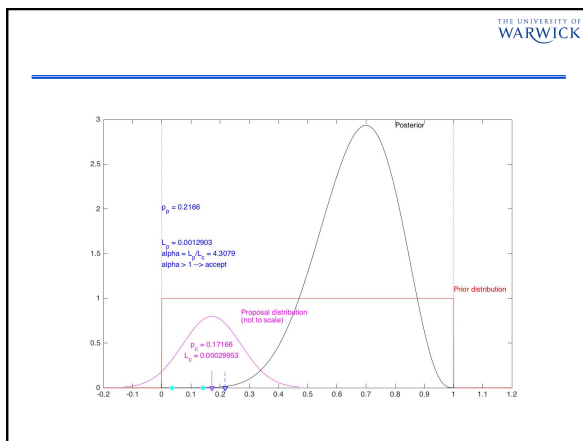
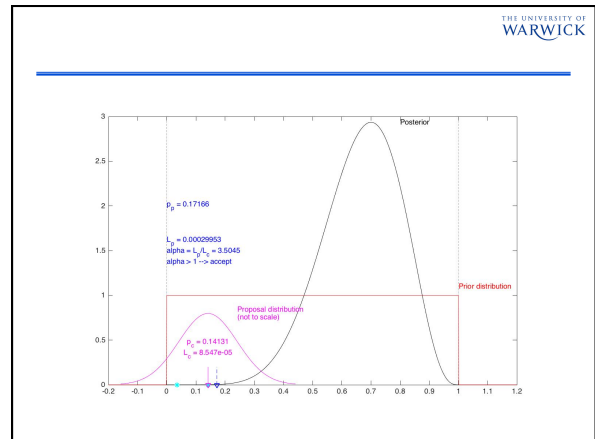
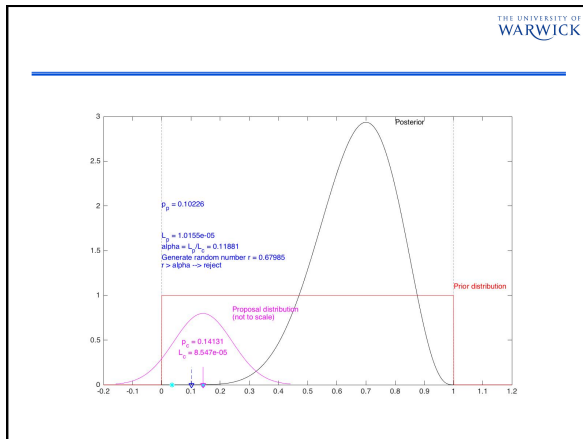
- ① **Propose new values** for the parameters
- ② **Compute the likelihood** at the new values
- ③ Decide whether to:
 - **accept**: move to the new values
 - or **reject**: stay where you are and count again the current values

and these three steps are repeated many times!

The most expensive step is typically the computation of the likelihood

MCMC





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- ### Where to start
- First, you need your **data** – this is given
 - Second, you need to work out how to compute the **likelihood** – this comes from the model you have assumed
 - Then you need to choose (once and for all):
 1. a **prior** distribution for your parameters
 2. a **proposal** distribution
 3. a **starting value** for the parameters (it should have no influence on the final result)
 - Finally you need to choose (and play around with):
 1. the length of your chain
 2. width of proposal distribution
 3. thinning and burn-in

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MCMC for coin tosses

- Rules of the game: n coin tosses
- Data:
 - number of heads k
- Goal: explore the **posterior distribution** for the probability p of the coin giving heads, given the data you have seen. This includes information from:
 - the prior distribution on p (my belief / expert opinion)
 - the data

Likelihood $\mathcal{L}_k(p)$ (which contains the data)

Posterior $\mathbb{P}(p|k) = \frac{\mathbb{P}(k|p)\mathbb{P}(p)}{\int_0^1 \mathbb{P}(k|p)\mathbb{P}(p) dp}$ Prior

Good news:
this you can ignore!

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The likelihood

- Our model assumes that the number of heads is binomially distributed. Implicitly, that means:
 - all tosses are independent of each other
 - output can only be head or tail (and nothing else)
 - head occurs with the same probability p each time
- I have tossed the coin n times and I have seen head k times:

$$\mathcal{L}_k(p) = \mathbb{P}(k \text{ heads} | p)$$

$$= \binom{n}{k} p^k (1-p)^{n-k}$$

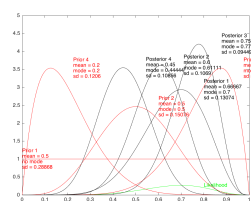
Prior distribution

- The prior reflects your knowledge (or expert opinion), e.g.
 - if you believe the coin is likely to be fair (maybe because you have seen many fair coins and very few non-fair ones), you will choose a prior highly peaked around $p = 0.5$
 - if you know nothing at all and don't trust anybody, or if you want all the information to come from your data, choose a flat one

- The choice of the prior matters:

- The difference between your prior and your posterior tells you how much you learnt from the data

- Simplest choice: flat



Common prior distributions

- On $[0,1]$ (e.g. for probabilities):
 - uniform, i.e. flat (the pdf is constant = 1 in $[0,1]$ and 0 outside)
 - Beta distribution
- On $[0,+\infty)$ (e.g. variances, infection rate, recovery rate...):
 - flat – this is an improper prior (the pdf is constant “= 0”)
 - exponential distribution
 - lognormal distribution
- On $\mathbb{R} = (-\infty, +\infty)$ (e.g. mean of normal distribution)
 - flat – again, improper (the pdf is constant “= 0”)
 - Normal
- The parameters describing your prior are called hyper-parameters

Proposal distribution

- In theory, it doesn't matter which one you choose
- In practice, you want one that guarantees your chain “mixes well”, i.e.
 - you move around (instead of staying for long on the same place)
 - you explore your parameter space quickly
- Unless you know what you are doing (e.g. Gibbs sampling), **choose a Normal distribution**:
 - with **mean** the previous value of your parameter
 - with a **standard deviation** you will tune by trial and error
- The Normal is convenient because it's symmetric (see below)
- In more than 1 dimension, use a multivariate Normal (you can play with the covariance matrix)

Acceptance probability

- This is the clever bit that allows the miracle to work
- At each step you have:
 - An old (current) parameter p and a new (proposed) one p'
 - The likelihood \mathcal{L} and the prior \mathbb{P} computed in both p and p'
 - The probability of your proposal distribution Q making you jump:
 - » from p to p' : $Q(p \rightarrow p')$
 - » and backwards: $Q(p' \rightarrow p)$
- Then you compute:

$$\tilde{\alpha} = \frac{\mathcal{L}(p') Q(p' \rightarrow p) \mathbb{P}(p')}{\mathcal{L}(p) Q(p \rightarrow p') \mathbb{P}(p)} = \frac{\mathcal{L}(p') \mathbb{P}(p')}{Q(p \rightarrow p')} \bigg/ \frac{\mathcal{L}(p) \mathbb{P}(p)}{Q(p' \rightarrow p)}$$
- and you accept p' with probability: $\alpha = \min\{1, \tilde{\alpha}\}$

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Simpler acceptance probability

- When computing

$$\tilde{\alpha} = \frac{\mathcal{L}(p') Q(p' \rightarrow p) \mathbb{P}(p')}{\mathcal{L}(p) Q(p \rightarrow p') \mathbb{P}(p)}$$

- If the prior is constant in the allowed range, it cancels out
- If you fall outside the allowed range of the prior $\mathbb{P}(p') = 0$, i.e. $\tilde{\alpha} = 0$ and you reject for sure
- If Q is symmetric, the probability of jumping in one direction or backwards are identical, and Q also cancels out
 - This is why the Normal distribution is a good choice
- If the likelihood has some common factors independent of p , they cancel out (e.g. the binomial coefficient)

Starting value for parameters

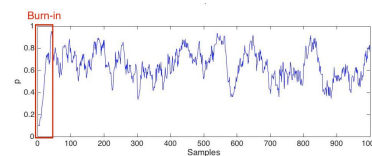
- When running MCMC, you have to wait until your chain has “converged”, i.e. has run long enough that:
 - you have forgotten your initial conditions
 - you are bouncing around the stationary distribution (which is exactly your posterior by construction!)
- Therefore, it doesn't matter where you start from – **choose what you prefer!**
- Further, it might be useful to choose different starting values to ensure that each run still converges to the same stationary distribution (as it should)

Length of chain

- You should run your chain long enough
- You want 1,000-10,000 (almost) independent samples (nice histogram)
- Rule of thumb:
 - run your chain for 1,000 steps
 - look at the autocorrelation plot
 - check after how many steps the correlation becomes small (i.e. between the horizontal lines in the plot), say 50
 - you want to run your chain 50 x how many (almost) independent samples
- If the chain is too big to save on your computer you can “thin” it by a factor τ , i.e. save one output every τ

Burn-in

- You only want a sample from the stationary distribution (= the posterior)
- The **burn-in** is the initial part of the chain, that depends of where you started from, and that looks “different” from the rest of the chain, because you haven't yet converged
- The burn-in should be identified by eye from the trace plot and discarded



Width of the proposal

- If your proposal is very wide, you want to jump very far, usually out of the range of the prior or into regions of low posterior probability:
 - high rejection rates
 - chain visibly constant in bits

⇒ Choose a smaller standard deviation
- If your proposal is very narrow, your proposals are almost always accepted, but you move very slowly around the parameter space:
 - high acceptance rates
 - chain with visible broad oscillations

⇒ Choose a larger standard deviation
- Both the problems above lead to large autocorrelation (bad)
- In 1 dim, acceptance rates should be between 20 and 60%

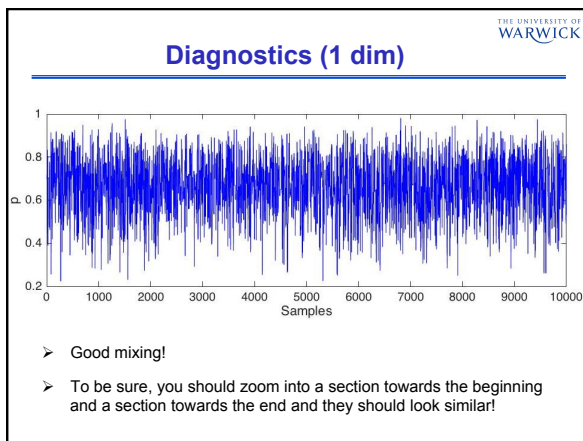
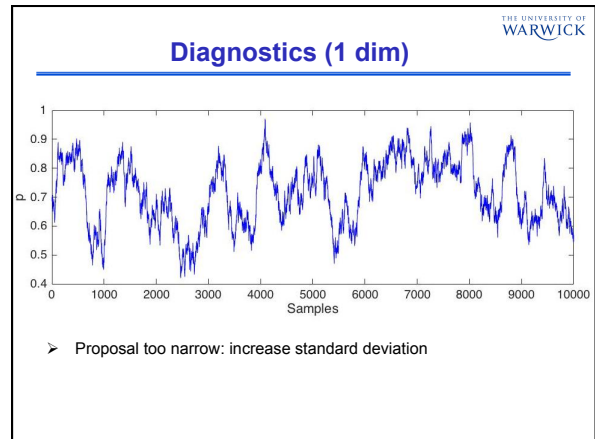
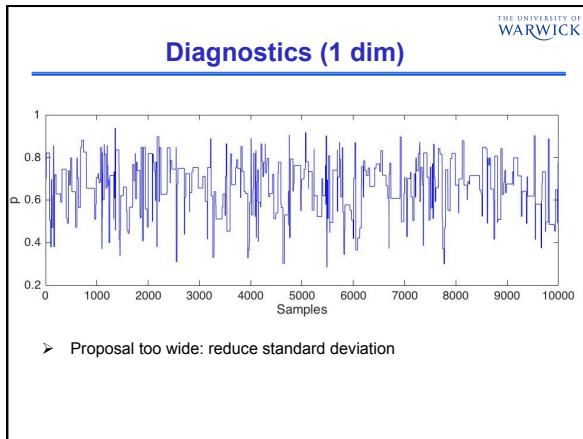
MCMC for coin tossing (1 dim)

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MCMC IN PRACTICE



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Trick 1: log-likelihood

Instead of using the likelihood, use the log-likelihood

- This should always be done:
 - it has no drawbacks
 - reduce numerical error (likelihood can have really small values)
 - cheaper computations (products become sums, exponentials become products)
- E.g. binomial likelihood $\mathcal{L}_k(p) = \binom{n}{k} p^k (1-p)^{n-k}$
 - Ignore constant factors independent of p (they cancel out in $\tilde{\alpha}$)
 - Take the log

$$\log \mathcal{L}_k(p) \propto k \log p + (n-k) \log(1-p)$$
- At this point, it is convenient to work with $\log \tilde{\alpha}$ and to use the log for all its factors (proposal and prior)

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Trick 2: avoid useless calculations

- Calculating the likelihood is usually very expensive
 - If you propose a new parameter where the prior is 0 (e.g. p outside $[0,1]$), reject immediately, before calculating $\tilde{\alpha}$
- Cheaper to test an "if" statement than to generate random numbers:
 - If $\tilde{\alpha} > 1$, accept without generating a random number to choose whether to accept or reject

Trick 3: Always plot the prior

- If your posterior is different, it tells you how much you have learnt from the data
- If your posterior is very similar, it means the data contains very little or no information about that parameters (unidentifiability issue)

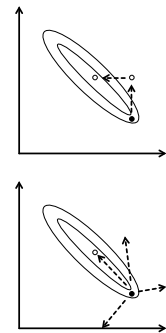
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MCMC IN PRACTICE

Proposal in 2 dimension

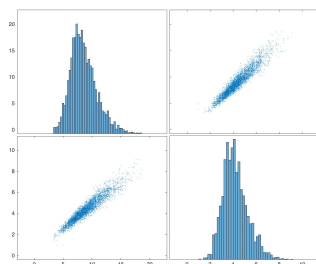
You can choose whether to:

- propose 1 at a time (e.g. from a simple Normal distribution in 1 dim), while keeping the other fixed:
 - OK if parameters are relatively uncorrelated
 - Bad if they are strongly correlated
 - Very good if you can specify analytically the conditional posterior (Gibbs sampling)
- or propose both parameters in one go (e.g. from a multivariate normal) – this is called block update
 - A good solution when the parameters are strongly correlated



Plotmatrix

- Plotmatrix is a command (in Matlab) that creates a fancy plot that can reveal correlation between parameters



Strongly correlated parameters

- Tricks to improve mixing:
 - Block updates, possibly from a multivariate normal "elongated" in the direction of the correlation
 - Re-parameterise your model with new parameters that are less correlated.



PLAY WITH MATLAB OR R



Codes

- “MCMCBinomial” file: play with
 - n_tosses
 - n_heads
 - n_iters
 - thinning
 - sd_proposal (try 0.01 or 5)
 - burnin
- “MCMCEpidemicFinalSizeLargePop” file: play also with
 - Updating in block or not
 - Tuning the sd_proposal for either parameter