Introduction

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Introduction to Bayesian Statistics

Bayes Rule

Bayes' theorem is at the heart of Bayesian statistics:

$$P(\theta|Y) = \frac{P(\theta) \times P(Y|\theta)}{P(Y)}$$

where:

- θ is our parameter value(s);
- Y is the data that we have observed;
- $P(\theta|Y)$ is the posterior probability of the parameter value(s);
- $P(\theta)$ is the prior probability of the parameters;
- $P(Y|\theta)$ is the likelihood of the data given the parameters value(s);
- P(Y) is the probability of the data, integrated over parameter space.

Bayesian statistics

• In practice we usually work with the following:

$$P(\theta|Y) \propto P(\theta) \times P(Y|\theta)$$

• Our Bayesian posterior is therefore always a combination of the likelihood of the data $P(Y|\theta)$, and the parameter priors $P(\theta)$.

How to get a posterior distribution?

- Analytical derivation
- Numerical approximation

Analytical derivation

Analytical derivation could be feasible in some simple cases (Beta-binomial model)

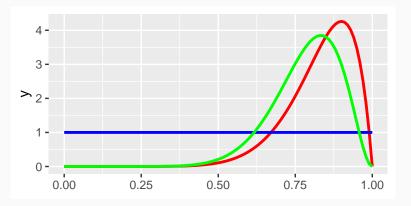
- Prior $p \sim Beta(\alpha, \beta)$
- Likelihood $Y|p \sim Bin(p, n)$
- Posterior $p|y \sim Beta(\alpha + y, \beta + n y)$

Example: Suppose we are testing the fairness of a coin. We observed n=12 flips and y=10 heads. We assume an uninformative prior.

- Prior $p \sim Beta(\alpha = 1, \beta = 1)$
- Likelihood $Y|p \sim Bin(p, 12)$
- Posterior $p|y \sim Beta(\alpha = 11, \beta = 3)$

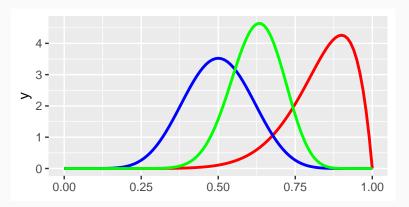
Analytical derivation

- Uniform Prior Beta(1,1)
- Likelihood *Bin*(10, 12)
- Posterior *Beta*(11, 3)



Analytical derivation

- If I change the Prior to Beta(10, 10)
- Likelihood *Bin*(10, 12)
- Posterior *Beta*(20, 12)



A quick look at the Beta distribution.

- The Beta distribution is a family of continuous probability distributions defined on the [0, 1] interval parameterized by two positive "shape" parameters α and β .
- Parameters of Beta distribution are commonly considered as "pseudo-counts" of successes (α) and failures (β)

•
$$Y \sim Beta(\alpha, \beta) = \frac{x^{\alpha-1}(1-x)^{\beta-1}}{B(\alpha, \beta)}$$

•
$$E(Y) = \frac{\alpha}{\alpha + \beta}$$

•
$$Var(Y) = \frac{\alpha\beta}{(\alpha+\beta)^2 + (\alpha+\beta+1)}$$

MCMC

- Markov chain Monte Carlo (MCMC) methods comprise a class of algorithms for sampling from a probability distribution.
- By constructing a Markov chain that has the desired distribution as its equilibrium distribution, one can obtain a sample of the desired distribution by recording states from the chain.
- The more steps are included, the more closely the distribution of the sample matches the actual desired distribution.
- Various algorithms exist for constructing chains, including the Metropolis—Hastings algorithm.

MCMC

- A way of obtaining a numerical approximation of the posterior
- Highly flexible
- Not inherently Bayesian but most widely used in this context
- Assessing convergence is essential, otherwise we may not be summarising the true posterior
- Our chains are correlated so we need to consider the effective sample size

Theory and application of MCMC

MCMC in practice

We can write a Metropolis–Hastings algorithm but this is complex and inefficient

There are a number of general purpose languages that allow us to define the problem and leave the details to the software:

- WinBUGS/OpenBUGS
- JAGS(Just Another Gibbs Sampler)
- Stan (named in honour of Stanislaw Ulam, pioneer of the Monte Carlo method)

JAGS uses the BUGS language

- This is a declarative (non-procedural) language
- The order of statements does not matter
- The compiler converts our model syntax into an MCMC algorithm with appropriately defined likelihood and priors
- You can only define each variable once!!!

Different ways to run JAGS from R: rjags, runjags, R2jags, jagsUI

A simple JAGS model might look like this:

```
basicjags <- "model{</pre>
  # Likelihood part:
  Positives ~ dbinom(prevalence, TotalTests)
  # Prior part:
  prevalence ~ dbeta(2, 2)
  # Hooks for automatic integration with R:
  #data# Positives, TotalTests
  #monitor# prevalence
  #inits# prevalence
}
```

Two model statements in this JAGS model:

 The number of *Positive* test samples is Binomially distributed with probability parameter *prevalence* and total trials *TotalTests*

```
Positives ~ dbinom(prevalence, TotalTests)
```

2. Our prior probability distribution for the parameter *prevalence* is a Beta(2,2)

```
prevalence ~ dbeta(2,2)
```

The other lines in this model are automated hooks that are only used by runjags for:

1. Loading data

#data# Positives, TotalTests

2. Monitoring the posterior distribution of interest

#monitor# prevalence

3. Initializing the chains

#data# Positives, TotalTests

This JAGS model is:

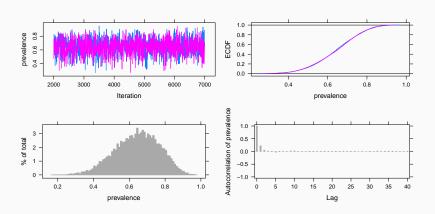
- Easy to write and understand
- Efficient (low autocorrelation)
- Fast to run

Let's run this model with some data.

```
# data to be retrieved by runjags:
Positives <- 7
TotalTests <- 10
# initial values to be retrieved by runjags:
prevalence <- list(chain1=0.05, chain2=0.95)</pre>
results <- run.jags(model = basicjags,
                     n.chains = 2,
                     burnin = 1000,
                     sample = 5000)
```

JAGS - Check the plots for convergence

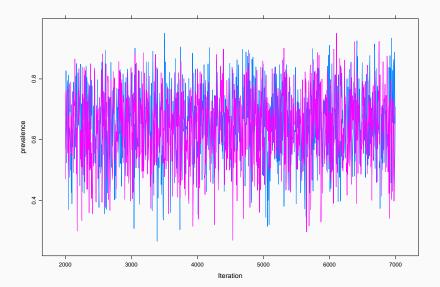
Generating plots...



Generating plots...

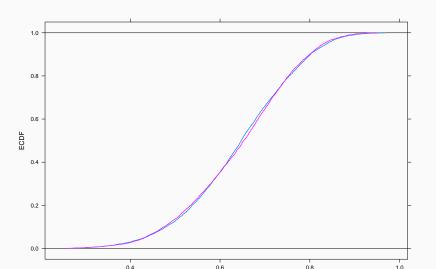
JAGS - Trace plots

The two chains should be stationary.



JAGS - Empirical Cumulative Distribution Function (ECDF) plots

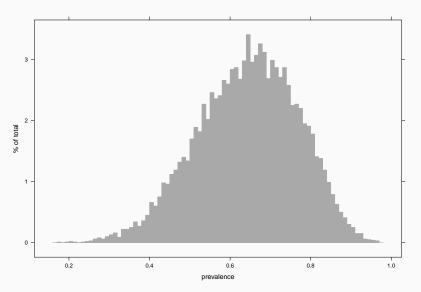
The two chains should be very close to each other.



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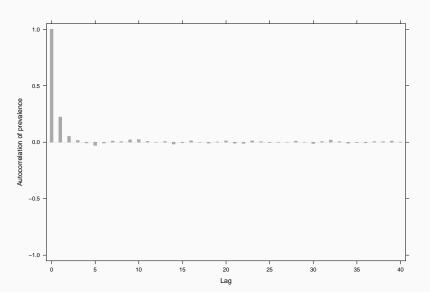
JAGS - Histograms

Histogram of the combined chains should appear smooth.



JAGS - Autocorrelation plots

Autocorrelation plot tells how well behaved the model.



JAGS - Diagnostics

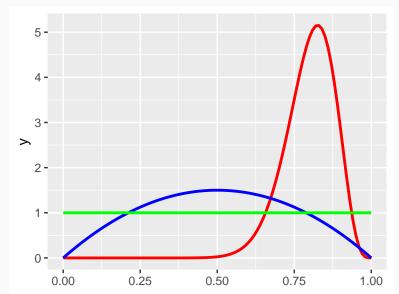
Then check the effective sample size (SSeff) and Gelman-Rubin statistic (psrf):

```
## Lower95 Median Upper95 SSeff psrf
## 0.402 0.649 0.869 6354.000 1.000
```

Reminder: we want psrf < 1.05 and SSeff > 1000

Priors: the $Beta(\alpha, \beta)$ distribution

Beta(2,2) Beta(20,5) Beta(1,1)



Priors: the $Beta(\alpha, \beta)$ distribution

Common choices:

- Uniform prior *Beta*(1,1) (Bayes-Laplace)
- Jeffreys prior $Beta(\frac{1}{2}, \frac{1}{2})$
- "Neutral" prior $Beta(\frac{1}{3}, \frac{1}{3})$ (Kerman 2011)
- Haldane prior Beta(0,0), or it's approximation $Beta(\epsilon > 0, \epsilon > 0)$

Exercise

- Run this model yourself in JAGS
- Change the initial values for the two chains and make sure it doesn't affect the results
- Reduce the burnin length does this make a difference?
- Change the sample length does this make a difference?
- Change the priors
- Increase the sample size