

Session 1

A practical introduction to MCMC

Matt Denwood

2021-06-28

Course Outline and Practicalities

Overview

Date/time:

- 28th June to 1st July 2021
- 09.00 - 12.30 daily
- Use the same Zoom link all week!

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Teachers:

- Matt Denwood (University Of Copenhagen)
- Nils Toft (IQinAbox)
- Søren Saxmose Nielsen (University Of Copenhagen)
- Maj Beldring Henningsen (University of Copenhagen)

COST action CA18208: [<https://harmony-net.eu/about/>]

Goals are to encourage the use of latent class models/methods for:

- Diagnostic test evaluation
- Determination of true prevalence
- Certification of disease freedom

Period: October 2019 - October 2023

Contact: info@harmony-net.eu

Practical information on the course

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 - We may tweak material as we go along
 - Remember to pull changes at the start of each day!

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 - Feel free to share this with your colleagues
- Attendance registration is necessary for COST meetings
 - We will take care of this via Zoom

Background

Diagnostic test evaluation: with gold standard = simple!

```
library("tidyverse")
se <- c(1, 0.6)
sp <- c(1, 0.9)
N <- 1000
prevalence <- 0.25

data <- tibble(Status = rbinom(N, 1, prevalence)) %>%
  mutate(Test1 = Status) %>%
  mutate(Test2 = rbinom(N, 1, se[2]*Status + (1-sp[2])*(1-Status)))

(twoXtwo <- with(data, table(Test1, Test2)))
##      Test2
## Test1   0   1
##      0 656  68
##      1 127 149
```

The true Status is always the same as the result of Test1 . . .

```
(sensitivity <- twoXtwo[2,2] / sum(twoXtwo[2,1:2]))
## [1] 0.5398551
(specificity <- twoXtwo[1,1] / sum(twoXtwo[1,1:2]))
## [1] 0.9060773
```

Diagnostic test evaluation: no gold standard

Now we have both values of sensitivity and specificity $< 1 \dots$

```
se <- c(0.9, 0.6)
sp <- c(0.95, 0.9)
N <- 1000
prevalence <- 0.25

data <- tibble(Status = rbinom(N, 1, prevalence)) %>%
  mutate(Test1 = rbinom(N, 1, se[1]*Status + (1-sp[1])*(1-Status))) %>%
  mutate(Test2 = rbinom(N, 1, se[2]*Status + (1-sp[2])*(1-Status)))

with(data, table(Status, Test1))
##           Test1
## Status    0    1
##      0 691  35
##      1  32 242
with(data, table(Status, Test2))
##           Test2
## Status    0    1
##      0 667  59
##      1 104 170
```

In real life we don't know what Status is...

```
(twoXtwo <- with(data, table(Test1, Test2)))  
##      Test2  
## Test1    0    1  
##      0 646  77  
##      1 125 152  
(sensitivity_1 <- twoXtwo[2,2] / sum(twoXtwo[1:2,2]))  
## [1] 0.6637555  
(sensitivity_2 <- twoXtwo[2,2] / sum(twoXtwo[2,1:2]))  
## [1] 0.5487365  
(specificity_1 <- twoXtwo[1,1] / sum(twoXtwo[1:2,1]))  
## [1] 0.8378729  
(specificity_2 <- twoXtwo[1,1] / sum(twoXtwo[1,1:2]))  
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So we will *always* under-estimate the Se and Sp of both tests!

The solution

- We need to assess the sensitivity and specificity of both tests against the true (but unknown) Status of each individual
- This unknown Status is called the latent class
 - Therefore we need to run a latent class model ...

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- This unknown Status is called the latent class
 - Therefore we need to run a latent class model ...
- How can we implement a latent class model?
 - Frequentist statistical methods:
 - possible, but difficult
 - Bayesian statistical methods:
 - easier and much more commonly done!

Learning outcomes

By the end of the course you should be able to:

- Understand what a latent class model is, and how they can be used for diagnostic test evaluation
- Run basic latent class models using R and JAGS for real-world problems
- Interpret the results
- Understand the nuances and complexities associated with these types of analysis and the interpretation of the latent class

Revision

Bayes Rule

Bayes' theorem is at the heart of Bayesian statistics:

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

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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.

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- Our Bayesian posterior is therefore always a combination of the likelihood of the data, and the parameter priors
- But for more complex models the distinction between what is 'data' and 'parameters' can get blurred!

- 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

Bayesian MCMC vs Frequentist ML

Advantages:

- Very flexible modelling framework
- More natural interpretation of confidence intervals (credible intervals)
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Disadvantages:

- More computationally intensive
- More emphasis on the practitioner to ensure the output is reliable
- Requirement to incorporate prior information

Everyone up to speed?

Any questions so far?

Anything unclear?

Session 1: A practical introduction to MCMC

- We can write a Metropolis algorithm ourselves, 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
 - Bayesian inference Using Gibbs Sampling
 - 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 prior
 - You can only define each variable once!!!

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 - This is a declarative (non-procedural) language
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- Different ways to run JAGS from R:
 - `rjags`, `runjags`, `R2jags`, `jagsUI`
- See <http://runjags.sourceforge.net/quickjags.html>
 - This is also in the GitHub folder

A simple JAGS model might look like this:

```
model{  
  # Likelihood part:  
  Positives ~ dbinom(prevalence, N)  
  
  # Prior part:  
  prevalence ~ dbeta(1, 1)  
  
  # Hooks for automatic integration with R:  
  #data# Positives, N  
  #monitor# prevalence  
  #inits# prevalence  
}
```

There are two model statements:

- The first:

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These are very similar to the likelihood and prior functions defined in the preparatory exercise (although this prior is less informative)

The other lines in this model:

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Compared to our Metropolis algorithm, this JAGS model is:

- Easier to write and understand
- More efficient (lower autocorrelation)
- Faster to run

To run this model, copy/paste the code above into a new text file called “basicjags.txt” in the same folder as your current working directory. Then run:

```
library('runjags')

# data to be retrieved by runjags
Positives <- 70
N <- 100

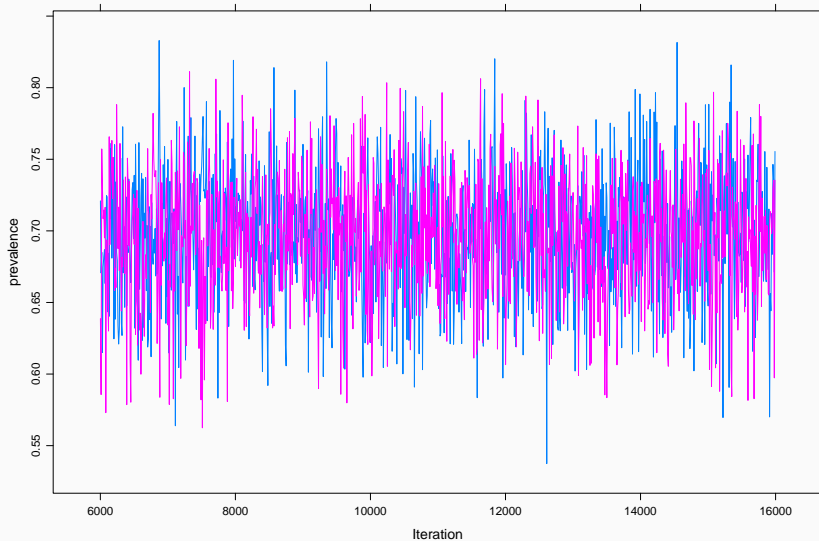
# initial values to be retrieved by runjags:
prevalence <- list(chain1=0.05, chain2=0.95)

results <- run.jags('basicjags.txt', n.chains=2, burnin=5000,
  ↪ sample=10000)
```

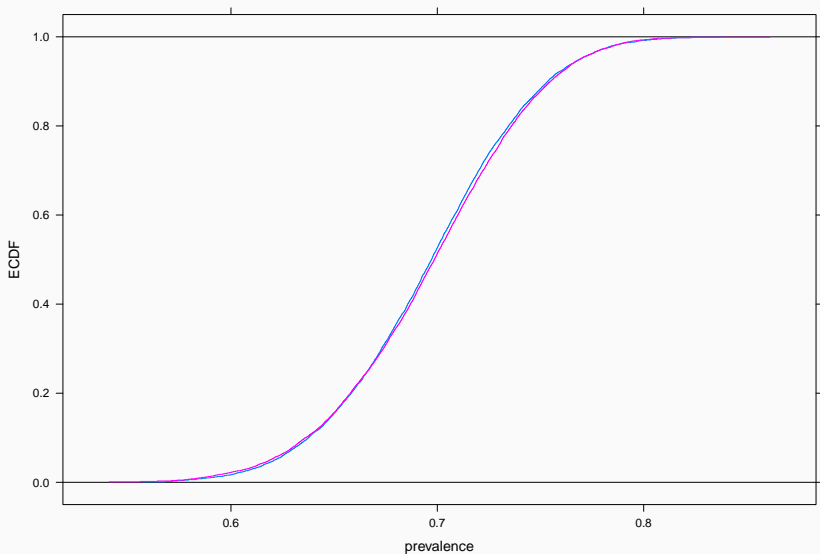
First check the plots for convergence:

```
plot(results)
```

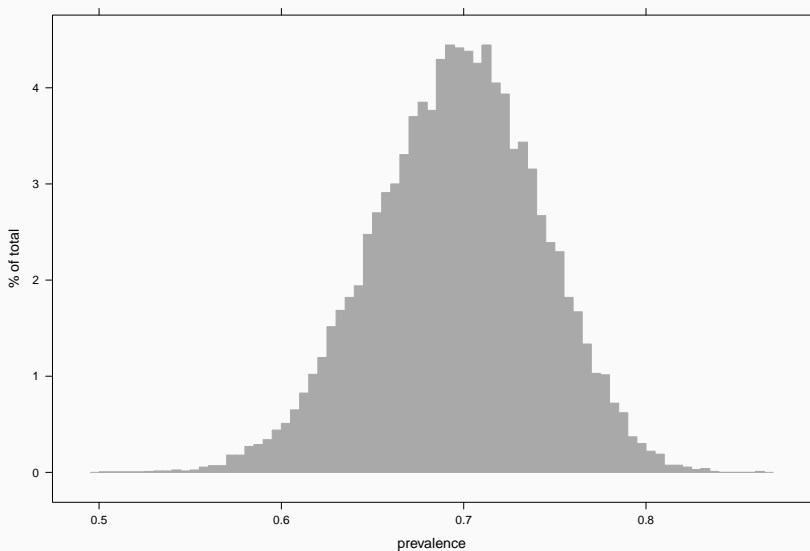
Trace plots: the two chains should be stationary:



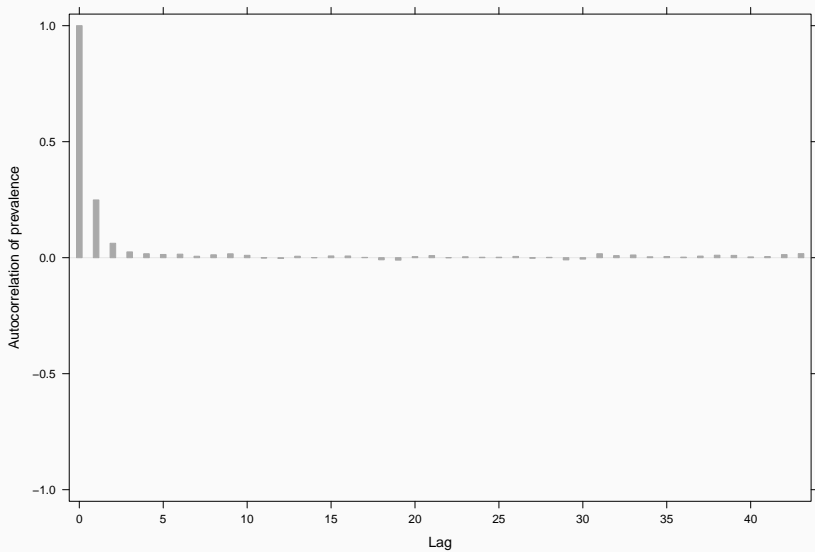
ECDF plots: the two chains should be very close to each other:



Histogram of the combined chains should appear smooth:



Autocorrelation plot tells you how well behaved the model is:



Then check the effective sample size (S_{Seff}) and Gelman-Rubin statistic (psrf):

```
results
##
## JAGS model summary statistics from 20000 samples (chains = 2;
↳ adapt+burnin = 6000):
##
##           Lower95  Median Upper95      Mean      SD Mode
## prevalence 0.60835 0.69782  0.7844 0.69637 0.045379  --
##
##           MCerr MC%ofSD SSeff      AC.10  psrf
## prevalence 0.00041321      0.9 12060 0.010246 1.0002
##
## Total time taken: 0.2 seconds
```

Reminder: we want $\text{psrf} < 1.05$ and $\text{SSeff} > 1000$

Introduction to practical sessions

Each practical session will consist of:

1. Some general/philosophical points to consider
2. One or more practical exercises for everyone to complete
3. One or more additional (optional) exercise for those that finish the main exercise early
4. A wrap-up discussion to reinforce the key messages

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Consideration points are given in the PDF

The exercises (and solutions) are only in the HTML versions

- We have approximately 1 hour per practical session
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- We will allocate you in pairs / threes to breakout rooms for the exercises (partly randomly, partly based on your institution)
 - If you need help please use the “Ask For Help” feature from your breakout room
 - Otherwise we will drop into the breakout rooms periodically to see how you are getting on!

Practical Session 1

Points to consider

1. What are the advantages and disadvantages of Bayesian MCMC relative to more standard frequentist likelihood-based methods?
2. Identifiability refers to the ability of a model to extract useful information from a dataset for a particular set of parameters. What 3 things affect whether or not a model/parameter will be identifiable?

The exercises can be found in [Session_1.html](#)!

Summary

- MCMC allows flexibility in models BUT requires more computational resource and user awareness
 - Convergence
 - Effective sample size
- Bayesian methods allow priors to be used BUT necessitate that priors are used
- Models are less likely to be identifiable if they:
 - Are more complex
 - Have less informative priors
 - Do not have sufficient data
- There is often a disparity between the model we would like to run and the model we can run given the data available