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!

Teachers:

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

HARMONY

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

- All of the material is on the GitHub repository
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  - Remember to pull changes at the start of each day!

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- 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")
## -- Attaching packages ---------------------------------------
↪  tidyverse 1.3.1 --
## v ggplot2 3.3.4     v purrr   0.3.4
## v tibble  3.1.2     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1
## -- Conflicts ------------------------------------------
↪  tidyverse_conflicts() --
## x tidyr::extract() masks runjags::extract()
## x dplyr::filter()  masks stats::filter()
## x dplyr::lag()     masks stats::lag()
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
```

Diagnostic test evaluation: no gold standard

Now we have both values of sensitivity and specificity <1...

```
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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  - 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:

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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.

- In practice we usually work with the following:

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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!

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

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Any questions so far? Anything unclear?

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Any problems: ask for help during the first practical session!

Session 1: A practical introduction to MCMC

MCMC in Practice

- We can write a Metropolis algorithm ourselves, but this is complex and inefficient
- There are a number of general purpose langauages 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

- 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
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  - 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!!!
- 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:

- Eaiser 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

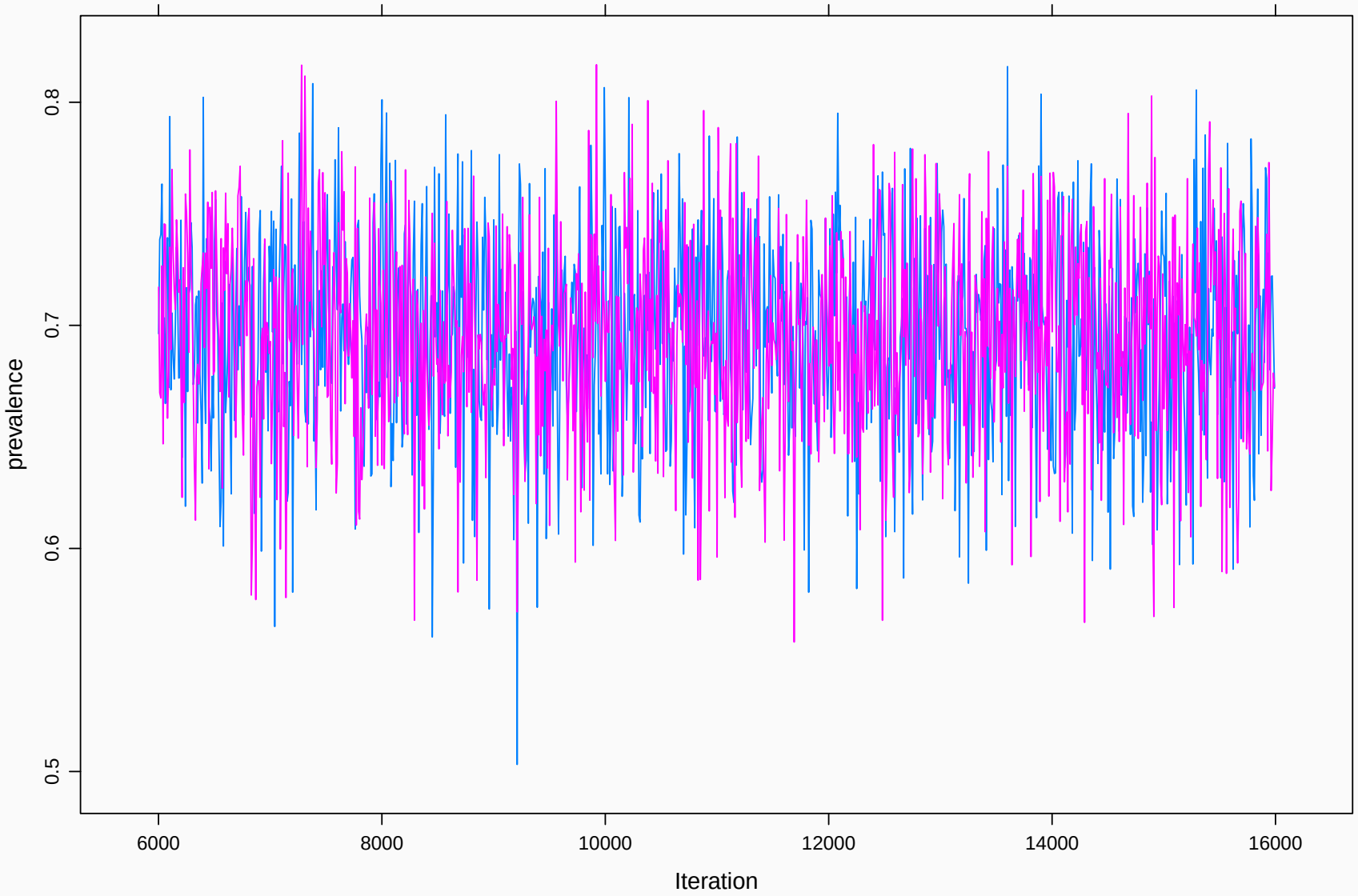
# initial values to be retrieved by runjags:
prevalence <- list(chain1=0.05, chain2=0.95)

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

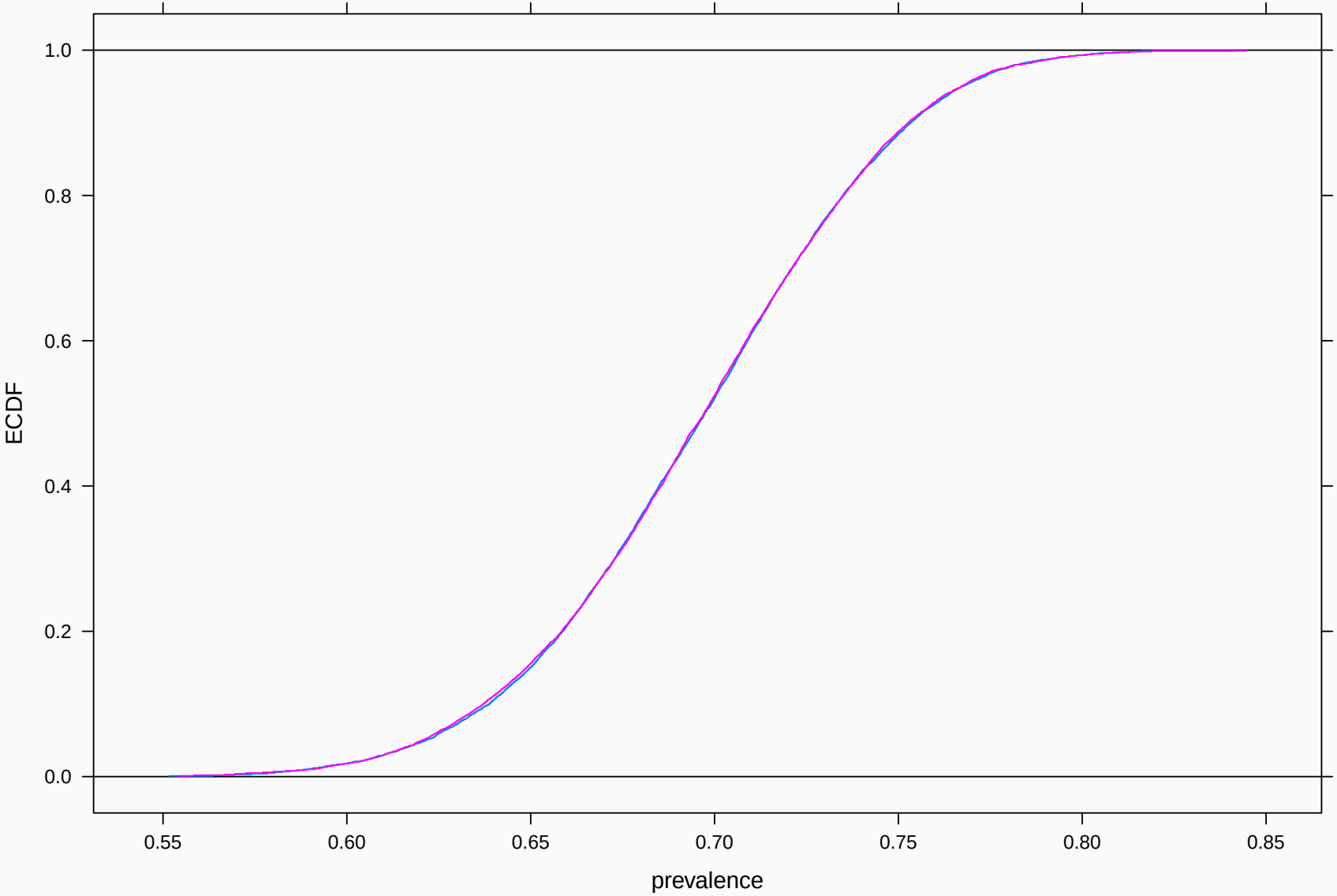
First check the plots for convergence:

```
plot(results)
```

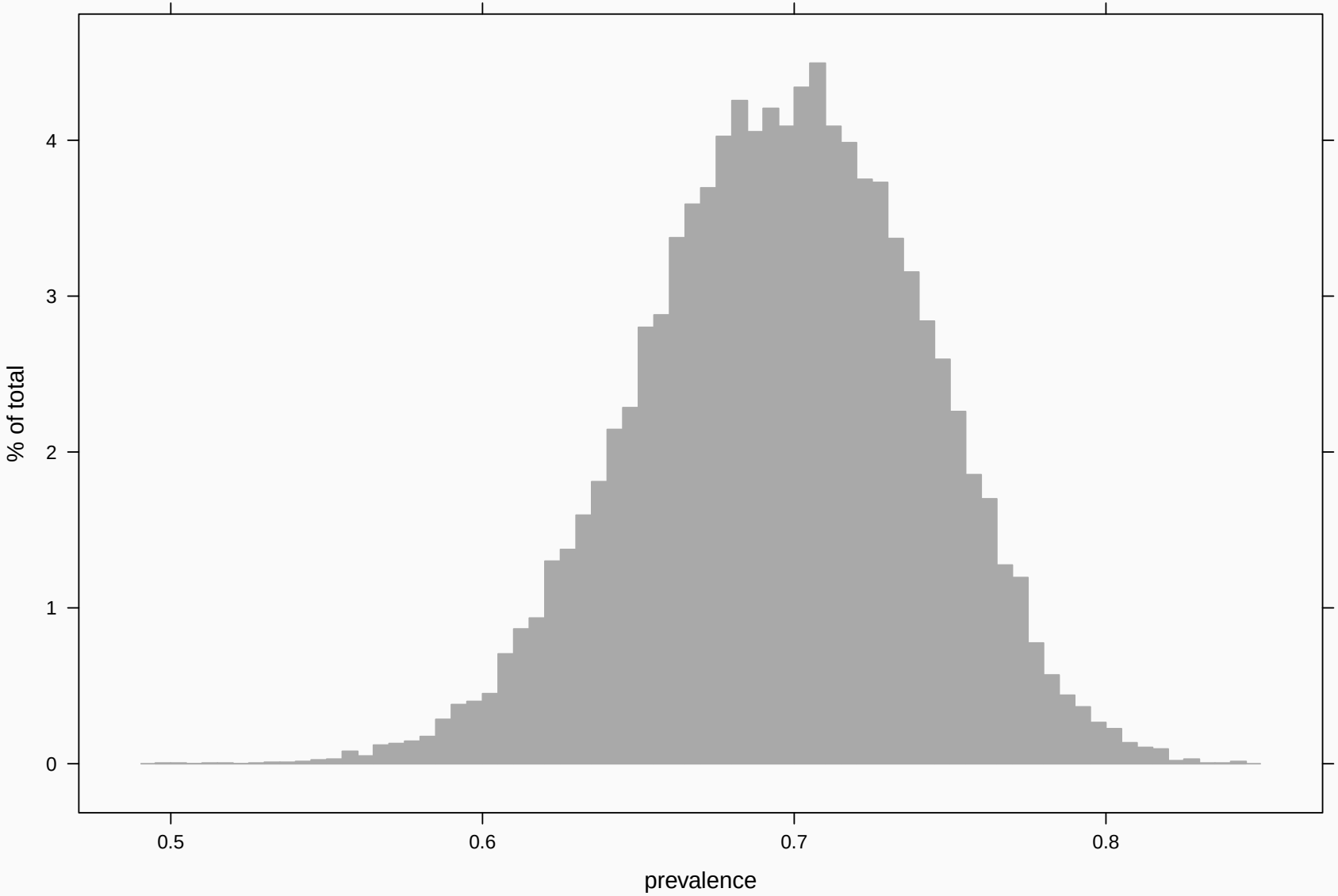
Trace plots: the two chains should be stationary:



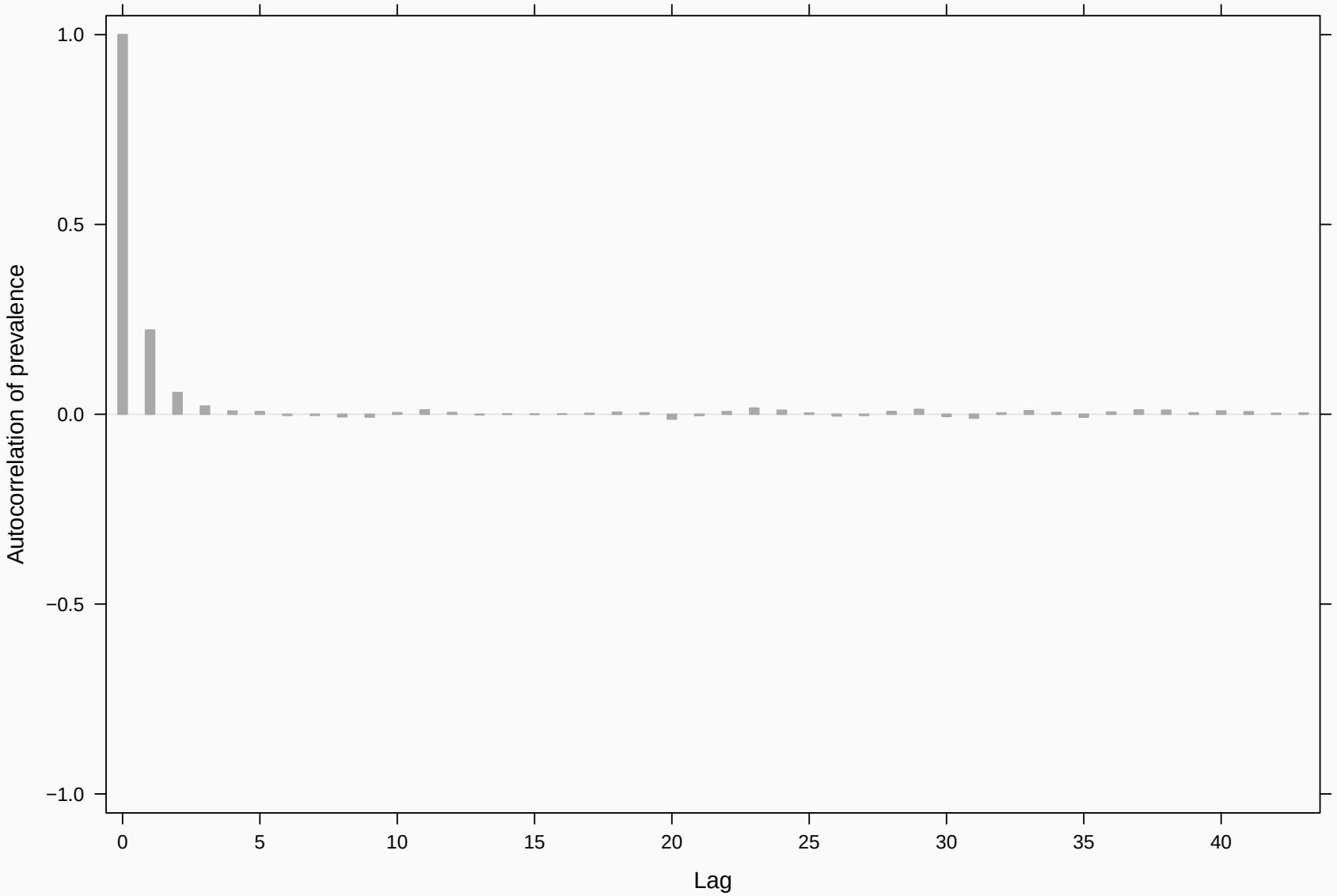
ECDF plots: the two chains should be very close to each other:



Histogram of the combined chains should appear smooth:



Autocorrelation plot tells you how well behaved the model is:



Then check the effective sample size (SSeff) 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  0.6098 0.69719 0.78159 0.696 0.044745   --
##
##                 MCerr MC%ofSD SSeff     AC.10    psrf
## prevalence 0.00040496     0.9 12209 0.0043318 0.99997
##
## Total time taken: 0.3 seconds
```

Reminder: we want psrf < 1.05 and 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

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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