Hands-on training session 2

Hui-Walter models for diagnostic test evaluation

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2020-02-11

Introduction

Overview

Date/time:

- 19th February 2020
- 16.00 - 17.00

Teachers:

- Matt Denwood (presenter)
- Giles Innocent

Recap

Important points from session 1

Session 2a: Hui-Walter models for 2 tests and 1 population

Hui-Walter Model

Background (not necessarily Bayesian)

Rabbits and hats

Model Specification

Care with order of combinations in dmultinom

Practicalities

Works best with strong priors for one of the tests

Label switching (se+sp > 0.5)

Lots of data needed

Convergence tricky

Simulating data

How to simulate data for this and checking we can recover
parameter values

```
1   # R code simulating data
2   # Parameters
3   Prev1 <- 0.8   # prevalence
4   Se1 <- 0.8     # test sensitivity
5   Sp1 <- 0.95    # test specificity
6   n.obs <- 50    # Number of individuals tested (number of
    ↪   observations)
7   n.burnin <- 2000  # number of burn-in iterations for MCMC
8   n.sample <- 2000  # number of samples to take after
    ↪   burn-in
9   # simulation
10  true.positive <- rbinom(1, n.obs, Prev1)
11  test.positive <- rbinom(1, true.positive, Se1)
12  test.positive <- test.positive + rbinom(1,
```

Exercise

Simulate data and recover parameters

Play around with different priors and watch autocorrelation etc

Session 2b: Hui-Walter models for 2 tests and N populations

Model specification 1

Independent intercepts for populations

Model specification 2

Random effect of population

Practicalities

Need to be very careful with tabulating the data

Works best when populations have very different prevalences

Auto Hui-Walter

Show autohuiwalter.R

Disable correlations by default

Modify so it allows Se/Sp priors to be defined as matrices?

And correlations on/off as matrices?

Will be in runjags at some point

Exercise

Play around with the autohuiwalter function