Session 2

Basic Hui-Walter models

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2021-06-28

Session 2: Basic Hui-Walter models

Hui-Walter Model

- A particular model formulation that was originally designed for evaluating diagnostic tests in the absence of a gold standard
- Not necessarily (or originally) Bayesian but often implemented using Bayesian MCMC
- But evaluating an imperfect test against another imperfect test is a bit like pulling a rabbit out of a hat
    - If we don't know the true disease status, how can we estimate sensitivity or specificity for either test?

Model Specification

```
model{
  Tally ~ dmulti(prob, N)

  # Test1- Test2-
    prob[1] <- (prev * ((1-se[1])*(1-se[2]))) + ((1-prev) *
    ↪  ((sp[1])*(sp[2])))

  # Test1+ Test2-
    prob[2] <- (prev * ((se[1])*(1-se[2]))) + ((1-prev) *
    ↪  ((1-sp[1])*(sp[2])))

  # Test1- Test2+
    prob[3] <- (prev * ((1-se[1])*(se[2]))) + ((1-prev) *
    ↪  ((sp[1])*(1-sp[2])))
  # Test1+ Test2+
    prob[4] <- (prev * ((se[1])*(se[2]))) + ((1-prev) *
    ↪  ((1-sp[1])*(1-sp[2])))

  prev ~ dbeta(1, 1)
  se[1] ~ dbeta(1, 1)
  sp[1] ~ dbeta(1, 1)
  se[2] ~ dbeta(1, 1)
  sp[2] ~ dbeta(1, 1)

  #data# Tally, N
  #monitor# prev, prob, se, sp
  #inits# prev, se, sp
}
```

```r
twoXtwo <- matrix(c(48, 12, 4, 36), ncol=2, nrow=2)
twoXtwo
##      [,1] [,2]
## [1,]   48    4
## [2,]   12   36
```

```r
library('runjags')

Tally <- as.numeric(twoXtwo)
N <- sum(Tally)

prev <- list(chain1=0.05, chain2=0.95)
se <- list(chain1=c(0.5,0.99), chain2=c(0.99,0.5))
sp <- list(chain1=c(0.5,0.99), chain2=c(0.99,0.5))

results <- run.jags('basic_hw.bug', n.chains=2)
```

[Remember to check convergence and effective sample size!]

```
results
```

	Lower95	Median	Upper95	SSeff	psrf
prev	0.309	0.441	0.574	3948	1.000
prob[1]	0.366	0.462	0.557	13968	1.000
prob[2]	0.073	0.133	0.202	14641	1.000
prob[3]	0.019	0.055	0.104	9869	1.000
prob[4]	0.253	0.344	0.434	13104	1.000
se[1]	0.824	0.933	1.000	5657	1.000
se[2]	0.689	0.847	1.000	3521	1.001
sp[1]	0.747	0.877	1.000	3419	1.001
sp[2]	0.863	0.948	1.000	5617	1.000

- Note the wide confidence intervals!

TODO: find/use initial values that give us label switching, and show trace plots

Practicalities

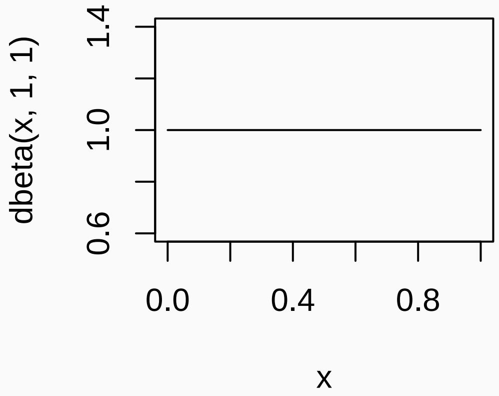
- Be **very** vareful with the order of combinations in dmultinom!
- Check your results carefully to ensure they make sense!
- Convergence is more problematic than usual
- These models need A LOT of data, and/or strong priors for one of the tests

Priors

A different prior

- A quick way to see the distribution of a prior:

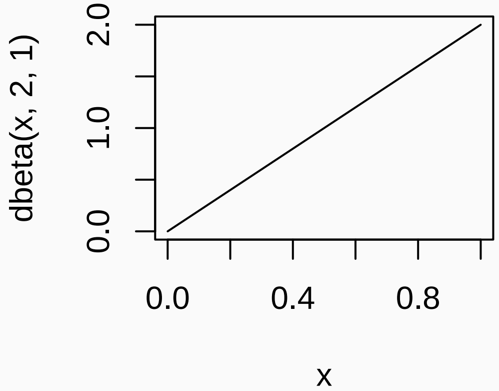
```
curve(dbeta(x, 1, 1), from=0, to=1)
```



```
qbeta(c(0.025,0.975), shape1=1, shape2=1)
## [1] 0.025 0.975
```

- This was minimally informative, but how does that compare to a weakly informative prior for e.g. sensitivity?

```r
curve(dbeta(x, 2, 1), from=0, to=1)
```

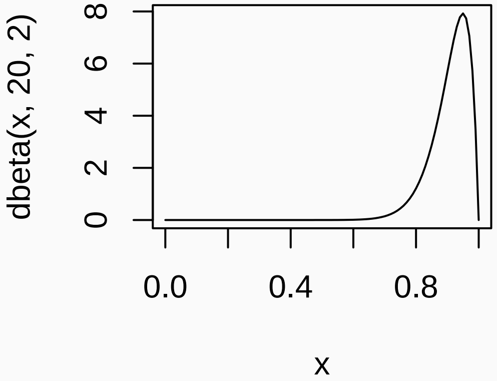


```r
qbeta(c(0.025,0.975), shape1=2, shape2=1)
## [1] 0.1581139 0.9874209
```

- Or more accurately:

- What about a more informative prior?

```
curve(dbeta(x, 20, 2), from=0, to=1)
```



```
hpd(qbeta, shape1=20, shape2=2)
## [1] 0.7919691 0.9973994
```

Choosing a prior

- Typically we are given median and 95% confidence intervals from a paper, e.g.:

"The median (95% CI) estimates of the sensitivity and specificity of the shiny new test were 94% (92-96%) and 99% (97-100%) respectively"

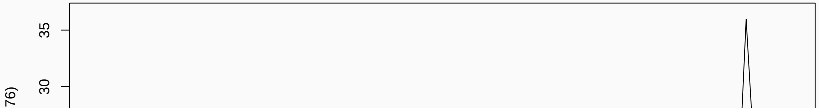
- How can we generate a prior from this?

The PriorGen package

"The median (95% CI) estimates of the sensitivity and specificity of the shiny new test were 94% (92-96%) and 99% (97-100%) respectively"

```
library("PriorGen")
## Loading required package: rootSolve
findbeta(themedian = 0.94, percentile=0.95, percentile.value = 0.92)
## [1] "The desired Beta distribution that satisfies the specified
↪  conditions is: Beta( 429.95 27.76 )"
## [1] "Here is a plot of the specified distribution."
## [1] "Descriptive statistics for this distribution are:"
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.8910  0.9322  0.9399  0.9393  0.9473  0.9749
## [1] "Verification: The percentile value 0.92 corresponds to the 0.05
↪  th percentile"
```

```
curve(dbeta(x, shape1=429.95, shape2=27.76))
```



Label Switching

How to interpret a test with Se=0% and Sp=0%?

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We can force se+sp >= 1:

```
se[1] ~ dbeta(1, 1)
sp[1] ~ dbeta(1, 1)T(1-se[1], )
```

Or:

```
se[1] ~ dbeta(1, 1)T(1-sp[1], )
sp[1] ~ dbeta(1, 1)
```

But not both!

This allows the test to be useless, but not worse than useless.

Alternatively we can have the weakly informative priors:

```
se[1] ~ dbeta(2, 1)
```

Analysing simulated data

This is useful to check that we can recover parameter values!

```
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)))

twoXtwo <- with(data, table(Test1, Test2))
Tally <- as.numeric(twoXtwo)
```

Practical Session 2

Points to consider

1. What is the typical autocorrelation (and therefore effective sample size) of Hui-Walter models compared to the simpler models we were running earlier? Is there any practical consequence of this?
2. When will a model be identifiable and when might it not be?
3. How does changing the prior distributions for the se and sp of one test affect the inference for the other test parameters?

Summary

- Using JAGS / runjags allows us to work with MCMC more easily, safely and efficiently than writing our own sampling algorithms
- But we must *never forget* to check convergence and effective sample size!
- More complex models become easy to implement
    - For example imperfect diagnostic tests
- But just because a model can be defined does not mean that it will be useful for our data
    - We need to be realistic about the information available in the data, what parameters are feasible to estimate, and where we will need to use strong priors