Session 7

Incorporating imperfect sensitivity and specificity into more complex models

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2022-06-10

Recap

Models for diagnostic test evaluation require:

- At least 2 tests
- At least 2 populations, but preferably 3 or more
- Quite a lot of data

Recap

Models for diagnostic test evaluation require:

- At least 2 tests
- At least 2 populations, but preferably 3 or more
- Quite a lot of data

Fitting the models is technically quite straightforward

The real difficulty lies in the interpretation

- What exactly is the latent class?

Incorporating coefficients: prevalence

Modelling variation in infection probability

- Individuals may be at higher/lower risk of being infected due to known characteristics e.g.:
  - Age
  - Sex
  - History
  - Presence of co-infections
  - Whatever

Modelling variation in infection probability

- Individuals may be at higher/lower risk of being infected due to known characteristics e.g.:
  - Age
  - Sex
  - History
  - Presence of co-infections
  - Whatever
- There are three ways to deal with this:
  1. Ignore it
  2. Group "populations" by these characteristics
  3. Embed a (preferably simple!) generalised linear model within your LCM

Logistic regression in JAGS

```
model{

  for(i in 1:N){
    Observation[i] ~ dbern(prob[i])
    logit(prob[i]) <- intercept + beta1[Category[i]] + beta2*Covariate[i]
  }

  intercept ~ dnorm(0, 0.01)
  beta1[1] <- 0
  for(c in 2:NC){
    beta1[c] ~ dnorm(0, 0.01)
  }
  beta2 ~ dnorm(0, 0.01)

  #data# N, Observation, NC, Category, Covariate
  #monitor# intercept, beta1, beta2
  #inits# intercept, beta1, beta2
}
```

```
model{

  for(i in 1:N){
    Observation[i] ~ dbern(obs_prob[i])
    obs_prob[i] <- prob[i]*se + (1-prob[i])*(1-sp)
    logit(prob[i]) <- intercept + beta1[Category[i]] + beta2*Covariate[i]
  }

  se ~ dbeta(148.43, 16.49)T(1-sp, )
  sp ~ dbeta(240.03, 12.63)

  intercept ~ dnorm(0, 0.01)
  beta1[1] <- 0
  for(c in 2:NC){
    beta1[c] ~ dnorm(0, 0.01)
  }
  beta2 ~ dnorm(0, 0.01)

  #data# N, Observation, NC, Category, Covariate
  #monitor# intercept, beta1, beta2, se, sp
  #inits# intercept, beta1, beta2, se, sp
}
```

```
model{

  for(i in 1:N){
    Observation[i] ~ dbern(obs_prob[i])
    obs_prob[i] <- prob[i]*se + (1-prob[i])*(1-sp)
    logit(prob[i]) <- intercept + beta1[Category[i]] + beta2*Covariate[i]
  }

  #data# se, sp

  intercept ~ dnorm(0, 0.01)
  beta1[1] <- 0
  for(c in 2:NC){
    beta1[c] ~ dnorm(0, 0.01)
  }
  beta2 ~ dnorm(0, 0.01)

  #data# N, Observation, NC, Category, Covariate
  #monitor# intercept, beta1, beta2
  #inits# intercept, beta1, beta2
}
```

```
model{

  for(i in 1:N){
    Observation[i] ~ dbern(obs_prob[i])
    obs_prob[i] <- prob[i]*se[Test[i]] + (1-prob[i])*(1-sp[Test[i]])
    logit(prob[i]) <- intercept + beta1[Category[i]] + beta2*Covariate[i]
  }

  #data# se, sp

  intercept ~ dnorm(0, 0.01)
  beta1[1] <- 0
  for(c in 2:NC){
    beta1[c] ~ dnorm(0, 0.01)
  }
  beta2 ~ dnorm(0, 0.01)

  #data# N, Observation, NC, Category, Covariate, Test
  #monitor# intercept, beta1, beta2
  #inits# intercept, beta1, beta2
}
```

```
model{

  for(i in 1:N){
    Observations[i,1:4] ~ dmulti(obs_probs[i,1:4], 1)

    obs_probs[i,1] <- (prob[i] * ((1-se[1])*(1-se[2]))) + ((1-prob[i]) * ((sp[1])*(sp[2])))
    obs_probs[i,2] <- (prob[i] * ((se[1])*(1-se[2]))) + ((1-prob[i]) * ((1-sp[1])*(sp[2])))
    obs_probs[i,3] <- (prob[i] * ((1-se[1])*(se[2]))) + ((1-prob[i]) * ((sp[1])*(1-sp[2])))
    obs_probs[i,4] <- (prob[i] * ((se[1])*(se[2]))) + ((1-prob[i]) * ((1-sp[1])*(1-sp[2])))

    logit(prob[i]) <- intercept + beta1[Category[i]] + beta2*Covariate[i]
  }

  #snip#

}
```

```
model{

  for(i in 1:G){
    Observations[i,1:4] ~ dmulti(obs_probs[i,1:4], Total[i])

    obs_probs[i,1] <- (prob[i] * ((1-se[1])*(1-se[2]))) + ((1-prob[i]) * ((sp[1])*(sp[2])))
    obs_probs[i,2] <- (prob[i] * ((se[1])*(1-se[2]))) + ((1-prob[i]) * ((1-sp[1])*(sp[2])))
    obs_probs[i,3] <- (prob[i] * ((1-se[1])*(se[2]))) + ((1-prob[i]) * ((sp[1])*(1-sp[2])))
    obs_probs[i,4] <- (prob[i] * ((se[1])*(se[2]))) + ((1-prob[i]) * ((1-sp[1])*(1-sp[2])))

    logit(prob[i]) <- intercept + beta1[Category[i]] + beta2*RoundedCovariate[i]
  }

  #snip#

}
```

Embedding a LR within a LCM

- Hierarchical modelling gives us the freedom to include "models within models" as needed for our specific application, but we usually have to write these ourselves!
- Remember that blocking at group level is much more efficient than looping through all individuals as fewer likelihood calculations are required

Embedding a LR within a LCM

- Hierarchical modelling gives us the freedom to include "models within models" as needed for our specific application, but we usually have to write these ourselves!
- Remember that blocking at group level is much more efficient than looping through all individuals as fewer likelihood calculations are required
- Autocorrelation may be problematic - if so try to use different contrast schemes eg:

```
sex_effect ~ dnorm(0, 0.01)
beta1[1] <- -sex_effect/2
beta1[2] <- sex_effect/2
```

- Random effects are kind of like fixed effects:

```
#snip#
  logit(prob[i]) <- intercept + beta1[Category[i]] + beta3[Group[i]]
#snip#

for(r in 1:NR){
  beta3[r] ~ dnorm(0, tau)
}
tau ~ dgamma(0.01, 0.01)

#inits# tau
#monitor# tau, beta3
```

Generating code for a LR

You can use template.jags as inspiration:

```
template.jags(weight ~ group, family="gaussian", data=data, file="linear_model.txt")
## Your model template was created at "linear_model.txt" - it is highly advisable to examine
↪  the model syntax to be sure it is as intended
## You can then run the model using run.jags("linear_model.txt")
results <- run.jags("linear_model.txt")
## Loading required namespace: rjags
## module glm loaded
## module dic loaded
```

```
##############################################################################################################
##############################################################################################################
#### JAGS model file written by runjags version 2.2.2-1 on 2022-06-07 22:29:30
##############################################################################################################
##############################################################################################################

### Model template as follows - ensure this is syntactically correct before running the
↪  model!

model{

# In the BUGS/JAGS language we must use an explicit for loop:
for(i in 1:N){
    # These lines describe the response distribution and linear model terms:
    weight[i] ~ dnorm(regression_fitted[i], regression_precision)
    regression_residual[i] <- weight[i] - regression_fitted[i]
    regression_fitted[i] <- intercept + group_effect[group[i]]
}

# These lines give the prior distributions for the parameters to be estimated:
regression_precision ~ dgamma(0.001, 0.001)
intercept ~ dnorm(0, 10^-6)
group_effect[1] <- 0    # Factor level "Ctl"
group_effect[2] ~ dnorm(0, 10^-6)    # Factor level "Trt"
resid.sum.sq <- sum(regression_residual^2)
```

Supported features:

- Gaussian, binomial, Poisson, negative binomial, ZIB, ZIP, ZINB
- Random intercepts
- Automatic centering of continuous variables

We can also add (currently manually):

- Random slopes
- Spline terms
- Interval censoring

Grouping populations

- This is much easier than writing a GLM within our LCM...
- We can also use the template_huiwalter function!
  - See Otero-Abad 2017 for a simple example
- If you have a lot of populations you could use a simple random effect:

```
# prev[p] ~ dbeta(1, 1)
logit(prev[p]) <- intercept + raneff[i]
raneff[i] ~ dnorm(0, tau)
```

Grouping populations

- This is much easier than writing a GLM within our LCM...
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- If you have a lot of populations you could use a simple random effect:

```
# prev[p] ~ dbeta(1, 1)
logit(prev[p]) <- intercept + raneff[i]
raneff[i] ~ dnorm(0, tau)
```

- Be careful that Se/Sp is still consistent across populations!

Do nothing?

What is the goal of your analysis?

- Estimating risk factors for disease?
- Estimating true prevalence?
- Estimating Se/Sp?

Do nothing?

What is the goal of your analysis?

- Estimating risk factors for disease?
- Estimating true prevalence?
- Estimating Se/Sp?

Inclusion of risk factors for disease is NOT necessary to estimate Se/Sp!

If you are interested in risk factors for disease (rather than the se/sp directly) then I would probably use a simpler model with fixed se/sp (+/- multiple imputation)

Covariates for Sensitivity / Specificity

What if diagnostic tests are not consistent across populations?

This time we can't just ignore it!

Solutions:

- Remove that population (and clearly state this in the paper..!)
- Allow the relevant parameter to vary between populations
- Use a (very simple) GLM on the relevant parameter(s)

What if diagnostic tests are not consistent across populations?

This time we can't just ignore it!

Solutions:

- Remove that population (and clearly state this in the paper..!)
- Allow the relevant parameter to vary between populations
- Use a (very simple) GLM on the relevant parameter(s)

But now we are no longer technically within the Hui-Walter framework...

Varying Se/Sp between populations

```
        Tally[1:4,p] ~ dmulti(prob[1:4,p], N[p])

        prob[1,p] <- prev[p] * ((1-se[1,SeGp[p]])*(1-se[2,SeGp[p]]))  +  (1-prev[p]) *
↪  (sp[1])*(sp[2])

        prob[2,p] <- prev[p] * (se[1,SeGp[p]]*(1-se[2,SeGp[p]]))  +  (1-prev[p]) *
↪  (1-sp[1])*sp[2]

        prob[3,p] <- prev[p] * ((1-se[1,SeGp[p]])*(se[2,SeGp[p]]))  +  (1-prev[p]) *
↪  (sp[1])*(1-sp[2])

        prob[4,p] <- prev[p] * (se[1,SeGp[p]]*se[2,SeGp[p]])  +  (1-prev[p]) *
↪  (1-sp[1])*(1-sp[2])

        prev[p] ~ dbeta(1,1)
```

Varying Se/Sp between populations

```
        Tally[1:4,p] ~ dmulti(prob[1:4,p], N[p])

        prob[1,p] <- prev[p] * ((1-se[1,SeGp[p]])*(1-se[2,SeGp[p]]))  +  (1-prev[p]) *
↪  (sp[1])*(sp[2])

        prob[2,p] <- prev[p] * (se[1,SeGp[p]]*(1-se[2,SeGp[p]]))  +  (1-prev[p]) *
↪  (1-sp[1])*sp[2]

        prob[3,p] <- prev[p] * ((1-se[1,SeGp[p]])*(se[2,SeGp[p]]))  +  (1-prev[p]) *
↪  (sp[1])*(1-sp[2])

        prob[4,p] <- prev[p] * (se[1,SeGp[p]]*se[2,SeGp[p]])  +  (1-prev[p]) *
↪  (1-sp[1])*(1-sp[2])

        prev[p] ~ dbeta(1,1)
```

See also: Stærk-Østergaard 2022

Embedded GLM for Se/Sp

```
  for(p in 1:Populations){
      Tally[1:4,p] ~ dmulti(prob[1:4,p], N[p])

      # Probability of observing test -/-
      prob[1,p] <- prev[p] * ((1-se[1,p])*(1-se[2,p]))  +  (1-prev[p]) * (sp[1])*(sp[2])

      #snip#

      logit(se[1,p]) <- se_intercept[1] + se1_beta[Se1Category[p]]
      logit(se[2,p]) <- se_intercept[2] + se2_beta[Se2Category[p]]

  }

# NB: tweak contrasts for convergence!
se_beta1[1] <- -se_eff/2
se_beta1[2] <- se_eff/2
se_eff ~ dnorm(0, 0.01)
```

Embedded GLM for Se/Sp

```
    for(p in 1:Populations){
        Tally[1:4,p] ~ dmulti(prob[1:4,p], N[p])

        # Probability of observing test -/-
        prob[1,p] <- prev[p] * ((1-se[1,p])*(1-se[2,p]))  +  (1-prev[p]) * (sp[1])*(sp[2])

        #snip#

        logit(se[1,p]) <- se_intercept[1] + se1_beta[Se1Category[p]]
        logit(se[2,p]) <- se_intercept[2] + se2_beta[Se2Category[p]]

    }

# NB: tweak contrasts for convergence!
se_beta1[1] <- -se_eff/2
se_beta1[2] <- se_eff/2
se_eff ~ dnorm(0, 0.01)
```

See also: Martinez 2008 (although they wrote the samplers themselves!)

Embedded GLM for Infection AND Se/Sp

```
  for(p in 1:Populations){
      Tally[1:4,p] ~ dmulti(prob[1:4,p], N[p])

      # Probability of observing test -/-
      prob[1,p] <- prob[p] * ((1-se[1,p])*(1-se[2,p]))  +  (1-prob[p]) * (sp[1])*(sp[2])

      #snip#

      logit(se[1,p]) <- se_intercept[1] + se1_beta[Se1Category[p]]
      logit(se[2,p]) <- se_intercept[2] + se2_beta[Se2Category[p]]

      logit(prob[i]) <- intercept + beta1[Category[i]]

  }

#snip#
se_eff ~ dnorm(0, 0.01)
pr_eff ~ dnorm(0, 0.01)
```

Embedded GLM for Infection AND Se/Sp

```
  for(p in 1:Populations){
      Tally[1:4,p] ~ dmulti(prob[1:4,p], N[p])

      # Probability of observing test -/-
      prob[1,p] <- prob[p] * ((1-se[1,p])*(1-se[2,p]))  +  (1-prob[p]) * (sp[1])*(sp[2])

      #snip#

      logit(se[1,p]) <- se_intercept[1] + se1_beta[Se1Category[p]]
      logit(se[2,p]) <- se_intercept[2] + se2_beta[Se2Category[p]]

      logit(prob[i]) <- intercept + beta1[Category[i]]

  }

#snip#
se_eff ~ dnorm(0, 0.01)
pr_eff ~ dnorm(0, 0.01)
```

But what happens if “Category” is confounded with “Se1Category” ??

General points

- Inconsistent se/sp may happen in e.g. laboratory vs field settings, blood vs milk samples, or due to biological effects such as age-aquired immunity
- Theoretically it is possible to incorporate this into the model, but...
  - It is not frequently done so the models are less well developed/understood
  - Great care is needed, and any additions should be based on known biological processes
  - If all populations have their own se/sp then the model collapses!

General points

- Inconsistent se/sp may happen in e.g. laboratory vs field settings, blood vs milk samples, or due to biological effects such as age-aquired immunity
- Theoretically it is possible to incorporate this into the model, but...
  - It is not frequently done so the models are less well developed/understood
  - Great care is needed, and any additions should be based on known biological processes
  - If all populations have their own se/sp then the model collapses!
- Be VERY careful when prevalence and se/sp have the same covariate
  - It may work if balancing populations by these covariates, and only including them as se/sp covariates?

Practical session 7

Points to consider

1. What is the optimal number of populations?
2. What happens to identifiability when you deviate from the standard Hui-Walter model?

Summary

- Adding populations (or equivalently, covariates on prevalence) adds parameters but may add information
  - But it is not always worthwile!
- Using covariates on sensitivity and specificity is tricky...
- Some further reading: Martinez et al 2008, Stærk-Østergaard et al 2022