Building your own SIMM and advanced topics

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Learning outcomes

- Revision on everything we've covered
- Tips for building your own SIMM in JAGS
- Splines, and using them in SIMMs
- Future extensions for SIMMs

Revision: a starter SIMM script

```
modelstring ='
model {
  for(i in 1:N) {
    for(j in 1:J) {
      y[i,j] ~ dnorm(inprod(p*q[,j],s[,j]+c[,j])/inprod(p,q
    }
  }
  for(k in 1:K) {
    for(j in 1:J) {
      s[k,j] ~ dnorm(s_mean[k,j],s_sd[k,j]^-2)
      c[k,j] ~ dnorm(c_mean[k,j],c_sd[k,j]^-2)
    }
  }
  p ~ ddirch(alpha)
  for(j in 1:J) { sigma[j] ~ dunif(0,10) }
}
'
```

Revision: a more advanced SIMM script

```
modelstring ='
model {
  for (i in 1:N) {
    for (j in 1:J) {
      y[i,j] ~ dnorm(inprod(p[i,]*q[,j], s_mean[,j]+c_mean
      var_y[i,j] <- inprod(pow(p[i,]*q[,j],2),s_sd[,j]^2+c_
        + pow(sigma[j],2)
    }
  }
  for(i in 1:N) {
    p[i,1:K] <- expf[i,]/sum(expf[i,])
    for(k in 1:K) {
      expf[i,k] <- exp(f[i,k])
      f[i,k] ~ dnorm(mu_f[k],sigma_f[k]^-2)
    }
  }
  for(k in 1:K) {
    mu_f[k] ~ dnorm(0,1)
```

Tips for building your own SIMM

- If your data are small and relatively simple, a standard Dirichlet/SIAR-type model will work fine
- If your data contain covariates or contain interestingly arranged sources (as evidenced by the iso-space plot) use the more advanced JAGS script or MixSIAR
- Think carefully about prior distributions. Which parameters do you have information about? Which parameters do you need to constrain to fit the model properly?
- Always check convergence, and see if the results match the iso-space plots

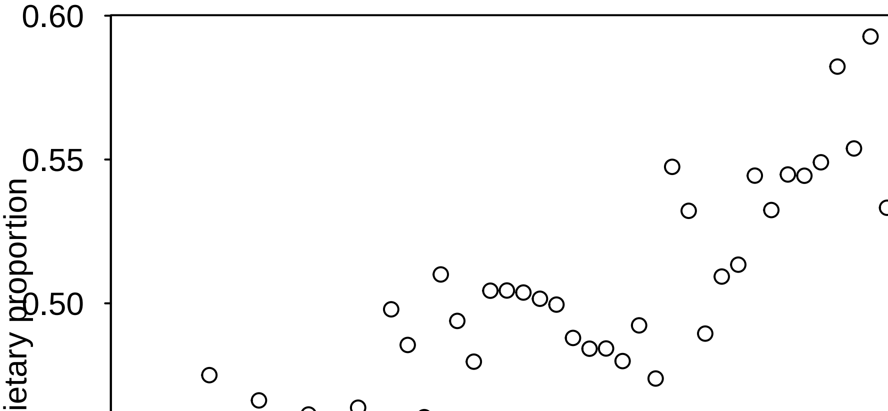
New topic: splines

- Often we don't want to fit a straight line relationship between our covariate(s) and our response
- For example, the relationship might be quadratic, cubic, or completely non-linear
- Splines are a neat method for exploring non-linear relationships between covariates and the response
- They work by replacing the covariate with *basis functions* defined at *knots*. A standard regression model is fitted to these basis functions with an extra constraint to make sure the results are smooth
- Often you will hear these types of models referred to as *non-parametric* which is a bit of a misnomer, since they contain lots of parameters!

Simple splines example

- Consider fitting a model to some data where the response is non-linear

```
par(mar=c(3,3,2,1), mgp=c(2,.7,0), tck=-.01,las=1)
plot(t,p,xlab='time',ylab='dietary proportion')
```



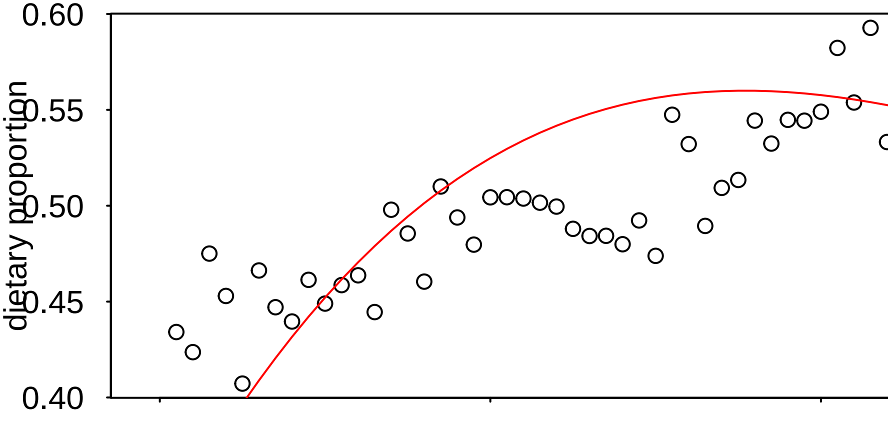
Fitting a model with polynomial regression

```
modelstring ='
model {
  for(i in 1:N) { p[i] ~ dnorm(mu[i],sigma^-2) }
  mu <- B%*%beta
  for(l in 1:L) { beta[l] ~ dnorm(0,0.01) }
  sigma ~ dunif(0,1000)
}'
B = cbind(1,t,t^2,t^3)
data=list(p=p,N=length(p),B=B,L=ncol(B))
model=jags.model(textConnection(modelstring), data=data,n.c
output=coda.samples(model=model,variable.names=c("beta","si
```

Look how many iterations are required for convergence! This also gets very unstable once you get beyond cubic

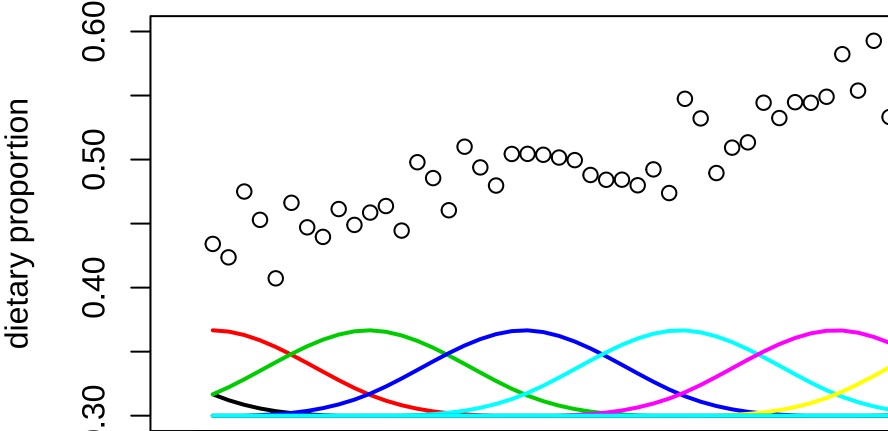
Output from polynomial regression

```
beta_mean = summary(output)$statistics[1:data$L,1]
par(mar=c(3,3,2,1), mgp=c(2,.7,0), tck=-.01,las=1)
plot(t,p,xlab='time',ylab='dietary proportion')
lines(t,B%*%beta_mean,col='red')
```



An alternative: B-spline basis functions

```
source('bases.r')
B = bbase(t)
plot(t,p,xlab='time',ylab='dietary proportion',ylim=c(0.3,0
for(i in 1:ncol(B)) lines(t,B[,i]/10+0.3,col=i,lwd=2)
```

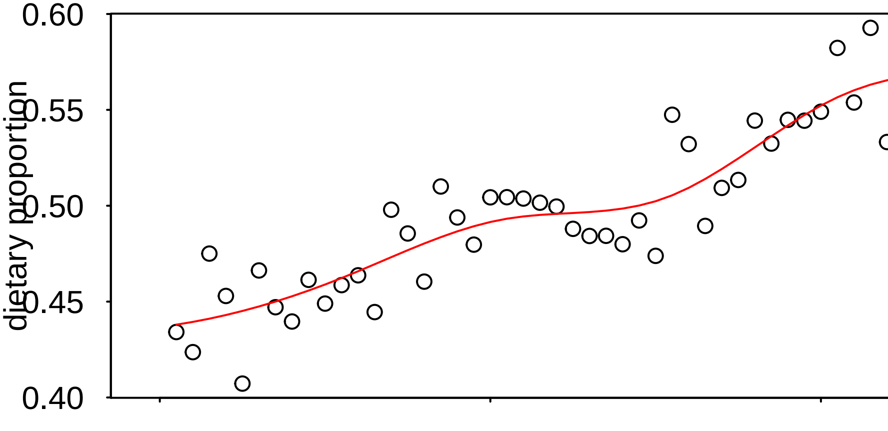


Splines in JAGS

```
modelstring ='
model {
  for(i in 1:N) { p[i] ~ dnorm(mu[i],sigma^-2) }
  mu <- B%*%beta
  beta[1] ~ dnorm(0,100^-2)
  for(l in 2:L) { beta[l] ~ dnorm(beta[l-1],sigma_beta^-2)
  sigma_beta ~ dunif(0,10)
  sigma ~ dunif(0,1000)
}'
B = bbase(t)
data=list(p=p,N=length(p),B=B,L=ncol(B))
model=jags.model(textConnection(modelstring), data=data,n.c
output=coda.samples(model=model,variable.names=c("beta","si
```

Output from spline model

```
beta_mean = summary(output)$statistics[1:data$L,1]
par(mar=c(3,3,2,1), mgp=c(2,.7,0), tck=-.01,las=1)
plot(t,p,xlab='time',ylab='dietary proportion')
lines(t,B%*%beta_mean,col='red')
```



Some more notes on splines

- You can vary the smoothness of the splines by increasing the number of basis functions (i.e. the number of knots), or changing the prior on the smoothness parameter (here `sigma_beta`)
- It's usually best to put more knots in than you need and to constrain the smoothness parameter
- This will converge to a neater result far, far, faster than the polynomial version, and be able to capture more wiggly behaviour
- Like, every other topics we have met, we can insert these ideas into a SIMM as the prior structure on the dietary proportions. . .

Splines and the Geese data

- Model available in file `run_spline_geese.R` file
- Main change in code is:

```
modelstring ='
model {
  ...
  for(k in 1:K) {
    f[1:N,k] <- B%*%beta[,k]
    beta[1,k] ~ dnorm(0,100^-2)
    for(l in 2:L) { beta[l,k] ~ dnorm(beta[l-1,k],sigma_bet
    sigma_beta[k] ~ dunif(0,10)
  }
  ...
}
'
```

Output from spline SIMM model

Some more advanced topics: time series models

- A standard way to analyse data that are observed over time is to use an *auto-regressive* model, e.g.

$$y_t = \alpha + \beta y_{t-1} + \epsilon_t$$

- Here each value of y at time t depends on the value of y at time $t-1$, known as an AR(1) model
- This type of model turns out to be very useful for analysing stocks and shares, climate change, etc, etc
- A related model is the *random walk*:

$$y_t = \alpha + y_{t-1} + \epsilon_t$$

- This can be extended in all kinds of ways to continuous time, stochastic volatility (changing variance of ϵ), multivariate

Time series and SIMMs

It's possible to put in an autoregressive term in a SIMM:

```
modelstring ='
model {
  ...
  for(i in 1:N) {
    p[i,1:K] <- expf[i,]/sum(expf[i,])
    for(k in 1:K) {
      expf[i,k] <- exp(f[time[i],k])
    }
  }
  for(k in 1:K) {
    f[1,k] ~ dnorm(0,100^-2)
    for(t in 2:N_t) { f[t,k] ~ dnorm(alpha[k] + beta[k]*f[t
    ...
  }
  ...
}
'
```

Advanced topics: clustering

- A popular method for clustering data in a Bayesian model is to use a *mixture model*:

$$\pi(y_i) = \sum_{g=1}^{G} \tau_g \pi_g(y_i|\theta_g)$$

  where π_g is an individual normal density, and τ_g are weights which sum to 1
- This looks a bit like our SIMM, except for in a SIMM we have a mixture on the means, whereas this is a mixture on the entire density
- Each normal distribution has its own mean/variance so acts like an individual cluster
- The idea is often to identify the number of clusters G

Clustering example

Clustering in SIMMs

- Various places where clustering might be useful in a SIMM
- Perhaps the sources/TEFs are unknown mixtures of two sources and you want to separate them
- Perhaps the consumers are from multiple (undefined) groups based on dietary proportion and you want to discover which group they belong to

Clustering dietary proportions

```
modelstring ='
model {
  ...
  for(k in 1:K) {
    for(i in 1:N) {
      mu_f[i,k] <- lambda[T[i,k],k]
      T[i,k] ~ dcat(pi[,k])
    }
    pi[,k] ~ ddirch(alpha)
  }
  ...
}
'
```

Advanced topics: zero-inflation

- What if some of the consumers aren't eating any of some sources?
- SIAR/MixSIAR will give this value a very small proportion, but it will never set the value to exactly zero
- If you could find a model that sets some dietary proportions to zero you could put in a larger number of sources and see which ones the model sets to zero
- 'Shrinkage' models very popular in statistics research
- No easy way to put these into JAGS!

Summary

- Ideally use a JAGS SIMM script to run your own SIMM model. If not use MixSIAR
- Splines a really useful way of doing non-linear smoothing
- Some advanced topics not yet implemented in SIMMs - very fertile avenue for further and collaboration

THANK YOU FOR LISTENING!