

The background of the slide is a dense, repeating pattern of various tropical leaves, including palm fronds and monstera leaves, rendered in a light green line-art style. A large, semi-transparent white circle is centered on the left side of the slide, serving as a backdrop for the text.

Synchrony Update: December 2020

Recent progress:

- Model comparison
- Plotting the better PPC
- Visualizing partial pooling

The models:

mdl – model used in Kharouba et al. paper

```
data {
  int<lower=0> N; //No. obs
  int<lower=0> Nspp; //No. spp
  int species[N]; // Grouping by species
  vector[N] year;
  //response
  real ypred[N]; //DOY of pheno event
}

parameters {
  real a[Nspp]; // intercept for each sp, but not partially pooled
  real b[Nspp]; // slopes for species

  real<lower=0> sigma_y; //measurement error, noise

  //hyperparameters
  real mu_b; // mean slope across sp
  real<lower=0> sigma_b; //var of slope among sp
}

transformed parameters{
  real mu_y[N]; //individual mean

  for(i in 1:N){
    mu_y[i]= a[species[i]] +b[species[i]]*year[i];
  }
}
```

mdslpint – partial pooling across species

```
data {
  int<lower=0> N; //No. obs
  int<lower=0> Nspp; //No. spp
  int species[N]; // Grouping by species
  vector[N] year;
  //response
  real ypred[N]; //DOY of pheno event
}

// The parameters accepted by the model. Our model accepts
parameters {
  real a[Nspp] ;// intercept for species, I will have Nspp
  real b[Nspp]; // slopes for species

  real mu_a; //mean int across sp -- with pooled inttth
  real<lower=0> sigma_a; // variation in int among sp
  real mu_b; // mean slope across sp
  real<lower=0> sigma_b; //var of slope among sp

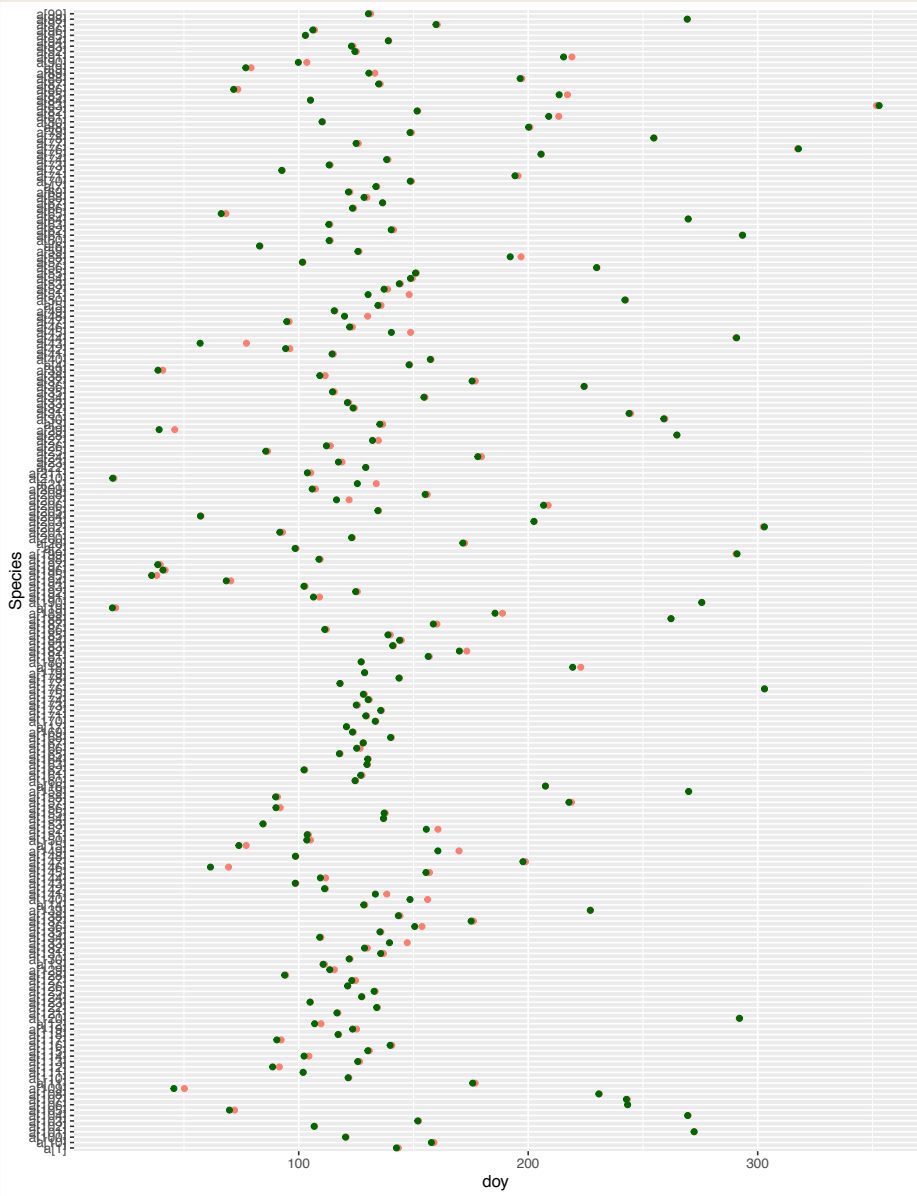
  real<lower=0> sigma_y; //measurement error, noise
}

transformed parameters{
  real mu_y[N]; //individual mean

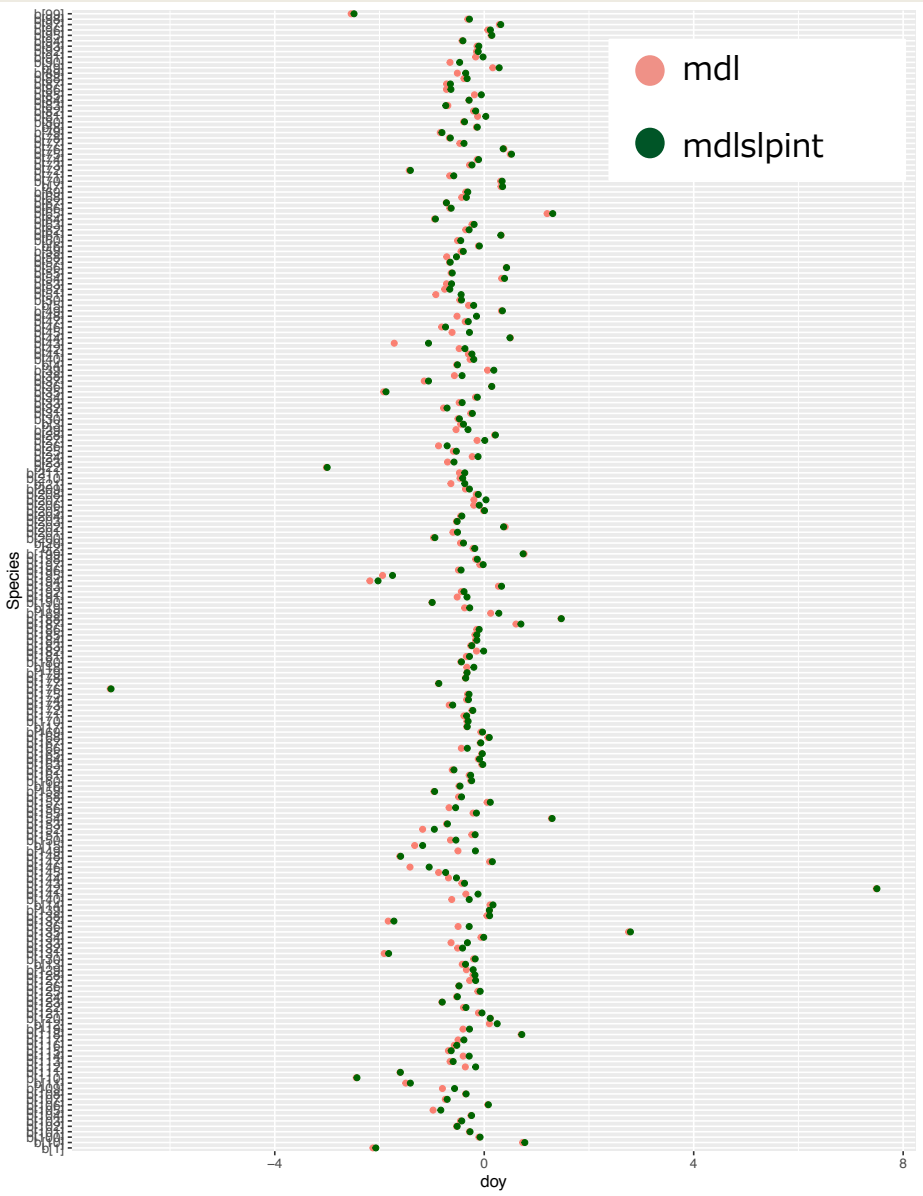
  for(i in 1:N){
    mu_y[i]=a[species[i]]+b[species[i]]*year[i];
  }
}
```

Model Comparison:

Intercepts

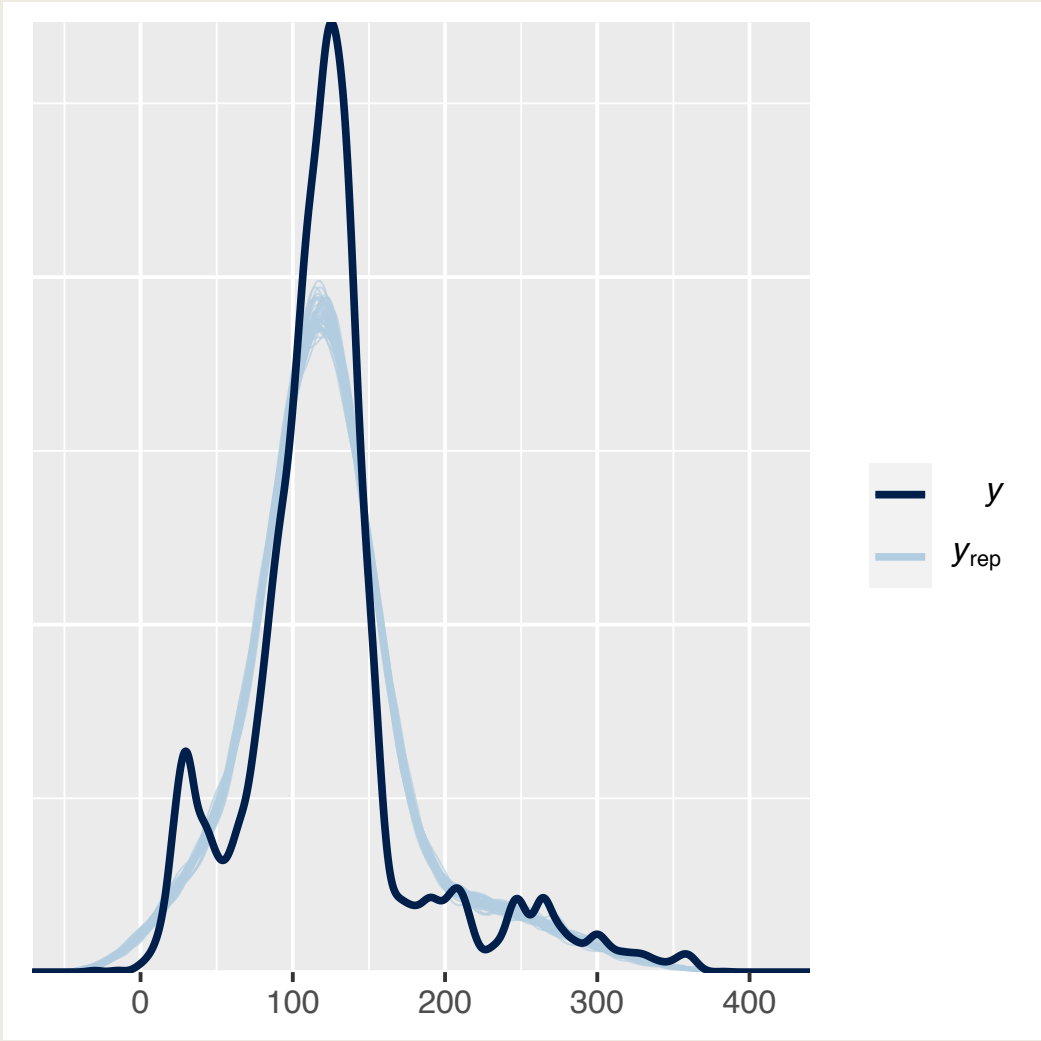


Slopes

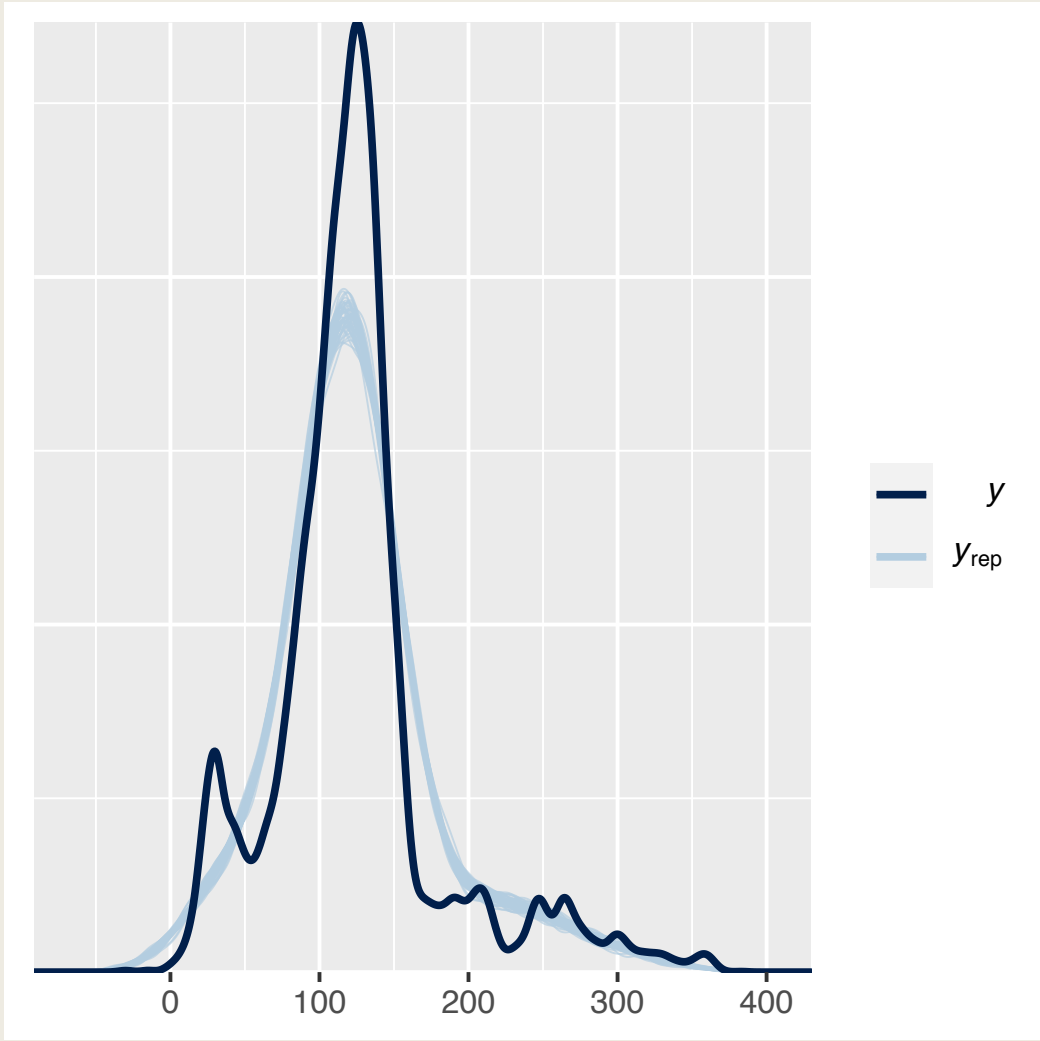


Model Comparison:

mdl:



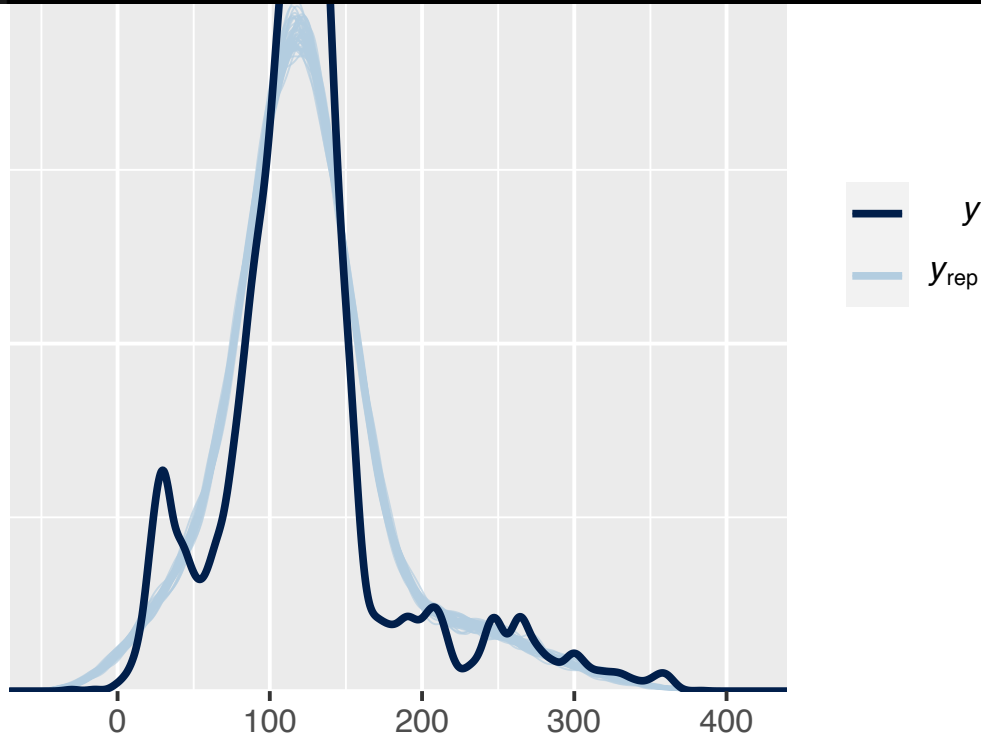
mdlslpint:



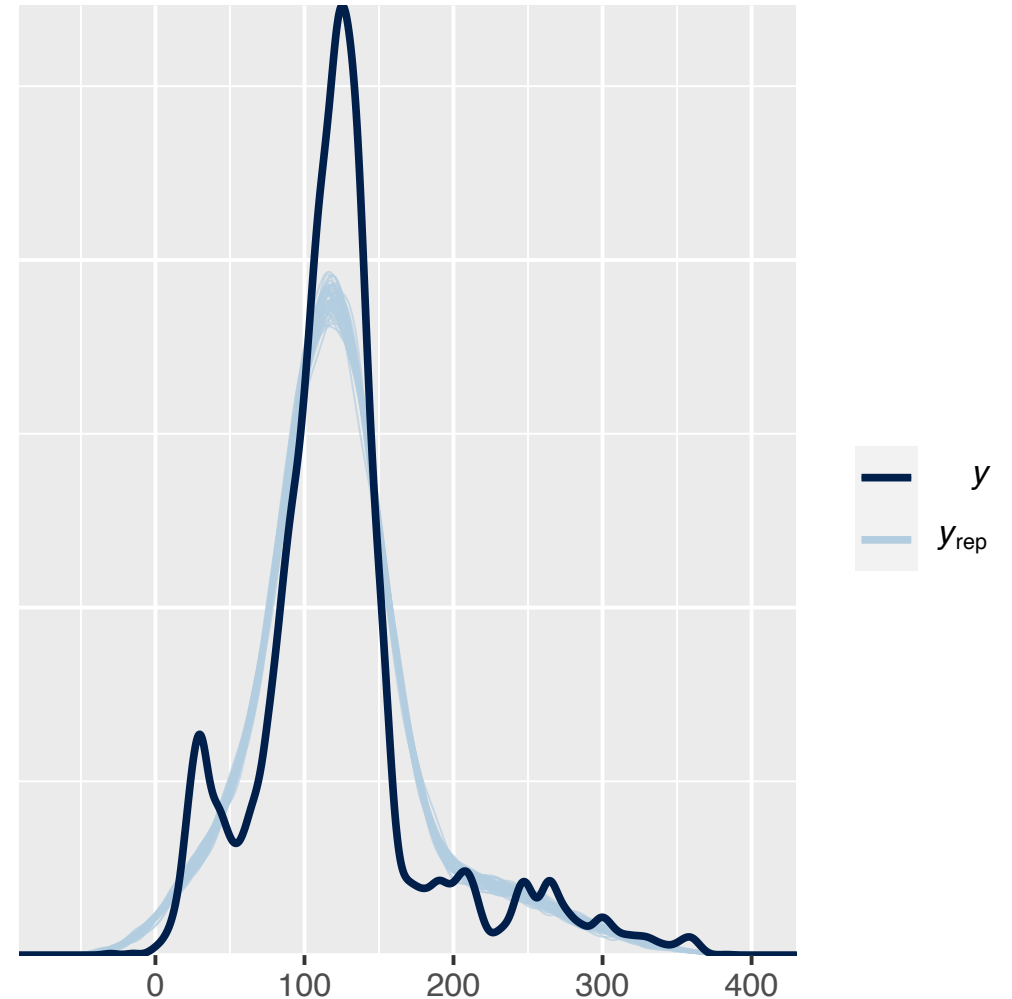
Model Comparison:

mdl:

```
real ypred_new[N];  
  
for (i in 1:N) // now over writing this with the sample dist, but this is al  
transformed para block  
  ypred_new[i] = normal_rng(mu_y[i], sigma_y);  
  // does include the partial pooling because the mu-y does this above  
}
```

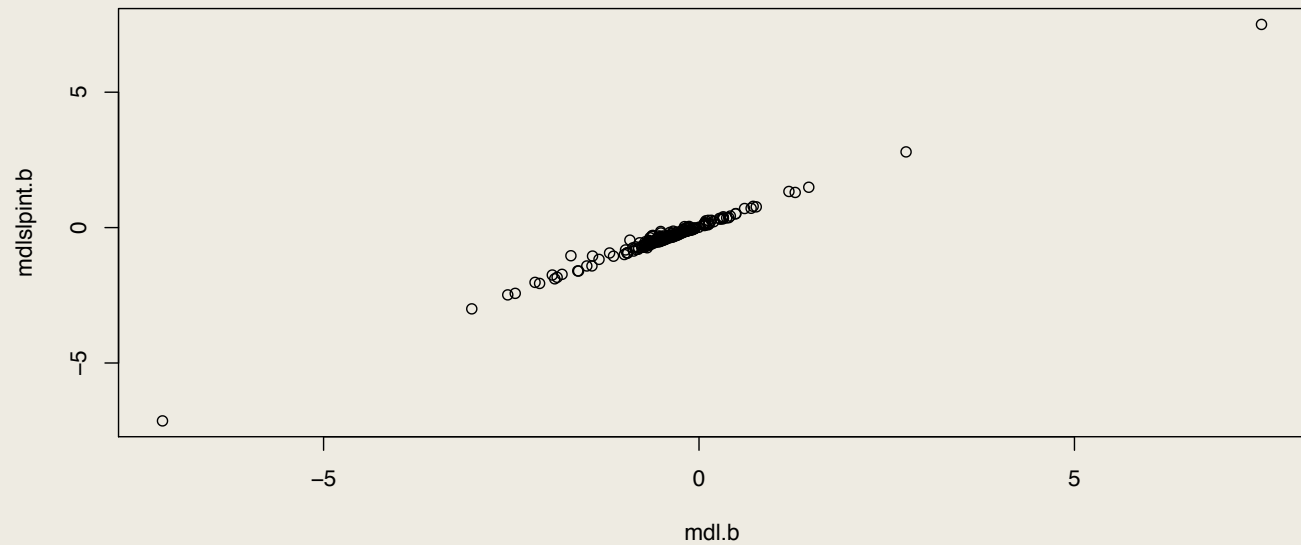
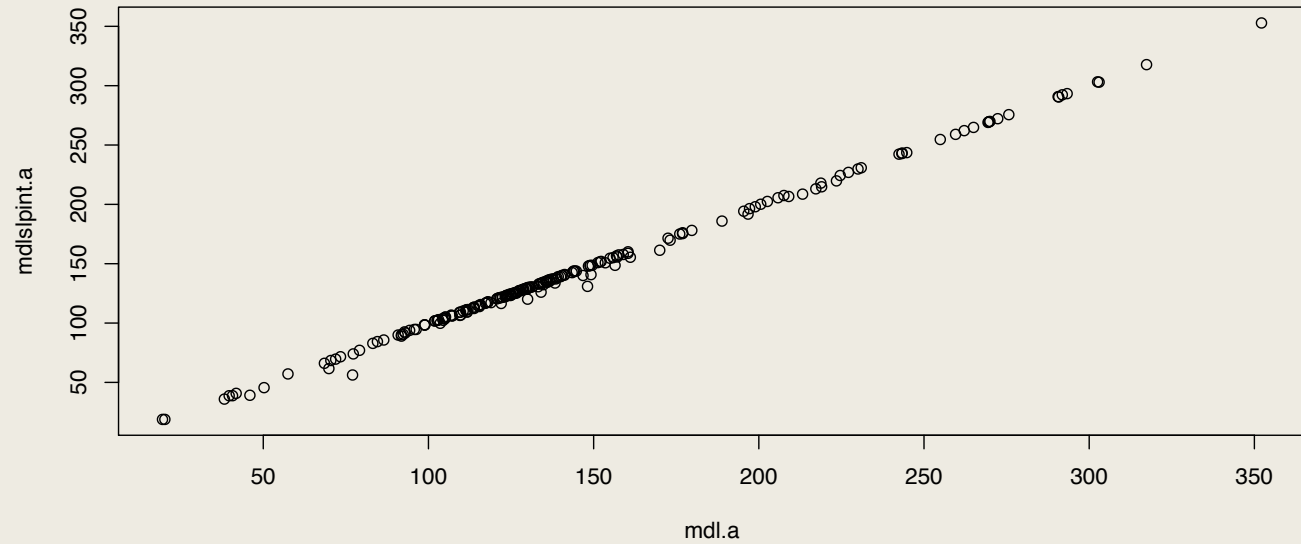


mdlslpint:



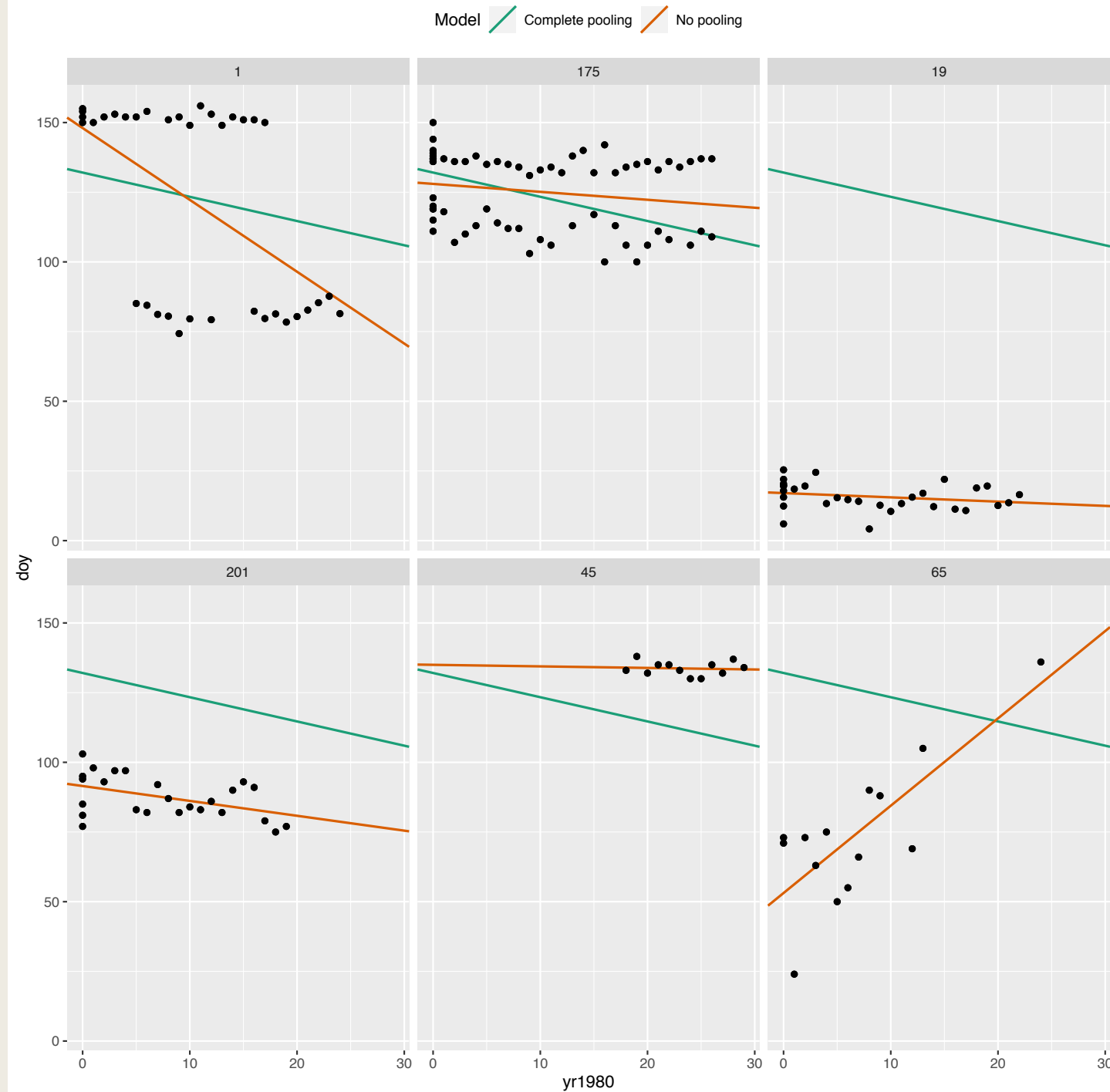
Model Comparison:

- mdl on the x-axis
- mdlspint on the y



Model Comparison:

- Haphazardly selected subset of the 211 unique species
- Partial pooling best fits the data on average
- Sp1: occurs in two datasets
- Sp175 has two phenological events



Pooling of regression:

- Full model with random slopes and intercepts fails to converge
 - Still played with random intercept model

For interest, a few of the species names:

- Sp142 is a Eurasian bullfinch
- Sp176 is a Common starling
- Sp83 is a white-throated needletail

