

```
Error in library(blme): there is no package called 'blme'
```

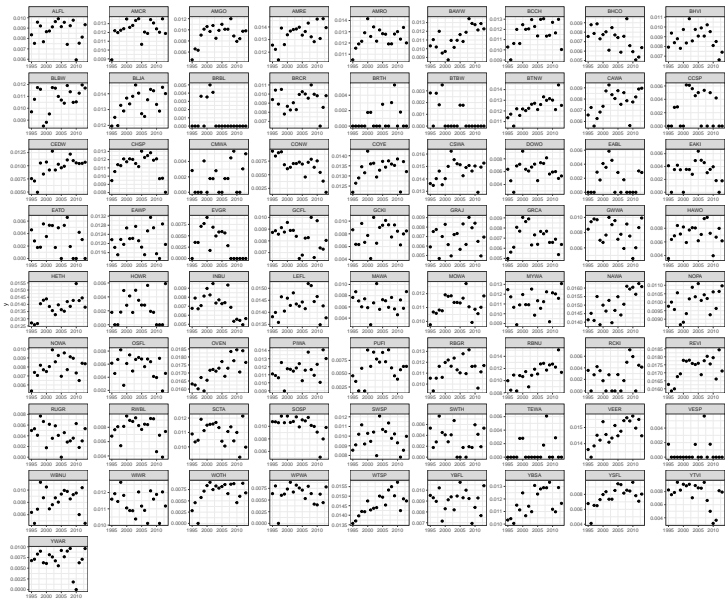
# Hierarchical linear models (cont.)

## Random intercept, random slope

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year

# Independent regressions

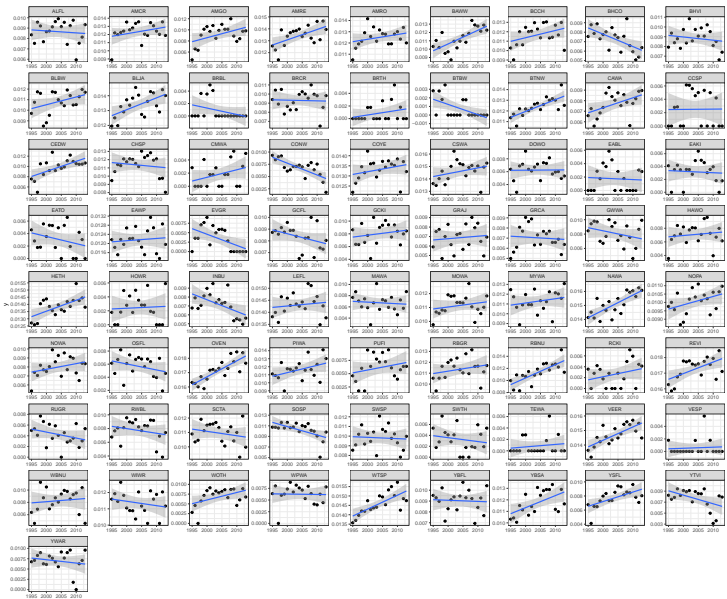
Initially, we could consider the model

$$y_{st} \overset{ind}{\sim} N(\beta_{s,0} + x_{st}\beta_{s,1}, \sigma_s^2)$$

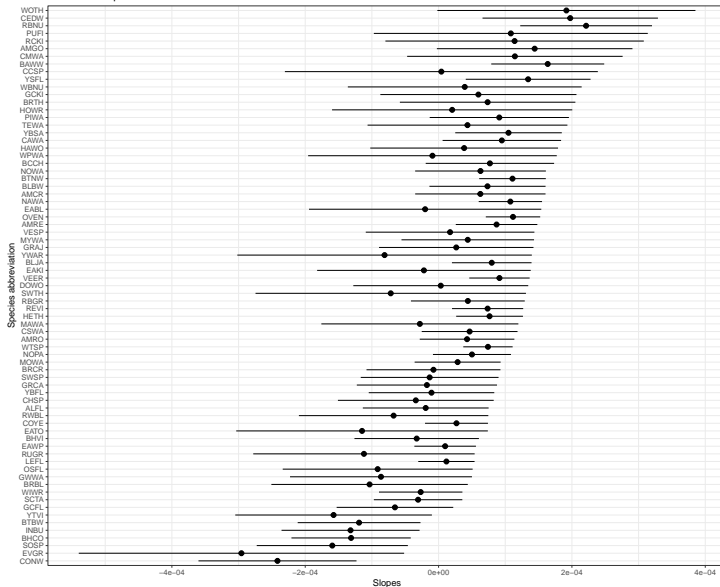
where

- $y_{st}$  is the mean log count (+1) for species  $s$  at time  $t$
- $x_{st}$  is the year (minus 2005) for species  $s$  at time  $t$

This model treats each species completely independently.



Estimated slopes and 95% confidence intervals



## Random intercept, random slope model

A reasonable assumption is to treat these species exchangeably and put a distribution on the intercept and slope.

Then a **random intercept, random slope model** is

$$\begin{aligned} y_{st} &\overset{\text{ind}}{\sim} N(\beta_{s,0} + x_{st}\beta_{s,1}, \sigma^2) \\ \beta_s &\overset{\text{ind}}{\sim} N(\mu_\beta, \Sigma_\beta) \end{aligned}$$

where  $\beta_s = (\beta_{s,0}, \beta_{s,1})'$  and  $\sigma^2$ ,  $\mu_\beta$ , and  $\Sigma_\beta$  are parameters to be estimated.

Notice that there is now a common variance for all species.

# Random intercept and random slope model in R

```
m2 = lmer(y~I(year-2005) + (I(year-2005)|abbrev), d)
```

```
Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model failed to converge with max|grad| = 0.00267938 (tol = 0.002, component 1)
```

```
summary(m2)
```

Linear mixed model fit by REML ['lmerMod']

Formula:  $y \sim I(\text{year} - 2005) + (I(\text{year} - 2005) \mid \text{abbrev})$

Data: d

REML criterion at convergence: -13786.6

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-4.6888	-0.5157	0.0381	0.5437	3.6364

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
abbrev	(Intercept)	1.799e-05	4.242e-03	
	I(year - 2005)	5.996e-09	7.743e-05	0.49
Residual		2.015e-06	1.419e-03	

Number of obs: 1387, groups: abbrev, 73

Fixed effects:

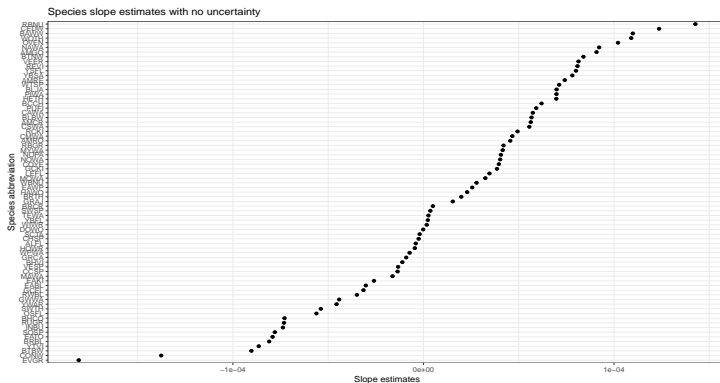
	Estimate	Std. Error	t value
(Intercept)	8.543e-03	4.979e-04	17.157
I(year - 2005)	1.502e-05	1.143e-05	1.314



Error: coord\_fixed doesn't support free scales

# Which species have significant decline?

The quantities of interest here are  $\beta_{s,1}$  and whether these quantities are negative, i.e. indicating an average decrease in counts over time. But how can we calculate pvalues or confidence intervals for the random effects themselves?



# Bayesian random intercept, random slope model

The model

$$\begin{aligned}y_{st} &\stackrel{\text{ind}}{\sim} N(\beta_{s,0} + x_{st}\beta_{s,1}, \sigma^2) \\ \beta_s &\stackrel{\text{ind}}{\sim} N(\mu_\beta, \Sigma_\beta)\end{aligned}$$

and a prior

$$p(\sigma, \mu_\beta, \Sigma_\beta) \propto p(\sigma)p(\mu_\beta)p(\Sigma_\beta)$$

and

- $\sigma \sim Ca^+(0, 1)$ ,
- $p(\mu_\beta) \propto 1$ , and
- $\Sigma_\beta \sim ?$

## Conjugate prior for a covariance matrix

The natural conjugate prior for a covariance matrix is the **inverse-Wishart** distribution, which has density

$$p(\Sigma) \propto |\Sigma|^{-(\nu+d+1)/2} \exp\left(-\frac{1}{2}\text{tr}(S\Sigma^{-1})\right)$$

with  $\nu > d - 1$  and  $S$  is a positive definite matrix. The expected value is

$$E[\Sigma] = \frac{S}{\nu - d - 1}$$

for  $\nu > d + 1$ . We write  $\Sigma \sim IW(\nu, S^{-1})$ .

Special cases:

- If  $\nu = d + 1$  and  $S$  is diagonal, then each of the correlations in  $\Sigma$  has a marginal uniform prior.
- Jeffreys prior

$$p(\Sigma) = |\Sigma|^{-(d+1)/2}$$

## Issues with the inverse-Wishart distribution

If  $\Sigma \sim IW(\nu, S)$ , then  $\Sigma_{ii} \sim IG([\nu - (d - 1)]/2, S_{ii}/2)$ . In particular, if  $\nu = d + 1$  and  $S = I$  (to ensure marginally uniform priors on the correlations), then  $\Sigma_{ii} \sim IG(1, 1/2)$ .

### The problems

- although the correlations are marginally uniform, they are not independent *a priori* of the variances (diagonal elements of  $\Sigma$ ),
- the inverse gamma distribution has a region near zero of extremely low density that can cause extreme bias toward larger values for truly small variances,
- this in turn causes the correlation to be shrunk toward zero.

# Deconstructing the covariance matrix

Let

$$\Sigma = \text{diag}(\sigma)\Omega\text{diag}(\sigma)$$

where

- $\sigma$  is a vector of standard deviations
- $\Omega$  is a correlation matrix

which results in the standard deviations and correlations being independent *a priori*.

Now we can put whatever prior we want on  $\sigma$  and  $\Omega$ , e.g.  $\sigma_i \stackrel{ind}{\sim} Ca^+(0, ?)$ .

## LKJ correlation matrix prior

The LKJ (Lewandowski, Kurowicka, and Joe 2009) distribution is

$$p(\Omega) = |\Omega|^{\eta-1}$$

where  $\Omega$  is a correlation matrix with implicit dimension  $d$  and  $\eta > 0$  is the shape parameter.

- if  $\eta = 1$ , then the density is uniform over correlation matrices of dimension  $d$
- if  $\eta > 1$ , the identity matrix is the modal correlation matrix with a sharper peak in the density for larger values of  $\eta$
- if  $\eta < 1$ , the density has a trough at the identity matrix.

```

model = "
data {
  int<lower=1> n_species;
  int<lower=1> n_years;
  vector[n_years] y[n_species];
  matrix[n_years,2] X;
}
parameters {
  real<lower=0> sigma;
  vector[2] beta[n_species];
  vector[2] mu_beta;
  vector<lower=0>[2] sigma_beta;
  corr_matrix[2] L;
}
model {
  sigma ~ cauchy(0,1);
  sigma_beta ~ cauchy(0,1);
  L ~ lkj_corr(1.0);
  beta ~ multi_normal(mu_beta, diag_matrix(sigma_beta) * L * diag_matrix(sigma_beta));
  for (s in 1:n_species) y[s] ~ normal(X*beta[s], sigma);
}
"

```



```

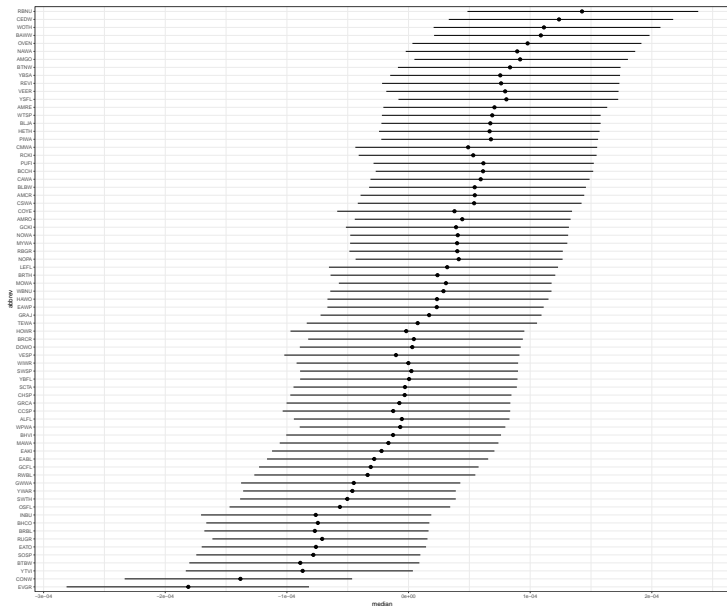
tmp = reshape2::dcast(d[,c('year','abbrev','y')], abbrev~year, value.var='y')
dat = list(n_species = nrow(tmp),
          n_years    = ncol(tmp)-1,
          y          = tmp[,-1],
          X          = cbind(1, as.numeric(names(tmp)[-1])-2005),
          prior_scale = 0.01)
m = stan_model(model_code=model)
r = sampling(m, dat, refresh=0)

```

Warning: There were 2 divergent transitions after warmup. Increasing adapt\_delta above 0.8 may help. See <http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup>

Warning: There were 97 transitions after warmup that exceeded the maximum treedepth. Increase max\_treedepth above 10. See <http://mc-stan.org/misc/warnings.html#maximum-treedepth-exceeded>

Warning: Examine the pairs() plot to diagnose sampling problems



# Hierarchical model for the variances

The model

$$\begin{aligned}y_{st} &\stackrel{\text{ind}}{\sim} N(\beta_{s,0} + x_{st}\beta_{s,1}, \sigma_s^2) \\ \beta_s &\stackrel{\text{ind}}{\sim} N(\mu_\beta, \Sigma_\beta) \\ \sigma_s &\stackrel{\text{ind}}{\sim} LN(\mu_\sigma, \tau_\sigma)\end{aligned}$$

and a prior

$$p(\mu_\sigma, \tau_\sigma, \mu_\beta, \Sigma_\beta) \propto p(\mu_\sigma)p(\tau_\sigma)p(\mu_\beta)p(\Sigma_\beta)$$

and

- $p(\mu_\sigma) \propto 1$ ,
- $\tau_\sigma \sim Ca^+(0, 1)$ ,
- $p(\mu_\beta) \propto 1$ , and
- $\Sigma_\beta$  as before

```

model2 = "
data {
  int<lower=1> n_species;
  int<lower=1> n_years;
  vector[n_years] y[n_species];
  matrix[n_years,2] X;
}
parameters {
  real<lower=0> sigma[n_species];
  real mu;
  real<lower=0> tau;
  vector[2] beta[n_species];
  vector[2] mu_beta;
  vector<lower=0>[2] sigma_beta;
  corr_matrix[2] L;
}
model {
  tau ~ cauchy(0,1);
  sigma ~ lognormal(mu,tau);
  sigma_beta ~ cauchy(0,1);
  L ~ lkj_corr(1.0);
  beta ~ multi_normal(mu_beta, diag_matrix(sigma_beta) * L * diag_matrix(sigma_beta));
  for (s in 1:n_species) y[s] ~ normal(X*beta[s], sigma[s]);
}
"

```

```
m2 = stan_model(model_code=model2)
r2 = sampling(m2, dat, refresh=0)
```

Warning: There were 3 divergent transitions after warmup. Increasing adapt\_delta above 0.8 may help. See <http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup>

Warning: There were 3997 transitions after warmup that exceeded the maximum treedepth. Increase max\_treedepth above 10. See

<http://mc-stan.org/misc/warnings.html#maximum-treedepth-exceeded>

Warning: There were 1 chains where the estimated Bayesian Fraction of Missing Information was low. See <http://mc-stan.org/misc/warnings.html#bfmi-low>

Warning: Examine the pairs() plot to diagnose sampling problems

