

Modeling changes in synchrony

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Study questions:

- ▶ How has the phenology of different trophic levels changed over time and are there differences across suites of interactions?
- ▶ Are the observed trends in shifts in interactions similar using data from single-species studies, or should we be using biologically relevant paired species data?

Building the model from simple to complex...

- ▶ How has the phenology of different trophic levels changed over time and what differences are there across suites of interactions?
 - ▶ To compare findings with those of Thackeray and Cohen, I am analyzing the data as single species using a simpler model

$$d\hat{y} = \alpha_{sp_i} + \beta(year_i)$$

$$\alpha_{sp} \sim N(\mu, \sigma)$$

$$doy_i \sim N(d\hat{y}, \sigma_i)$$

Building the model from simple to complex...

- Are the observed trends in shifts in interactions similar using data from single-species studies, or should we be using biologically relevant paired species data?

$$doy_{r_i} = \alpha_{r_i} + \beta_{r_i}(year_i)$$

$$\beta_{r_i} \sim N(\mu_r, \sigma_r)$$

$$doy_{r_i} \sim N(doy_{r_i}, \sigma_{doy})$$

$$doy_{c_i} = \alpha_{c_i} + \beta_{shift}(year_i)$$

$$\beta_{shift} \sim (\beta_{c_i} - \beta_{r_i})$$

$$\beta_{c_i} \sim N(\mu_c, \sigma_c)$$

$$doy_{c_i} \sim N(doy_{c_i}, \sigma_{doy})$$

Generating data:

Test data variables:

- ▶ Study
- ▶ Species
- ▶ Event
- ▶ Year
- ▶ DOY

	Study	Species	Event	Year	DOY S
1	1	51	4	1	206.9588
2	1	51	4	2	208.6147
3	1	51	4	3	212.5579
4	1	51	4	4	222.5058
5	1	51	4	5	223.9829
6	1	51	4	6	232.6540

Stan model:

```
// The input data is a vector 'y' of length 'N'.
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 two parameters 'mu' and 'sigma'.
parameters {
  //setting random values for intercepts
  real mu_a_sp;
  real<lower=0> sigma_a_sp;
  real<lower=0,upper=365> a[Nspp]; // intercept for species

  real mu_b_sp;
  real<lower=0> sigma_b_sp;
  real b[Nspp]; // slopes for species

  real<lower=0> sigma_y;
}

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

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

// The model to be estimated. We model the outputn'y' to be normally distributed
// with deviation 'sigma'.
model {
  a ~ normal(mu_a_sp, sigma_a_sp); //using the previously defined values here
  b ~ normal(mu_b_sp, sigma_b_sp);
  ypred ~ normal(mu_y, sigma_y);

  //Priors
  mu_a_sp ~normal(188, 20);
  sigma_a_sp ~normal(0,20);
  mu_b_sp ~normal(5,2);
  sigma_b_sp ~normal(0,2);
  sigma_y ~normal(0,2);
}
```

Stan model output:

Priors:

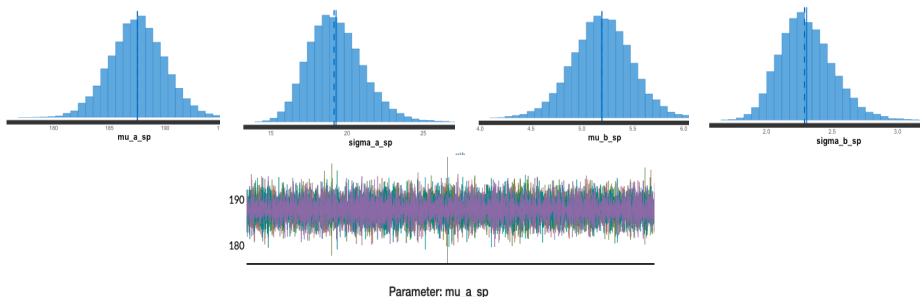
```
//Priors
mu_a_sp ~normal(188, 20);
sigma_a_sp ~normal(0,20);
mu_b_sp ~normal(5,2);
sigma_b_sp ~normal(0,2);
sigma_y ~normal(0,2);
```

Model output:

```
Inference for Stan model: singlesp_randslopes_goo.
4 chains, each with iter=8000; warmup=4000; thin=1;
post-warmup draws per chain=4000, total post-warmup draws=16000.
```

	mean	se_mean	sd	2.5%	25%	50%	75%	97.5%	n_eff	Rhat
mu_a_sp	187.50	0.01	2.43	182.70	185.87	187.51	189.12	192.31	37664	1
sigma_a_sp	19.28	0.01	1.78	16.17	18.02	19.15	20.39	23.14	34550	1
mu_b_sp	5.20	0.00	0.29	4.62	5.01	5.20	5.39	5.77	36173	1
sigma_b_sp	2.31	0.00	0.21	1.95	2.16	2.29	2.43	2.75	29629	1
sigma_y	1.98	0.00	0.04	1.91	1.96	1.98	2.00	2.05	29038	1
a[1]	145.99	0.01	1.51	143.02	144.97	145.99	147.01	148.97	26578	1
a[2]	175.20	0.00	0.73	173.78	174.71	175.20	175.69	176.62	28136	1
a[3]	161.39	0.01	1.36	158.71	160.49	161.38	162.30	164.03	23124	1
a[4]	143.18	0.00	0.56	142.09	142.80	143.19	143.56	144.28	26531	1
a[5]	199.39	0.01	0.94	197.53	198.76	199.40	200.03	201.22	26292	1
a[6]	201.77	0.01	1.07	199.64	201.05	201.78	202.49	203.86	24036	1

Shiny stan diagnostic plots:



Next Steps:

- ▶ More accurately represent slopes in the test data
- ▶ Manipulate posteriors to detect differences across groups
- ▶ Test on real data
- ▶ Repeat for a joint model