Elevated temperatures have a greater effect on herbivore survival than a viral pathogen

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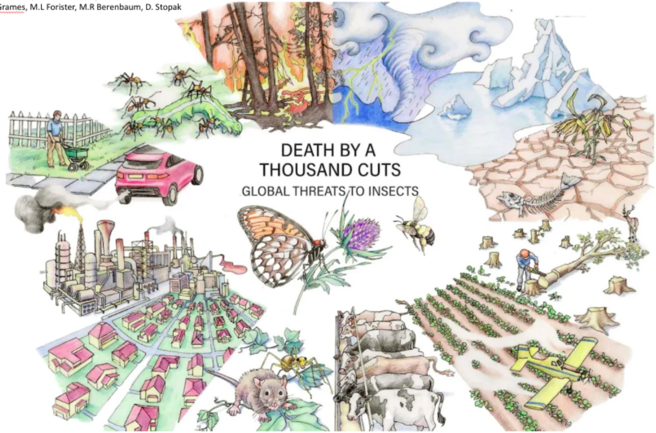
Background

Insect decline in the Anthropocene: Death by a thousand cuts
D.L. Wagner, E.M. Grames, M.L Forister, M.R Berenbaum, D. Stopak
PNAS 2021



Questions

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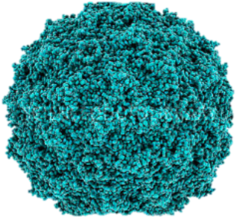
- Does viral infection and temperature interact to effect the development and survival of an insect herbivore?
- Is there a threshold temperature at which insect herbivores can survive with infection of the virus?

Study System

Junonia coenia densovirus
(Parvoviridae: Densovirinae)



Junonia coenia
Common Buckeye

Plantago lanceolata
Plantain

Field Work

Factorial Experiment Design

	Temp 1 (25/20)	Temp 2 (28/23)	Temp 3 (31/26)	Temp 4 (35/29)
Infected	60	60	60	60
Control	60	60	60	60

Model Statements

$$y_i \sim Bernoulli(\mu_i)$$

Model 1:

$$\mu_i = logit^{-1}(\beta_0 + \beta_1 virus_i + \beta_2 temp_{2i} + \beta_3 temp_{3i} + \beta_4 temp_{4i})$$

Model 2:

$$\mu_i = logit^{-1}(\beta_0 + \beta_1 virus_i + \beta_2 temp_{2i} virus_i + \beta_3 temp_{3i} virus_i + \beta_4 temp_{4i} virus$$

Model 3:

$$\mu_i = logit^{-1}(\beta_0 + \beta_1 virus_i + \beta_2 temp_{2i} + \beta_3 temp_{3i} + \beta_4 temp_{4i})$$

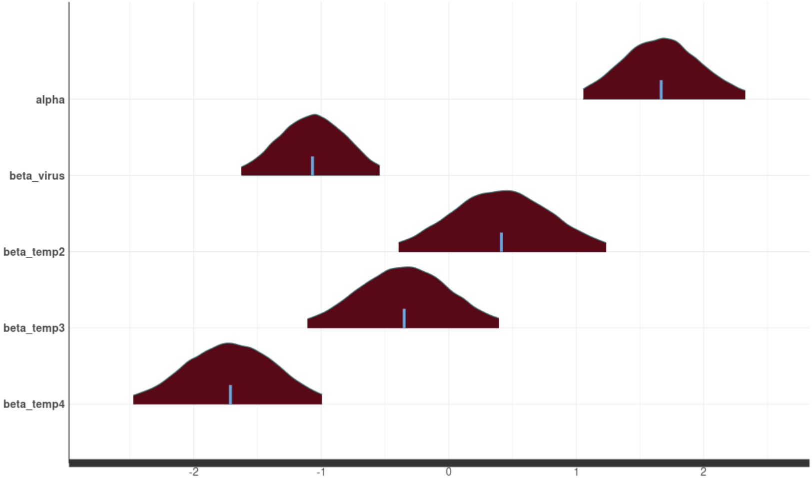
$$\beta_1 \sim Normal(-1.3, 1.5)$$

Model 1 Results

Model 1:

Parameter	Rhat	n_eff	mean	sd	se_mean	2.5%	97.5%
alpha	1.0	12011	1.7	0.3	0.0	1.1	2.3
beta_virus	1.0	18817	-1.1	0.3	0.0	-1.6	-0.5
beta_temp2	1.0	15785	0.4	0.4	0.0	-0.4	1.2
beta_temp3	1.0	15259	-0.4	0.4	0.0	-1.1	0.4
beta_temp4	1.0	14106	-1.7	0.4	0.0	-2.5	-1.0

Model 1 Posterior Distributions

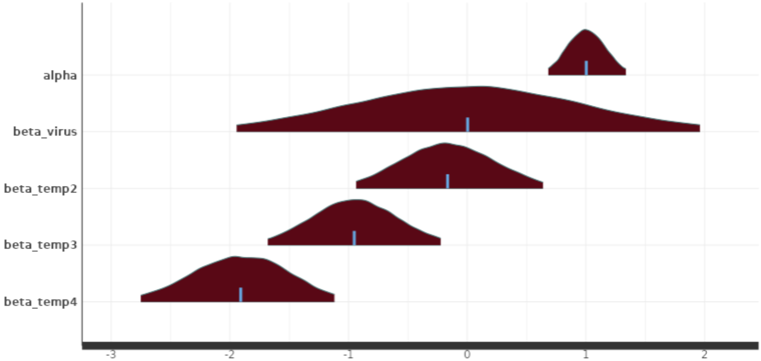


Model 2 Results

Model 2:

Parameter	Rhat	n_eff	mean	sd	2.5%	97.5%
alpha	1.0	28490	1.0	0.2	0.7	1.3
beta_virus	1.0	36956	0.0	1.0	-2.0	2.0
beta_temp2	1.0	33795	-0.2	0.4	-0.9	0.6
beta_temp3	1.0	34062	-0.9	0.4	-1.7	-0.2
beta_temp4	1.0	32972	-1.9	0.4	-2.7	-1.1

Model 2 Posterior Distributions

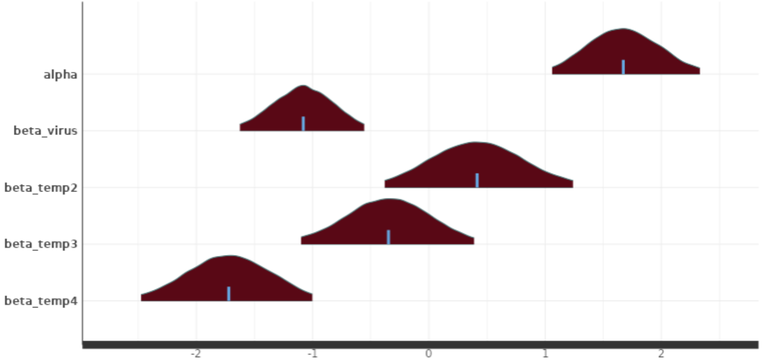


Model 3 Results

Model 3:

Parameter	Rhat	n_eff	mean	sd	2.5%	97.5%
alpha	1.0	12776	1.7	0.3	1.1	2.3
beta_virus	1.0	17718	-1.1	0.3	-1.6	-0.6
beta_temp2	1.0	16688	0.4	0.4	-0.4	1.2
beta_temp3	1.0	16386	-0.4	0.4	-1.1	0.4
beta_temp4	1.0	15455	-1.7	0.4	-2.5	-1.0

Model 3 Posterior Distributions



Model Checking

The loo package is used to carry out Pareto smoothed importance-sampling leave-one-out cross-validation (PSIS-LOO) for purposes of model checking and model comparison.

- $\widehat{elpd_{loo}}$
  - expected log predictive density
- $\widehat{p_{loo}}$
  - effective number of parameters
- $looic = -2\widehat{elpd_{loo}}$
  - the LOO information criterion

Model Checking

Model	$\Delta\widehat{elpd}_{loo}$	Δse	*looic*
Model 3	0.0	0.0	331.3
Model 1	-0.1	0.0	331.4
Model 2	-11.9	4.6	355.0

The compare function makes an object that contains the estimated difference of expected leave-one-out prediction errors between the two models, along with the standard error.

Conclusions

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- The highest temperature treatment group had a greater negative effect on the survival of Buckeyes than viral infection.
- There may not be a strong interaction between temperature and virus, but there might be some interaction in the lower temperature treatment groups.
- Prior data did not really change the results, but made the posterior predictive check perform slightly better.

Model 3

```
data {
  int N; // Number of observations
  real virus[N]; // Virus dummy variable (0 or 1)
  real temp_2[N]; // Temperature dummy variable (0 or 1)
  real temp_3[N];
  real temp_4[N];
  int surv[N]; // Response variable: survivorship
}
parameters {
  real alpha; // Intercept
  real beta_virus; // Coefficient for virus variable
  real beta_temp2;
  real beta_temp3;
  real beta_temp4;
}
```

Model 3

```
model {
  // Priors
  alpha ~ normal(0, 1); // Prior for intercept
  beta_virus ~ normal(-1.3, 1.5);// Prior for virus coefficient
  // Likelihood
  for (i in 1:N) {
    real mu = alpha +
              beta_virus * virus[i] +
              beta_temp2 * temp_2[i] +
              beta_temp3 * temp_3[i] +
              beta_temp4 * temp_4[i]; // Linear predictor
    surv[i] ~ bernoulli_logit(mu); // Likelihood function*
  }
```