**Model fitting notes**

Mean detections by species (poisson model, no species pooling): does a really great job at tracking counts on average!



Max detections by species (poisson model, no species pooling): fails to capture the variability in high counts, we sometimes see high numbers for each species above and beyond the high numbers generated by the fitted poisson model. Too much dispersion in the counts?



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Mean detections by species (negative binomial model, no species pooling): now we actually do a little bit worse in terms of being able to predict counts on average, slightly underpredicting impatiens counts and overpredicting flavifrons and melanopygus counts.



Max detections by species (negative binomial model, no species pooling): doing a lot better in terms of predicting the weird outlier high counts, but still sometimes we actually see a bit more impatiens than our model is able to estimate. We are also overpredicting flavifrons and melanopygus by a bit here.



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Mean detections by species (poisson model with hierarchical (species-specific) overdispersion, no species pooling): does a really great job at tracking counts on average!



Max detections by species (poisson model with hierarchical (species-specific) overdispersion, no species pooling): also now is able to track the high variance that we see in our counts!



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Mean detections by species (poisson model with hierarchical (species-specific) overdispersion, no species pooling) – with more species: does a really great job at tracking counts on average! HOWEVER, rhat is too high and there are divergent transitions. Maybe setting hierarchical priors to partially pool data among species would help solve estimation issues?



Max detections by species (poisson model with hierarchical (species-specific) overdispersion, no species pooling) – with more species: everything still looks good here as well, but still need to overcome the pathology issues above^



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Overall phenology model structure:

Y[i,j,k] ~ poisson(lambda[i,j,k])

lambda[i,j,k] = β0 + βspecies[i] + βsite[j] + βyear[k] + βdate[i] \* date + βdate\_sq[i] \* date2 + ε[i]

βsite[j] ~ Normal(0, σsite)

ε[i]~ Normal(0, σε[i])

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**Figure 1: Species-specific phenology.** 95% BCI’s for expected abundance by julian date (a) illustrate the phenological differences among the five most common bumble bee species encountered during our surveys. Expected abundances are displayed for the average site, for the year 2022, and without extra-poisson dispersion that we accounted for with our model. Posterior model estimates indicate that the peak abundance earlier for all species relative to *Bombus impatiens* (b), with 50% (bold) and 95% (light) BCI’s for all species < 0.

Model diagnostic plots:

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