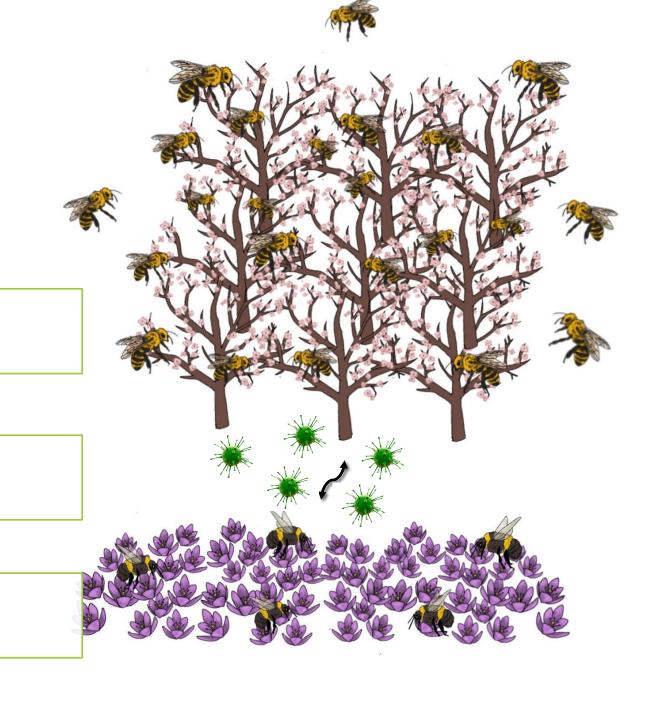
Impact of commercial honey bee importation on disease dynamics in wild bees

Nina Sokolov

Large populations of honey bees are regularly imported into California for crop pollination with an unknown impact on disease dynamics in wild bees.

What factors influence the disease status of deformed wing virus (DWV) in wild bees?

How does a fluctuating source population of honey bees impact disease dynamics in wild bees through time?



What factors influence the disease status of deformed wing virus (DWV) in wild bees?

Model: Generalized linear mixed model with random effect of site within year

Response Variable: DWV disease status in wild bees

Predictor Variables: Honey bee density, honey bee disease status, distance to crop site, pesticides, temperature, species, vector presence, solitary vs social

Family: Binomial

Link: logit

R Function: glmer(viral_prevalence_wb ~ hb_density + distance + pesticides + temp + species + ..., family= 'binomial', data = bee.data)

Hypothesis: The closer wild bees are to crop sites with high commercial honey bee density, the more wild bees will be diseased.

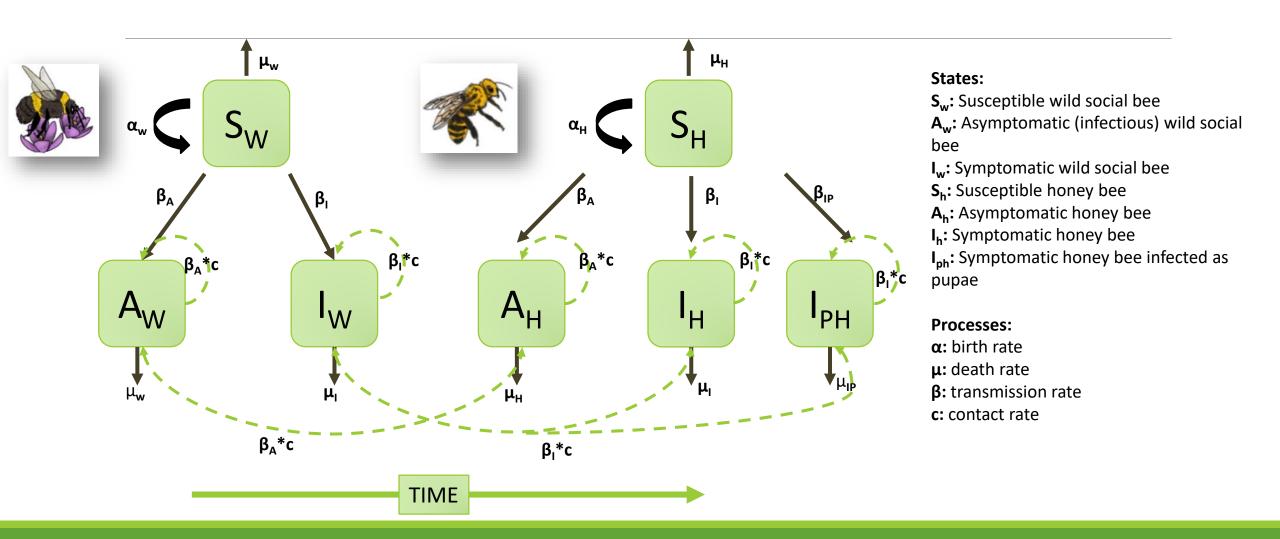




Increasing pollinator requirement

- □ Honey and wild bees will be collected at increasing distances away from crop sites, across the span of multiple years.
- ☐ Samples will be analyzed as whether they have the virus actively replicating (1) or not (0).
- ☐ The (a)biotic characteristics will be quantified

How does the timing of a fluctuating source population of honey bees impact disease dynamics in wild social bees?



Next Steps

- □ Field + Lab Data: Collect field data and bee samples at sites that vary in commercial honey bee density across California + RtPCR to detect virus actively replicating in the bee samples
- ☐ Fit my model to the data
 - ☐ Model solitary bee species
 - ☐ Sensitivity analysis
- Spatially map the infectious status information
 - ☐ Check for spatial auto correlation

