**Outline of Rusty Patched Bumble Bee population genetics manuscript**

**Potential titles**

* Analysis of Rusty Patched Bumble Bee (Bombus affinis) population genetics suggests evidence for spatially structured populations and warrants caution in captive breeding efforts
* Patterns of low colony abundance, isolation by distance, and male diploidy across the range of a federally endangered bumble bee (*Bombus affinis*)
* Rangewide genetic analysis of Rusty Patched Bumble Bee (*Bombus affinis*) reveals population structure, male diploidy, and low colony abundances

**Main message**

We document evidence for isolation by distance, low observed heterozygosity, male diploidy, and low colony abundance for the endangered *Bombus affinis*. We contextualize our results for imperiled bumble bee conservation.

**Working abstract**

* Why are you doing this? [context and aim]

Well-documented declines in bumble bee species across multiple continents have prompted the need for informed management plans to aid in species recovery. The Rusty Patched Bumble Bee (*Bombus affinis*) is the first federally-listed bumble bee species in North America. There is substantial interest in understanding range-wide patterns of population structure to determine appropriate conservation units and inform priority areas for potential interventions. Additionally, site-level knowledge on colony abundance is needed to understand the potential impact of development or captive rearing efforts.

* What did you do? [methods]

To inform these conservation priorities, we conducted a coordinated collection of non-lethal *B. affinis* genetic samples from across all extant conservation units. We conduct our analysis of rangewide population genetic analysis using standard methodologies. Additionally, we conduct site-level analyses of colony abundance at a subset of locations.

* What did you find? [core results – say something useful – no motherhood statements or deference to the main text!]

We find substantial evidence of isolation by distance, low observed heterozygosity, and ???. We detect male diploidy at a rate of XXX. Site-level analyses suggests low colony abundance estimates for *B. affinis* when compared to similar datasets of common or stable species. We find high-levels of private alleles in the Appalachian population and ????, suggesting this population may be substantially differentiation from the upper Midwest core.

* What does this mean? [interpretation in context]
* What is it good for? [application]

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