

# Characterization of and selection on compound within-individual floral variation in *Vicia americana* (Fabaceae)

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June 16, 2025

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## Abstract

This document provides code to reproduce all results from the manuscript `Characterization of and selection on compound within-individual floral variation in *Vicia americana*` (Fabaceae).

## 1 R

- The version of R used to make this document is 4.5.0.
- The version of the `rmarkdown` package used to make this document is 2.29.
- The version of the `bookdown` package used to make this document is 0.43.
- The version of the `dplyr` package used to make this document is 1.1.4.
- The version of the `glmmTMB` package used to make this document is 1.1.11.
- The version of the `DHARMA` package used to make this document is 0.4.7.
- The version of the `car` package used to make this document is 3.1.3.
- The version of the `caret` package used to make this document is 7.0.1.
- The version of the `Hmisc` package used to make this document is 5.2.3.
- The version of the `tidyr` package used to make this document is 1.3.1.
- The version of the `viridis` package used to make this document is 0.6.5.

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- The version of the **refund** package used to make this document is 0.1.37.

Attach packages.

```
suppressMessages(library("dplyr"))
suppressMessages(library("glmmTMB"))
suppressMessages(library("ggplot2"))
suppressMessages(library("DHARMa"))
suppressMessages(library("car"))
suppressMessages(library("caret"))
suppressMessages(library("Hmisc"))
suppressMessages(library("tidyr"))
suppressMessages(library("viridis"))
suppressMessages(library("refund"))
```

Need at least version 1.3-4 of R package **aster** for R generic function `vcov` to work on results of calls to R functions **aster** and **reaster**.

*#Nope*

where the variables are

- **Germ** is germination indicator (0 = no, 1 = yes), conditionally Bernoulli.
- **flw** is survival to flowering (0 = no, 1 = yes), conditionally Bernoulli.
- **total.pods** is total number of pods produced, conditionally Poisson.
- **total.pods.collected** is number of pods collected, conditionally Bernoulli (i.e. each pod may be collected or not). The arrow leading to this node is a subsampling arrow. The number of pods collected is a random sample of the pods produced.
- **totalseeds** is total number of seeds counted from collected pods, conditionally Poisson.

As always with **aster** models, the name of the distribution for an arrow is the name of the conditional distribution of the successor variable given the predecessor variable. The arrow labeled **samp** is a subsampling arrow. It is a Bernoulli arrow but the sampling is experimental rather than biological. This arrow may be [missing in some analyses](#).

Set graphical model description in R.

```
vars <- c("Germ", "flw", "total.pods", "total.pods.collected", "totalseeds")
pred <- c(0, 1, 2, 3, 4)
fam <- c(1, 1, 2, 1, 2)
```

## 1.1 Alternative Structure