

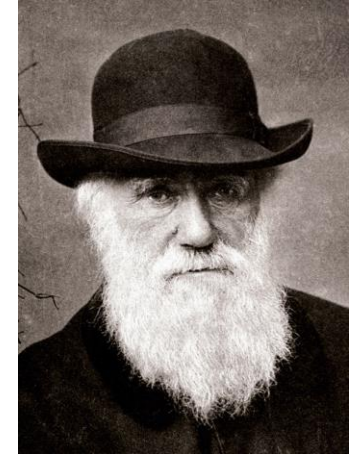
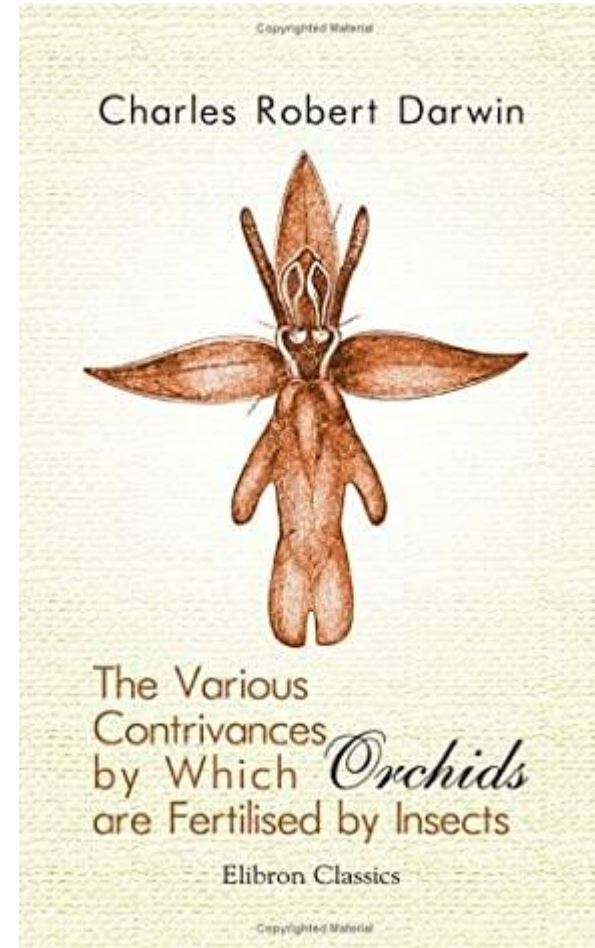
# Extending latent-variable modelling of plant-pollinator interactions

A close-up photograph of a bumblebee with a black and orange body, positioned on a white, tubular flower. The bee is facing left, and its legs are visible as it interacts with the flower. The background is a soft-focus green, showing other leaves and stems of the plant.

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# The study of floral evolution: Darwin's 'flank movement on the enemy'

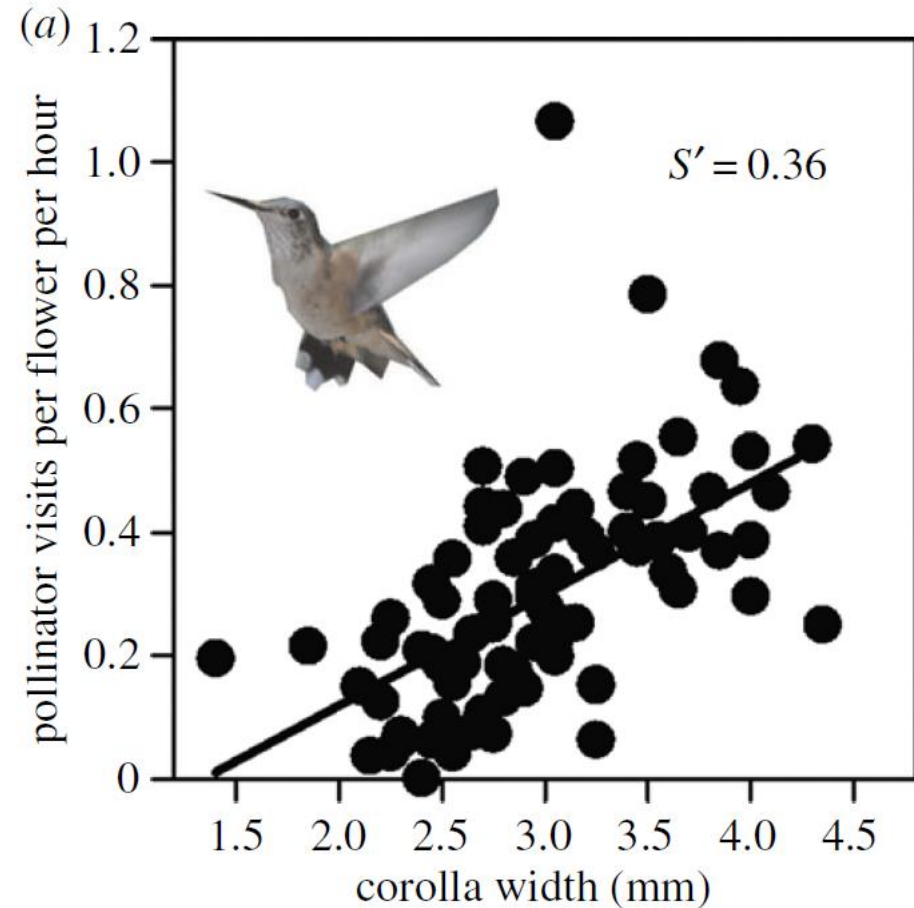
- 'no one else has perceived that my chief interest in my orchid book, has been that it was a "flank movement" on the enemy' (Darwin to Asa Gray, July 23<sup>rd</sup> 1862)
- 'If you grant an intelligent designer anywhere in Nature, you may be confident that he has had something to do with the "contrivances" in your Orchids.' (Gray to Darwin, July 2<sup>nd</sup> 1862)





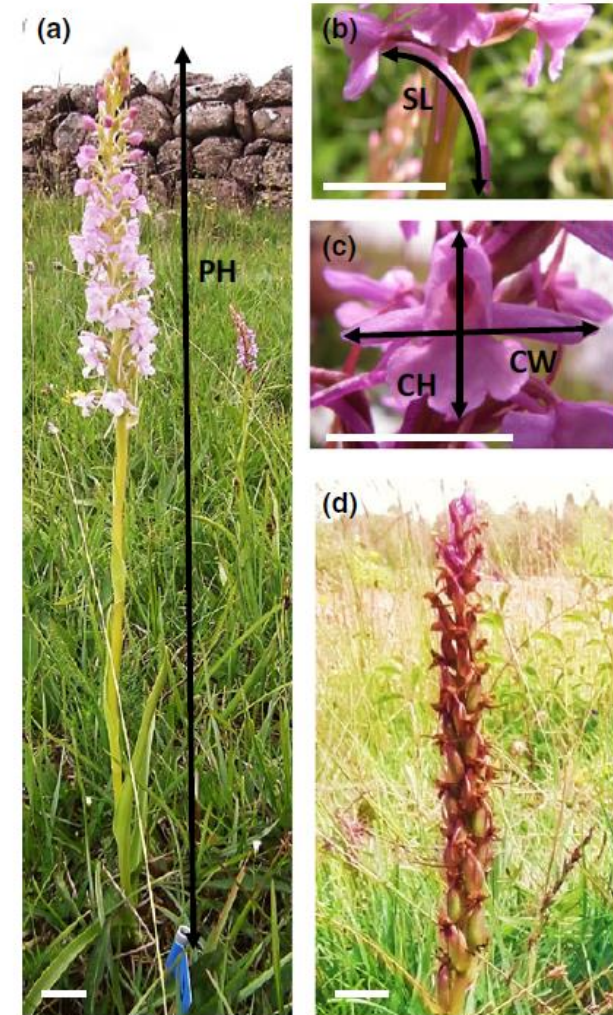
# Measuring Natural Selection

- Positive (or negative) relationship between a trait and a fitness component
- Pollinator-mediated selection arise when pollinators prefer some flowers over others, or when floral traits affect the efficiency of pollen transfer



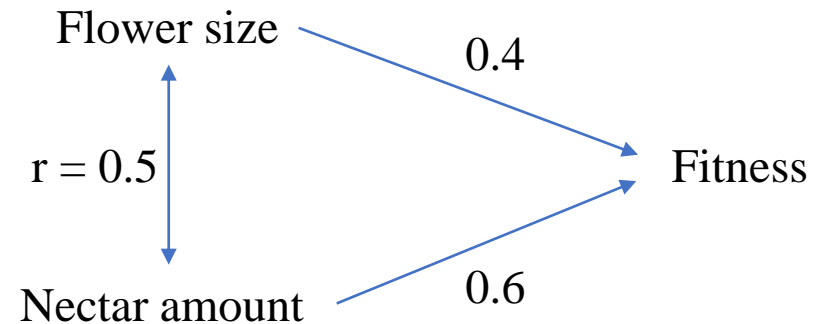
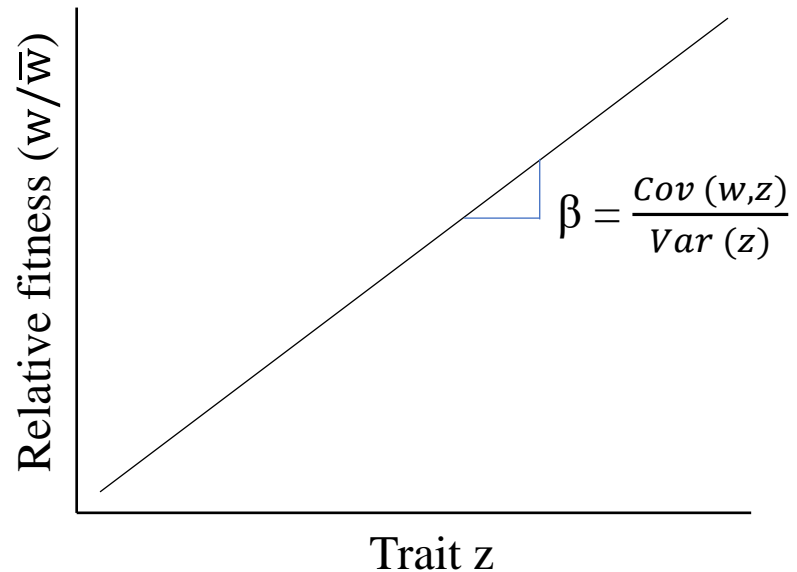
# Traits are not independent

- To account for (measured) correlated traits, linear selection gradients are estimated as the partial regression coefficients of relative fitness on a set of traits.
- Relative fitness =  
individual fitness/population mean fitness
- In plants, we often know or can hypothesize the functions of specific traits in the pollination process



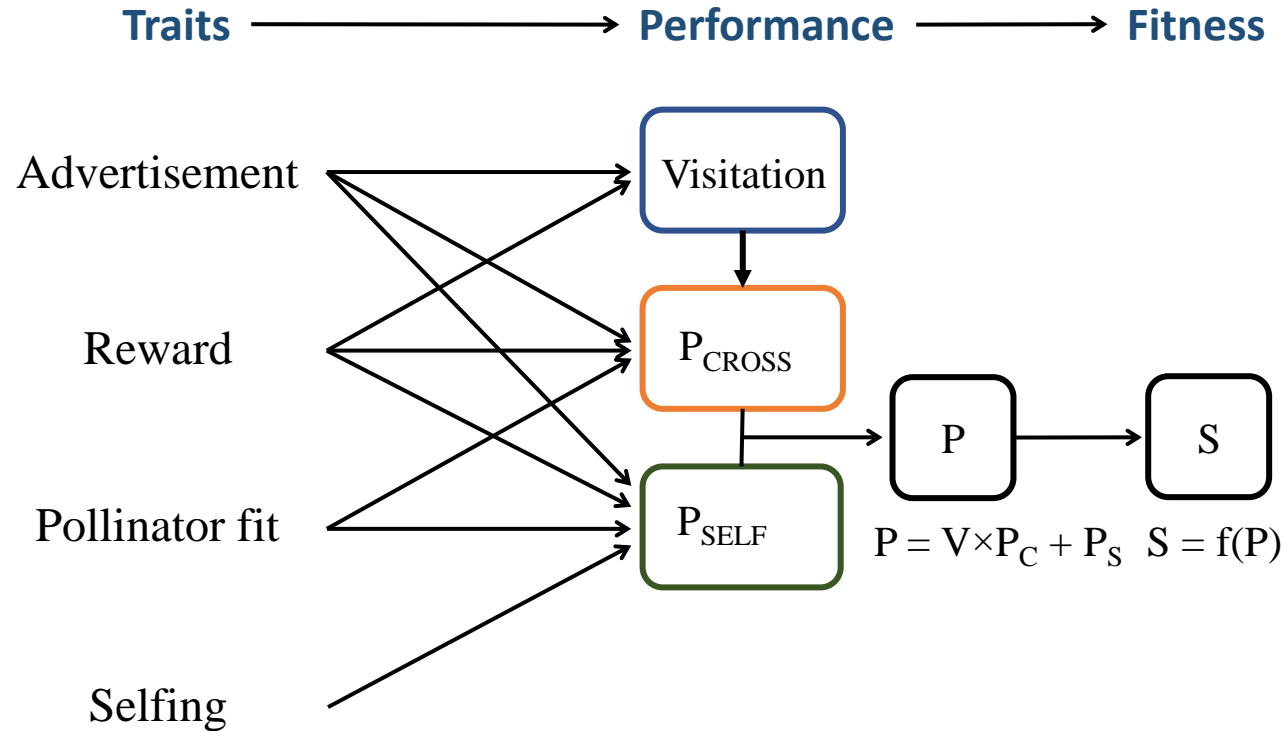
# The Lande-Arnold approach to measuring selection

- Total selection on a trait is the sum of direct selection on the focal trait, and indirect selection on phenotypically correlated traits



$$\text{Net selection on flower size} = 0.4 + 0.5 \times 0.6 = 0.7$$

# Building a fitness function



Visitation ( $V$ ) =  $f(\text{Advertisement, Reward})$

Cross-pollen arrival ( $P_{\text{CROSS}}$ ) =  $f(\text{Advertisement, Reward, Fit})$

Self-pollen arrival ( $P_{\text{SELF}}$ ) =  $f(\text{Advertisement, Reward, Fit, Herkogamy})$

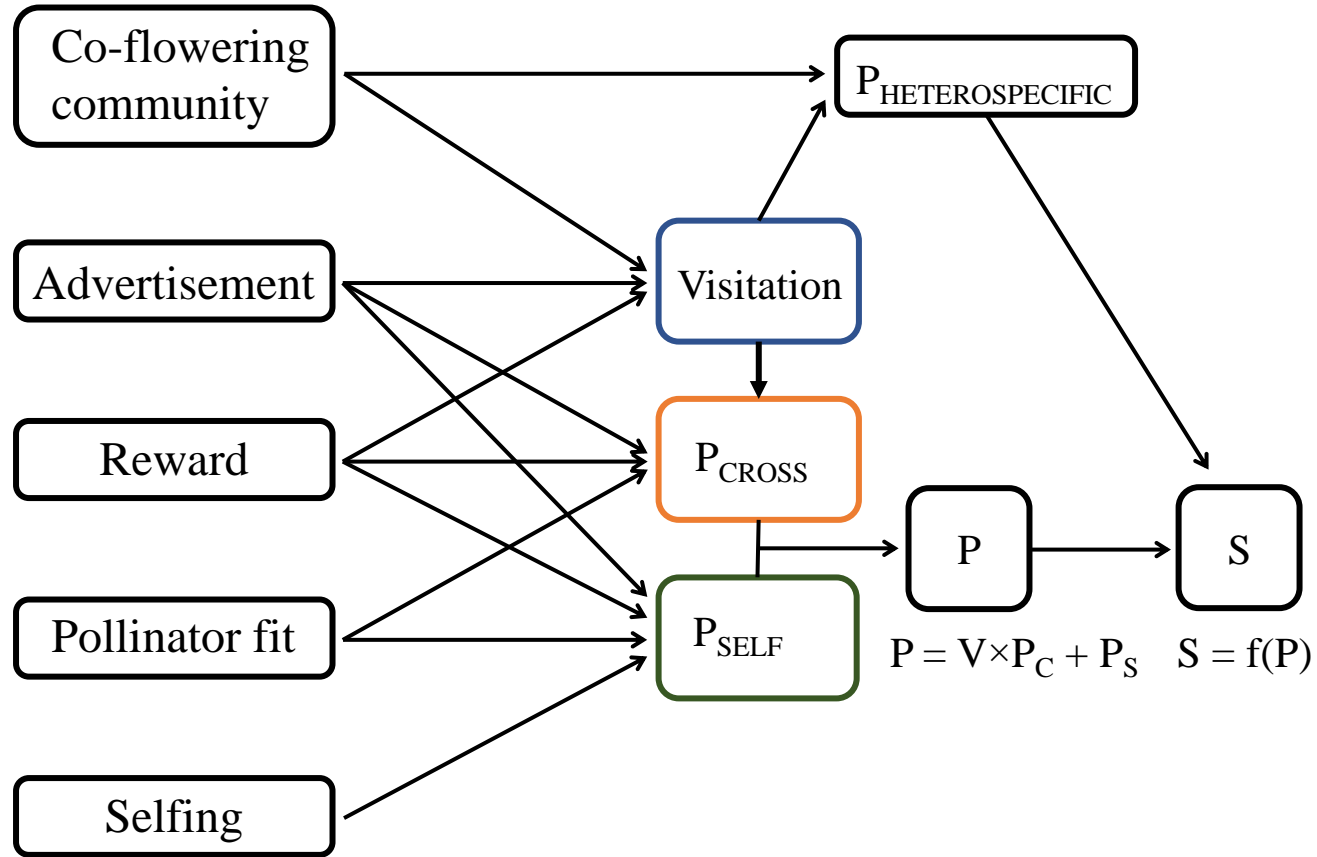




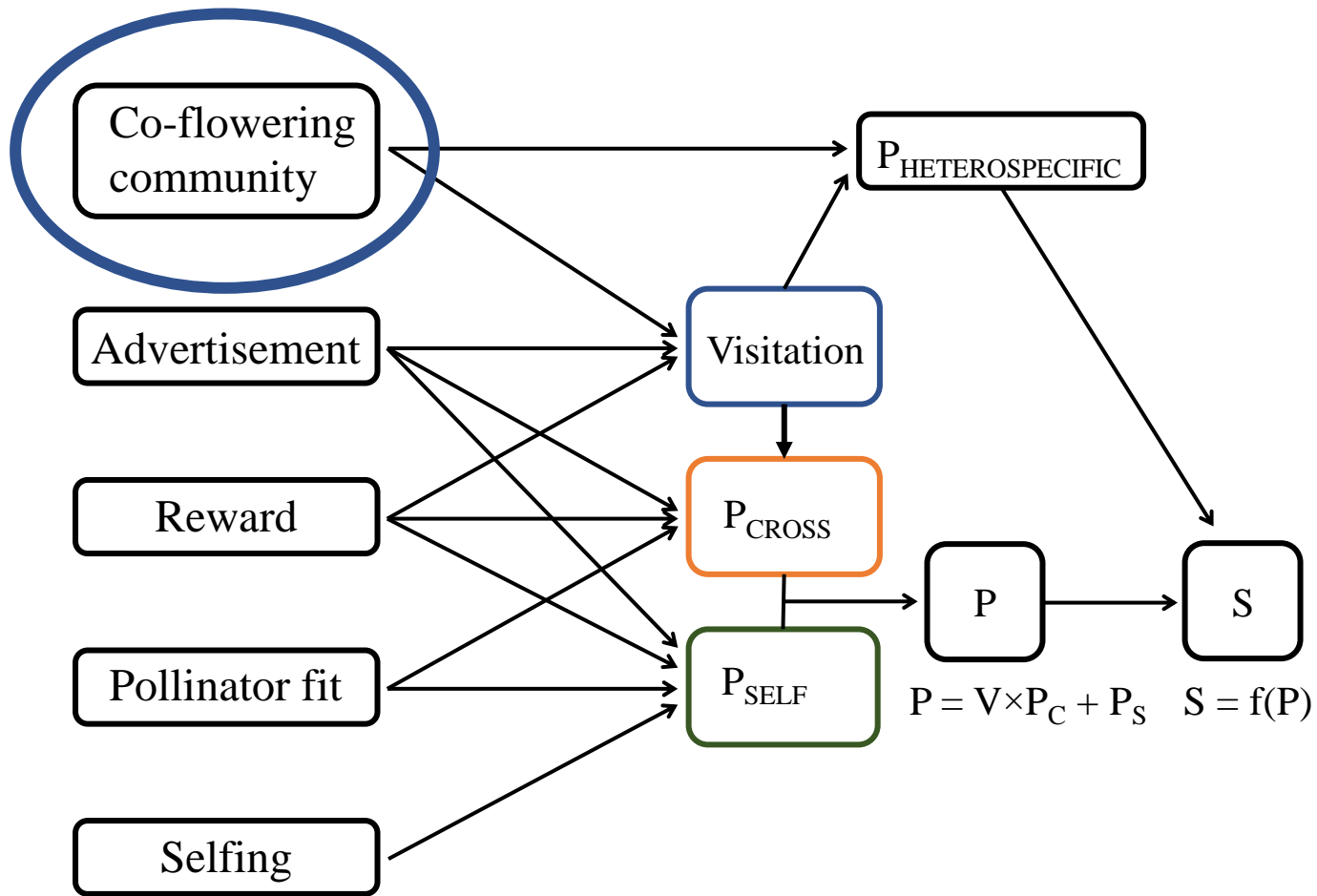
Plants do not interact with their  
pollinators in isolation

How can we extend single-species  
analyses to the community level?



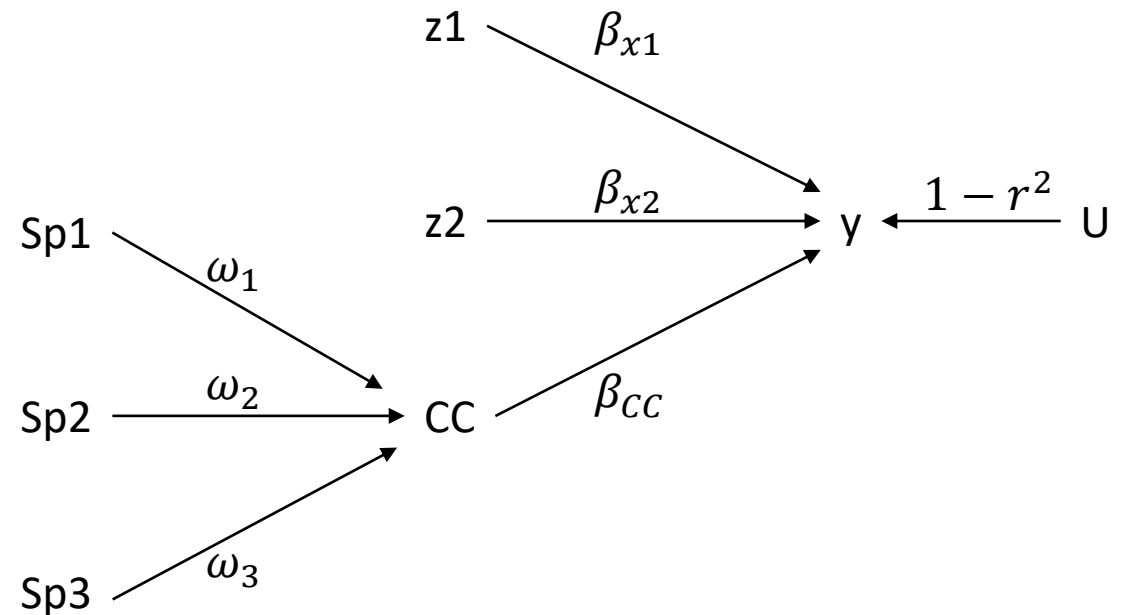






# Treating the coflowering community as a unmeasured (latent) variable

- With many coflowering species, it becomes untractable to model the effect of each separately
- Alternative approach is to consider the community as a composite variable representing all coflowering species







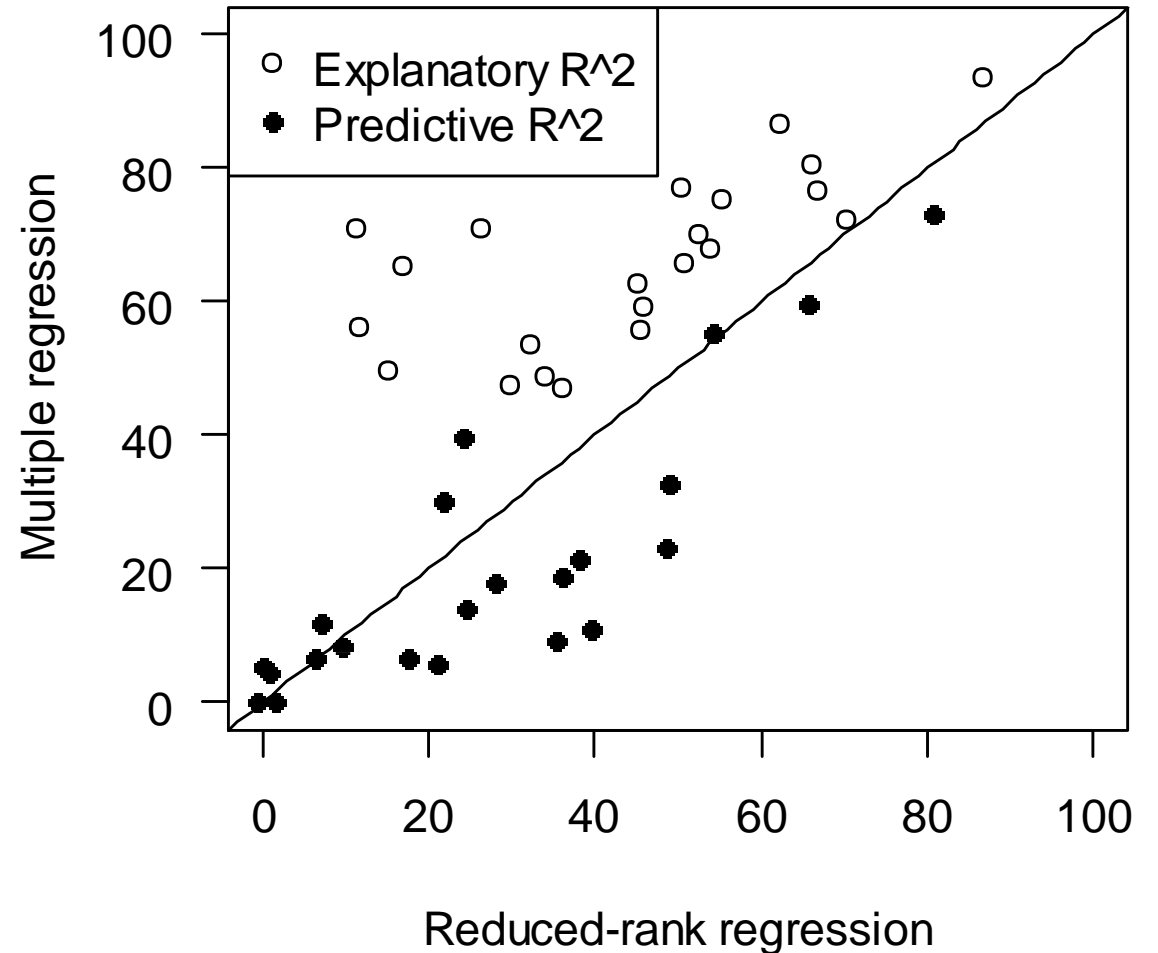
# Theory: selection analysis with reduced-rank regression

- Reduced-rank regression (Anderson 1951; Izenman 1975) achieves dimension reduction of multivariate problems by projecting an original set of covariates onto a reduced set of composite variables that best explains variance in the response variable. In our case, **the composite scent trait under selection**
- The reduced-rank regression covariates (**scent selection axis**) are obtained as linear combinations of the original covariates,  $x_{i(n_c+k)} = \sum_{l=1}^{n_c^{O,RRR}} w_{kl} \tilde{x}_{il}$ , where the weights  $w_{kl}$  determine the contribution of the original covariates (**volatiles**)  $\tilde{x}_{il}$  to the new covariate  $x_{i(n_c+k)}$ .
- The weights  $w_{kl}$  and the regression coefficients  $\beta_{kj}$  are estimated during model fitting (posterior sampling). For the weights, we apply a multiplicative Gamma process shrinkage prior to ensure that the leading axis explains the most variation. Thus, **our approach jointly estimates the structure of the scent selection axis, and selection acting on it.**

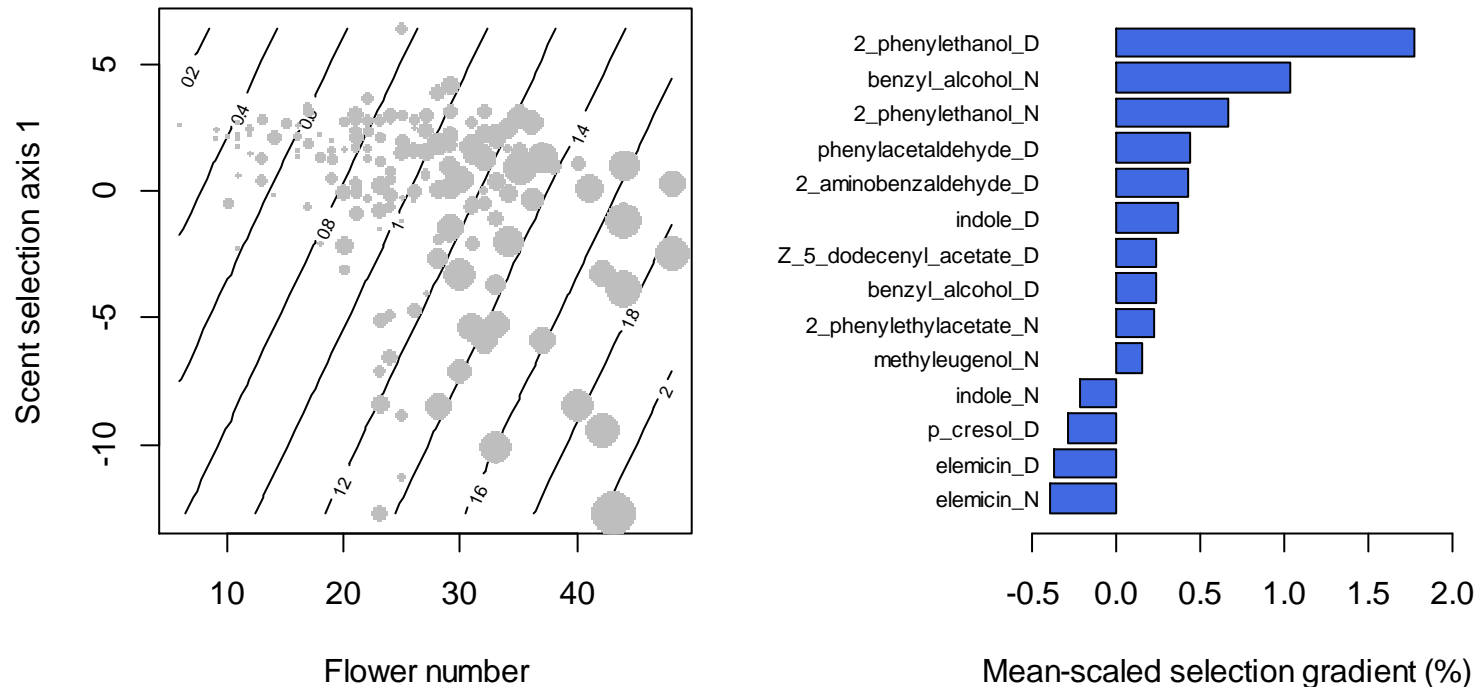


# Is the 'scent selection axis' a reasonable approximation?

- Explanatory power always higher for multiple-regression: fully expected
- Predictive power tends to be higher for reduced-rank regression: less overfitting



# Characterizing the scent selection axis



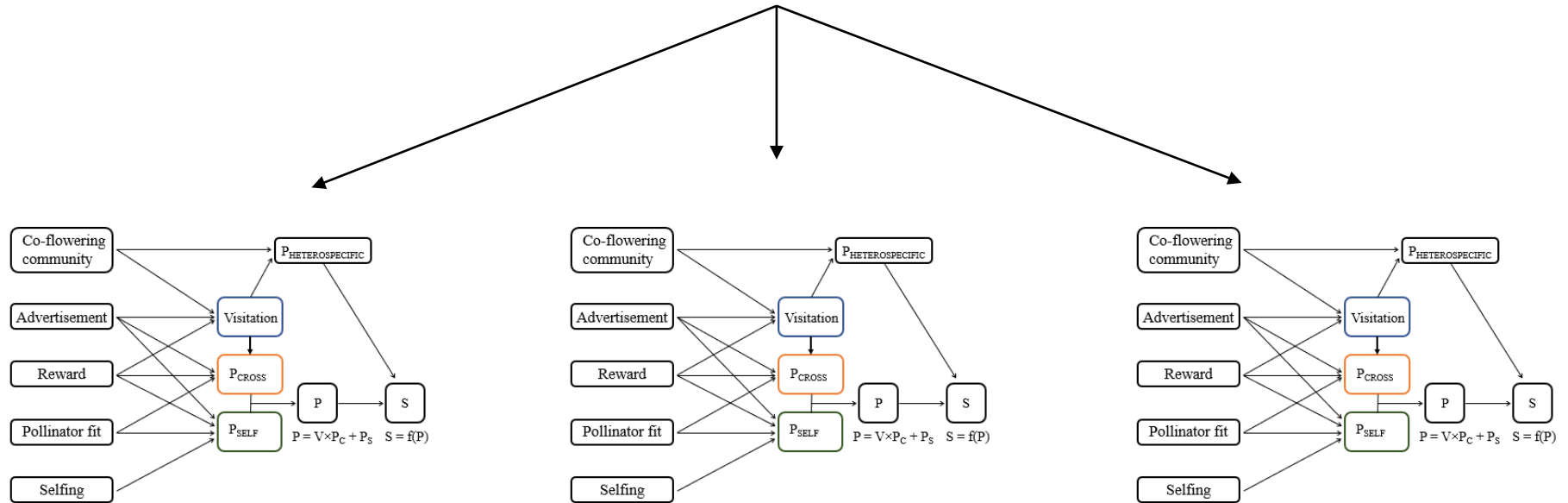


# Theory: co-flowering community analysis with reduced-rank regression

- Reduced-rank regression (Anderson 1951; Izenman 1975) achieves dimension reduction of multivariate problems by projecting an original set of covariates onto a reduced set of composite variables that best explains variance in the response variable. In our case, **the combination of co-flowering species associated with pollination success of a focal plant**
- The co-flowering community variables are obtained as linear combinations of the original covariates,  $x_{i(n_c+k)} = \sum_{l=1}^{n_c^{O,RRR}} w_{kl} \tilde{x}_{il}$ , where the weights  $w_{kl}$  determine the contribution of the original covariates (**species**)  $\tilde{x}_{il}$  to the new covariate  $x_{i(n_c+k)}$ .
- The weights  $w_{kl}$  and the regression coefficients  $\beta_{kj}$  are estimated during model fitting (posterior sampling). For the weights, we apply a multiplicative Gamma process shrinkage prior to ensure that the leading axis explains the most variation. Thus, **our approach jointly estimates the structure of the community variable, and its effect on a focal species**

# Still a single focal species, what about multiple?

“Hierarchical structure linking species together”








# Methodological advances towards community-level analyses

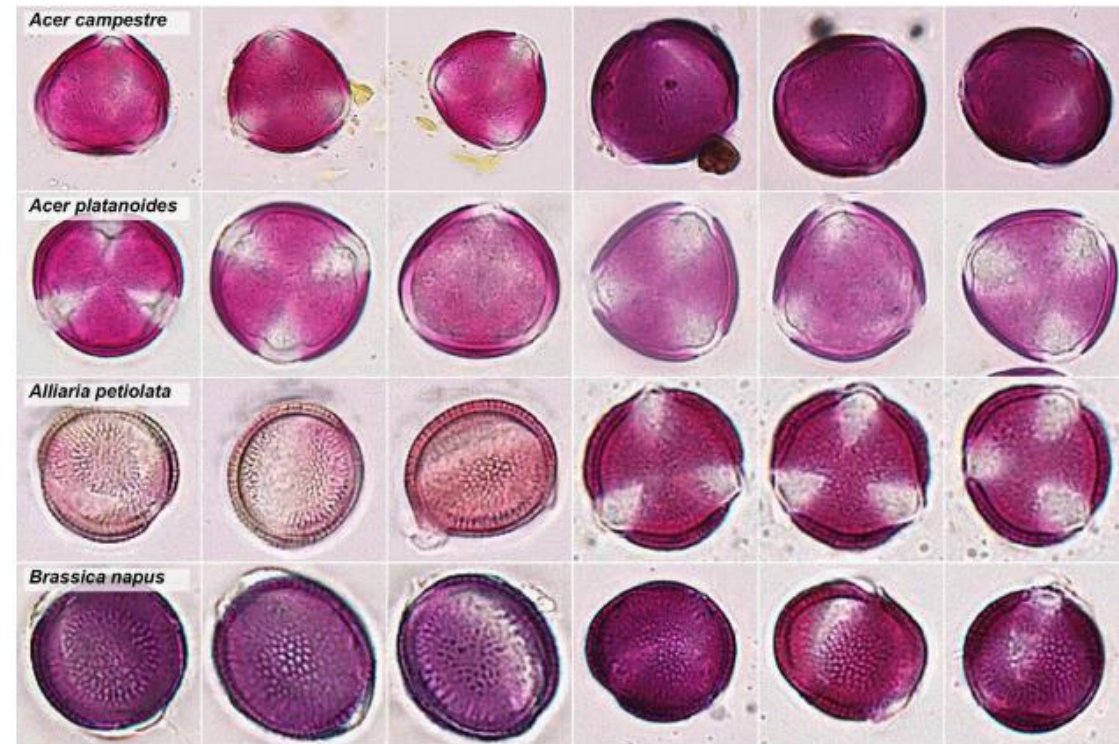
- Analysing plant-pollinator interactions and selection at the community level is complex
- Advances in automated pollen identification and joint modelling paves the way forward

RESEARCH ARTICLE

Methods in Ecology and Evolution 

## Efficient, automated and robust pollen analysis using deep learning

Ola Olsson<sup>1</sup>  | Melanie Karlsson<sup>2</sup>  | Anna S. Persson<sup>2</sup>  | Henrik G. Smith<sup>1,2</sup>  | Vidula Varadarajan<sup>1</sup> | Johanna Yourstone<sup>1</sup>  | Martin Stjernman<sup>1</sup> 



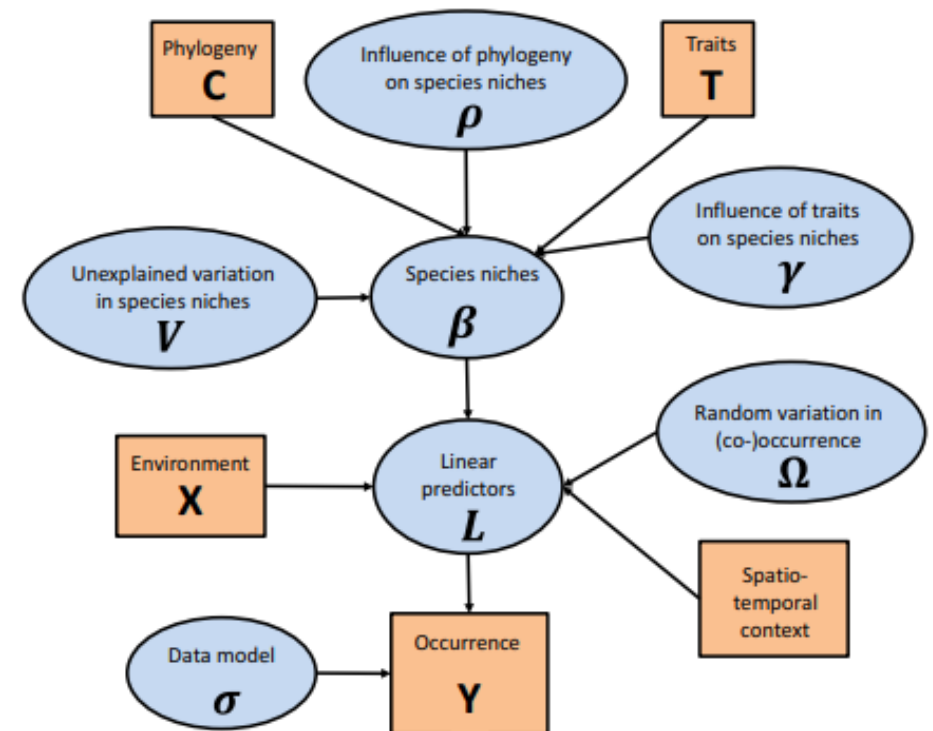
# Methodological advances towards community-level analyses

- Analysing plant-pollinator interactions and selection at the community level is complex
- Advances in automated pollen identification and joint modelling paves the way forward

## APPLICATION

### Joint species distribution modelling with the R-package HMSC

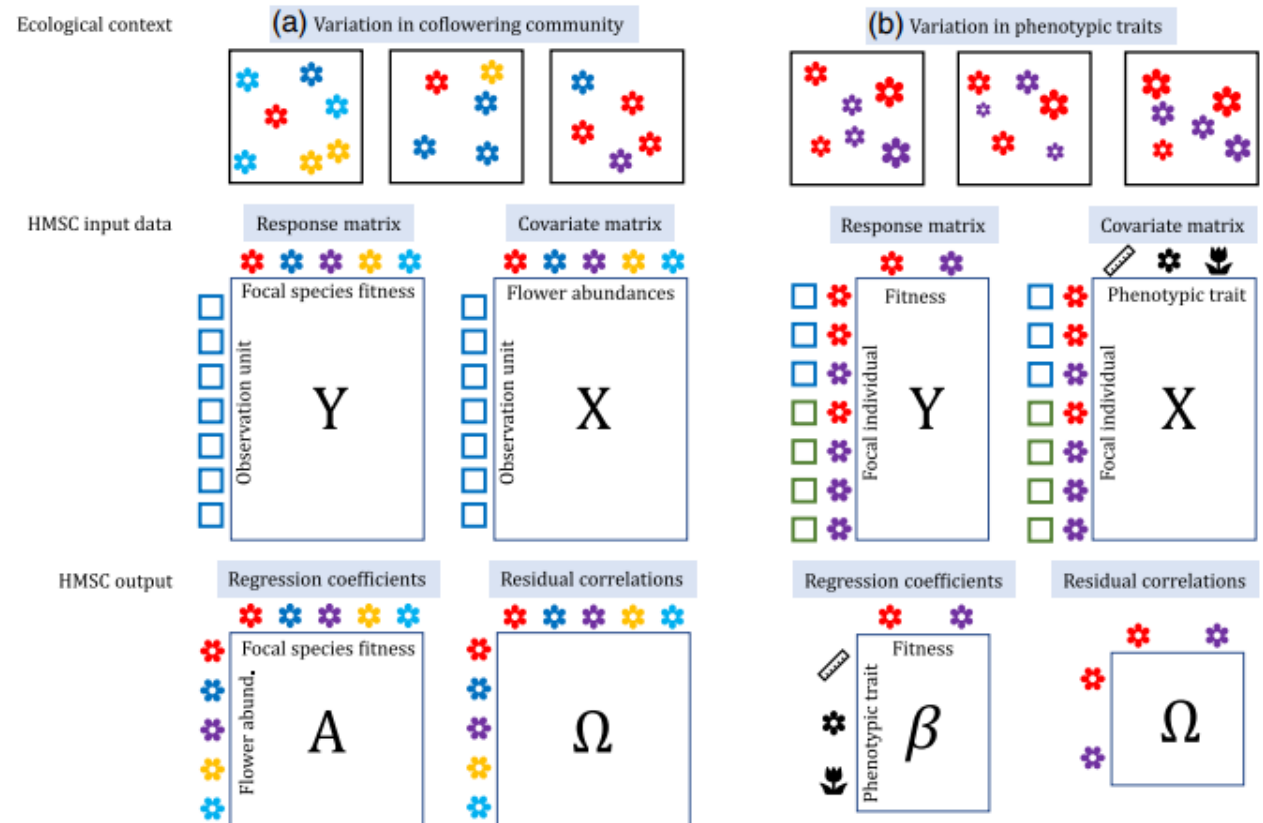
Gleb Tikhonov<sup>1,2</sup> | Øystein H. Opedal<sup>2,3</sup>  | Nerea Abrego<sup>4</sup> | Aleksi Lehikoinen<sup>5</sup> | Melinda M. J. de Jonge<sup>6</sup> | Jari Oksanen<sup>7</sup> | Otso Ovaskainen<sup>2,3</sup> 





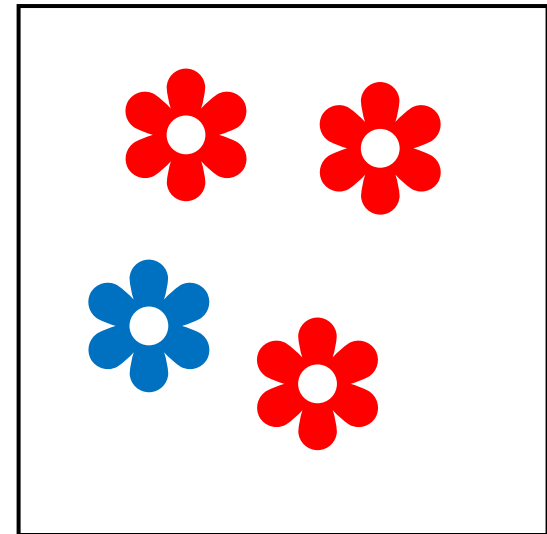
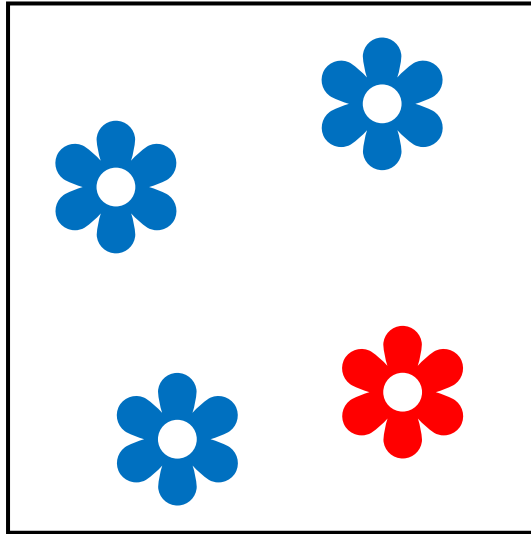
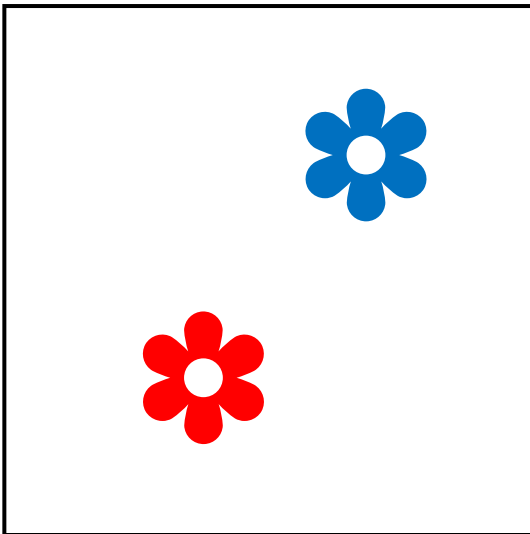
# Hierarchical joint models

- Hierarchical joint models allows analysing multiple response variables (e.g. pollinator species) while inferring joint responses
- Also allows inferring residual associations after accounting for relevant covariates (e.g. phenotype)

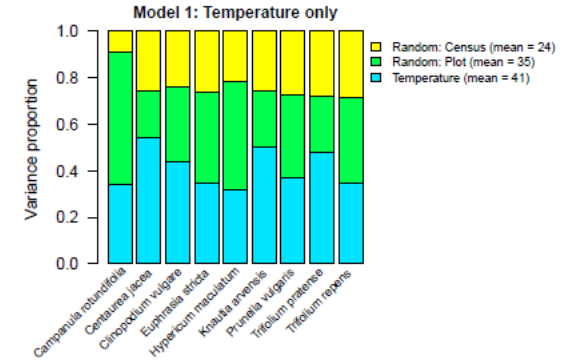
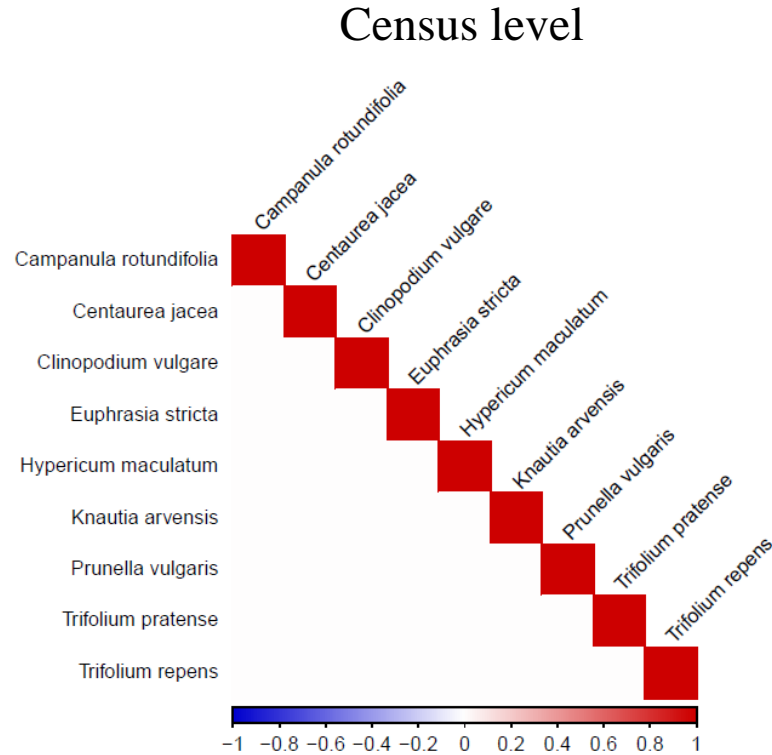
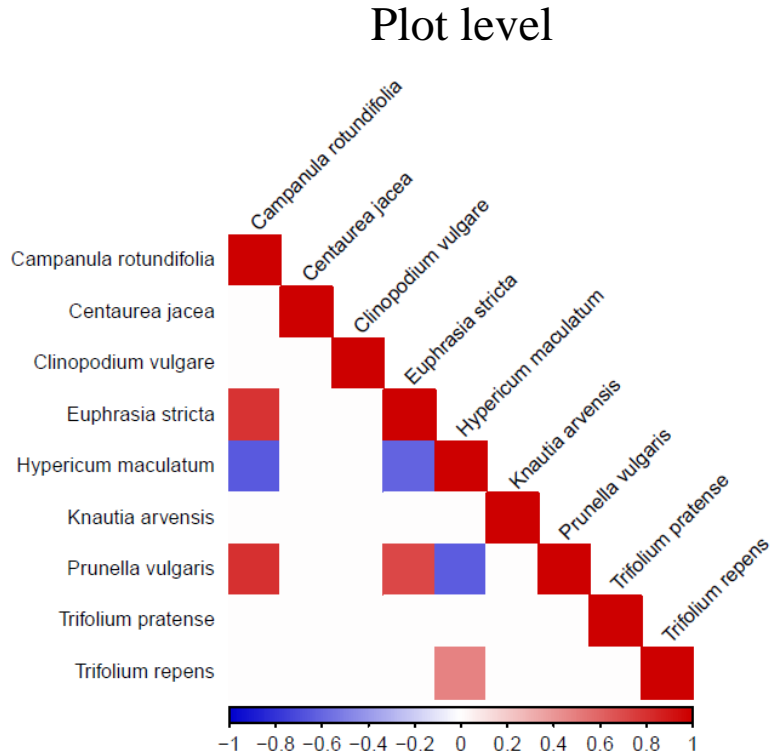


# The Rudsviki data

- 20 plots
- 9 bumblebee-pollinated plant species
- 200 censuses, each 10 min
- Number of visits to each species

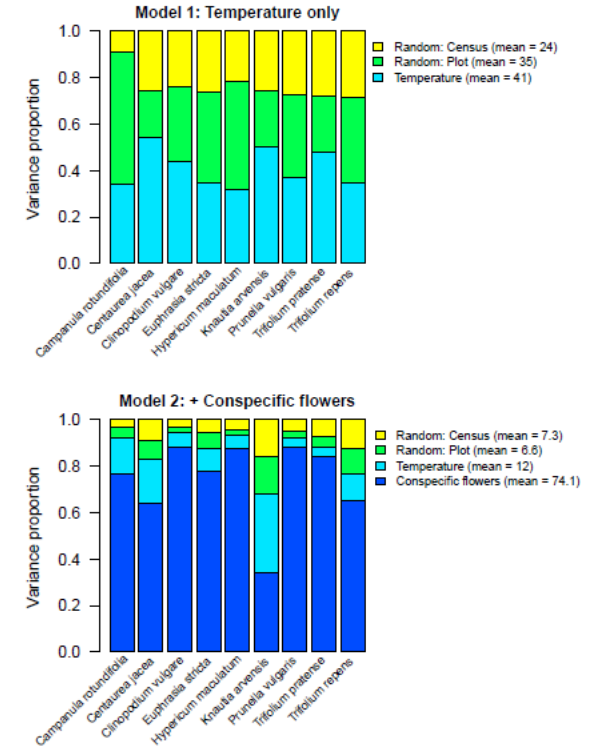
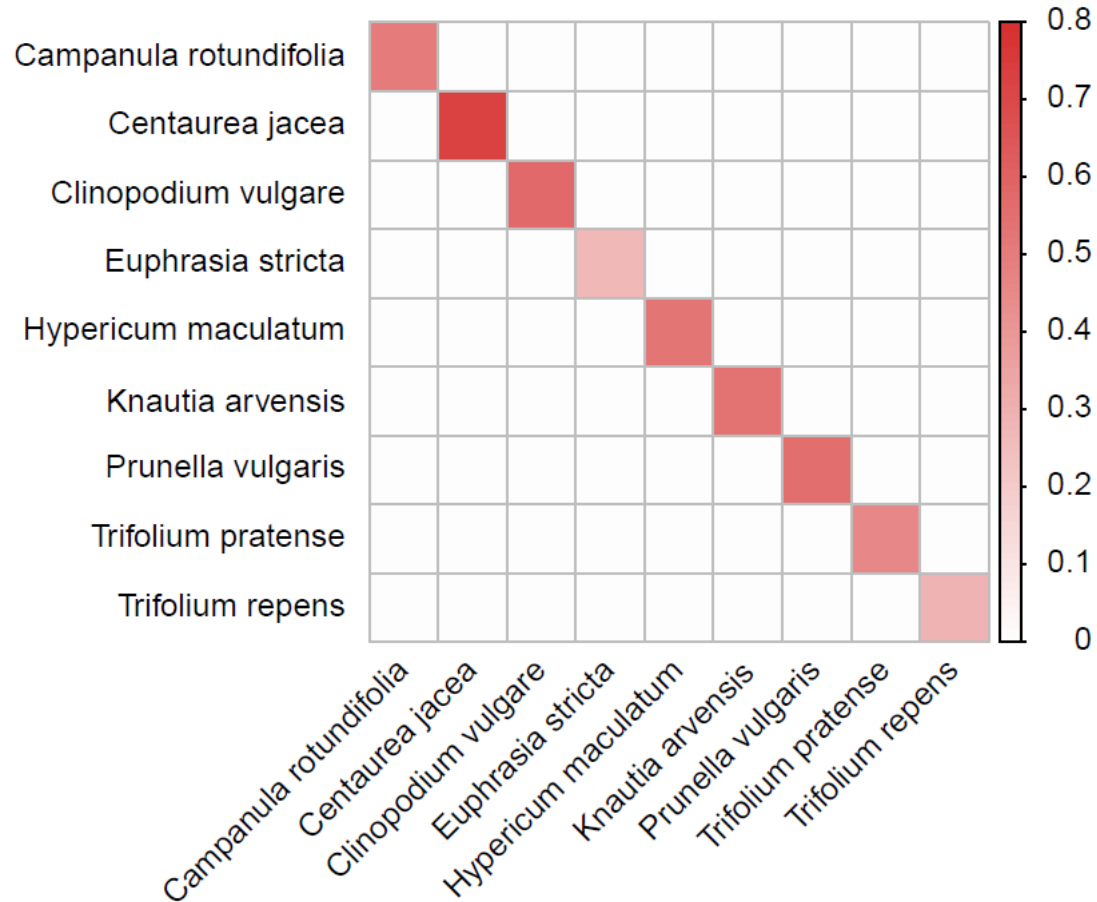


# Model 1: Latent variables only

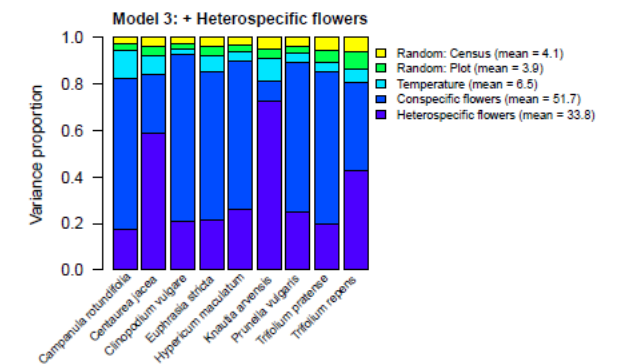
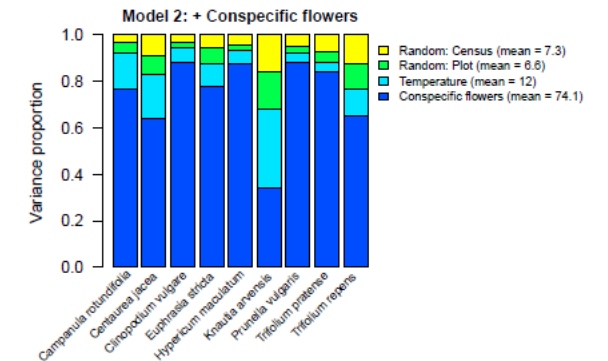
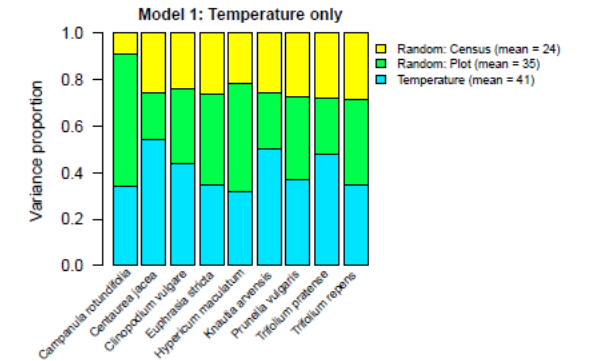
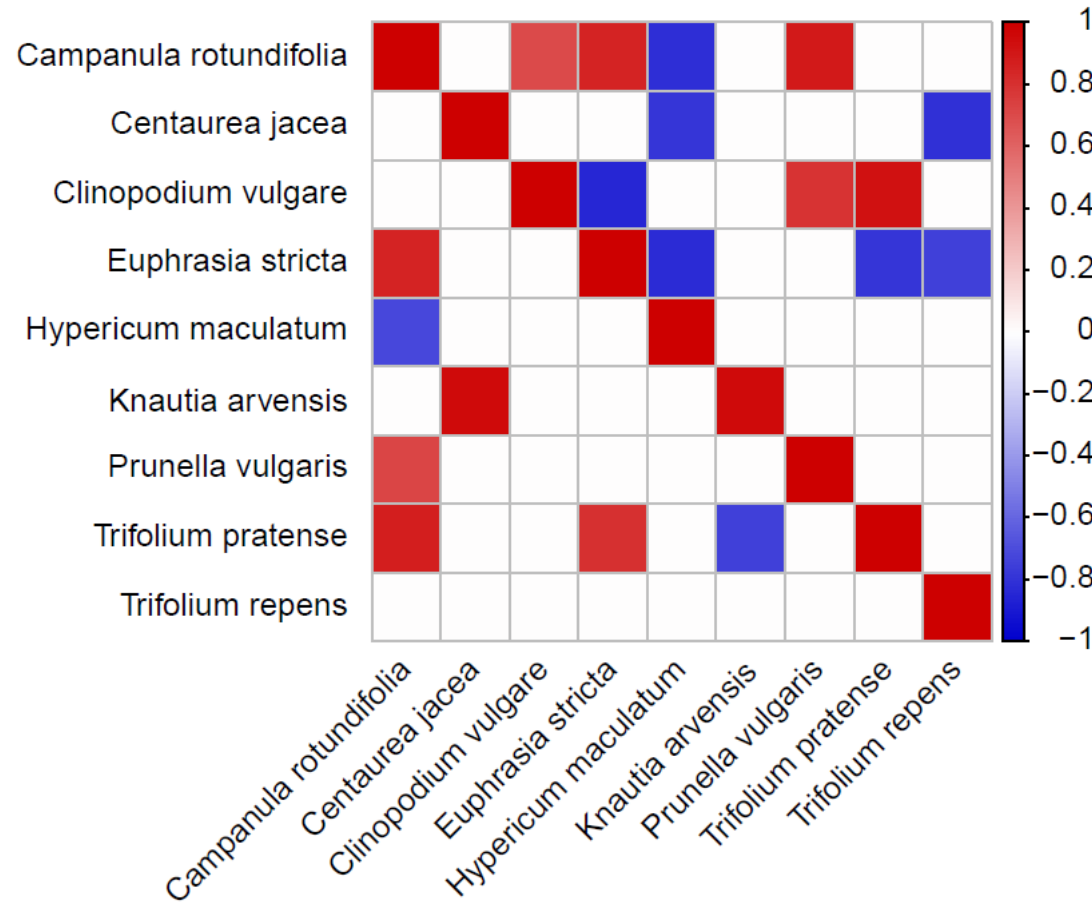




# Model 2: Conspecific floral abundances



# Model 3: All floral abundances





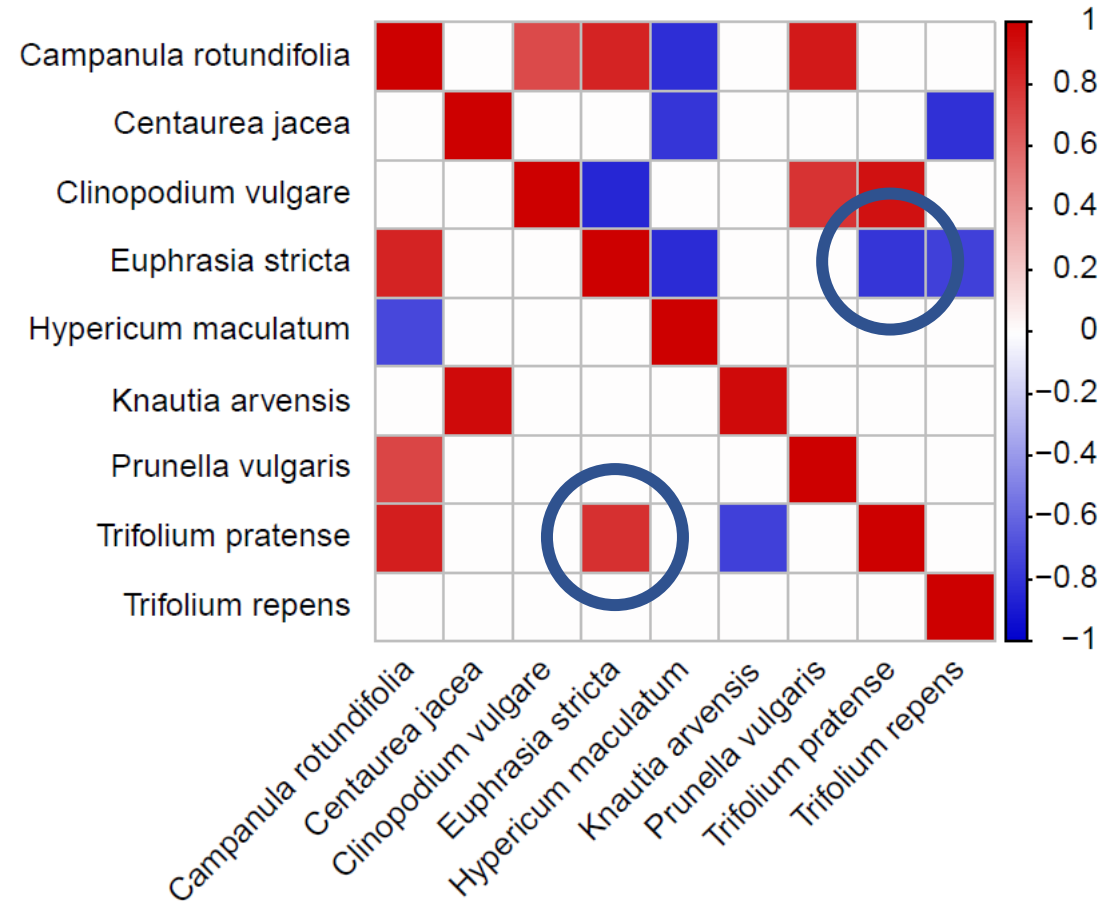




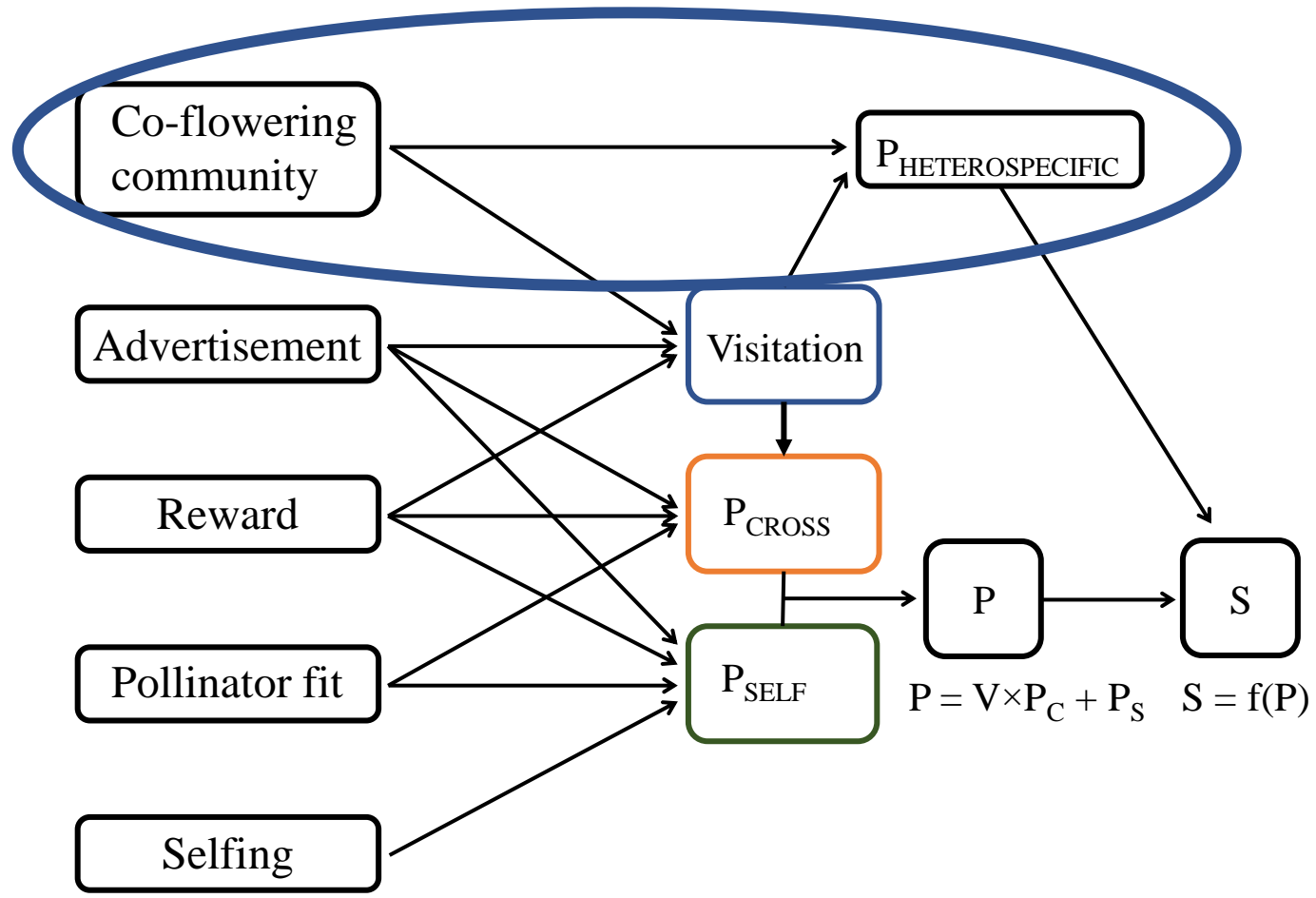


# Model 3: All floral abundances

- Directionality:
- Two-way positive
- One-way positive
- One-way negative
- Two-way positive-negative





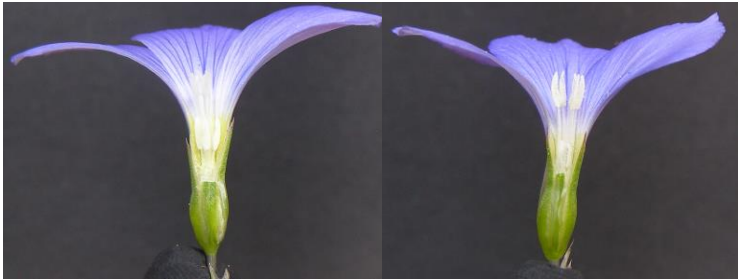


# Coflowering *Linum* species in southern Spain

*Linum suffruticosum*



*Linum suffruticosum*



*Linum viscosum*

