



# How much are wild vertebrate populations evolving right now?

Timothée Bonnet & Loeske Kruuk  
Australian National University

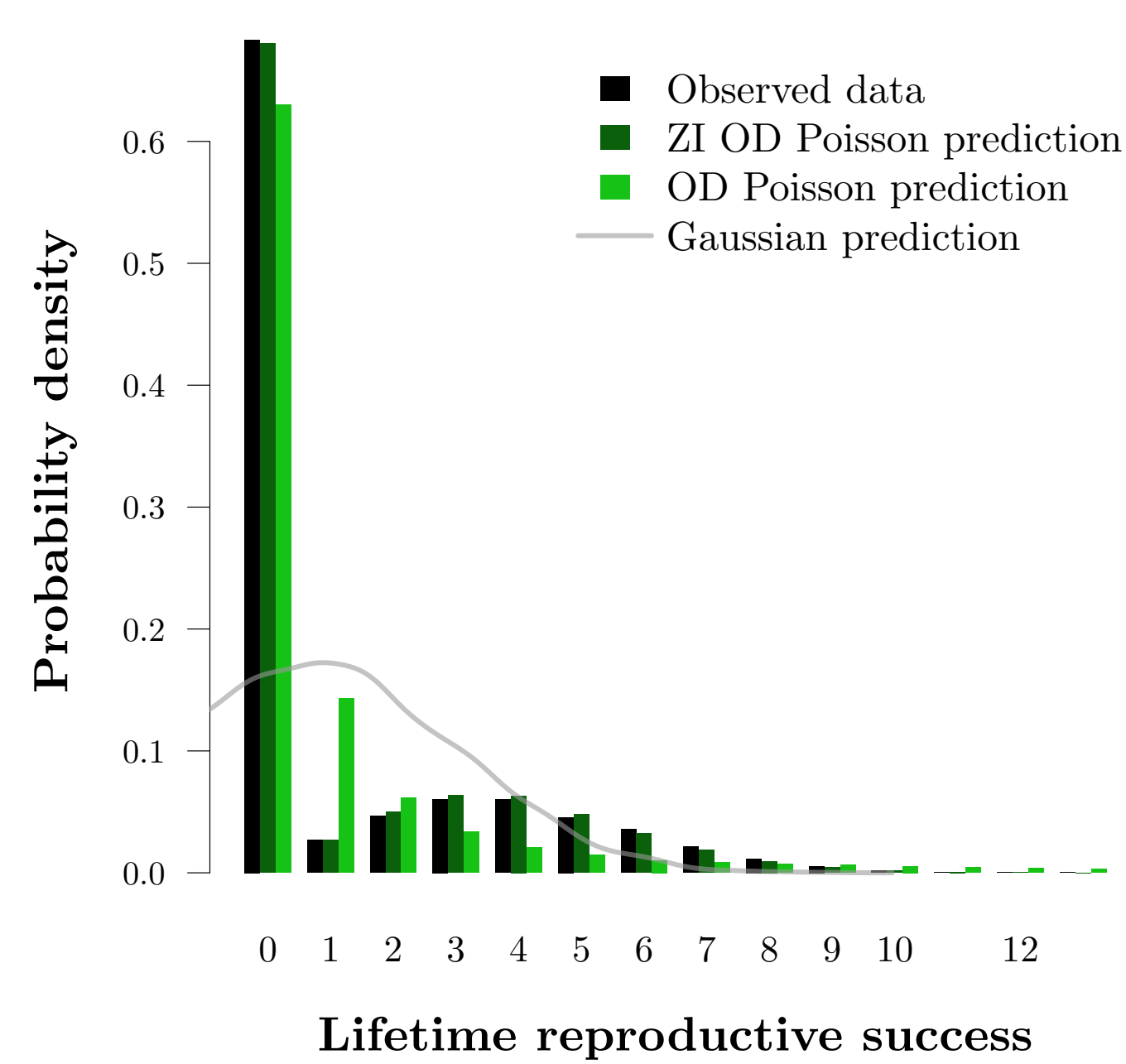


## THE BIG PROBLEM: We do not know how much wild organisms are currently evolving!

Fisher's fundamental theorem of natural selection states that **additive genetic variation in fitness measures evolution across all traits and all the genome**. That is just what we need\*! Yet, there are few estimates in free-ranging populations, and most may be unreliable. Indeed, it is difficult to measure fitness, difficult to estimate genetic variance, statistical models tend not to fit the data, and it is unclear how to interpret estimates from generalized linear models. We assemble data from the monitoring of a dozen pedigreed populations,

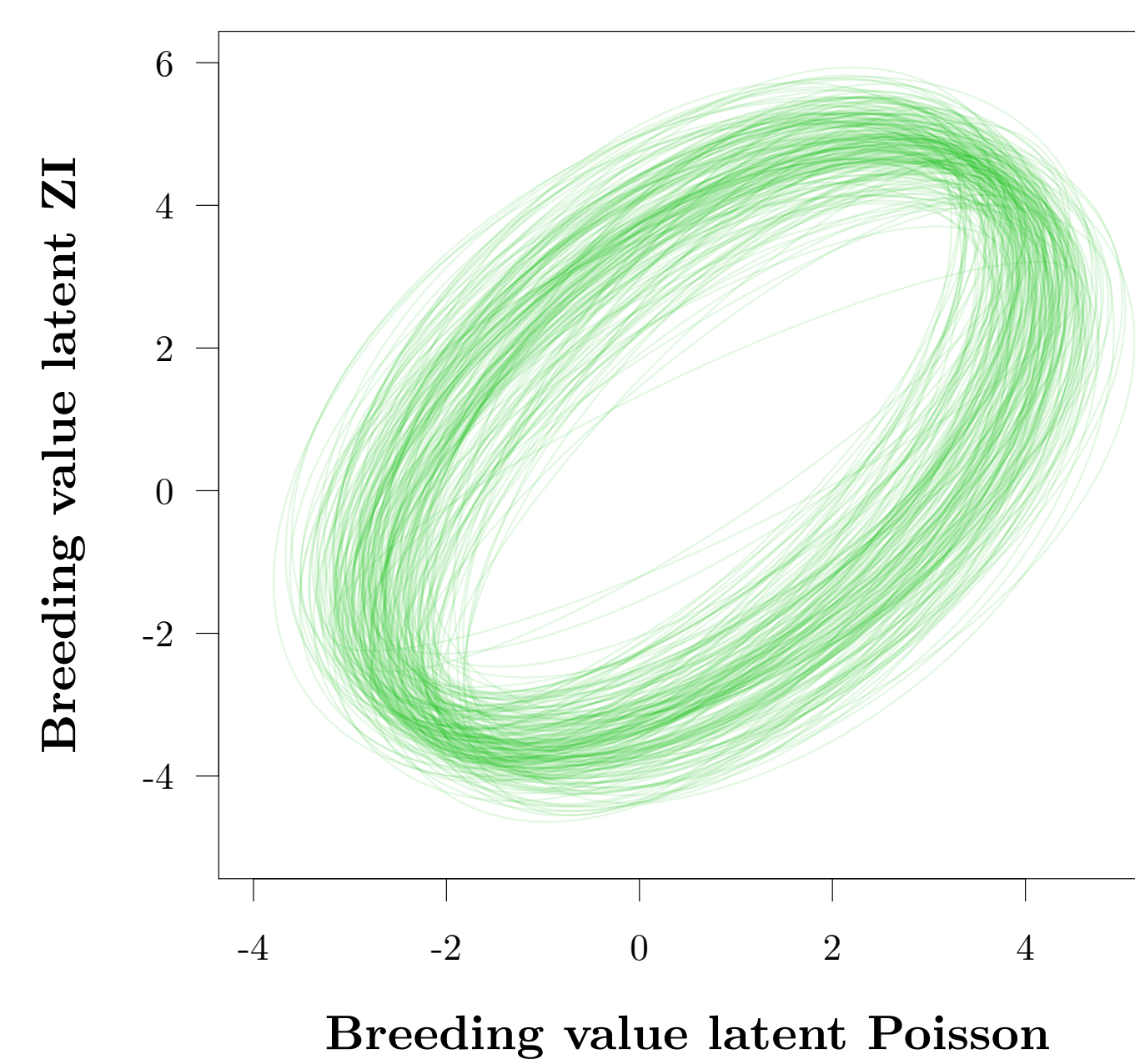
## THEORY: How to estimate additive genetic variance in relative fitness ( $V_A(\omega)$ ) ?

### HOW TO MODEL FITNESS?



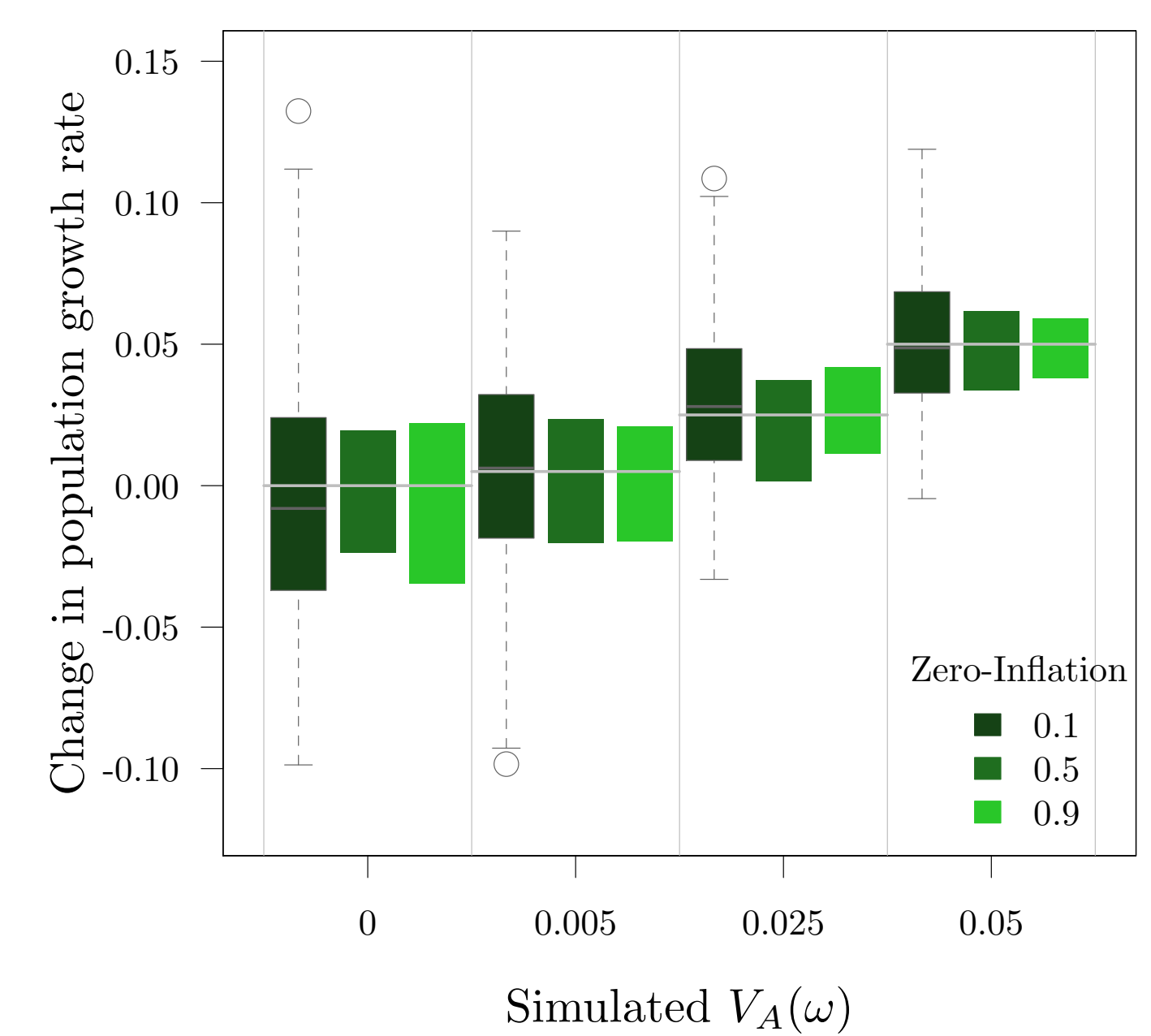
Zero-Inflated Over-Dispersed Poisson models tend to fit well lifetime fitness data. Quantitative genetic estimates may be more precise than with Gaussian or Poisson models.

### HOW TO ESTIMATE GENETIC VARIATION?



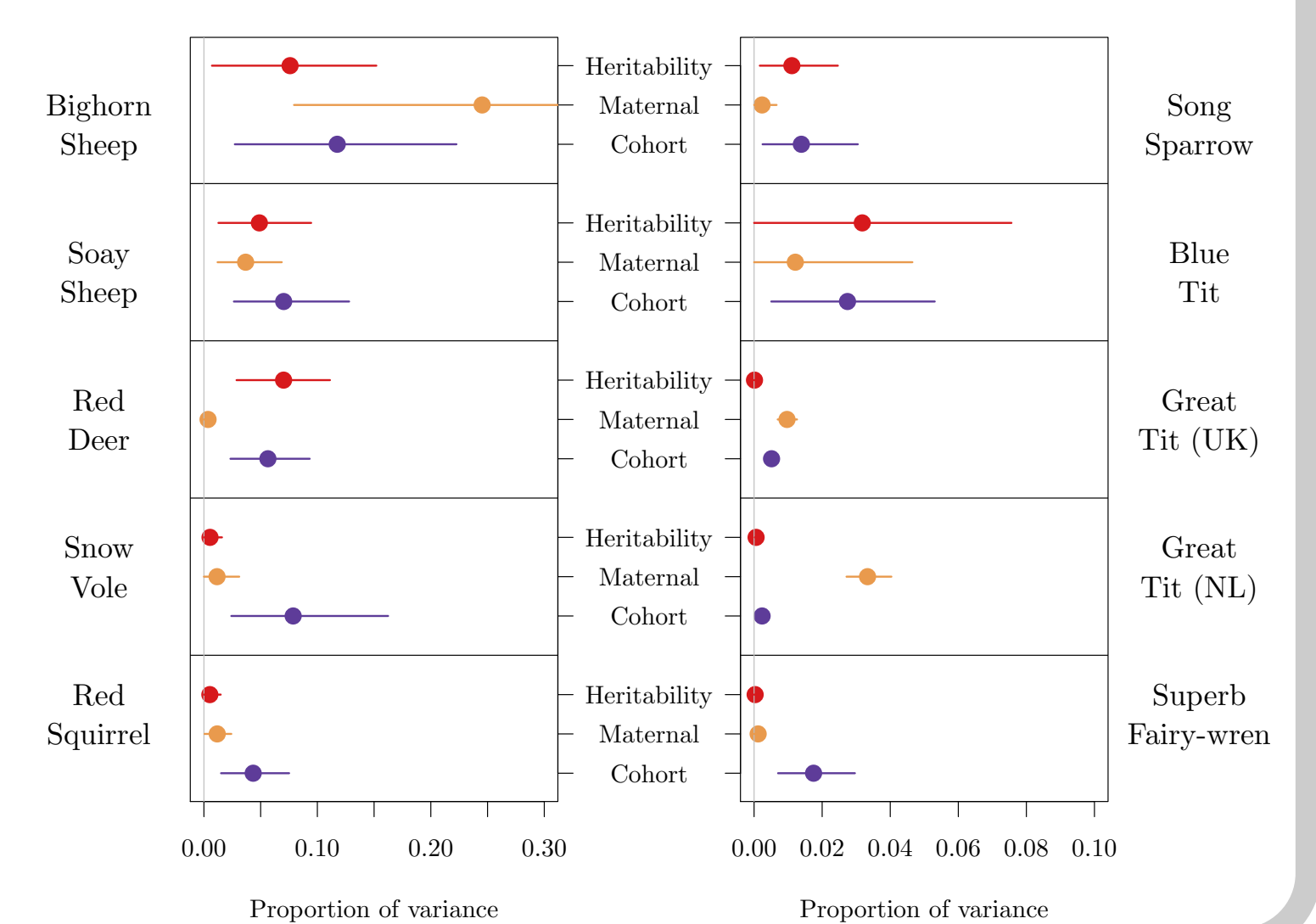
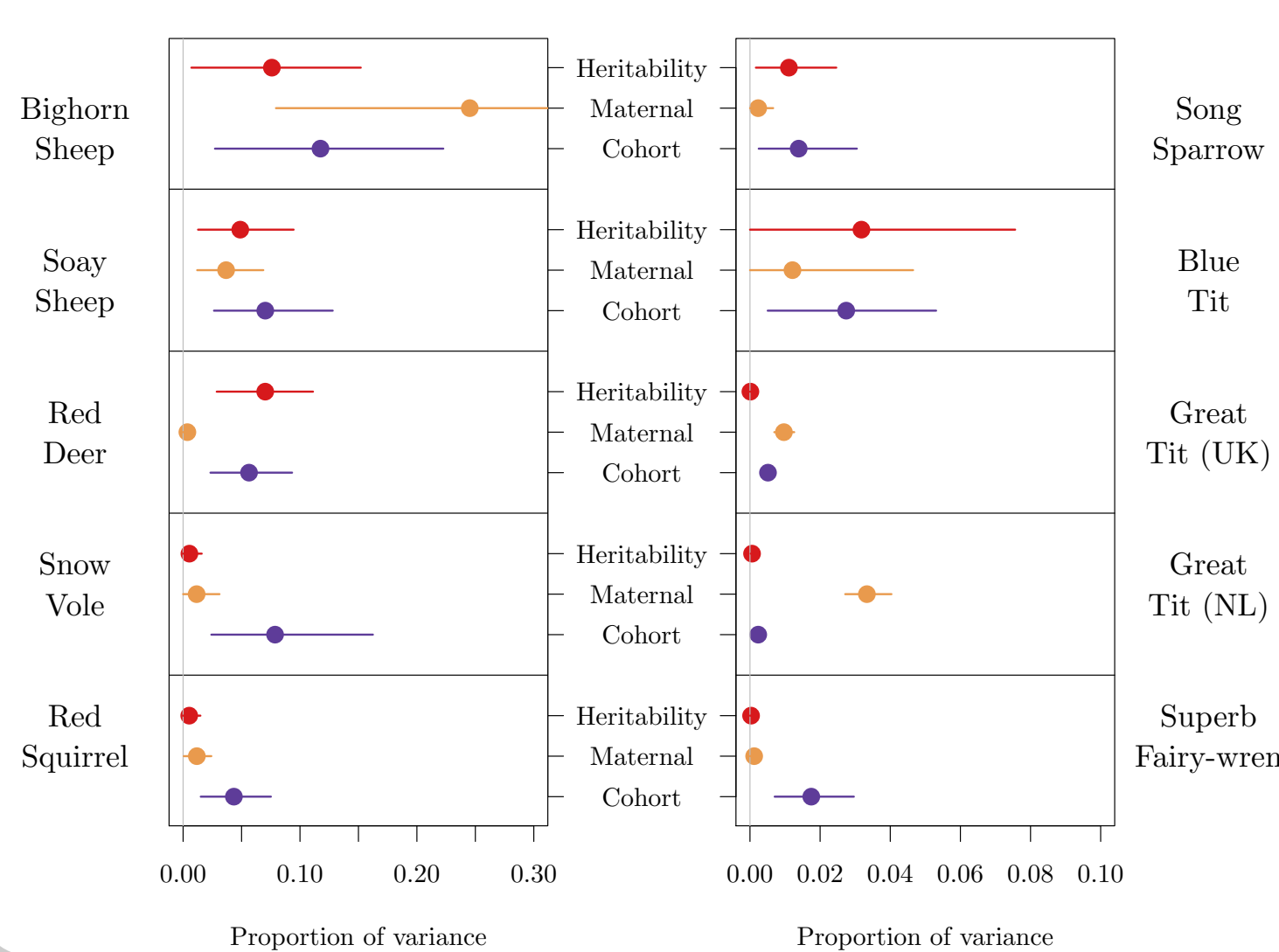
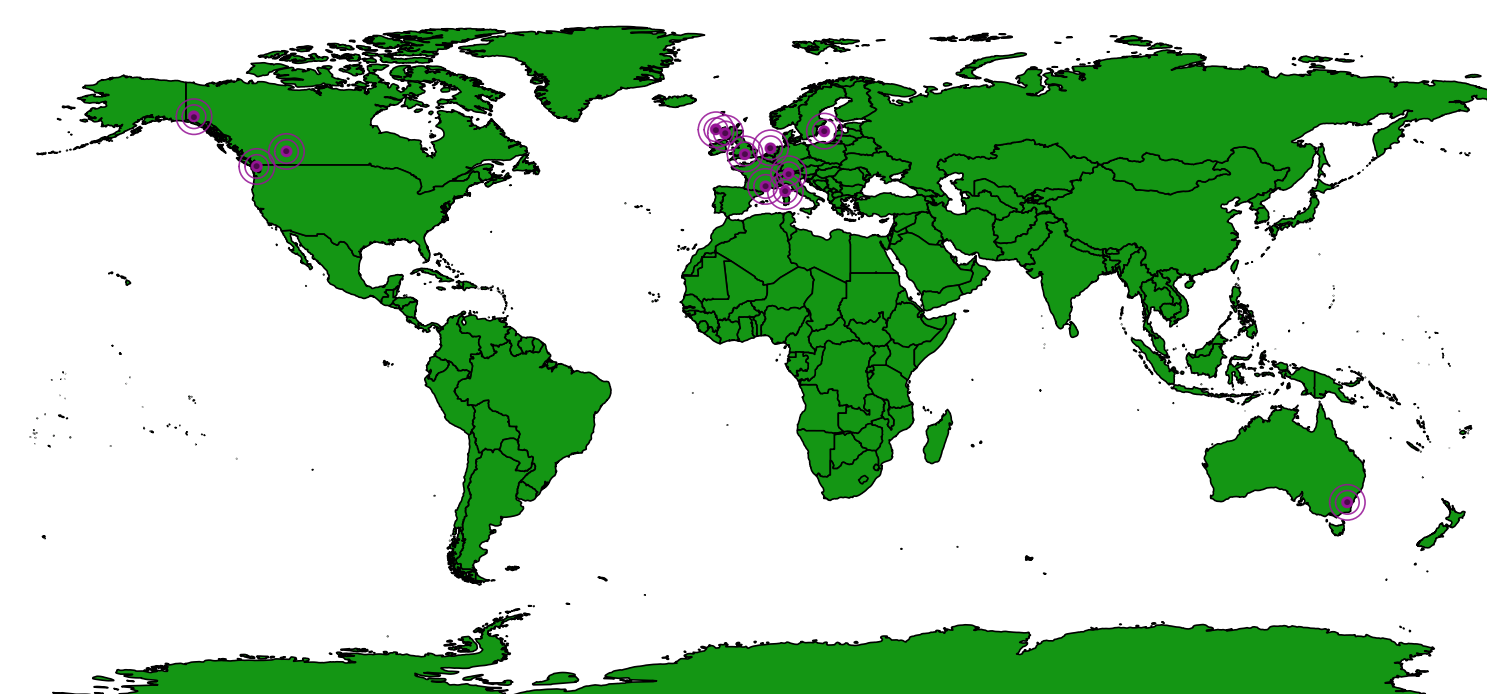
Quantitative genetic ANIMAL MODELS use relatedness matrix to estimate G-matrix for the zero-inflation and the over-dispersed Poisson processes on two latent scales (log and logit).

### HOW TO CONVERT ESTIMATES TO $V_A(\omega)$



Monte-Carlo integration of latent breeding values to the scale of data. Back-transformation works: with simulations  $V_A(\omega)$  equals the increase in population growth rate.

## EMPERICAL RESULTS:



### Website



timotheenivalis.github.io

### Co-AUTHORS:

Michael Morrissey, Josephine Pemberton, Tim Clutton-Brock, Marco Festa-Bianchet, Andrew McAdam, Stan Boutin, Anne Charmantier, Céline Teplisky, Christophe de Franceschi, Erik Postma, Glauco Camenisch, Marcel Visser, Ben Sheldon, Simon Evans, Lars Gustafsson, Jane Reid, Matthew Wolack & Andrew Cockburn

### R and $\LaTeX$ code



\* Fisher's theorem relies on stringent assumptions, or alternatively on a specific meaning of evolution. In the absence of competition and gene-by-environment interactions,  $V_A(\omega)$  is the increase in expected population growth rate. This clean link between evolution and demography probably doesn't apply (for long) in nature.

github.com/timotheenivalis/VAWisWOW