

How much are wild vertebrate populations evolving right now?

Timothée Bonnet, Michael Morrissey & Loeske Kruuk
Australian National University & University of St Andrews

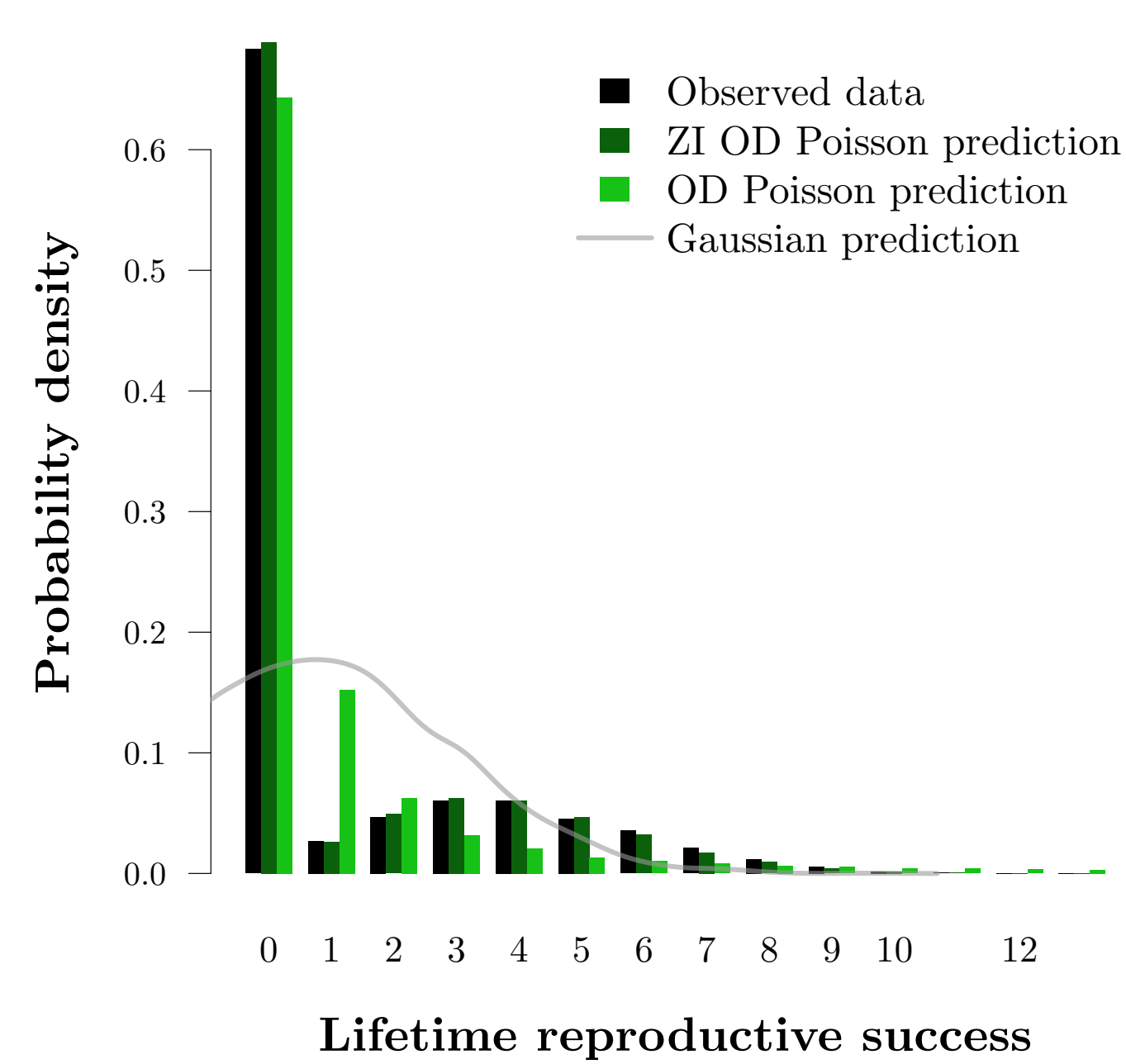


THE BIG PROBLEM: We do not know how much wild organisms are currently evolving!

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 use a dozen long-term monitored populations with high quality fitness (measured as lifetime breeding success) and relatedness measurements to tackle these issues. How to make the most of these data? Are birds and mammals currently evolving?

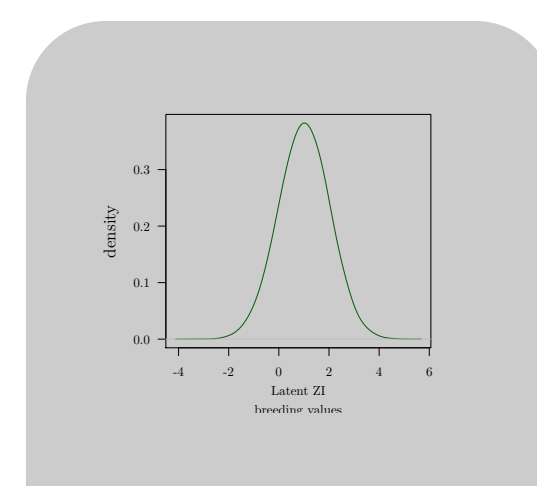
THEORY: How to estimate additive genetic variance in relative fitness ($V_A(\omega)$) ?

MODEL DISTRIBUTIONS FOR FITNESS



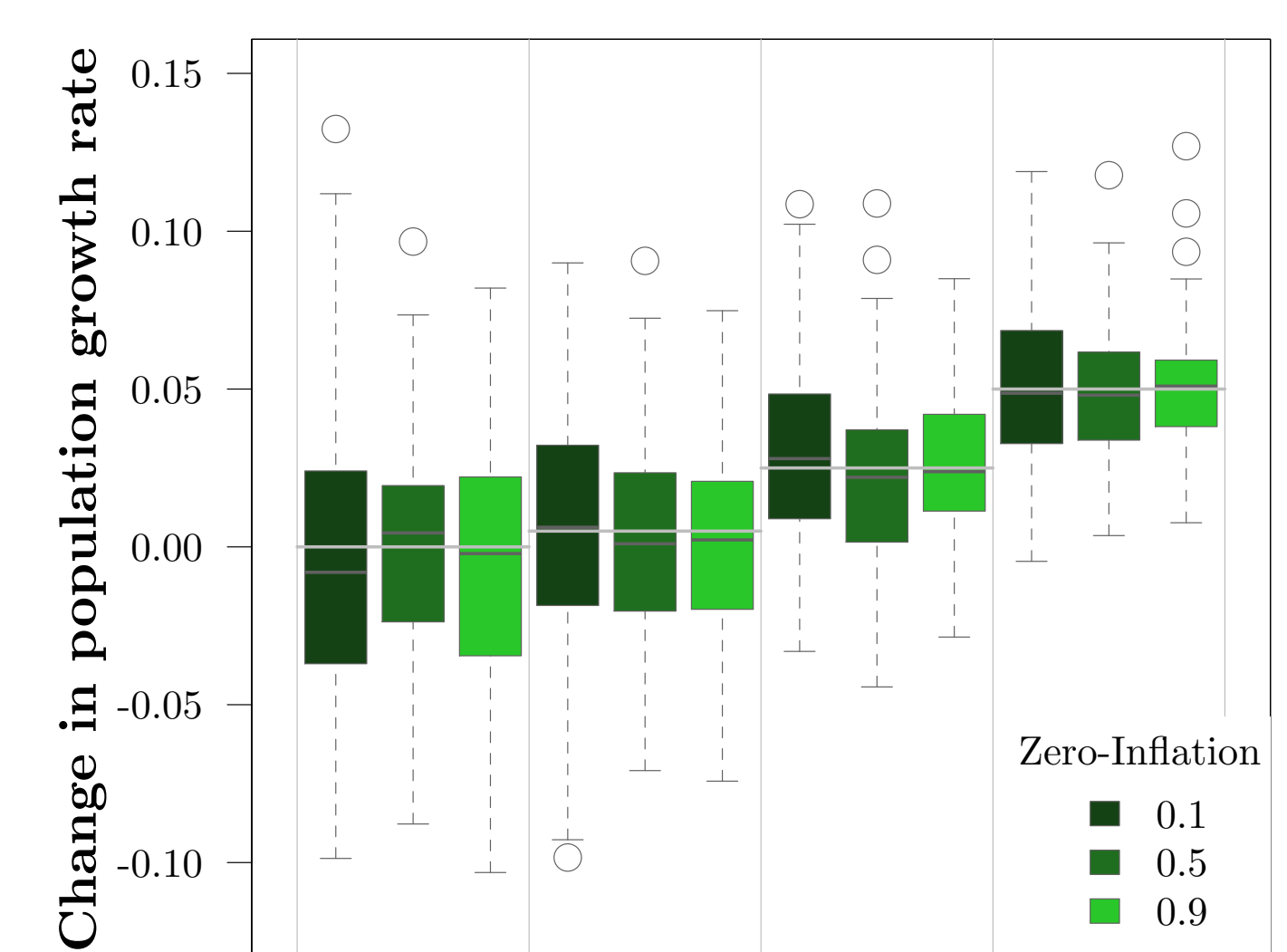
Zero-Inflated Over-Dispersed Poisson models tend to fit well lifetime fitness data. Quantitative genetic estimates may be more precise than with Gaussian or Poisson models.

ESTIMATE LATENT 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).

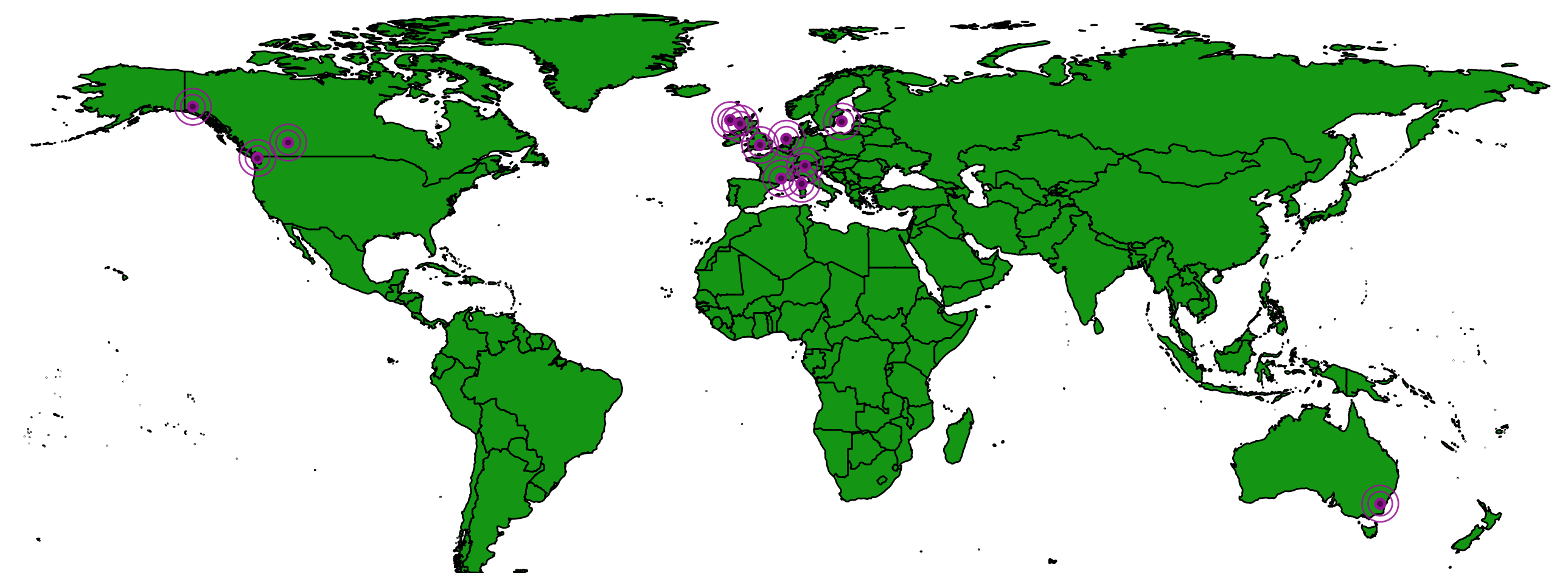
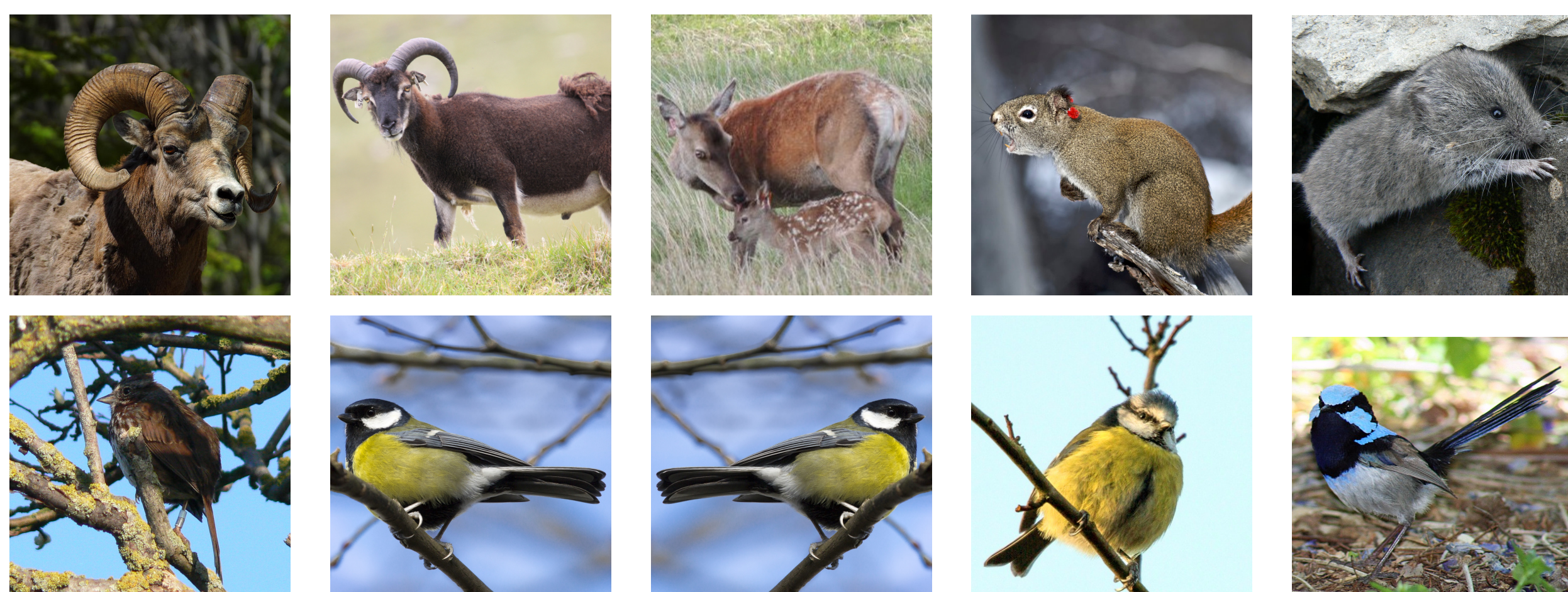
CONVERT LATENT PARAMETERS TO $V_A(\omega)$



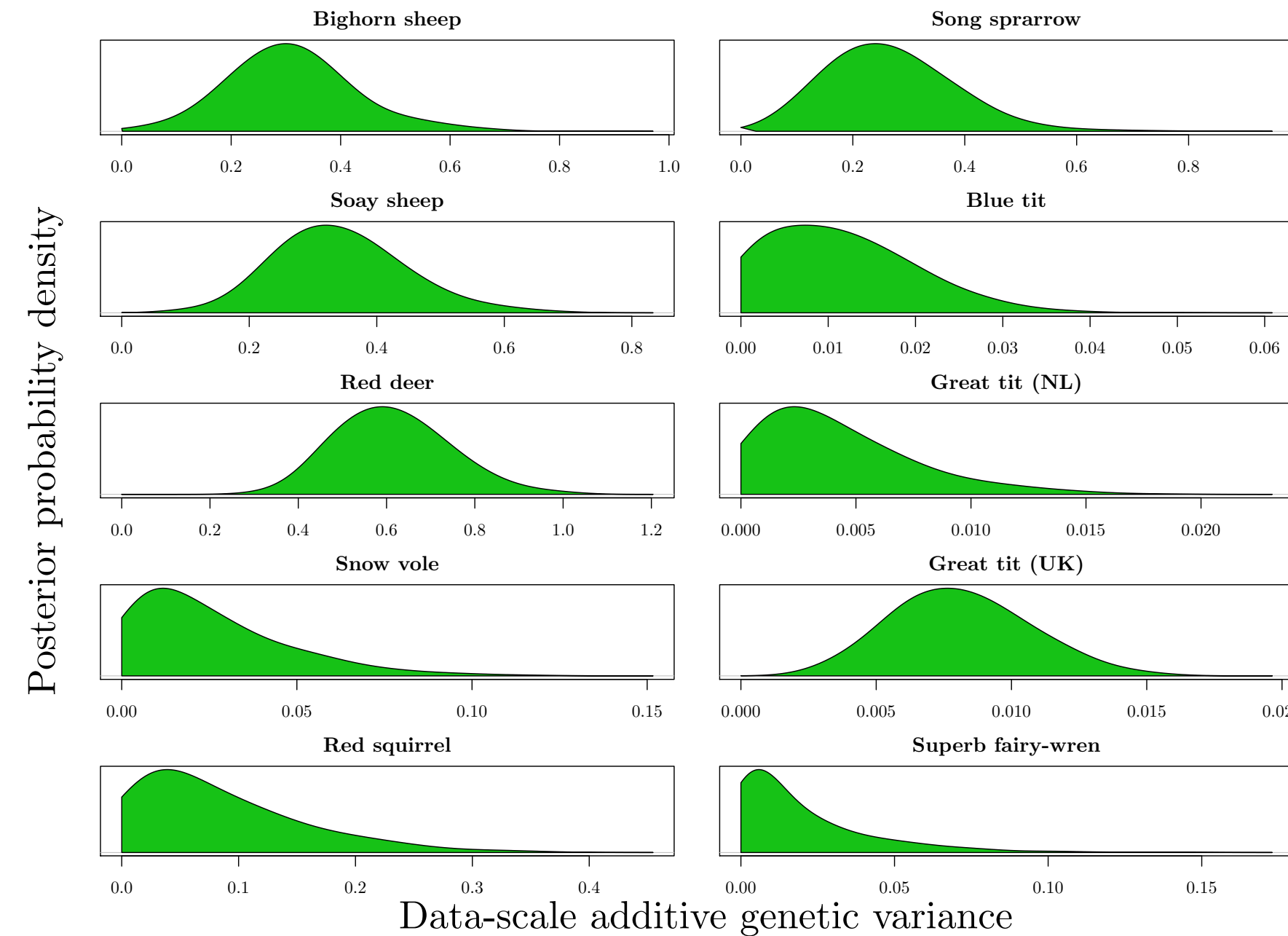
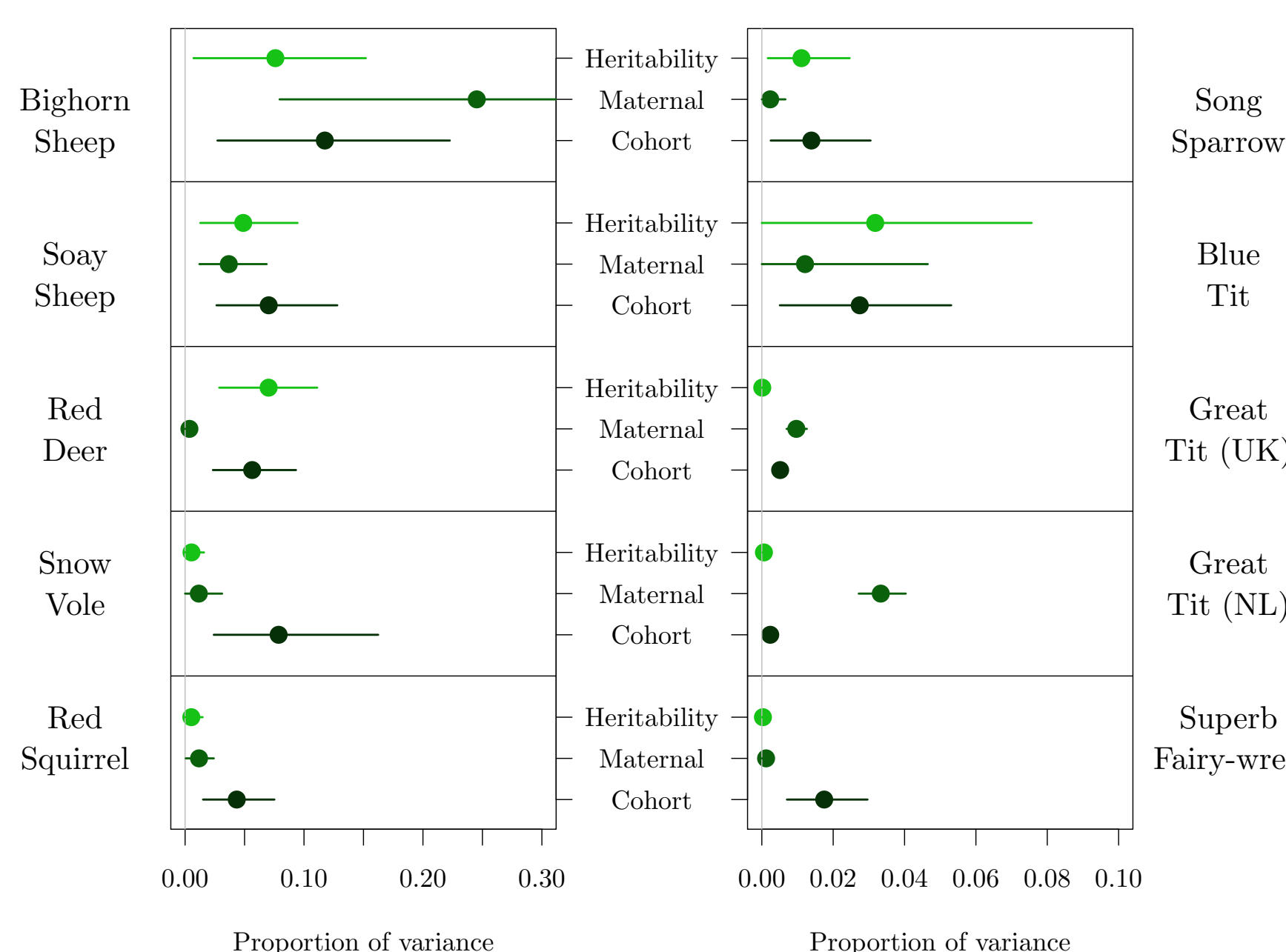
Simulated $V_A(\omega)$ after back-transformation

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

EMPERICAL RESULTS: Additive genetic variation in fitness detectable in most populations



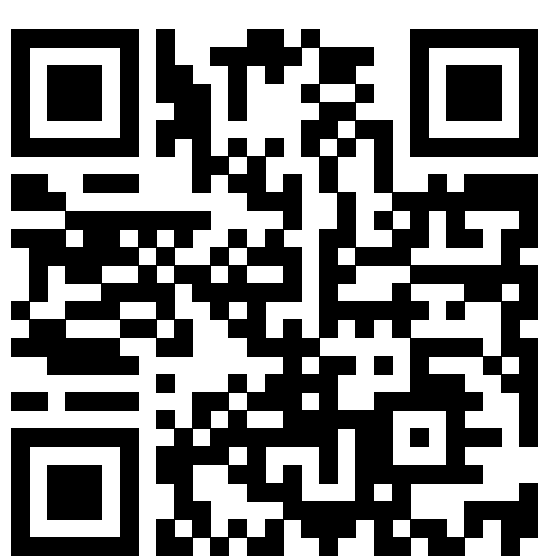
Preliminary models suggest small heritabilities of fitness on the data-scale (average 2.4%). Cohort effects, maternal effects and stochasticity dominate variation. However, credibility intervals of $V_A(\omega)$ exclude 0 in 5 out of 10 populations, and the posterior mode exceeds 0.1% in all of them, suggesting widespread on-going evolution.



NEXT, WE WILL EXPLORE:

- Influence of priors on estimation
- Influence of missing data and immigration
- Sex-specific fitness. Does cross-sex genetic correlation constrain or enhance evolution?
- Relative importance of ZI, Poisson and their covariance
- Significance for population dynamics

Website



timotheenivalis.github.io

Co-AUTHORS:

Josephine Pemberton, Tim Clutton-Brock, Marco Festa-Bianchet, David Coltman, Fanie Pelletier, 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, Peter Arcese & Andrew Cockburn

* 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.

R and L^AT_EXcode



github.com/timotheenivalis/VAWisWOW