



HAL
open science

Tools for estimating and comparing behavioral variation

Raphaël Royauté, Petri Niemelä

► **To cite this version:**

Raphaël Royauté, Petri Niemelä. Tools for estimating and comparing behavioral variation. 15th annual meeting of the Ethological Society, Feb 2020, Tübingen Germany, Germany. 10.17605/OSF.IO/CG3Y5 . hal-04168210

HAL Id: hal-04168210

<https://hal.science/hal-04168210>

Submitted on 21 Jul 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Comparing behavioral variation requires multiple approaches

Tools for estimating and comparing behavioral variation

Raphaël Royauté¹, Petri Niemelä¹

¹ LMU München/Department Biology II

CONTEXT

- Understanding how behavioral variation is generated is important
- Repeatability is a common metric for **reporting behavioral variation**
- Is repeatability the best metric for **comparing variation** among populations, sexes or studies?

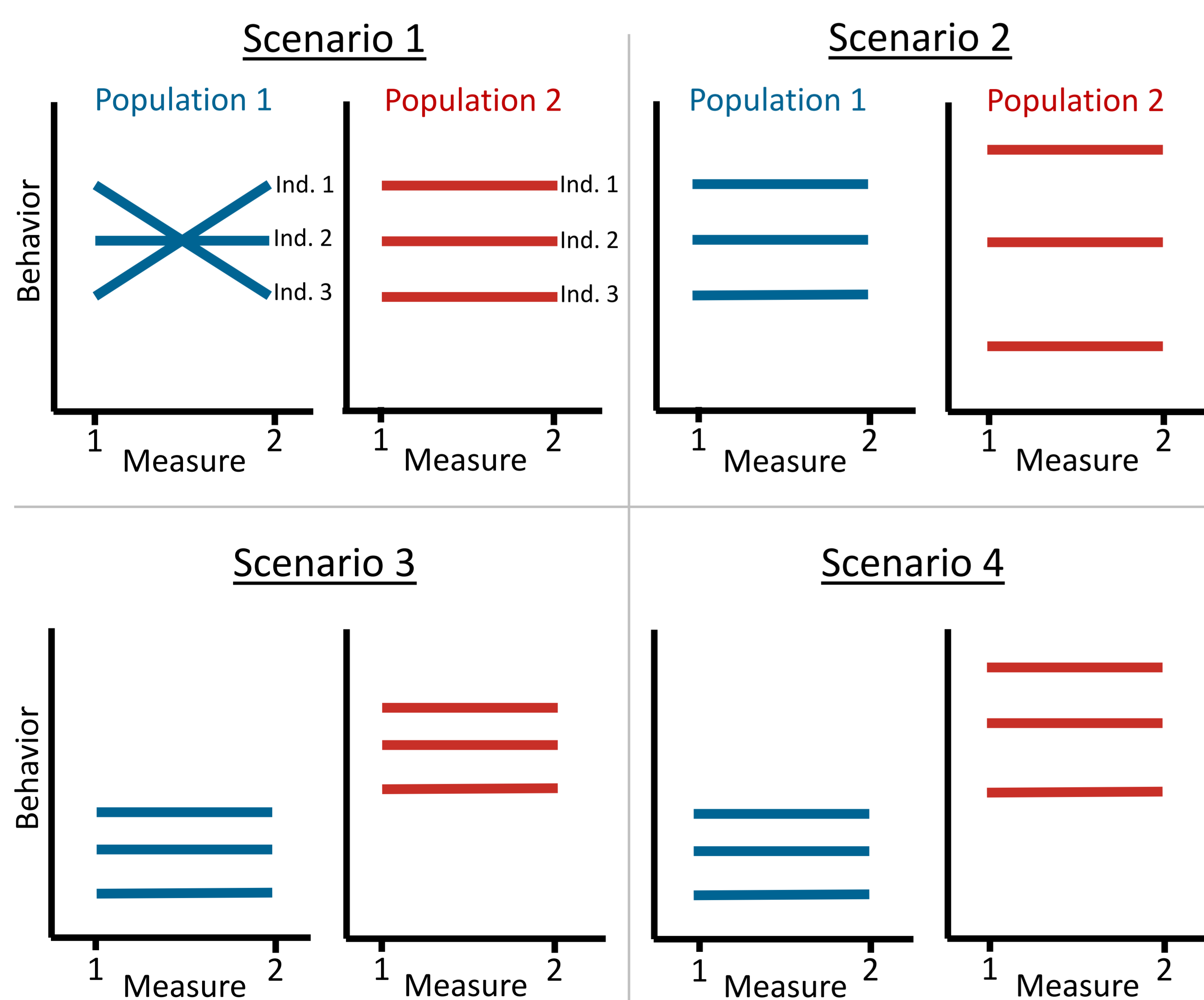
Repeatability: proportion of variation due to individual differences in behavior

Measured as a ratio of among (V_i) and within-individual (V_w) variances

$$R = \frac{V_i}{V_i + V_w}$$

V_i → Inference on genetic variation and irreversible plasticity
 V_w → Inference on reversible plasticity

QUESTION: In each scenario, which population has the highest repeatability?



HOW SHOULD WE COMPARE BEHAVIORAL VARIATION?

TOOL 1: DIFFERENCES IN REPETABILITY

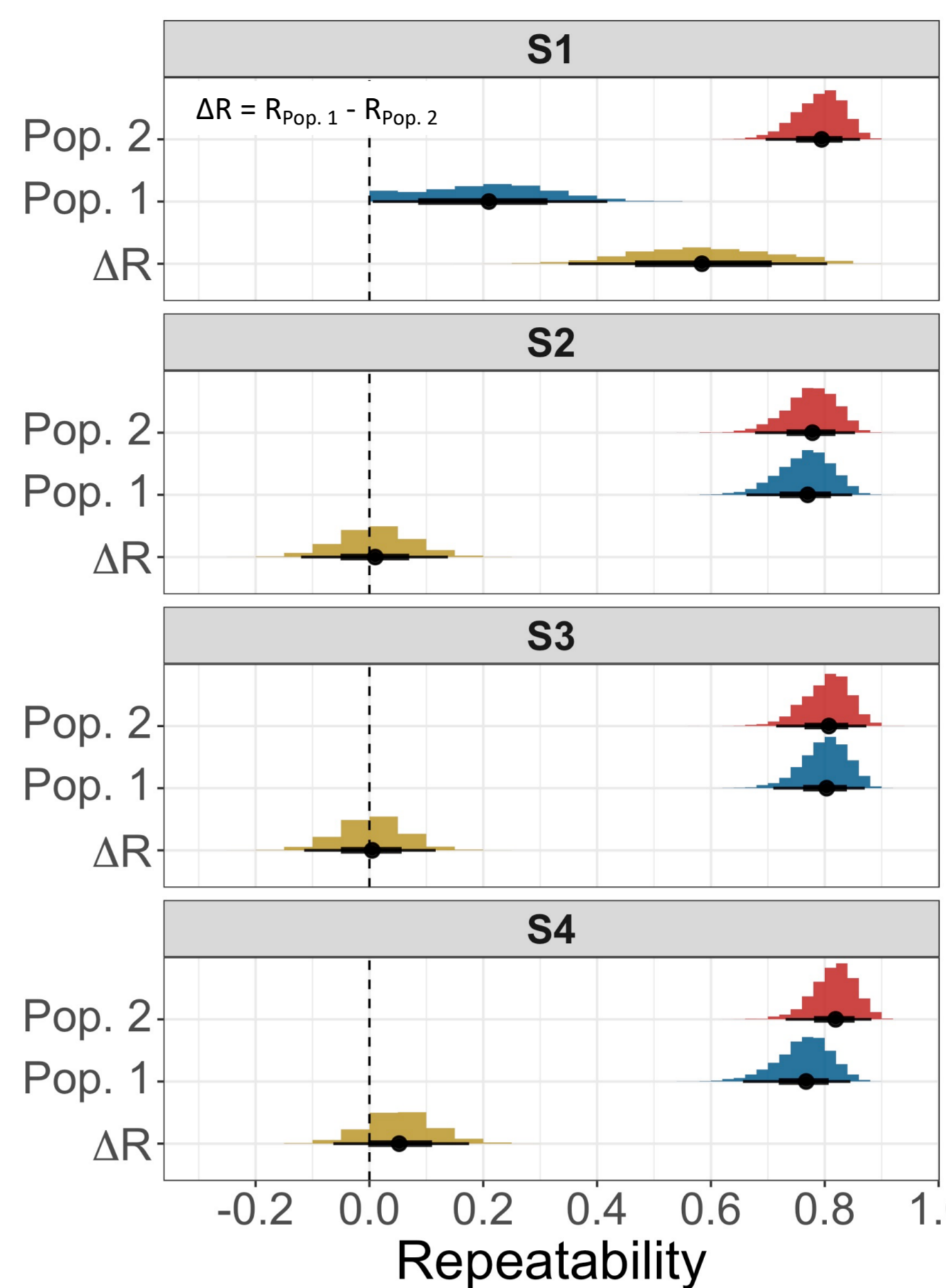


Fig. 1. Posterior distribution of repeatability (R) and the difference in repeatability (ΔR) by scenario.

Data simulated according to each scenario with 100 individuals per populations and 2 measures per individual. The data was analyzed using a Bayesian hierarchical mixed model in brms.

Repeatability fails to detect meaningful differences between populations in some scenarios (S2, S3, S4)

Problem: Repeatability can lead to misleading inferences

Solution: Compare among-individual variances

TOOL 2: DIFFERENCES IN VARIANCE

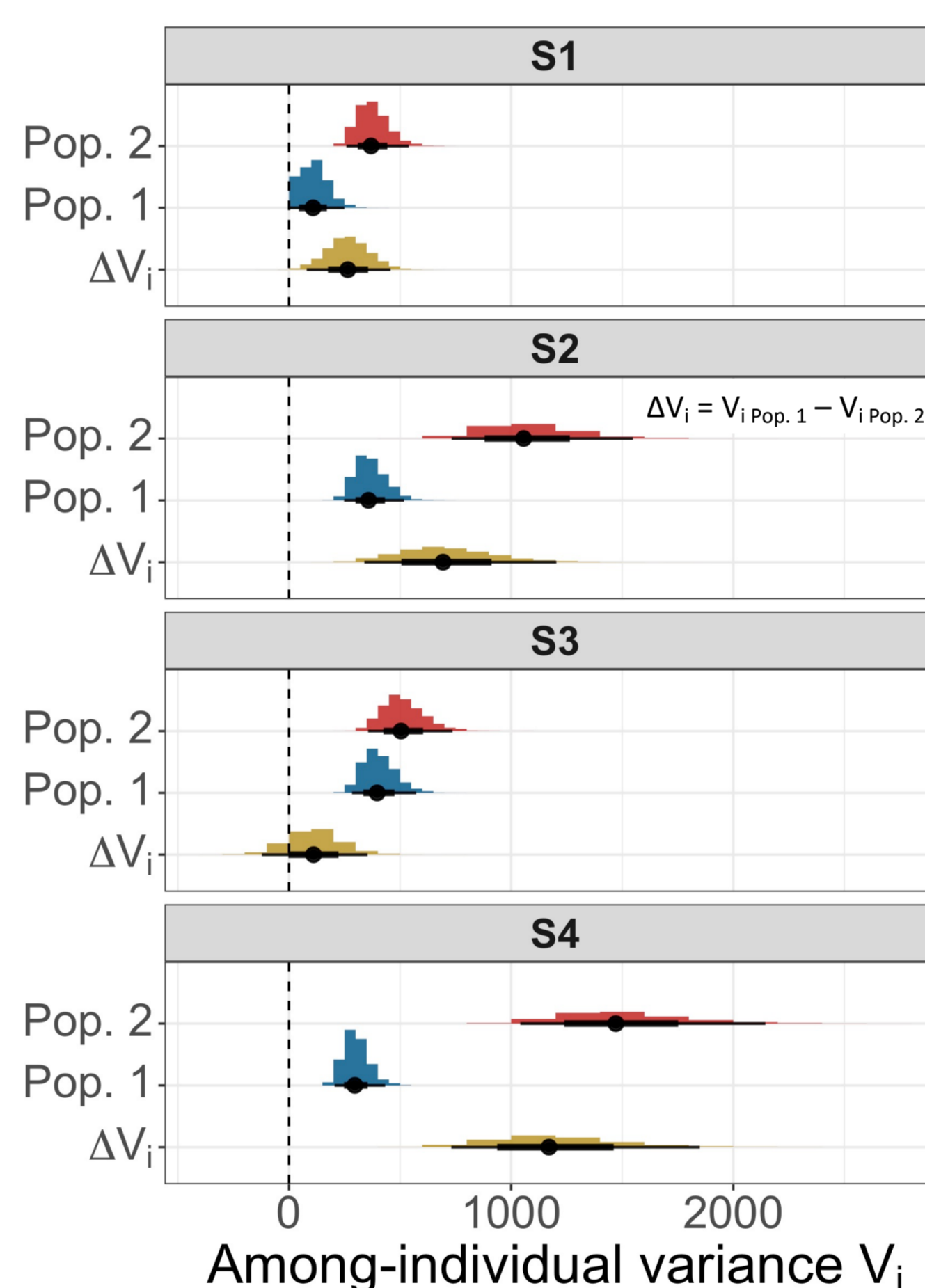


Fig. 2. Posterior distribution of among-individual variance (V_i) and the difference in variance (ΔV_i) by scenario.

Strong differences detected in S1, S2, S4.

Problem: Are these differences biologically meaningful?

Solution: Compare the variation relative to the mean with the coefficient of variation (CV)

TOOL 3: DIFFERENCES IN COEFFICIENT OF VARIATION

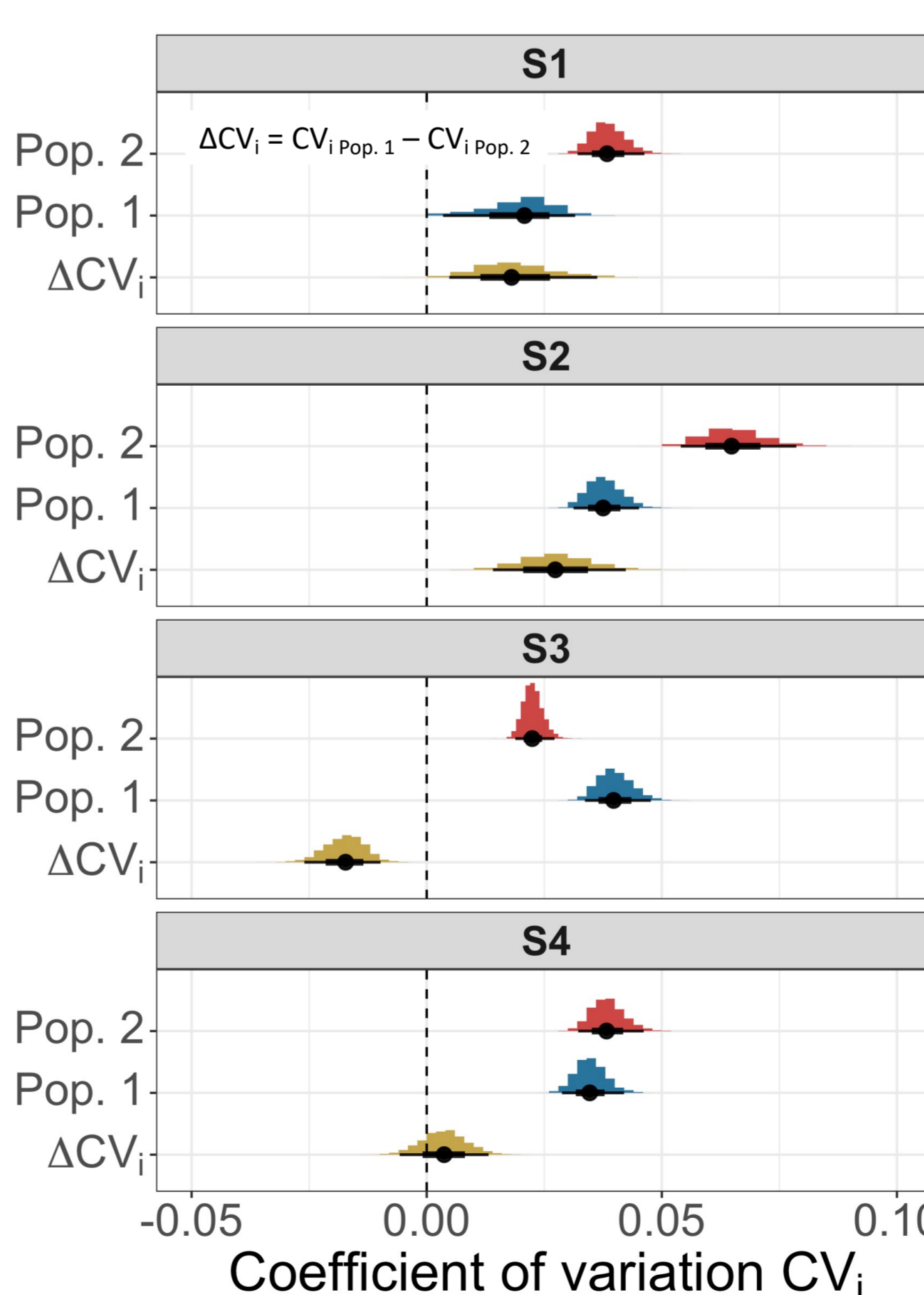


Fig. 3. Posterior distribution of the coefficient of variation in among-individual differences (CV_i) and its difference among population (ΔCV_i) by scenario.

$$CV_i = \frac{\sqrt{V_i}}{\mu}$$

Conclusions

- Populations can differ because of behavioral differences in mean and/or variance
- To fully understand biological variation, we recommend to report all three types of estimates.

