

Data S1 caption

The compressed file DataS1.zip contains all data necessary to reproduce the analyses. Decompress it to access one folder for each of the 19 populations: bsR = bighorn sheep on Ram Mountain, btM = blue tits at Muro, btP = blue tits at Pirio, btR = blue tits at la Rouvière, cfG = collared flycatchers on Gotland, gtH = great tits in Hoge Veluwe, gtW = great tits in Wytham Woods, hhT = hihi on Tiritiri Matangi Island, hhK = hihi at Karori, mkK = meerkats in the Kalahari, rdR = red deer on the Isle of Rum, rmC = rhesus macaques at Cayo Santiago, rsK=red squirrels in Kluane, sfC = superb fairy-wrens in Canberra, shN = spotted hyenas in the Ngorongoro Crater, spM=song sparrows on Mandarte Island, ssS = Soay sheep on St Kilda, ,svG = snow voles in Graubünden, ybA = yellow baboons at Amboseli.

Each folder contains a .csv file, containing the phenotypic data, where each row corresponds to an individual and with the following columns:

- LBS, the lifetime breeding success
- inbreeding, the pedigree inbreeding
- Qgg, the expected proportion of immigrant genetic ancestry
- SexU, a variable indicating the sex of the individual (including random assignment for individuals of unknown sex)
- stcohort, a standardized covariate indicating birth year
- id, the individual identifier linked to entries in the inverse additive relatedness matrix
- dam, the identity of an individual's mother
- cohort, the birth year
- DamCohort, the interaction of dam and cohort
- plus potentially other variables to be fitted as fixed and random effects that are specific to each population

This file can be opened in many ways, including in a text editor, in a spreadsheet editor, or in R using the base-R function `read.csv()`.

Each folder also contains a file called `Ainv_XXX`, where XXX is the population code. This file can be loaded into R using the base-R function `load()`. It contains the inverse additive relatedness matrix derived from the pedigree using the function `MCMCglmm::inverseA()` in R, and necessary to fit an animal model. The matrix is most easily used to fit models in `MCMCglmm`. The dimension names correspond to individuals in the population and are label in a way consistent with the labelling of the column `id` in the phenotypic data file.