

Supplementary Material S3. Prior analysis and model diagnostics

Prior testing

In the Bayesian analysis, choosing the prior is an important step in modeling, as this influences the model results [45, 46]. We conducted an analysis over multiple priors, choosing for the G structure of the models (random effects) two inverse Wishart priors [45] and a parameter-expanded prior [47]. For the R structure of the models (the residual variance), we set a prior where we fixed the bottom right of the diagonal matrix (fix = 2, zero-inflation variance).

```
library(MCMCglmm)

# Inverse-Wishart prior
prior_1 <-
  list(
    G = list(
      G1 = list(V = diag(2), nu = 0.002),
      G2 = list(V = diag(2), nu = 0.002),
      G3 = list(V = diag(2), nu = 0.002)),
    R = list(V = diag(2), nu = 0.002, fix = 2)
  )

# Inverse-Wishart prior (increased nu)
prior_2 <-
  list(
    G = list(
      G1 = list(V = diag(2), nu = 0.02),
      G2 = list(V = diag(2), nu = 0.02),
      G3 = list(V = diag(2), nu = 0.02)),
    R = list(V = diag(2), nu = 0.02, fix = 2)
  )

# Parameter expanded prior ( $\chi^2$  distribution)
prior_3 <- list(
  G = list(
    G1 = list(V = diag(2), nu = 1000, alpha.mu = c(0,0), alpha.V = diag(2)),
    G2 = list(V = diag(2), nu = 1000, alpha.mu = c(0,0), alpha.V = diag(2)),
    G3 = list(V = diag(2), nu = 1000, alpha.mu = c(0,0), alpha.V = diag(2))),
  R = list(V = diag(2), nu = 1, fix = 2)
)

# Number of samples and iterations
sampling <- 3000
burn <- 5000
thin <- 2500
nitt <- burn + thin * sampling
```

```
# Example of a multi-year model
mcy_1 <- MCMCglmm(
  Cones ~ trait -1 + Provenance,
  random = ~
    idh(trait):Clone+
    idh(trait):Year+
    idh(trait):Clone:Year,
  rcov=~idh(trait):units,
  family = "zipoisson",
  data = data,
  prior = prior_1,
  pr = TRUE,
  pl = TRUE,
  saveX = TRUE,
  saveZ = TRUE,
  nitt = nitt,
  thin = thin,
  burnin = burnin)
```

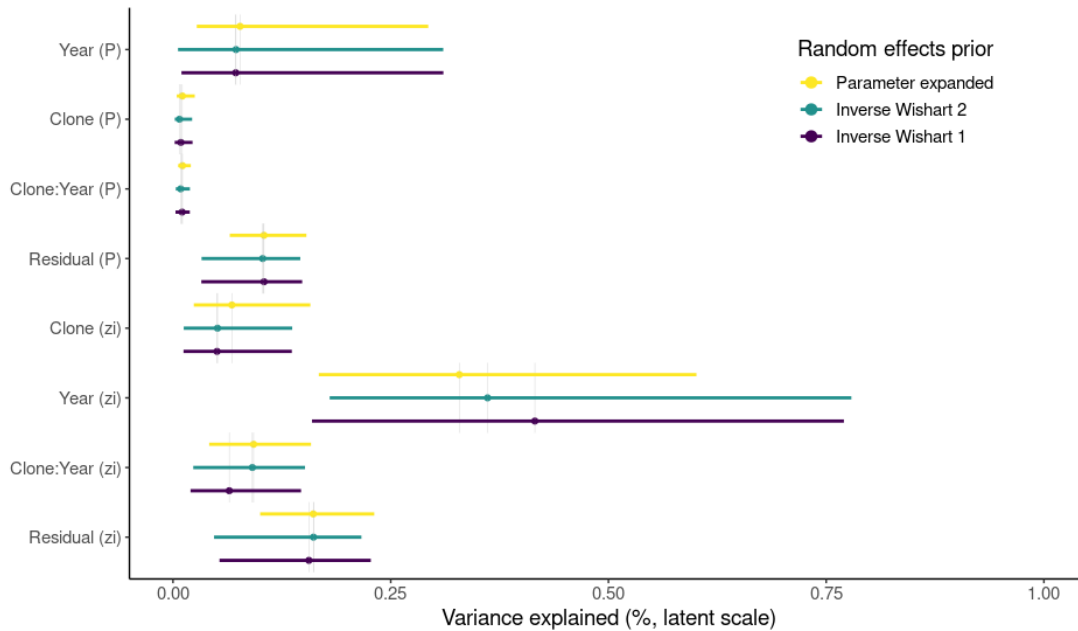


Figure S3.1. Variance explained by random effects in the Poisson and zero-inflated components of the multi-year model. The data in latent scale.

The comparison (Figure S3.1) indicated differences in the zero-inflated component of the multi-year model (clone and clone-year interaction) due to the inverse Wishart priors. Similar findings were reported before [48], and we preferred further the parameter expanded prior (χ^2 distribution), as recommended for cases where the expected heritability values are small [47] to inverse Wishart priors [49].

Diagnostic plots

Trace plots

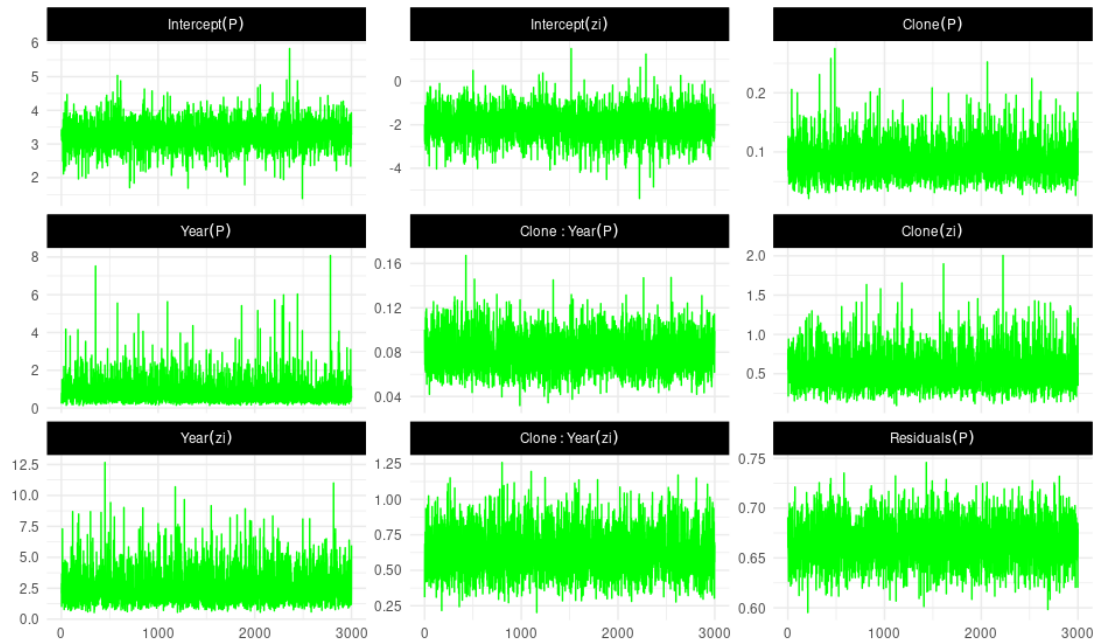


Figure S3. 2. The trace plot for each variable of the Bayesian multi-year model.

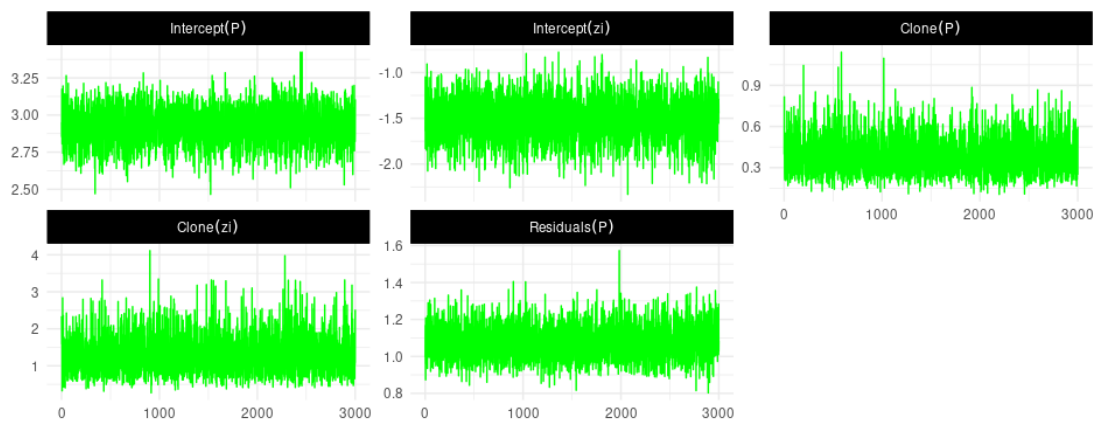


Figure S3. 3. The trace plot for each variable of the Bayesian model - year 2013.

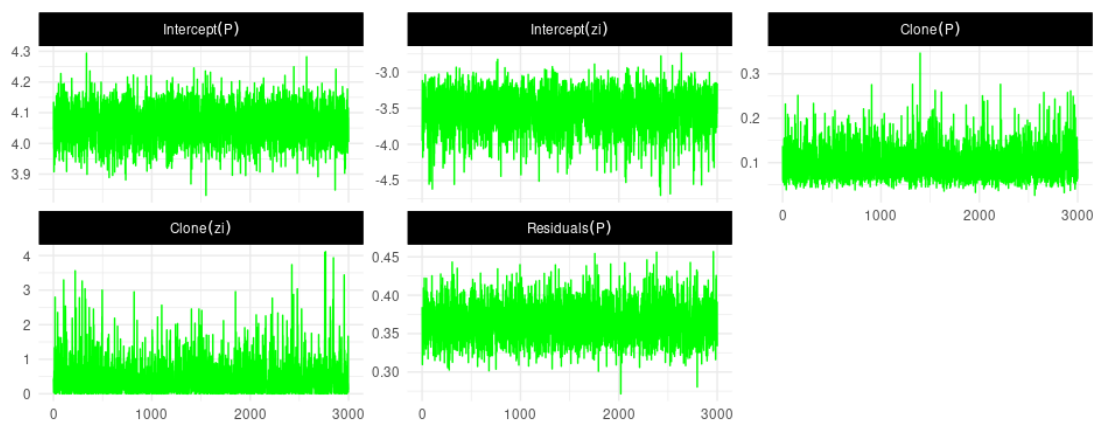


Figure S3. 4. The trace plot for each variable of the Bayesian model - year 2015.

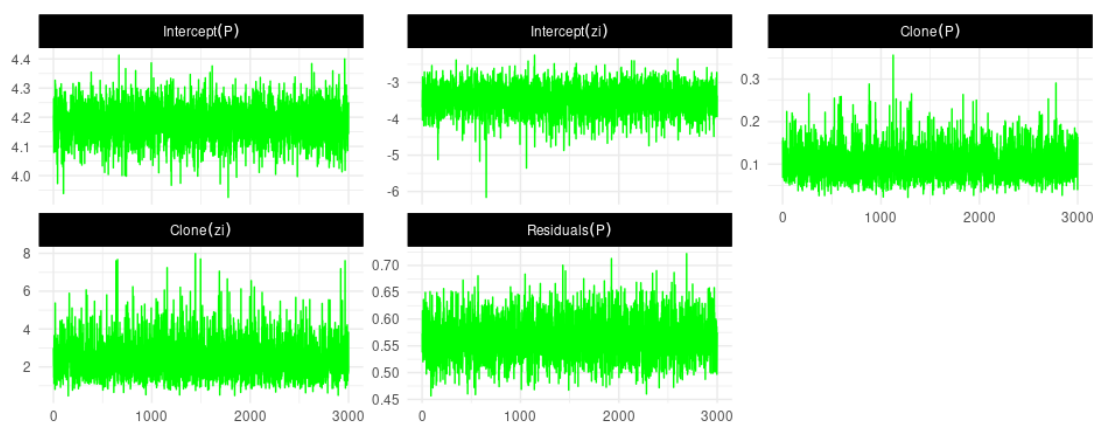


Figure S3. 5. The trace plot for each variable of the Bayesian model - year 2018.

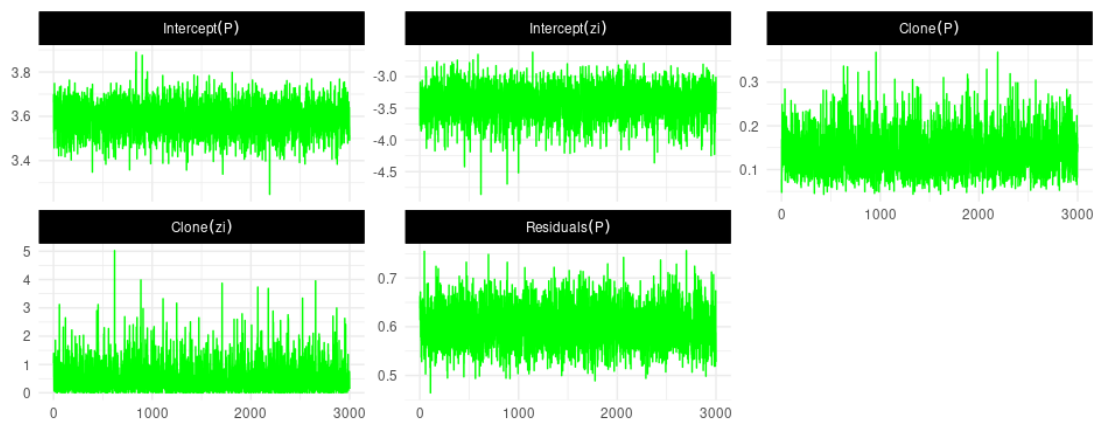


Figure S3. 6. The trace plot for each variable of the Bayesian model - year 2020.

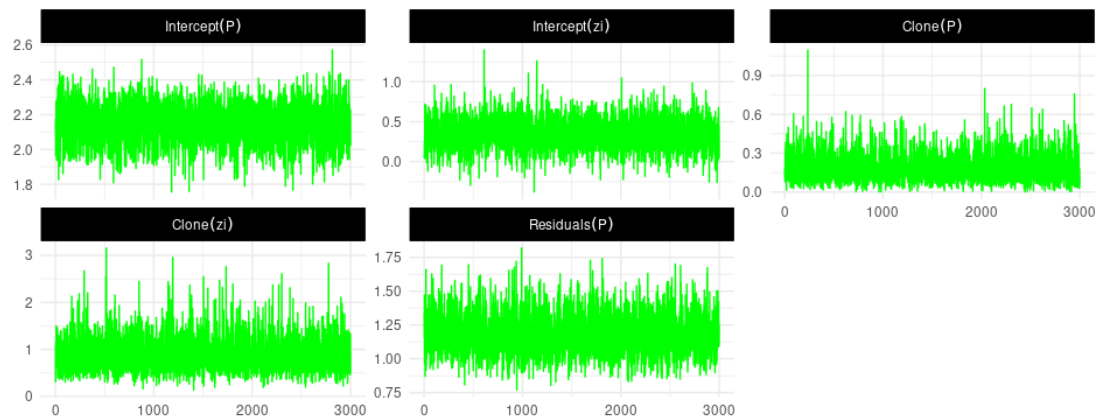


Figure S3. 7. The trace plot for each variable of the Bayesian model - year 2021.

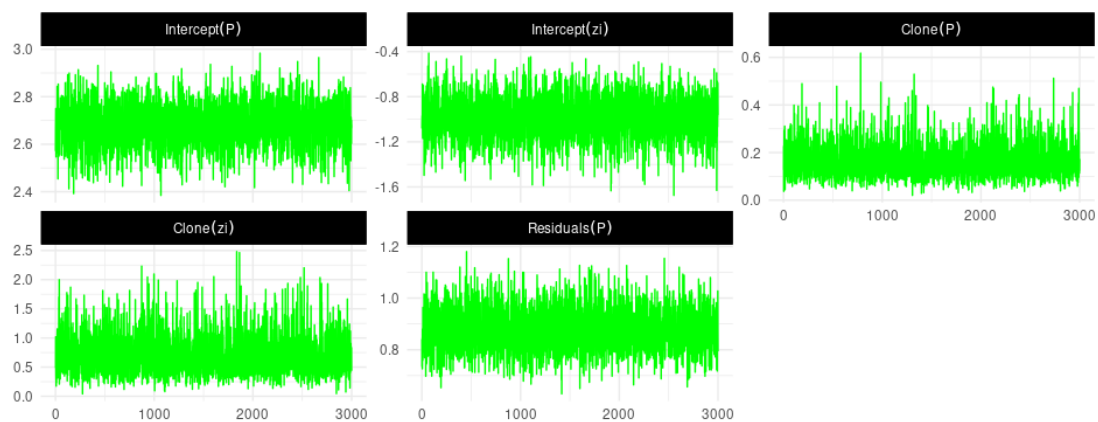


Figure S3. 8. The trace plot for each variable of the Bayesian model - year 2022.

Autocorrelation plots

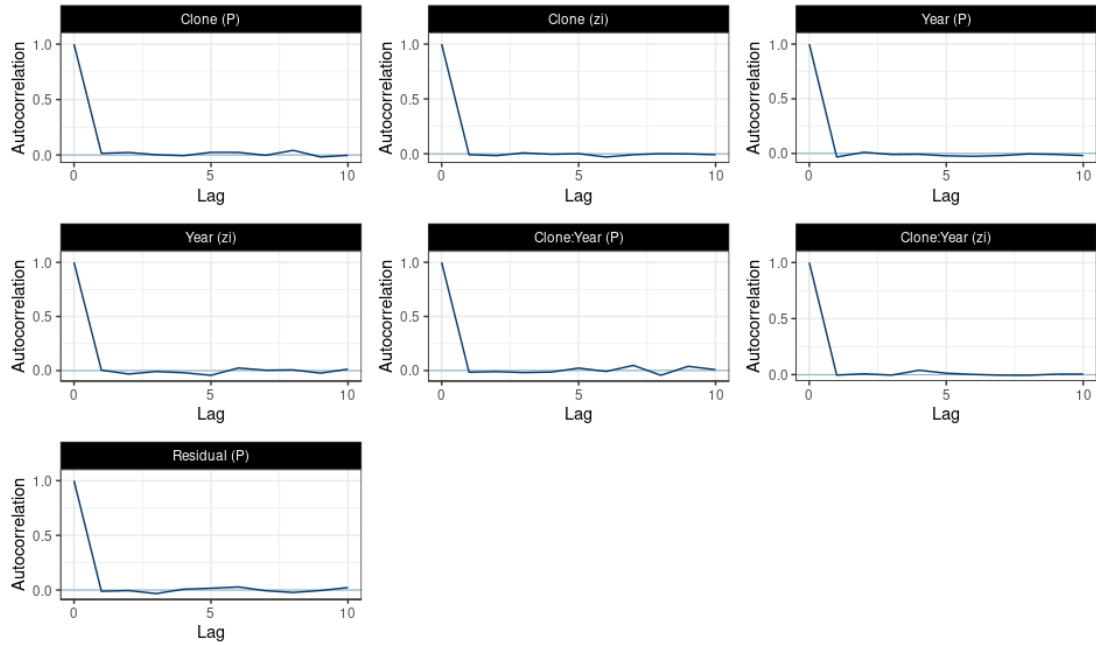


Figure S3. 9. The autocorrelation plot for each variable of the Bayesian multi-year model.

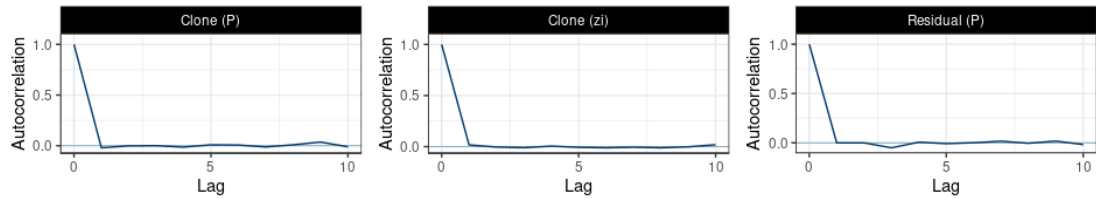


Figure S3. 10. The autocorrelation plot for each variable of the Bayesian model of year 2013.

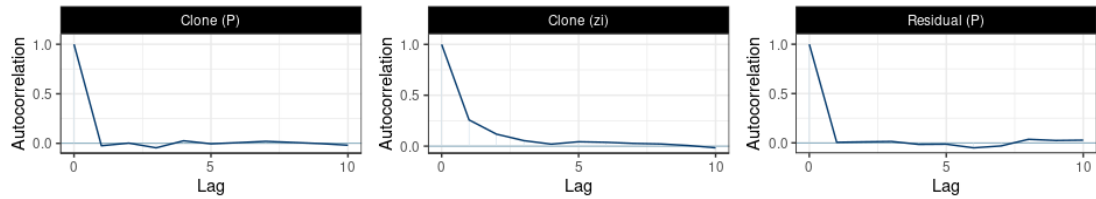


Figure S3. 11. The autocorrelation plot for each variable of the Bayesian model of year 2015.

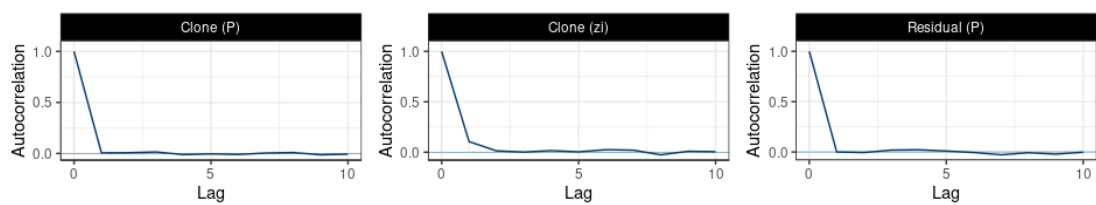


Figure S3. 12. The autocorrelation plot for each variable of the Bayesian model of year 2018.

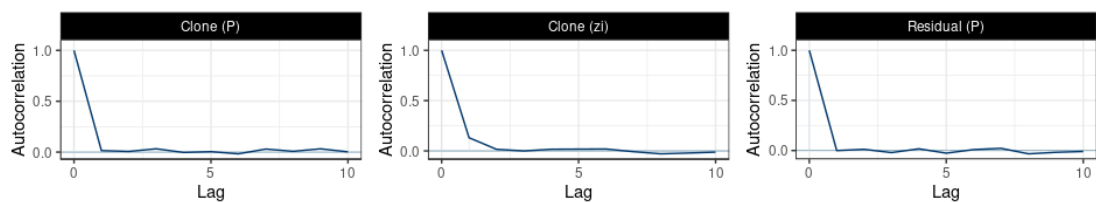


Figure S3. 13. The autocorrelation plot for each variable of the Bayesian model of year 2020.

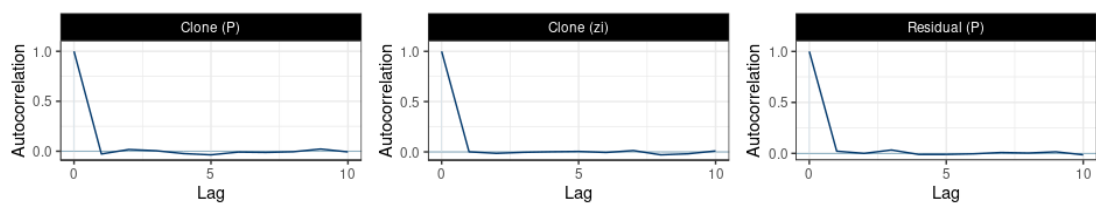


Figure S3. 14. The autocorrelation plot for each variable of the Bayesian model of year 2021.

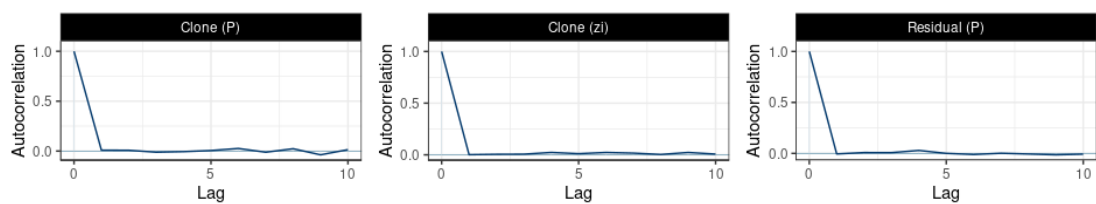


Figure S3. 15. The autocorrelation plot for each variable of the Bayesian model of year 2022.

References

46. Hadfield, J.D. MCMC Methods for Multi-Response Generalized Linear Mixed Models: The MCMCglmm R Package. *J. Stat. Soft.* **2010**, *33*, 1–22. <https://doi.org/10.18637/jss.v033.i02>.
47. Banner, K.M.; Irvine, K.M.; Rodhouse, T.J. The Use of Bayesian Priors in Ecology: The Good, the Bad and the Not Great. *Methods Ecol. Evol.* **2020**, *11*, 882–889. <https://doi.org/10.1111/2041-210X.13407>.
48. de Villemereuil, P.; Gimenez, O.; Doligez, B. Comparing Parent-Offspring Regression with Frequentist and Bayesian Animal Models to Estimate Heritability in Wild Populations: A Simulation Study for Gaussian and Binary Traits. *Methods Ecol. Evol.* **2013**, *4*, 260–275. <https://doi.org/10.1111/2041-210X.12011>.
49. Hadfield, J. MCMCglmm Course Notes. **2022**. Available online: <https://mran.microsoft.com/snapshot/2018-08-24/web/packages/MCMCglmm/Vignettes/CourseNotes.Pdf> (accessed on 22 July 2022).