

# Appendix S1. Linear regression models and non-linear population dynamics

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20 April, 2024

## 1 species, logistic growth

Population growth over time in a single species is first modelled using a Beverton-Holt (discrete-time, logistic) model (Beverton and Holt (1957); Leslie and Gower (1958)).

### 1.1 Generating the data frames

For the diagnosis first need to convert the chains into a coda object and extract the effective sample size (ESS), which denotes how many MCMC iteration were independent (e.g. having no autocorrelation) from previous iterations, and potential scale reduction factors (PSRF), which describe how well the MCMC chains converged around a value and if the two chains differ from each other. Therefore a high value for ESS (close to the number of actual iterations multiplied by the number of chains) is preferable and a PSRF value of 1 represents both chains converging on the same mean. Note we do not check the predictive and explanatory power of the model, as we have a perfect data set by the time series data of the simulations, which leads to  $R^2 > .98$ .

```
load("../output/h_01_d_minus3_hmsc_v01.RData")  
  
m.post <- convertToCodaObject(m.1)
```

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```
ess.beta <- effectiveSize(m.post$Beta)

psrf.beta <- gelman.diag(m.post$Beta, multivariate = FALSE)$psrf
```

## 2 References

```
1 + 1

#> [1] 2

knitr::knit_exit()
```

- 18 Beverton, R. J., and S. J. Holt. 1957. On the dynamics of exploited fish populations (Vol. 11). Springer  
19 Science & Business Media.
- 20 Leslie, P. H., and J. C. Gower. 1958. [The properties of a stochastic model for two competing species.](#)  
21 Biometrika 45:316–330.