**Population dynamics of the proboscis monkey *Nasalis larvatus* in the Lower Kinabatangan, Sabah, Borneo, Malaysia**

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Supplementary Material 1 Statistical modelling of population dynamics at long-term monitoring areas

We developed a Bayesian state space model to fit time series data of the proboscis monkey *Nasalis larvatus* populations. In this data analysis, the observed number of monkeys at observation *i* is $Y\_{i} $where *i* ($\in ${1, 2, …, *N*}) is a serial number in the population. The observation $Y\_{i} $ is supposed to follow the Poisson distribution *D* of mean $μ\_{i}$ (i.e. $Y\_{i} \~ D\left(μ\_{i}\right)$ where the binomial operator *Y* ~ *D* represents a random variable *Y* and follows a probability distribution *D.* The mean value $μ\_{i}$ is given as $μ\_{i }=exp⁡(x\_{i}+β+ ϵ\_{i})$, where $x\_{i}$ is the time-autocorrelation term (described later), and $β$ is the trend term to represent monotonic time change. The last term $ϵ\_{i}$ is an independent noise at observation *i* that follows the normal distribution of mean zero and standard deviation $σ\_{e}$.

The autocorrelated time series $\left\{x\_{i}\right\}$ is generated by a simple random walk model, $x\_{i}\~N\left(x\_{i-1}, σ\_{x}^{2}ΔT \right)$ , that is, $x\_{i}$ follows the normal distribution $N\left(x\_{i-1}, σ\_{x}^{2}ΔT \right)$ of mean $x\_{i-1}$ and variance $σ\_{x}^{2}ΔT,$ where $σ\_{x}^{2}$ is the proportionality constant and $ΔT$ is the interval length (d) between observation *i* and *i*-1. The previous distributions of all standard deviations $\{σ\_{\*}\}$ are the uniform distribution ranging over $\left[0,10^{4}\right]$, while that of $δ$ is the uniform distributions ranging over$\left[-10^{4},10^{4}\right]$.

The Markov chain Monte Carlo method was used to sample from the posterior distributions of the parameters with *JAGS 4.2.0* ([Plummer, 2016](#_ENREF_2)) and *R 3.2.4* (R Development Core Team, 2016). The posterior samples were obtained from three independent Markov chains in which 15,000 values (i.e. 5,000 samples for each parameter) were sampled with an interval of 100 after a burn-in of 10,000 iterations. We evaluated the convergence of the triple sampling chains using $\hat{R}$ statistics ([Gelman et al., 2013](#_ENREF_1)) for each parameter. The sampling details described above were chosen such that all $\hat{R}$ statistics were < 1.1 or all posterior distributions were well converged.

**References**

Gelman, A., Carlin, J.B., Stern, H.S., Vehtari, A. & Rubin, D.B. (2013) *Bayesian Data Analysis,* Chapman & Hall/CRC, Boca Raton, USA.

Plummer, M. (2016) *JAGS: Just Another Gibbs Sampler*. [Http://mcmc-jags.sourceforge.net/](http://mcmc-jags.sourceforge.net/) [accessed 03 August 2018].

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