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Appendix D from I. Martínez et al., "Disentangling the Formation of Contrasting Tree-Line Physiognomies Combining Model Selection and Bayesian Parameterization for Simulation Models"

(Am. Nat., vol. 177, no. 5, p. E136)

Pseudocode for the Model-Fitting Procedure

Step 1. Generate a random vector ψ_0 from the prior distributions and run the model.

if the model does not converge, repeat Step 1

else estimate the negative log likelihood, $\mathcal{L}_0$, and proceed

Main loop

for $j = 1 \ldots N$

Step 2. Propose a vector of candidate parameters, ψ_j, by sampling a truncated normal distribution centred on a random subset of previous values, ψ_{j-1}, and with standard deviations δ_j.

Step 3. Run the model.

if the model does not converge, go back to Step 2

else estimate the negative log likelihood, $\mathcal{L}_j$, and proceed

Step 4. Compare model fits to the previous step, $\alpha = \mathcal{L}_{j-1} - \mathcal{L}_j$

Step 5. Accept or reject the proposal ψ_j,

if $\alpha < 0$, the proposal provides a worse fit,

if $Unif > \exp(\alpha)$, reject the proposal, $\psi_j = \psi_{j-1}$,

else, accept the proposal

else the proposal provides at least an equal fit, so it is automatically accepted

Step 5. Update the vector of acceptance rates, γ_j, for the subset of parameters proposed at Step 2. Update the vector δ_j containing the standard deviations used to propose candidate values in the next iteration, $\delta_j = \delta_{j-1}\left(\gamma_j/(1-\gamma_j)\right)(0.3/(1-0.3))$, where 0.3 is the objective acceptance rate.

Figure D1: Pseudocode for the model-fitting procedure.