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**Phylogenetic occupancy models integrate imperfect detection and phylogenetic signal to analyze community structure**

*Ecology*

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**Data S1**  
**Phylogenetic Occupancy Model functions**

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**File list (files found within DataS1.zip)**

pom.R  
hpp.R

**Description**

pom.R - Core Phylogenetic Occupancy Model written as R function in JAGS language.  
A tutorial on running a POM in JAGS is available at: <https://github.com/lofrishkoff/pom>.

hpp.R - Function to calculate highest posterior probability for a bounded variable.

Arguments are as follows:

'sample' is the full MCMC posterior sample (*e.g.*, of lambda)

'lower' is a lower bound (for lambda this is 0, but can take -Inf)

'upper' is upper bound (for lambda this is 1, but can take Inf)

'mode = TRUE' if you want the posterior mode (highest posterior probability)

'HPDcoverage' is the percentage coverage by kernel method, or 'FALSE' if no interval is desired

'codaHPD = TRUE' if interval wanted with same HPDcoverage amount or a number if a different amount wanted. Coda HPDs can not equal 0 or 1 when these are the bounds, so its purpose here is for comparison with custom HPD coverage.

'n' is the number of points that determine the resolution of the density function

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