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

`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