

# Package ‘nimbleEcology’

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**Type** Package

**Title** Distributions for Ecological Models in 'nimble'

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**Description**

Common ecological distributions for 'nimble' models in the form of nimbleFunction objects. Includes Cormack-Jolly-Seber, occupancy, dynamic occupancy, hidden Markov, dynamic hidden Markov, and N-mixture models. (Jolly (1965) <DOI:10.2307/2333826>, Seber (1965) <DOI:10.2307/2333827>, Turek et al. (2016) <doi:10.1007/s10651-016-0353-z>).

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**Depends** R (>= 3.4.0), nimble

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**VignetteBuilder** knitr

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**Collate** utils.R dBetaBinom.R dCJS.R dDynOcc.R dDHMM.R dHMM.R dOcc.R dNmixture.R zzz.R

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dBetaBinom	<i>A beta binomial distribution and beta function for use in nimble models</i>
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### Description

dBetaBinom and dBetaBinom\_One provide a beta binomial distribution that can be used directly from R or in nimble models. These are also used by beta binomial variations of dNmixture distributions. nimBetaFun is the beta function.

### Usage

```
nimBetaFun(a, b, log)

dBetaBinom(x, N, shape1, shape2, log = 0)

dBetaBinom_One(x, N, shape1, shape2, log = 0)

rBetaBinom(n, N, shape1, shape2)

rBetaBinom_One(n, N, shape1, shape2)
```

### Arguments

a	shape1 argument of the beta function nimBetaFun.
b	shape2 argument of the beta function nimBetaFun.
log	TRUE or 1 to return log probability. FALSE or 0 to return probability.
x	vector of integer counts.
N	number of trials, sometimes called "size".
shape1	shape1 parameter of the beta-binomial distribution.
shape2	shape2 parameter of the beta-binomial distribution.
n	number of random draws, each returning a vector of length len. Currently only n = 1 is supported, but the argument exists for standardization of "r" functions.

## Details

These nimbleFunctions provide distributions that can be used directly in R or in nimble hierarchical models (via [nimbleCode](#) and [nimbleModel](#)). They were originally written for the beta binomial N-mixture extensions.

The beta binomial distribution is equivalent to a binomial distribution whose probability is itself a beta distributed random variable.

The probability mass function of the beta binomial is  $\text{choose}(N, x) * B(x + \text{shape1}, N - x + \text{shape2}) / B(\text{shape1}, \text{shape2})$ , where  $B(\text{shape1}, \text{shape2})$  is the beta function.

The beta binomial distribution is provided in two forms. `dBetaBinom` and `rBetaBinom` are used when `x` is a vector (i.e. `length(x) > 1`), in which case the parameters `alpha` and `beta` must also be vectors. When `x` is scalar, `dBetaBinom_One` and `rBetaBinom_One` are used.

## Author(s)

Ben Goldstein and Perry de Valpine

## See Also

For beta binomial N-mixture models, see [dNmixture](#). For documentation on the beta function, use `?stats::dbeta`

## Examples

```
# Calculate a beta binomial probability
dBetaBinom(x = c(4, 0, 0, 3), N = 10,
  shape1 = c(0.5, 0.5, 0.3, 0.5), shape2 = c(0.2, 0.4, 1, 1.2))
# Same for case with one observation
dBetaBinom_One(x = 3, N = 10, shape1 = 0.5, shape2 = 0.5, log = TRUE)
```

---

dCJS

*Cormack-Jolly-Seber distribution for use in nimble models*

---

## Description

`dCJS_**` and `rCJS_**` provide Cormack-Jolly-Seber capture-recapture distributions that can be used directly from R or in nimble models.

## Usage

```
dCJS_ss(x, probSurvive, probCapture, len = 0, log = 0)
```

```
dCJS_sv(x, probSurvive, probCapture, len = 0, log = 0)
```

```
dCJS_vs(x, probSurvive, probCapture, len = 0, log = 0)
```

```
dCJS_vv(x, probSurvive, probCapture, len = 0, log = 0)
```

```
rCJS_ss(n, probSurvive, probCapture, len = 0)
```

```
rCJS_sv(n, probSurvive, probCapture, len = 0)
```

```
rCJS_vs(n, probSurvive, probCapture, len = 0)
```

```
rCJS_vv(n, probSurvive, probCapture, len = 0)
```

### Arguments

x	capture history vector of 0s (not captured) and 1s (captured). Include the initial capture, so x[1] should equal 1.
probSurvive	survival probability, either a time-independent scalar (for dCJS_s*) or a time-dependent vector (for dCJS_v*) with length len - 1.
probCapture	capture probability, either a time-independent scalar (for dCJS_*s) or a time-dependent vector (for dCJS_*v) with length len. If a vector, first element is ignored, as the total probability is conditioned on the capture at t = 1.
len	length of capture history. Should equal length(x)
log	TRUE or 1 to return log probability. FALSE or 0 to return probability.
n	number of random draws, each returning a vector of length len. Currently only n = 1 is supported, but the argument exists for standardization of "r" functions.

### Details

These nimbleFunctions provide distributions that can be used directly in R or in nimble hierarchical models (via [nimbleCode](#) and [nimbleModel](#)).

The letters following the 'dCJS\_' indicate whether survival and/or capture probabilities, in that order, are scalar (s, meaning the probability applies to every x[t]) or vector (v, meaning the probability is a vector aligned with x). When probCapture and/or probSurvive is a vector, they must be the same length as x.

It is important to use the time indexing correctly for survival. probSurvive[t] is the survival probability from time t to time t + 1. When a vector, probSurvive may have length greater than length(x) - 1, but all values beyond that index are ignored.

Time indexing for detection is more obvious: probDetect[t] is the detection probability at time t.

When called from R, the len argument to dCJS\_\*\* is not necessary. It will default to the length of x. When used in nimble model code (via [nimbleCode](#)), len must be provided (even though it may seem redundant).

For more explanation, see package vignette (`vignette("Introduction_to_nimbleEcology")`).

Compared to writing nimble models with a discrete latent state for true alive/dead status at each time and a separate scalar datum for each observation, use of these distributions allows one to directly sum (marginalize) over the discrete latent states and calculate the probability of the detection history for one individual jointly.

These are nimbleFunctions written in the format of user-defined distributions for NIMBLE's extension of the BUGS model language. More information can be found in the NIMBLE User Manual at <https://r-nimble.org>.

When using these distributions in a nimble model, the left-hand side will be used as  $x$ , and the user should not provide the log argument.

For example, in nimble model code,

```
captures[i, 1:T] ~ dCSJ_ss(survive, capture, T)
```

declares a vector node, `captures[i, 1:T]`, (detection history for individual  $i$ , for example) that follows a CJS distribution with scalar survival probability `survive` and scalar capture probability `capture` (assuming `survive` and `capture` are defined elsewhere in the model).

This will invoke (something like) the following call to `dCJS_ss` when nimble uses the model such as for MCMC:

```
dCJS_ss(captures[i, 1:T], survive, capture, len = T, log = TRUE)
```

If an algorithm using a nimble model with this declaration needs to generate a random draw for `captures[i, 1:T]`, it will make a similar invocation of `rCJS_ss`, with  $n = 1$ .

If both survival and capture probabilities are time-dependent, use

```
captures[i, 1:T] ~ dCSJ_vv(survive[1:(T-1)], capture[1:T], T)
```

and so on for each combination of time-dependent and time-independent parameters.

### Value

For `dCJS_**`: the probability (or likelihood) or log probability of observation vector  $x$ .

For `rCJS_**`: a simulated capture history,  $x$ .

### Author(s)

Ben Goldstein, Perry de Valpine, and Daniel Turek

### References

D. Turek, P. de Valpine and C. J. Paciorek. 2016. Efficient Markov chain Monte Carlo sampling for hierarchical hidden Markov models. *Environmental and Ecological Statistics* 23:549–564. DOI 10.1007/s10651-016-0353-z

### See Also

For multi-state or multi-event capture-recapture models, see [dHMM](#) or [dDHMM](#).

### Examples

```
# Set up constants and initial values for defining the model
dat <- c(1,1,0,0,0) # A vector of observations
probSurvive <- c(0.6, 0.3, 0.3, 0.1)
probCapture <- 0.4
```

```
# Define code for a nimbleModel
nc <- nimbleCode({
  x[1:4] ~ dCJS_vs(probSurvive[1:4], probCapture, len = 4)
  probCapture ~ dunif(0,1)
```

```

  for (i in 1:4) probSurvive[i] ~ dunif(0, 1)
})

# Build the model, providing data and initial values
CJS_model <- nimbleModel(nc, data = list(x = dat),
                        inits = list(probSurvive = probSurvive,
                                     probCapture = probCapture))

# Calculate log probability of data from the model
CJS_model$calculate()
# Use the model for a variety of other purposes...

```

---

dDHMM

*Dynamic Hidden Markov Model distribution for use in nimble models*


---

## Description

dDHMM and dDHMMo provide Dynamic hidden Markov model distributions for nimble models.

## Usage

```
dDHMM(x, init, probObs, probTrans, len, checkRowSums = 1, log = 0)
```

```
dDHMMo(x, init, probObs, probTrans, len, checkRowSums = 1, log = 0)
```

```
rDHMM(n, init, probObs, probTrans, len, checkRowSums = 1)
```

```
rDHMMo(n, init, probObs, probTrans, len, checkRowSums = 1)
```

## Arguments

x	vector of observations, each one a positive integer corresponding to an observation state (one value of which could correspond to "not observed", and another value of which can correspond to "dead" or "removed from system").
init	vector of initial state probabilities. Must sum to 1
probObs	time-independent matrix (dDHMM and rDHMM) or time-dependent 3D array (dDHMMo and rDHMMo) of observation probabilities. First two dimensions of probObs are of size x (number of possible system states) x (number of possible observation classes). dDHMMo and rDHMMo expect an additional third dimension of size (number of observation times). probObs[i, j, (t)] is the probability that an individual in the ith latent state is recorded as being in the jth detection state (at time t). See Details for more information.
probTrans	time-dependent array of system state transition probabilities. Dimension of probTrans is (number of possible system states) x (number of possible system states) x (number of observation times). probTrans[i,j,t] is the probability that an individual truly in state i at time t will be in state j at time t+1. See Details for more information.

len	length of observations (needed for rDHMM)
checkRowSums	should validity of probObs and probTrans be checked? Both of these are required to have each set of probabilities sum to 1 (over each row, or second dimension). If checkRowSums is non-zero (or TRUE), these conditions will be checked within a tolerance of 1e-6. If it is 0 (or FALSE), they will not be checked. Not checking should result in faster execution, but whether that is appreciable will be case-specific.
log	TRUE or 1 to return log probability. FALSE or 0 to return probability
n	number of random draws, each returning a vector of length len. Currently only n = 1 is supported, but the argument exists for standardization of "r" functions

## Details

These nimbleFunctions provide distributions that can be used directly in R or in nimble hierarchical models (via [nimbleCode](#) and [nimbleModel](#)).

The probability (or likelihood) of observation  $x[t, o]$  depends on the previous true latent state, the time-dependent probability of transitioning to a new state probTrans, and the probability of observation states given the true latent state probObs.

The distribution has two forms, dDHMM and dDHMMo. dDHMM takes a time-independent observation probability matrix with dimension  $S \times O$ , while dDHMMo expects a three-dimensional array of time-dependent observation probabilities with dimension  $S \times O \times T$ , where  $O$  is the number of possible occupancy states,  $S$  is the number of true latent states, and  $T$  is the number of time intervals.

probTrans has dimension  $S \times S \times (T - 1)$ . probTrans[i, j, t] is the probability that an individual in state  $i$  at time  $t$  takes on state  $j$  at time  $t+1$ . The length of the third dimension may be greater than  $(T - 1)$  but all values indexed greater than  $T - 1$  will be ignored.

init has length  $S$ . init[i] is the probability of being in state  $i$  at the first observation time. That means that the first observations arise from the initial state probabilities.

For more explanation, see package vignette (vignette("Introduction\_to\_nimbleEcology")).

Compared to writing nimble models with a discrete true latent state and a separate scalar datum for each observation, use of these distributions allows one to directly sum (marginalize) over the discrete latent state and calculate the probability of all observations from one site jointly.

These are nimbleFunctions written in the format of user-defined distributions for NIMBLE's extension of the BUGS model language. More information can be found in the NIMBLE User Manual at <https://r-nimble.org>.

When using these distributions in a nimble model, the left-hand side will be used as  $x$ , and the user should not provide the log argument.

For example, in a NIMBLE model,

```
observedStates[1:T] ~ dDHMM(initStates[1:S], observationProbs[1:S, 1:O], transitionProbs[1:S, 1:S, 1:(T-1)])
```

declares that the observedStates[1:T] vector follows a dynamic hidden Markov model distribution with parameters as indicated, assuming all the parameters have been declared elsewhere in the model. In this case,  $S$  is the number of system states,  $O$  is the number of observation classes, and  $T$  is the number of observation occasions. This will invoke (something like) the following call to dDHMM when nimble uses the model such as for MCMC:

```
rDHMM(observedStates[1:T],initStates[1:S],observationProbs[1:S,1:0],transitionProbs[1:S,1:S,1:(T-1)
= TRUE)
```

If an algorithm using a nimble model with this declaration needs to generate a random draw for `observedStates[1:T]`, it will make a similar invocation of `rDHMM`, with `n = 1`.

If the observation probabilities are time-dependent, one would use:

```
observedStates[1:T] ~ dDHMMo(initStates[1:S],observationProbs[1:S,1:0,1:T],transitionProbs[1:S,1:S,1
```

### Value

For `dDHMM` and `dDHMMo`: the probability (or likelihood) or log probability of observation vector `x`.  
For `rDHMM` and `rDHMMo`: a simulated detection history, `x`.

### Author(s)

Perry de Valpine, Daniel Turek, and Ben Goldstein

### References

D. Turek, P. de Valpine and C. J. Paciorek. 2016. Efficient Markov chain Monte Carlo sampling for hierarchical hidden Markov models. *Environmental and Ecological Statistics* 23:549–564. DOI 10.1007/s10651-016-0353-z

### See Also

For hidden Markov models with time-independent transitions, see [dHMM](#) and [dHMMo](#). For simple capture-recapture, see [dCJS](#).

### Examples

```
# Set up constants and initial values for defining the model
dat <- c(1,2,1,1) # A vector of observations
init <- c(0.4, 0.2, 0.4) # A vector of initial state probabilities
probObs <- t(array( # A matrix of observation probabilities
  c(1, 0,
    0, 1,
    0.8, 0.2), c(2, 3)))

probTrans <- array(rep(1/3, 27), # A matrix of time-indexed transition probabilities
  c(3,3,3))

# Define code for a nimbleModel
nc <- nimbleCode({
  x[1:4] ~ dDHMM(init[1:3], probObs = probObs[1:3, 1:2],
    probTrans = probTrans[1:3, 1:3, 1:3], len = 4, checkRowSums = 1)

  for (i in 1:3) {
    init[i] ~ dunif(0,1)

    for (j in 1:3) {
      for (t in 1:3) {
```



```

        probTrans[i,j,t] ~ dunif(0,1)
      }
    }

    probObs[i, 1] ~ dunif(0,1)
    probObs[i, 2] <- 1 - probObs[i,1]
  }
})

# Build the model, providing data and initial values
DHMM_model <- nimbleModel(nc,
  data = list(x = dat),
  inits = list(init = init,
               probObs = probObs,
               probTrans = probTrans))

# Calculate log probability of x from the model
DHMM_model$calculate()

# Use the model for a variety of other purposes...

```

---

dDynOcc	<i>Dynamic occupancy distribution for use in nimble models dDynOcc_** and rDynOcc_** provide dynamic occupancy model distributions that can be used directly from R or in nimble models.</i>
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---

## Description

Dynamic occupancy distribution for use in nimble models dDynOcc\_\*\* and rDynOcc\_\*\* provide dynamic occupancy model distributions that can be used directly from R or in nimble models.

## Usage

```

dDynOcc_vvm(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_vsm(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_svm(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_ssm(x, init, probPersist, probColonize, p, start, end, log = 0)
rDynOcc_vvm(n, init, probPersist, probColonize, p, start, end)
rDynOcc_vsm(n, init, probPersist, probColonize, p, start, end)
rDynOcc_svm(n, init, probPersist, probColonize, p, start, end)
rDynOcc_ssm(n, init, probPersist, probColonize, p, start, end)
dDynOcc_vvv(x, init, probPersist, probColonize, p, start, end, log = 0)

```

```

dDynOcc_vsv(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_svv(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_ssv(x, init, probPersist, probColonize, p, start, end, log = 0)
rDynOcc_vvv(n, init, probPersist, probColonize, p, start, end)
rDynOcc_vsv(n, init, probPersist, probColonize, p, start, end)
rDynOcc_svv(n, init, probPersist, probColonize, p, start, end)
rDynOcc_ssv(n, init, probPersist, probColonize, p, start, end)
dDynOcc_vvs(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_vss(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_svs(x, init, probPersist, probColonize, p, start, end, log = 0)
dDynOcc_sss(x, init, probPersist, probColonize, p, start, end, log = 0)
rDynOcc_vvs(n, init, probPersist, probColonize, p, start, end)
rDynOcc_vss(n, init, probPersist, probColonize, p, start, end)
rDynOcc_svs(n, init, probPersist, probColonize, p, start, end)
rDynOcc_sss(n, init, probPersist, probColonize, p, start, end)

```

### Arguments

x	detection/non-detection matrix of 0s (not detected) and 1s (detected). Rows represent primary sampling occasions (e.g. different seasons). Columns are secondary sampling locations (e.g. replicate visits within a season) that may be different for each row
init	probability of occupancy in the first sampling period
probPersist	persistence probability—probability an occupied cell remains occupied. 1-extinction probability. Scalar for dDynOcc_s**, vector for dDynOcc_v**. If vector, should have length $\dim(x)[1] - 1$ since no transition occurs after the last observation
probColonize	colonization probability. Probability that an unoccupied cell becomes occupied. Scalar for dDynOcc_**s, vector for dDynOcc_**v. If vector, should have length $\dim(x)[1] - 1$ since no transition occurs after the last observation
p	Detection probabilities. Scalar for dDynOcc_**s, vector for dDynOcc_**v, matrix for dDynOcc_**m. If a matrix, dimensions should match x
start	indicates the column number of the first observation in each row of x. A vector

	of length $\text{dim}(x)[1]$ . This allows for different time periods to have different numbers of sampling occasions
end	indicates the column number of the last observation in each row of $x$ . A vector of length $\text{dim}(x)[1]$ . This allows for different time periods to have different numbers of sampling occasions
log	TRUE (return log probability) or FALSE (return probability)
n	number of random draws, each returning a matrix of dimension $c(\min(\text{start}), \max(\text{end}))$ . Currently only $n = 1$ is supported, but the argument exists for standardization of "r" functions

## Details

These `nimbleFunctions` provide distributions that can be used directly in R or in `nimble` hierarchical models (via `nimbleCode` and `nimbleModel`).

The probability (or likelihood) of observation  $x[t, o]$  depends on the occupancy status of the site at time  $t-1$ , the transition probability of persistence (`probPersist` or `probPersist[t-1]`), colonization (`probColonize` or `probColonize[t-1]`), and a detection probability ( $p$ ,  $p[t]$ , or  $p[t, o]$ ).

The first two letters following the 'dDynOcc\_' indicate whether the probabilities of persistence and colonization are a constant scalar ( $s$ ) or time-indexed vector ( $v$ ). For example, `dDynOcc_svm` takes scalar persistence probability `probPersist` with a vector of colonization probabilities `probColonize[1:(T-1)]`.

When vectors, `probColonize` and `probPersist` may be of any length greater than or equal to  $\text{length}(x) - 1$ . Only the first  $\text{length}(x) - 1$  indices are used, each corresponding to the transition from time  $t$  to  $t+1$  (e.g. `probColonize[2]` describes the transition probability from  $t = 2$  to  $t = 3$ ). All extra values are ignored. This is to make it easier to use one distribution for many sites, some requiring probabilities of length 1.

The third letter in the suffix indicates whether the detection probability is a constant (scalar), time-dependent (vector), or both time-dependent and dependent on observation occasion (matrix). For example, `dDynOcc_svm` takes a matrix of detection probabilities  $p[1:T, 1:0]$ .

The arguments `start` and `end` allow different time periods to contain different numbers of sampling events. Suppose you have observations for samples in three seasons; in the first two seasons, there are four observations, but in the third, there are only three. The `start` and `end` could be provided as `start = c(1, 1, 1)` and `end = c(4, 4, 3)`. In this case, the value of  $x[4, 4]$  would be ignored.

For more explanation, see package vignette (`vignette("Introduction_to_nimbleEcology")`).

Compared to writing `nimble` models with a discrete latent state for true occupancy status and a separate scalar datum for each observation, use of these distributions allows one to directly sum (marginalize) over the discrete latent state and calculate the probability of all observations from one site jointly.

These are `nimbleFunctions` written in the format of user-defined distributions for NIMBLE's extension of the BUGS model language. More information can be found in the NIMBLE User Manual at <https://r-nimble.org>.

When using these distributions in a `nimble` model, the left-hand side will be used as  $x$ , and the user should not provide the `log` argument.

For example, in `nimble` model code,

```
detections[1:T, 1:0] ~ dDynOcc_ssm(init, probPersist = persistence_prob, probColonize =
  colonization_prob, p = p[1:T, 1:0], start = start[1:T], end = end[1:T])
```

declares that the `detections[1:T]` vector follows a dynamic occupancy model distribution with parameters as indicated, assuming all the parameters have been declared elsewhere in the model. This will invoke (something like) the following call to `dDynOcc_ssm` when `nimble` uses the model such as for MCMC:

```
dDynOcc_ssm(detections[1:T,1:0],init,probPersist = persistence_prob,probColonize =
colonization_prob,p = p[1:T,1:0],start = start[1:T],end = end[1:T],log = TRUE)
```

If an algorithm using a `nimble` model with this declaration needs to generate a random draw for `detections[1:T,1:0]`, it will make a similar invocation of `rDynOcc_ssm`, with `n = 1`.

If the colonization probabilities are time-dependent, one would use:

```
detections[1:T] ~ dDynOcc_svm(nrep,init = init_prob,probPersist = persistence_prob,probColonize
= colonization_prob[1:(T-1)],p = p[1:T,1:0])
```

### Value

For `dDynOcc_***`: the probability (or likelihood) or log probability of observation vector `x`. For `rDynOcc_***`: a simulated detection history, `x`.

### Author(s)

Ben Goldstein, Perry de Valpine and Lauren Ponisio

### See Also

For basic occupancy models, see documentation for [dOcc](#).

### Examples

```
# Set up constants and initial values for defining the model
x <- matrix(c(0,0,0,0,
              1,1,1,0,
              0,0,0,0,
              0,0,1,0,
              0,0,0,0), nrow = 4)
start <- c(1,1,2,1,1)
end <- c(5,5,5,4,5)
init <- 0.7
probPersist <- 0.5
probColonize <- 0.2
p <- matrix(rep(0.5, 20), nrow = 4)

# Define code for a nimbleModel
nc <- nimbleCode({

  x[1:2, 1:5] ~ dDynOcc_vvm(init,
    probPersist[1:2], probColonize[1:2], p[1:2,1:5],
    start = start[1:4], end = end[1:4])

  init ~ dunif(0,1)
```

```

for (i in 1:2) {
  probPersist[i] ~ dunif(0,1)
  probColonize[i] ~ dunif(0,1)
}

for (i in 1:2) {
  for (j in 1:5) {
    p[i,j] ~ dunif(0,1)
  }
}
})

# Build the model, providing data and initial values
DynOcc_model <- nimbleModel(nc, data = list(x = x),
                           constants = list(start = start, end = end),
                           inits = list(p = p, probPersist = probPersist,
                                         init = init, probColonize = probColonize))

# Calculate log probability of data from the model
DynOcc_model$calculate("x")
# Use the model for a variety of other purposes...

```

---

dHMM

*Hidden Markov Model distribution for use in nimble models*


---

## Description

dHMM and dHMMo provide hidden Markov model distributions that can be used directly from R or in nimble models.

## Usage

```
dHMM(x, init, probObs, probTrans, len = 0, checkRowSums = 1, log = 0)
```

```
dHMMo(x, init, probObs, probTrans, len = 0, checkRowSums = 1, log = 0)
```

```
rHMM(n, init, probObs, probTrans, len = 0, checkRowSums = 1)
```

```
rHMMo(n, init, probObs, probTrans, len = 0, checkRowSums = 1)
```

## Arguments

x	vector of observations, each one a positive integer corresponding to an observation state (one value of which could correspond to "not observed", and another value of which can correspond to "dead" or "removed from system").
init	vector of initial state probabilities. Must sum to 1

probObs	time-independent matrix (dHMM and rHMM) or time-dependent array (dHMMo and rHMMo) of observation probabilities. First two dimensions of probObs are of size $x$ (number of possible system states) $\times$ (number of possible observation classes). dDHMMo and rDHMMo expects an additional third dimension of size (number of observation times). $\text{probObs}[i, j, t]$ is the probability that an individual in the $i$ th latent state is recorded as being in the $j$ th detection state (at time $t$ ). See Details for more information.
probTrans	time-independent matrix of state transition probabilities. $\text{probTrans}[i, j]$ is the probability that an individual in latent state $i$ transitions to latent state $j$ at the next timestep. See Details for more information.
len	length of $x$ (see below).
checkRowSums	should validity of probObs and probTrans be checked? Both of these are required to have each set of probabilities sum to 1 (over each row, or second dimension). If checkRowSums is non-zero (or TRUE), these conditions will be checked within a tolerance of $1e-6$ . If it is 0 (or FALSE), they will not be checked. Not checking should result in faster execution, but whether that is appreciable will be case-specific.
log	TRUE or 1 to return log probability. FALSE or 0 to return probability.
n	number of random draws, each returning a vector of length len. Currently only $n = 1$ is supported, but the argument exists for standardization of "r" functions.

## Details

These nimbleFunctions provide distributions that can be used directly in R or in nimble hierarchical models (via `nimbleCode` and `nimbleModel`).

The distribution has two forms, dHMM and dHMMo. Define  $S$  as the number of latent state categories (maximum possible value for elements of  $x$ ),  $O$  as the number of possible observation state categories, and  $T$  as the number of observation times (length of  $x$ ). In dHMM, probObs is a time-independent observation probability matrix with dimension  $S \times O$ . In dHMMo, probObs is a three-dimensional array of time-dependent observation probabilities with dimension  $S \times O \times T$ . The first index of probObs indexes the true latent state. The second index of probObs indexes the observed state. For example, in the time-dependent case,  $\text{probObs}[i, j, t]$  is the probability at time  $t$  that an individual in state  $i$  is observed in state  $j$ .

probTrans has dimension  $S \times S$ .  $\text{probTrans}[i, j]$  is the time-independent probability that an individual in state  $i$  at time  $t$  transitions to state  $j$  time  $t+1$ .

init has length  $S$ .  $\text{init}[i]$  is the probability of being in state  $i$  at the first observation time. That means that the first observations arise from the initial state probabilities.

For more explanation, see package vignette (`vignette("Introduction_to_nimbleEcology")`).

Compared to writing nimble models with a discrete latent state and a separate scalar datum for each observation time, use of these distributions allows one to directly sum (marginalize) over the discrete latent state and calculate the probability of all observations for one individual (or other HMM unit) jointly.

These are nimbleFunctions written in the format of user-defined distributions for NIMBLE's extension of the BUGS model language. More information can be found in the NIMBLE User Manual at <https://r-nimble.org>.

When using these distributions in a `nimble` model, the left-hand side will be used as `x`, and the user should not provide the `log` argument.

For example, in `nimble` model code,

```
observedStates[i, 1:T] ~ dHMM(initStates[1:S], observationProbs[1:S, 1:O], transitionProbs[1:S, 1:S], 1, T)
```

declares that the `observedStates[i, 1:T]` (observation history for individual `i`, for example) vector follows a hidden Markov model distribution with parameters as indicated, assuming all the parameters have been declared elsewhere in the model. As above, `S` is the number of system state categories, `O` is the number of observation state categories, and `T` is the number of observation occasions. This will invoke (something like) the following call to `dHMM` when `nimble` uses the model such as for MCMC:

```
dHMM(observedStates[1:T], initStates[1:S], observationProbs[1:S, 1:O], transitionProbs[1:S, 1:S], 1, T, log = TRUE)
```

If an algorithm using a `nimble` model with this declaration needs to generate a random draw for `observedStates[1:T]`, it will make a similar invocation of `rHMM`, with `n = 1`.

If the observation probabilities are time-dependent, one would use:

```
observedStates[1:T] ~ dHMMo(initStates[1:S], observationProbs[1:S, 1:O, 1:T], transitionProbs[1:S, 1:S], 1, T)
```

### Value

For `dHMM` and `dHMMo`: the probability (or likelihood) or log probability of observation vector `x`.

For `rHMM` and `rHMMo`: a simulated detection history, `x`.

### Author(s)

Ben Goldstein, Perry de Valpine, and Daniel Turek

### References

D. Turek, P. de Valpine and C. J. Paciorek. 2016. Efficient Markov chain Monte Carlo sampling for hierarchical hidden Markov models. *Environmental and Ecological Statistics* 23:549–564. DOI 10.1007/s10651-016-0353-z

### See Also

For dynamic hidden Markov models with time-dependent transitions, see [dDHMM](#) and [dDHMMo](#). For simple capture-recapture, see [dCJS](#).

### Examples

```
# Set up constants and initial values for defining the model
len <- 5 # length of dataset
dat <- c(1,2,1,1,2) # A vector of observations
init <- c(0.4, 0.2, 0.4) # A vector of initial state probabilities
probObs <- t(array( # A matrix of observation probabilities
  c(1, 0,
    0, 1,
    0.2, 0.8), c(2, 3)))
probTrans <- t(array( # A matrix of transition probabilities
```

```

      c(0.6, 0.3, 0.1,
        0, 0.7, 0.3,
        0, 0, 1), c(3,3)))

# Define code for a nimbleModel
nc <- nimbleCode({
  x[1:5] ~ dHMM(init[1:3], probObs = probObs[1:3,1:2],
               probTrans = probTrans[1:3, 1:3], len = 5, checkRowSums = 1)

  for (i in 1:3) {
    for (j in 1:3) {
      probTrans[i,j] ~ dunif(0,1)
    }

    probObs[i, 1] ~ dunif(0,1)
    probObs[i, 2] <- 1 - probObs[i, 1]
  }
})

# Build the model
HMM_model <- nimbleModel(nc,
                        data = list(x = dat),
                        inits = list(init = init,
                                     probObs = probObs,
                                     probTrans = probTrans))

# Calculate log probability of data from the model
HMM_model$calculate()
# Use the model for a variety of other purposes...

```

---

dNmixture

*N-mixture distribution for use in nimble models*


---

## Description

dNmixture\_s and dNmixture\_v provide Poisson-Binomial mixture distributions of abundance ("N-mixture") for use in nimble models. Overdispersion alternatives are also provided.

## Usage

```
dNmixture_v(x, lambda, prob, Nmin = -1, Nmax = -1, len, log = 0)
```

```
dNmixture_s(x, lambda, prob, Nmin = -1, Nmax = -1, len, log = 0)
```

```
rNmixture_v(n, lambda, prob, Nmin = -1, Nmax = -1, len)
```

```
rNmixture_s(n, lambda, prob, Nmin = -1, Nmax = -1, len)
```

```
dNmixture_BNB_v(x, lambda, theta, prob, Nmin = -1, Nmax = -1, len, log = 0)
```



```
dNmixture_BNB_s(x, lambda, theta, prob, Nmin = -1, Nmax = -1, len, log = 0)

dNmixture_BNB_oneObs(
  x,
  lambda,
  theta,
  prob,
  Nmin = -1,
  Nmax = -1,
  len,
  log = 0
)

dNmixture_BBP_v(x, lambda, prob, s, Nmin = -1, Nmax = -1, len, log = 0)

dNmixture_BBP_s(x, lambda, prob, s, Nmin = -1, Nmax = -1, len, log = 0)

dNmixture_BBP_oneObs(x, lambda, prob, s, Nmin = -1, Nmax = -1, len, log = 0)

dNmixture_BBNB_v(x, lambda, theta, prob, s, Nmin = -1, Nmax = -1, len, log = 0)

dNmixture_BBNB_s(x, lambda, theta, prob, s, Nmin = -1, Nmax = -1, len, log = 0)

dNmixture_BBNB_oneObs(
  x,
  lambda,
  theta,
  prob,
  s,
  Nmin = -1,
  Nmax = -1,
  len,
  log = 0
)

rNmixture_BNB_v(n, lambda, theta, prob, Nmin = -1, Nmax = -1, len)

rNmixture_BNB_s(n, lambda, theta, prob, Nmin = -1, Nmax = -1, len)

rNmixture_BNB_oneObs(n, lambda, theta, prob, Nmin = -1, Nmax = -1, len)

rNmixture_BBP_v(n, lambda, prob, s, Nmin = -1, Nmax = -1, len)

rNmixture_BBP_s(n, lambda, prob, s, Nmin = -1, Nmax = -1, len)

rNmixture_BBP_oneObs(n, lambda, prob, s, Nmin = -1, Nmax = -1, len)

rNmixture_BBNB_v(n, lambda, theta, prob, s, Nmin = -1, Nmax = -1, len)
```

```
rNmixture_BBNB_s(n, lambda, theta, prob, s, Nmin = -1, Nmax = -1, len)
```

```
rNmixture_BBNB_oneObs(n, lambda, theta, prob, s, Nmin = -1, Nmax = -1, len)
```

### Arguments

x	vector of integer counts from a series of sampling occasions.
lambda	expected value of the Poisson distribution of true abundance
prob	detection probability (scalar for dNmixture_s, vector for dNmixture_v).
Nmin	minimum abundance to sum over for the mixture probability. Set to -1 to select automatically (not available for beta binomial variations; see Details).
Nmax	maximum abundance to sum over for the mixture probability. Set to -1 to select automatically (not available for beta binomial variations; see Details).
len	The length of the x vector
log	TRUE or 1 to return log probability. FALSE or 0 to return probability.
n	number of random draws, each returning a vector of length len. Currently only n = 1 is supported, but the argument exists for standardization of "r" functions.
theta	abundance overdispersion parameter required for negative binomial (*NB) N-mixture models. theta is parameterized such that variance of the negative binomial variable x is $\lambda^2 * \theta + \lambda$
s	detection overdispersion parameter required for beta binomial (BB*) N-mixture models. s is parameterized such that variance of the beta binomial variable x is $V(x) = N * \text{prob} * (1 - \text{prob}) * (N + s) / (s + 1)$

### Details

These nimbleFunctions provide distributions that can be used directly in R or in nimble hierarchical models (via [nimbleCode](#) and [nimbleModel](#)).

An N-mixture model defines a distribution for multiple counts (typically of animals, typically made at a sequence of visits to the same site). The latent number of animals available to be counted, N, follows a Poisson or negative binomial distribution. Each count,  $x[i]$  for visit i, follows a binomial or beta-binomial distribution. The N-mixture distributions calculate the marginal probability of observed counts by summing over the range of latent abundance values.

The basic N-mixture model uses Poisson latent abundance with mean lambda and binomial observed counts with size (number of trials) N and probability of success (being counted)  $\text{prob}[i]$ . This distribution is available in two forms, dNmixture\_s and dNmixture\_v. With dNmixture\_s, detection probability is a scalar, independent of visit, so  $\text{prob}[i]$  should be replaced with prob above. With dNmixture\_v, detection probability is a vector, with one element for each visit, as written above.

We also provide three important variations on the traditional N-mixture model: dNmixture\_BNB, dNmixture\_BBP, and dNmixture\_BBNB. These distributions allow you to replace the Poisson (P) abundance distribution with the negative binomial (NB) and the binomial (B) detection distribution with the beta binomial (BB).

**NOTE: These variants should work but are considered to be in development. Their function names, parameter names, and implementations are subject to change. Use with caution while this message is present. Please contact the authors on the nimble-users listserv if you have any questions. dNmixture\_v and dNmixture\_s are *not* considered to be in development.**

Binomial-negative binomial: BNB N-mixture models use a binomial distribution for detection and a negative binomial distribution for abundance with scalar overdispersion parameter  $\theta$  (0-Inf). We parameterize such that the variance of the negative binomial is  $\lambda^2 * \theta + \lambda$ , so large  $\theta$  indicates a large amount of overdispersion in abundance. The BNB is available in three suffixed forms: dNmixture\_BNB\_v is used if prob varies between observations, dNmixture\_BNB\_s is used if prob is scalar (constant across observations), and dNmixture\_BNB\_oneObs is used if only one observation is available at the site (so both  $x$  and prob are scalar).

Beta-binomial-Poisson: BBP N-mixture uses a beta binomial distribution for detection probabilities and a Poisson distribution for abundance. The beta binomial distribution has scalar overdispersion parameter  $s$  (0-Inf). We parameterize such that the variance of the beta binomial is  $N * \text{prob} * (1-\text{prob}) * (N + s) / (s + 1)$ , with greater  $s$  indicating less variance (greater-than-binomial relatedness between observations at the site) and  $s \rightarrow 0$  indicating the binomial. The BBP is available in three suffixed forms: dNmixture\_BBP\_v is used if prob varies between observations, dNmixture\_BBP\_s is used if prob is scalar (constant across observations), and dNmixture\_BBP\_oneObs is used if only one observation is available at the site (so both  $x$  and prob are scalar).

Beta-binomial-negative-binomial: dNmixture\_BBNB is available using a negative binomial abundance distribution and a beta binomial detection distribution. dNmixture\_BBNB is available with \_s, \_v, and \_oneObs suffixes as above and requires both arguments  $s$  and  $\theta$  as parameterized above.

The distribution dNmixture\_oneObs is not provided as the probability given by the traditional N-mixture distribution for  $\text{length}(x) = 1$  is equivalent to  $\text{dpois}(\text{prob} * \lambda)$ .

For more explanation, see package vignette (`vignette("Introduction_to_nimbleEcology")`).

Compared to writing nimble models with a discrete latent state of abundance  $N$  and a separate scalar datum for each count, use of these distributions allows one to directly sum (marginalize) over the discrete latent state  $N$  and calculate the probability of all observations for a site jointly.

If one knows a reasonable range for summation over possible values of  $N$ , the start and end of the range can be provided as  $N_{\min}$  and  $N_{\max}$ . Otherwise one can set both to -1, in which case values for  $N_{\min}$  and  $N_{\max}$  will be chosen based on the 0.0001 and 0.9999 quantiles of the marginal distributions of each count, using the minimum over counts of the former and the maximum over counts of the latter.

The summation over  $N$  uses the efficient method given by Meehan et al. (2020). See Appendix B for the algorithm.

These are nimbleFunctions written in the format of user-defined distributions for NIMBLE's extension of the BUGS model language. More information can be found in the NIMBLE User Manual at <https://r-nimble.org>.

When using these distributions in a nimble model, the left-hand side will be used as  $x$ , and the user should not provide the log argument.

For example, in nimble model code,

```
observedCounts[i,1:T] ~ dNmixture_v(lambda[i],prob[i,1:T],Nmin,Nmax,T)
```

declares that the `observedCounts[i,1:T]` (observed counts for site  $i$ , for example) vector follows an N-mixture distribution with parameters as indicated, assuming all the parameters have been

declared elsewhere in the model. As above, `lambda[i]` is the mean of the abundance distribution at site `i`, `prob[i, 1:T]` is a vector of detection probabilities at site `i`, and `T` is the number of observation occasions. This will invoke (something like) the following call to `dNmixture_v` when `nimble` uses the model such as for MCMC:

```
dNmixture_v(observedCounts[i, 1:T], lambda[i], prob[i, 1:T], Nmin, Nmax, T, log = TRUE)
```

If an algorithm using a `nimble` model with this declaration needs to generate a random draw for `observedCounts[1:T]`, it will make a similar invocation of `rNmixture_v`, with `n = 1`.

If the observation probabilities are visit-independent, one would use:

```
observedCounts[1:T] ~ dNmixture_s(observedCounts[i, 1:T], lambda[i], prob[i], Nmin, Nmax, T)
```

## Value

For `dNmixture_s` and `dNmixture_v`: the probability (or likelihood) or log probability of observation vector `x`.

For `rNmixture_s` and `rNmixture_v`: a simulated detection history, `x`.

## Author(s)

Ben Goldstein, Lauren Ponisio, and Perry de Valpine

## References

D. Turek, P. de Valpine and C. J. Paciorek. 2016. Efficient Markov chain Monte Carlo sampling for hierarchical hidden Markov models. *Environmental and Ecological Statistics* 23:549–564. DOI 10.1007/s10651-016-0353-z

Meehan, T. D., Michel, N. L., & Rue, H. (2020). Estimating Animal Abundance with N-Mixture Models Using the R—INLA Package for R. *Journal of Statistical Software*, 95(2). <https://doi.org/10.18637/jss.v095.i02>

## See Also

For occupancy models dealing with detection/nondetection data, see [dOcc](#). For dynamic occupancy, see [dDynOcc](#).

## Examples

```
# Set up constants and initial values for defining the model
len <- 5 # length of dataset
dat <- c(1,2,0,1,5) # A vector of observations
lambda <- 10 # mean abundance
prob <- c(0.2, 0.3, 0.2, 0.1, 0.4) # A vector of detection probabilities

# Define code for a nimbleModel
nc <- nimbleCode({
  x[1:5] ~ dNmixture_v(lambda, prob = prob[1:5],
                      Nmin = -1, Nmax = -1, len = 5)

  lambda ~ dunif(0, 1000)

  for (i in 1:5) {
```

```

      prob[i] ~ dunif(0, 1)
    }
  })

# Build the model
nmix <- nimbleModel(nc,
  data = list(x = dat),
  inits = list(lambda = lambda,
               prob = prob))
# Calculate log probability of data from the model
nmix$calculate()
# Use the model for a variety of other purposes...

```

dOcc

*Occupancy distribution suitable for use in nimble models***Description**

dOcc\_\* and rOcc\_\* provide occupancy model distributions that can be used directly from R or in nimble models.

**Usage**

```
dOcc_s(x, probOcc, probDetect, len = 0, log = 0)
```

```
dOcc_v(x, probOcc, probDetect, len = 0, log = 0)
```

```
rOcc_s(n, probOcc, probDetect, len = 0)
```

```
rOcc_v(n, probOcc, probDetect, len = 0)
```

**Arguments**

x	detection/non-detection vector of 0s (not detected) and 1s (detected).
probOcc	occupancy probability (scalar).
probDetect	detection probability (scalar for dOcc_s, vector for dOcc_v).
len	length of detection/non-detection vector (see below).
log	TRUE or 1 to return log probability. FALSE or 0 to return probability.
n	number of random draws, each returning a vector of length len. Currently only n = 1 is supported, but the argument exists for standardization of "r" functions.

**Details**

These nimbleFunctions provide distributions that can be used directly in R or in nimble hierarchical models (via [nimbleCode](#) and [nimbleModel](#)).

The probability of observation vector x depends on occupancy probability, probOcc, and detection probability, probDetect or probDetect[1:T].

The letter following the 'dOcc\_' indicates whether detection probability is scalar (s, meaning probDetect is detection probability for every  $x[t]$ ) or vector (v, meaning probDetect[t] is detection probability for  $x[t]$ ).

When used directly from R, the len argument to dOcc\_\* is not necessary. It will default to the length of x. When used in nimble model code (via nimbleCode), len must be provided (even though it may seem redundant).

For more explanation, see package vignette (vignette("Introduction\_to\_nimbleEcology")).

Compared to writing nimble models with a discrete latent state for true occupancy status and a separate scalar datum for each observation, use of these distributions allows one to directly sum (marginalize) over the discrete latent state and calculate the probability of all observations from one site jointly.

These are nimbleFunctions written in the format of user-defined distributions for NIMBLE's extension of the BUGS model language. More information can be found in the NIMBLE User Manual at <https://r-nimble.org>.

When using these distributions in a nimble model, the left-hand side will be used as x, and the user should not provide the log argument.

For example, in nimble model code,

```
detections[i,1:T] ~ dOcc_s(occupancyProbability,detectionProbability,T)
```

declares that detections[i,1:T] (detection history at site i, for example) follows an occupancy distribution with parameters as indicated, assuming all the parameters have been declared elsewhere in the model. This will invoke (something like) the following call to dOcc\_s when nimble uses the model such as for MCMC:

```
dOcc_s(detections[i,1:T],occupancyProbability,detectionProbability,len = T,log = TRUE)
```

If an algorithm using a nimble model with this declaration needs to generate a random draw for detections[i,1:T], it will make a similar invocation of rOcc\_s, with n = 1.

If the detection probabilities are time-dependent, use:

```
detections[i,1:T] ~ dOcc_v(occupancyProbability,detectionProbability[1:T],len = T)
```

## Value

For dOcc\_\*: the probability (or likelihood) or log probability of observation vector x.

For rOcc\_\*: a simulated detection history, x.

## Author(s)

Ben Goldstein, Perry de Valpine, and Lauren Ponisio

## See Also

For dynamic occupancy models, see documentation for [dDynOcc](#).

**Examples**

```

# Set up constants and initial values for defining the model
dat <- c(1,1,0,0) # A vector of observations
probOcc <- 0.6
probDetect <- 0.4

# Define code for a nimbleModel
nc <- nimbleCode({
  x[1:4] ~ dOcc_s(probOcc, probDetect, len = 4)
  probOcc ~ dunif(0,1)
  probDetect ~ dunif(0,1)
})

# Build the model, providing data and initial values
Occ_model <- nimbleModel(nc, data = list(x = dat),
                        inits = list(probOcc = probOcc,
                                     probDetect = probDetect))

# Calculate log probability of data from the model
Occ_model$calculate()
# Use the model for a variety of other purposes...

```

---

nimNmixPois\_logFac      *Helper function for fast N-mixture calculation*

---

**Description**

Helper function for fast N-mixture calculation

**Usage**

```
nimNmixPois_logFac(numN, ff)
```

**Arguments**

numN	first argument for helper function <code>nimNmixPois_logFac</code> , representing the number of indices in the truncated sum for the N-mixture.
ff	second argument for helper function <code>nimNmixPois_logFac</code> , a derived vector of units calculated partway through the fast N-mixture algorithm.

**Details**

This is a helper function for the fast N-mixture calculation. It runs an iterative calculation present in all N-mixture varieties. It doesn't have an interpretation outside of that context.

**See Also**

[dNmixture](#)

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