

# Package: mpbutils (via r-universe)

September 15, 2024

**Type** Package

**Title** Utilities for Mountain Pine Beetle Simulation Modelling

**Description** Utilities for mountain pine beetle (MPB) simulation modelling.

**Date** 2024-07-16

**Version** 0.1.3.9002

**Depends** R (>= 3.6)

**Imports** amc, data.table (>= 1.10.4), ggplot2, magrittr, methods, reproducible, sf, stats, terra, utils

**Suggests** roxygen2

**Remotes** achubaty/amc@development

**Encoding** UTF-8

**Language** en-CA

**License** GPL-3

**VignetteBuilder** knitr, rmarkdown

**BugReports** <https://github.com/PredictiveEcology/mpbutils/issues>

**ByteCompile** yes

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Repository** <https://predictiveecology.r-universe.dev>

**RemoteUrl** <https://github.com/PredictiveEcology/mpbutils>

**RemoteRef** HEAD

**RemoteSha** 36289d879b1c3f22c5a3352e39327e1c3d81959c

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binaryStacks	<i>Create a set of binary stacks from quantitative stacks</i>
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### Description

This is for converting forecasted abundance stacks in a list of simList objects into a list of binary stacks (presence/absence)

This is for converting forecasted abundance stack in a simList object into a binary stack (presence/absence)

The mask will occur with values of NA or values of 0.

### Usage

```
binaryStacks(
  sims,
  thresholdAttackTreesMinDetectable = 1.4,
  thresholdPineProportion = 0.3,
  stackName = "predictedStack",
  propPineRasName = "propPineRas"
)

binaryStack(
  stk,
  propPineRas,
  thresholdAttackTreesMinDetectable = 1.4,
  thresholdPineProportion = 0.3
)

maskWPine(ras, propPineRas, thresholdPineProportion)
```

### Arguments

sims	a list of simLists
thresholdAttackTreesMinDetectable	A scalar that delineates presence from an absence. Default is 1.4, which was derived from initial efforts to find a single value that works in all years.
thresholdPineProportion	A scalar. Values on the propPineRas that are below this threshold will be masked out, i.e., set to NA.
stackName	Character string. The name of the stack inside the simLists to use

propPineRasName	Character string. The name of the RasterLayer inside the simLists to use for proportion Pine.
stk	A stack of abundance
propPineRas	A RasterLayer that has values between 0 and 1, representing the proportion of pine cover in the pixel.
ras	A RasterLayer of abundance

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cleanUpPredictionRas *Cleans the predicted raster*

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### Description

Cleans the predicted raster

### Usage

```
cleanUpPredictionRas(
  rasLog,
  propPineRas,
  thresholdAttackTreesMinDetectable = 1.4,
  thresholdPineProportion = 0.3
)
```

### Arguments

rasLog            A RasterLayer of predicted mass attack, on a log scale

propPineRas      A RasterLayer of proportion pine cover.

thresholdAttackTreesMinDetectable  
                   A scalar. This will have come from an optim call to estimate this using AUC and ROC. THIS IS NOT ON A LOG SCALE. It will be logged internally.

thresholdPineProportion  
                   A scalar. The proportion of pine

years             A scalar indicating how many years are included in the rasLog

### Value

A RasterLayer with ever

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cumulativeMap	<i>Calculate cumulative sum of a stack, with optional log</i>
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**Description**

Calculate cumulative sum of a stack, with optional log

**Usage**

```
cumulativeMap(stk, log = TRUE)
```

**Arguments**

stk	a RasterStack
log	Logical. Will take $\log(\text{map}) + 1$

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growthFunction	<i>MPB red top growth function</i>
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**Description**

From Cooke and Carroll (2017).

**Usage**

```
growthFunction(x, s, dataset, growthData)
```

**Arguments**

x	beetle density
s	climate suitability factor
dataset	dataset name used for fitting: one of "Berryman1979_fit", "Berryman1979_forced", "Boone2011".
growthData	MPB red top growth data with which to fit.

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kernel_twoDT	<i>2Dt kernel</i>
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### Description

This is a 2-dimensional t-distribution that can be used for dispersal of natural entities. It has many characteristics (see Clark et al 1999)

### Usage

```
kernel_twoDT(dist, mu, p)
```

```
kernel_twoDT_mean(mu, m)
```

### Arguments

dist	A vector of distances
mu	The first parameter of the 2Dt kernel. This represents about 0.9 of the mean dispersal distance
p	The second parameter of the 2Dt kernel. This changes the shape.

### Value

A vector of probabilities

### References

Clark, J. S., M. Silman, R. Kern, E. Macklin, and J. HilleRisLambers. 1999. Seed dispersal near and far: patterns across temperate and tropical forests. *Ecology* 80:1475–1494.

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mpbStudyArea	<i>Create study area based o ecoregion selection</i>
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### Description

Create study area based o ecoregion selection

### Usage

```
mpbStudyArea(ecoregions = c(112, 120, 122, 124, 126), targetCRS, cPath, dPath)
```

**Arguments**

ecoregions	numeric vector indicating which ecoregions to be included as part of the study area. Derived from <a href="http://sis.agr.gc.ca/cansis/nsdb/ecostrat/region/ecoregion_shp.zip">http://sis.agr.gc.ca/cansis/nsdb/ecostrat/region/ecoregion_shp.zip</a> .
targetCRS	target CRS string to use for reprojecting ecodistrict (study area) polygons.
cPath	cache path
dPath	destination path

**Value**

an sf object

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xt	<i>MPB recruitment function</i>
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**Description**

From Cooke & Carroll (2017).

**Usage**

```
xt(xtminus1, cs, dataset, massAttacksMap, growthData)
```

**Arguments**

xtminus1	previous year's attack density
cs	climate suitability factor
dataset	dataset name used for fitting: one of "Berryman1979_fit", "Berryman1979_forced", "Boone2011".
massAttacksMap	RasterLayer of red attack densities
growthData	MPB red top growth data with which to fit.

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