

# Package ‘MixFishSim’

October 12, 2016

**Title** Mixed Fishery fleet dynamics simulation tool

**Version** 0.0.0.9000

**Description** A simulation framework for evaluating fleet dynamics in mixed fisheries.

**Depends** R (>= 3.3.1),

**Imports** spat

**License** What license is it under?

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 5.0.1

**Suggests** testthat

## R topics documented:

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|               |   |
|---------------|---|
| create_fields | <i>Create species distribution fields</i> |
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## Description

create\_fields parametrises and returns the spatio-temporal fields used for the spatial distribution of fish populations and movement in space and time for the simulations.

The spatio-temporal fields are generated using `spate.sim` function from the *spate* package using an advective-diffusion Stochastic Partial Differential Equation (SPDE). See *Lindgren 2011 and Sigrist 2015* for further detail.

**Usage**

```
create_fields(npt = 1000, t = 1, seed = 123, n.spp = NULL,
             spp.ctrl = NULL, plot.dist = FALSE, plot.file = getwd())
```

**Arguments**

|           |   |
|-----------|---|
| npt       | Numeric integer with the dimensions of the field in $npt * npt$   |
| t         | Numeric integer with the number of time-steps in the simulation   |
| seed      | (Optional) Numeric integer with the seed for the simulation   |
| n.spp     | Numeric integer with the number of species to be simulated. Each species must have an individual control list as detailed below.  |
| spp.ctrl  | List of controls to generate each species spatio-temporal distribution. Must be of the form <code>spp.ctrl = list(spp.1 = c(rho0 = 0.001, ...), spp.2 = c(rho0 = 0.001, ..),...)</code> and contain the following: <ul style="list-style-type: none"> <li>• <b>rho0</b> (<math>\geq 0</math>) Controls the range in a matern covariance structure.</li> <li>• <b>sigma2</b> (<math>\geq 0</math>) Controls the marginal variance (i.e. process error) in the matern (<math>\geq 0</math>) covariance structure.</li> <li>• <b>zeta</b> (<math>\geq 0</math>) Damping parameter; regulates the temporal correlation.</li> <li>• <b>rho1</b> (<math>\geq 0</math>) Range parameter for the diffusion process</li> <li>• <b>gamma</b> (<math>\geq 0</math>) Controls the level of anisotropy</li> <li>• <b>alpha</b> (<math>[0, \pi/2]</math>) Controls the direction of anisotropy</li> <li>• <b>muX</b> (<math>[-0.5, 0.5]</math>) x component of drift effect</li> <li>• <b>muY</b> (<math>[-0.5, 0.5]</math>) y component of drift effect</li> <li>• <b>tau2</b> (<math>\geq 0</math>) Nugget effect (measurement error)</li> <li>• <b>nu</b> Smoothness parameter for the matern covariance function</li> </ul> |
| plot.dist | Boolean, whether to plot the distributions to file  |
| plot.file | path to save the plots of the species distributions   |

**Value**

Silently returns a list of spatial distributions (0 -> 1) with first level of the list being the population (1 -> n.spp) and the second being time (1 -> t). If `plot.dist = TRUE` it produces an image of the spatial distributions at each time step for each of the populations saved to the working directory (unless specified otherwise in `plot.file`)

**Examples**

```
fields <- create_fields(n.spp = 1, t = 2,
                      spp.ctrl = list(
                        'spp.1' = c('rho0' = 0.1, 'sigma2' = 1, 'zeta' = 0.1,
                                   'rho1' = 0.01, 'gamma' = 0.3, 'alpha' = pi/4,
                                   'muX' = -0.05, 'muY' = -0.05, 'tau2' = 0, 'nu' = 1.5)),
                      plot.dist = TRUE, plot.file = getwd())
```

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|            |                                  |
|------------|----------------------------------|
| delay_diff | <i>Delay-difference (weekly)</i> |
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### Description

delay\_difference implements a two-stage delay-difference model with a weekly time-step after *Dichmont 2003*. Given the starting biomass, overall mortality and recruitment it returns the biomass in  $wk+1$ .

### Usage

```
delay_diff(K = 0.3, F = NULL, M = 0.2, wt = 1, wtm1 = 0.1, R = NULL,
           B = NULL, Bm1 = NULL, al = NULL, alm1 = NULL)
```

### Arguments

|      |   |
|------|---|
| K    | is a Numeric vector describing growth @param F is the weekly. Note: K is transformed to rho with $\rho = \exp(-K)$ for the model. estimate of instantaneous fishing mortality (obtained elsewhere, via <a href="#">find_f</a> and <a href="#">BaranovF</a> functions. |
| M    | is a Numeric vector of the instantaneous rate of natural mortality for the population   |
| wt   | is a Numeric vector of the weight of a fish when fully recruited  |
| wtm1 | is a Numeric vector of the weight of a fish before its recruited  |
| R    | is a Numeric vector of the annual recruitment for the population in numbers   |
| B    | is the biomass of the population during $wk_t$  |
| Bm1  | is a Numeric vector of the biomass of the population in the previous week $wk_{t-1}$  |
| al   | is a Numeric vector of the proportion of recruits to the fishery in $wk_t$  |
| alm1 | is a Numeric vector of the proportion of recruits to the fishery in $wk_{t-1}$  |

### Value

Returns the biomass at the beginning of the following week,  $wk_{t+1}$

### Examples

```
delay_diff(K = 0.3, F = 0.2, M = 0.2, wt = 1, wtm1 = 0.1, R = 1e6, B = 1e5,
           Bm1 = 1e4, al = 0.5, alm1 = 0.1)
```

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