Package 'fastmaRching'

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Type Package

Title Fast Marching Method for Modelling Evolving Boundaries

Version 1.1.0

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Description Fast Marching Method (FMM) first developed by Sethian (1996) <http://www.pnas.org/content/93/4/1591.short>, and further extended by including a second-order approximation, the first-arrival rule, additive weights, and non-homogeneous domains following Silva and Steele (2012) <doi:10.1142/S0219525911003293> and Silva and Steele (2014) <doi:10.1016/j.jas.2014.04.02

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Imports compiler, sp, raster, rgdal

NeedsCompilation no

Repository CRAN

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R topics documented:

| gridFastMarch | *Runs the grid version of the Modified Fast Marching Method* |

Description

This function runs the Modified Fast Marching Method of Silva and Steele (2012,2014) on a gridded domain.

Usage

```
gridFastMarch(domain, seeds, spatial.res = 1)
```

Arguments

domain	Grid (matrix) of chosen dimension with diffusivity values for every grid cell. Values above 1 will boost diffusivity, below 1 will inhibit it. Values of 0 should mark cells that block diffusion.
seeds	A (4 x n) array containing the x-coordinate, y-coordinate, incept time and rate-of-spread for each of the n seeds.
spatial.res	(Optional) Spatial resolution of the grid, necessary only to correct the rate-of-spread unit. See example below. Defaults to 1.

References

Sethian, J.A. (1996), A fast marching level set method for monotonically advancing fronts, *Proc. Natl. Acad. Sci.* 93 (4), 1591-1595.

Silva, F. and Steele, J. (2012), Modeling Boundaries Between Converging Fronts in Prehistory, *Advances in Complex Systems*, 15(1-2), 1150005, <doi:10.1142/S0219525911003293>

Silva, F. and Steele, J. (2014), New methods for reconstructing geographical effects on dispersal rates and routes from large-scale radiocarbon databases, *Journal of Archaeological Science* 52, 609-620, <doi:10.1016/j.jas.2014.04.021>

Examples

```
# Single process
grid <- matrix(1,10,10)
seed <- c(5,5,0,1)
fm <- gridFastMarch(grid, seed)
image(fm$arrival.time)

# Two processes with same incept time
seeds <- cbind(c(7,7,0,1),c(2,2,0,1))
fm2 <- gridFastMarch(grid, seeds)
par(mfrow=c(1,3))
image(fm2$process, main='process')
image(fm2$arrival.time, main='arrival time')
image(fm2$cost.distance, main='distance')
```

```
# Same as before but changing spatial.res parameter
fm3 <- gridFastMarch(grid, seeds, spatial.res=10)

# Same as before but with a barrier in middle
grid[5,2:9] <- 0
fm4 <- gridFastMarch(grid, seeds, spatial.res=10)
par(mfrow=c(1,3))
image(fm4$process, main='process')
image(fm4$arrival.time, main='arrival time')
image(fm4$cost.distance, main='distance')

# Same as before but with different incept times and speeds
seeds <- cbind(c(7,7,0,1),c(2,2,1,0.5))
fm5 <- gridFastMarch(grid, seeds, spatial.res=10)
par(mfrow=c(1,3))
image(fm5$process, main='process')
image(fm5$arrival.time, main='arrival time')
image(fm5$cost.distance, main='distance')
```

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spFastMarch   *Runs the spatial version of the Modified Fast Marching Method*

Description

This function runs the Modified Fast Marching Method of Silva and Steele (2012,2014) from *sp* and
raster objects and outputs results in the same formats, makin it more convenient for (geo)spatial
analyses and simulation.

Usage

```
spFastMarch(domain, seeds, spatial.res)
```

Arguments

domain	A raster object of chosen dimension and resolution with diffusivity values for every cell. Values above 1 will boost diffusivity, below 1 will inhibit it. Values of 0 should mark cells that block diffusion.
seeds	A SpatialPointsDataFrame object containing the incept time and rate-of-spread for each of the n seeds in its data.frame, in columns named exactly *incept* (for incept time) and *speed* (for rate-of-spread). This object will be automatically transformed to the projection of *domain*.
spatial.res	(Optional) Spatial resolution of the raster, necessary only to correct the rate-of-spread unit. Defaults to that of the raster used for domain.

References

Sethian, J.A. (1996), A fast marching level set method for monotonically advancing fronts, *Proc. Natl. Acad. Sci.* 93 (4), 1591-1595, doi:

Silva, F. and Steele, J. (2012), Modeling Boundaries Between Converging Fronts in Prehistory, *Advances in Complex Systems*, 15(1-2), 1150005, doi: 10.1142/S0219525911003293

Silva, F. and Steele, J. (2014), New methods for reconstructing geographical effects on dispersal rates and routes from large-scale radiocarbon databases, *Journal of Archaeological Science* 52, 609-620, doi: 10.1016/j.jas.2014.04.021

Examples

```
library(raster); library(sp); library(rgdal)
domain <- raster(system.file("external/test.grd", package="raster")) # sample raster
domain <- domain > 0 # flattening elevation data
coords <- cbind(c(179000,181200), c(330000, 333000)) # coordinates for seeds
seed.df <- data.frame(incept=c(0,10), speed=c(.1,.1)) # incept time and speed for each seed
seeds <- SpatialPointsDataFrame(coords, seed.df, proj4string=crs(domain))

fm <- spFastMarch(domain, seeds)
par(mfrow=c(1,3))
plot(fm$process, main='process')
plot(fm$arrival.time, main='arrival time')
plot(fm$cost.distance, main='distance')
```

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