

Package ‘eco.buffer’

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Title Delineates Ecologically-Defined Buffers Around Target Conservation Areas

Version 0.9.0

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Description # Delineates ecologically-defined buffers around target conservation areas using resistant kernels. Given conservation areas of interest ('seeds'), and a resistant surface (either one or more rasters or a landcover and table with a resistance for each class), eco.buffer builds resistant kernel polygons or rasters around each seed to delineate areas of conservation interest for seeds. Seeds may be point, line, or polygon shapefiles, typically delineating known locations for species of concern, rare ecological communities, or conservation cores.

License GPL-3

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Imports gridprocess,
raster,
rgdal,
rgeos,
utils

R topics documented:

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eco.buffer	<i>Ecological Buffer Tool Delineates ecologically-defined buffers around target conservation areas using a resistant kernel</i>
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Description

Ecological Buffer Tool Delineates ecologically-defined buffers around target conservation areas using a resistant kernel

Usage

```
eco.buffer(
  seeds,
  bandwidth,
  seedid = "Id",
  result = NULL,
  resultgrid = NULL,
  resist = NULL,
  resist.table = NULL,
  default.resist = NULL,
  landcover = "",
  barrier = NULL,
  passage = NULL,
  resist.mult = 1,
  resist.table.mult = 1,
  barrier.mult = 1,
  passage.mult = 1,
  save.resist = NULL,
  path = "",
  density = 1,
  expand = 0,
  screen = NULL,
  broccoli = NULL,
  flow = NULL,
  accumulation = NULL,
  streams = NULL,
  clip = NULL,
  fullextent = FALSE,
  simplify = TRUE,
  simplify.tolerance = 30,
  verbose = TRUE,
  timing = TRUE
)
```

Arguments

seeds	a shapefile of points, lines, or polygons designating conservation targets
bandwidth	maximum distance (m) to spread through cells of resistance = 1.
seedid	name of numeric ID column in seeds shapefile.
result	name of result polygon shapefile of ecological buffers.
resultgrid	name of result kernel grid (optional). If resultgrid is supplied, a graduated kernel representation of buffers will be created, useful for exploring parameterization and visualizing kernel-creation process.
resist	landscape resistance grid. Optional if landcover and resist.table are used to assign resistance by landcover type. Resistance values should range from 1 to infinity. Use resist.mult to invert positive grids.
resist.table	optional tab-delimited text file. Defines resistance value for each landcover class (ranging from 1 to infinity). Columns must include class (numeric landcover class) and resist (resistance value); additional columns may include landcover name for reference (highly recommended) and comments. Resistance ranges

	from 1 to infinity. If both resist and resist.table are supplied, the values from the resist raster will be used for values that are absent in the table.
default.resist	value to use for classes not included in table, or NULL to throw error if any values in landcover are missing from table. Nodata cells (outside of the landscape) always get a high resistance.
landcover	landcover grid. May be used to designate resistance values with resist.table; also used with screen option.
barrier	grid with resistance values for barriers, used as a complement to resist or resist.table, the maximum resistance of resist/resist.table will be used for each cell. Use to supply values for aquatic barriers (bridges, culverts, and dams), with nodata for other cells.
passage	grid with resistance values for cells that provide passage, reducing resistance, used as a complement to resist or resist.table. The minimum of resist/resist.table and passage will be used for each cell. Use to supply terrestrial passage over or under roads (bridges and wildlife passage structures), with nodata for other cells.
resist.mult	multiplier on resistance grid, such that such that resistance values that originally range from 0 to n or 1 to n will range from 1 to approximately $n * \text{resist.mult}$ after multiplying. Use a negative multiplier to invert the resistances when using a positive grid, where higher values denote lower resistance. The minimum and maximum resistances are needed for this procedure. They are obtained from the entire raster before any clipping. If you are running on tiled data, you may need to supply the overall minimum and maximum as the 2nd and 3rd elements. The default multiplier is 1, thus resistance values are used directly (or 1 is added if the minimum is 0).
resist.table.mult	multiplier on resistances from a table. See resist.mult.
barrier.mult	multiplier on barrier resistances. See resist.mult.
passage.mult	multiplier on passage resistances. See resist.mult.
save.resist	specify a result TIFF to write the realized resistance grid to, for assessing complex combinations of resistance sources.
path	base path prepended to input and result names/paths. Inputs that include a complete path (starting with / or a drive letter) don't use path. This option helps keep the inputs cleaner, and makes for easy switching to different sets of inputs and results.
density	build kernels for every nth cell to speed things up. By default, density = 1, and resistant kernels are built from each edge cell in seeds; a larger value will decrease runtime (by density2) at the cost of precision. You can get away with higher values for density when using larger bandwidths.
expand	distance to expand seeds (m). Use with screen to apply lines to wide streams, for example. If expanded seeds overlap, the overlapping area will be arbitrarily assigned the seedid of one of the seeds.
screen	limit seeds to these landcover classes (requires landcover). Use this if seeds are sloppy, e.g. when designating stream cores from vector data that don't correspond exactly to streams in landcover, or to exclude development classes from conservation target polygons.
broccoli	include entire watershed above point in stream if watershed area at point is $\leq x \text{ km}^2$ (requires flow, accumulation, and streams grids). Used to include the entirety of small watersheds.

flow	flow direction grid, used with broccoli option. Grid is a standard D8 grid.
accumulation	flow accumulation grid, used with broccoli option.
streams	stream centerline grid, used with the broccoli option.
clip	a polygon shapefile to clip the analysis to. Use this when developing parameters and testing to speed runs up immensely.
fullextent	if TRUE, produces a result grid at the full extent of the landscape. This runs more slowly, so use the default of FALSE unless you have a good reason not to. If TRUE, all grids are clipped to the reference grid (landcover if it exists, otherwise, reference grid) to enforce alignment.
simplify	if TRUE, simplify result polygons; if FALSE, polygons exactly match raster.
simplify.tolerance	polygon smoothing parameter used if simplify = TRUE. Larger values give simpler polygons.
verbose	set to FALSE to suppress informational chatter.
timing	display timing messages if TRUE (verbose must be TRUE too).

Details

The ecological buffer tool **eco.buffer** is a stand-alone R package for delineating ecologically-defined buffers around target conservation areas. Targeted areas are designated by point, line, or polygon shapefiles. Buffers are based on resistant kernels with flexible parameters to accommodate terrestrial or aquatic settings. Landscape resistance can be defined by a landcover raster and a table of classes and resistance values, directly from resistance rasters, or from a combination of a resistance table and rasters. Results are a polygon shapefile of ecological buffers and an optional geoTIFF raster of the resistant kernels.

The buffer tool is based on resistant kernels (Compton et. al 2007), which have been used in a number of conservation applications since 2003, including estimating local and regional connectivity (McGarigal et al. 2018) and building terrestrial and aquatic conservation cores in Designing Sustainable Landscapes/Nature's Network (McGarigal et al. 2017); they have also been used in TNC's Resilient Sites for Terrestrial Conservation and Massachusetts Natural Heritage's Living Waters and BioMap 2.

Notes

1. Resistance values must range from 1 to infinity. The spread value starts in each focal cell (all edge cells of each seed) at bandwidth / cell size. At each cell, the cell's resistance x multiplier is subtracted from the spread value. For example, a bandwidth of 5000 m when the cell size is 30 m gives a spread value of 166.67. The spread will stop once it has passed through cells with a cumulative resistance * multiplier of 166.67. Resistances greater than or equal to this value will stop the spread at a single cell, thus these cells act as complete barriers.
2. Raster inputs may be either Arc grids or geoTIFFs (other formats will likely work).
3. The seeds shapefile may be singlepart or multipart.
4. The seed id field (specified with the seedid option) will be preserved in the resulting buffer polygon. When result buffers overlap, the id of the seed with a shortest cost-distance to each point will be used.
5. When using the CAPS landcover for terrestrial cores, make sure to set the resistance of classes 60 (Bridge or culvert) and 61 (Dam) to the maximum road resistance, as these classes interrupt roads, thus with a lower resistance, they can allow a kernel to spread across roads where they occur.

6. When using the CAPS landcover for aquatic cores, you may want to use the Aquatic Barriers (abarriers) grid as a secondary resistance grid using the barriers option, to assign resistance to each bridge or culvert and each dam based on estimates of their aquatic passability.
7. If both a resistance raster (resist option) and resistance table (resist.table and landcover options) are supplied, the table is used for all classes in the table, and the raster is used for any classes not in the table (default.resist will be ignored).
8. When testing and developing parameters, runtime will be much faster if you limit seeds to a relatively small geographic area, or use the clip option select a small area of the landscape.
9. All input grids will be snapped and clipped to the reference grid—the landcover, if supplied, or else the resistance grid.

References

Compton, B.W., K. McGarigal, S.A. Cushman, and L.R. Gamble. 2007. A resistant-kernel model of connectivity for amphibians that breed in vernal pools. *Conservation Biology* 21:788-799. doi: [10.1111/j.15231739.2007.00674.x](https://doi.org/10.1111/j.15231739.2007.00674.x).

McGarigal, K., B.W. Compton, E.B. Plunkett, W.V. DeLuca, J. Grand, E. Ene, and S.D. Jackson. 2018. A landscape index of ecological integrity to inform landscape conservation. *Landscape Ecology* 33:1029-1048. doi: [10.1007/s1098001806539](https://doi.org/10.1007/s1098001806539).

McGarigal K., B.W. Compton, E.B. Plunkett, W.V. DeLuca, and J. Grand. 2017. Designing sustainable landscapes: landscape conservation design. Report to the North Atlantic Conservation Cooperative, US Fish and Wildlife Service, Northeast Region. http://landeco.umass.edu/web/lcc/dsl/technical/DSL_documentation_landscape_design.pdf

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Examples

```
### Set up temporary directory for examples
require(eco.buffer)
dp <- paste(shortPathName(system.file('exampledata', package='eco.buffer')), '/', sep = '')
dir <- tempdir()
if(!file.exists(dir)) dir.create(dir)
file.copy(dp, dir, recursive=TRUE)
cat('Example data and results will be in', dir)

### 1. terrestrial kernels (creates test1.shp and testg1.tif)
eco.buffer('seed_points', bandwidth = 2000, landcover = 'capsland.tif',
resist.table = 'resistance.txt', result = 'test1', resultgrid = 'testg1.tif', path = dir)

### 2. WMA poly example (creates WMAtest2.shp)
eco.buffer('wma_seeds', 5000, landcover = 'capsland.tif', resist = 'iei.tif', resist.mult = -30,
resist.table = 'resist_dev.txt', result = 'WMAtest2', path = dir)

### 3. stream cores (creates stream_test3.tif)
eco.buffer('stream_seeds', bandwidth = 3000, landcover = 'capsland.tif',
resist.table = 'resist_streams.txt', default.resist = 999, barrier = 'abarriers.tif',
barrier.mult = 100, result = 'stream_test3', simplify = FALSE, path = dir)
```

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