

# Package ‘neighborhood’

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**Type** A package

**Title** An R package to determine the neighborhood competitive environment of trees

**Version** 0.1.0

**Author** Aitor Ameztegui - Universitat de Lleida

**Maintainer** Aitor Ameztegui <aitor.ameztegui@udl.cat>

**Description**

Functions to define and characterize neighborhoods and estimate their effects on forest dynamics

**License** MIT

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

**Imports** dplyr, tidyr, likelihood

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create_nci_files	<i>create_nci_files</i>
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## Description

function to create the files needed to estimate NCI-growth equations using the anneal function of the likelihood package.

## Usage

```
create_nci_files(df, dbh, sp, x, y, plot_ID, self_del = T)
```

**Arguments**

df	the data frame containing information about the target trees.
dbh	variable in 'df' that contains the diameter of the trees.
sp	variable in 'df' that contains the specific identity of trees
x	variable in 'df' that contains the X coordinate of the trees. Coordinates can be referred to any reference point (typically they will refer to either one of the plot corners or the plot center), but all of them must be referred to the same point to allow calculating distances between trees.
y	variable in 'df' that contains the Y coordinate of the trees. Coordinates can be referred to any reference point (typically they will refer to either one of the plot corners or the plot center), but all of them must be referred to the same point to allow calculating distances between trees.
plot_ID	optional. Variable that identifies the plots, or experimental units, within which the neighbors will be considered. This information is used to split the calculations per plot, and the results are merged back into a single data frame. A tree 'b' will not be considered as a neighbor of tree 'a' unless they belong to the same 'plot_ID'. If this argument is missing, all trees in 'df' will be considered both targets and neighbors.
self_del	If 'TRUE', a tree is not included as a neighbor of itself. If 'FALSE' the attribute if the target tree will be also included in the output as a neighbor of itself.

**Details**

create\_nci\_files

**Value**

a list containing three data frames with the values of dbh, species and distance to target tree for each neighbor tree. Each data frame will contain as many rows as target trees, and as many columns as the maximum number of neighbors per tree. Missing values are coded as 'NA'.

**Examples**

```
data(tree_data)

files <- create_nci_files(tree_data, dbh = dbh, sp = sps, x = x, y = y, plot)
```

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get_neighbors	<i>get_neighbors</i>
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**Description**

Function to obtain the neighbors of each tree from a file containing the identities of the trees and, optionally, a variable that identifies the plots.

**Usage**

```
get_neighbors(df, plot_ID, coords, suffixes, max_dist = 10000)
```

**Arguments**

df	the data frame containing the trees for which we want to identify the neighbors, and their associated information
plot_ID	<b>**optional**</b> . Variable that identifies the plots, or experimental units, within which the neighbors will be searched. If this variable exists, a tree "a" can only be a neighbor of another tree "b", if it is fulfilled that plot(a) == plot(b).
coords	<b>**optional**</b> Character vector containing the names of the columns in 'df' containing the x and y coordinates of the trees. By default 'coords = c("x", "y")', i.e. it assumes that the columns are called "x" and "y"
suffixes	<b>**optional**</b> character vector containing the suffixes that will be added to the variables in 'df' to identify target trees and neighbours. By default it takes the value 'suffixes = c("_target", "_neighbor")', but can take any other value defined by user.
max_dist	numeric Maximum distance to search for neighbours of target trees. It takes value 10000 by default.

**Value**

This function identifies the neighbors of each potential "target" tree and creates a data frame that contains a row for each neighbor of each tree in the original data frame. Variables characterizing target and neighbor trees are identified with the suffixes "\_target" and "\_neighbour", respectively. It also computes the distance between each target - neighbor pair, in the same units as provided by the "x" and "y" coordinates.

**Examples**

```
data(tree_data)

neighbors <- get_neighbors(tree_data, plot)

# If not plots are to be considered
all_neighbors <- get_neighbors(tree_data)

# specify suffix for target and neighbors, and maximum distance
neighbors2 <- get_neighbors(tree_data, plot, suffixes = c("cible", "voisin"), max_dist = 10)
```

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```
get_neighbor_variables
      get_neighbor_variables
```

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**Description**

function to obtain the attributes of all the neighbors of a given set of target trees

**Usage**

```
get_neighbor_variables(df, plot_ID, var, self_del = T)
```

Arguments

df	the data frame containing information about the target trees.
plot_ID	optional. Variable that identifies the plots, or experimental units, within which the neighbors will be considered. This information is used to split the calculations per plot, and the results are merged back into a single data frame. A tree 'b' will not be considered as a neighbor of tree 'a' unless they belong to the same 'plot_ID'. If this argument is missing, all trees in 'df' will be considered both targets and neighbors.
var	The variable that we want to extract from the neighbors. It can be either a numeric, logical or character variable.
self_del	If 'TRUE', a tree is not included as a neighbor of itself. If 'FALSE' the attribute if the target tree will be also included in the output as a neighbor of itself.

Details

get\_neighbor\_variables

Value

a data frame containing as many rows as target trees, and as many columns as the maximum number of neighbors per tree. Cells contain values of the variable "var" for each neighbor tree, and missing values are coded as 'NA'.

Examples

```
data(tree_data)

# Get dbhs of all the neighbors
dbhs <-get_neighbor_variables(tree_data, plot, dbh, self_del = T)

# Get species of all the neighbors (including target tree as its own neighbor)
species <-get_neighbor_variables(tree_data, plot, sps, self_del = F)
```

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neighbors	<i>Forest inventory data in Pyrenean forests</i>
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Description

Forest inventory data in Pyrenean forests

Usage

neighbors

**Format**

A data frame with columns:

**plot** Plot identifier

**sps\_target** Target tree species, with 3 possible values: ABAL, PINI or PISY

**dbh\_target** Target tree diameter(cm).

**x\_target** x coordinates of the target tree within the plot, as measured from the plot center (m).

**y\_target** y coordinates of the target tree within the plot, as measured from the plot center (m).

**n\_target** Correlative number identifying target tree position within the plot.

**ID\_target** Unique identifier for target trees

**sps\_neighbor** Neighbor tree species, with 3 possible values: ABAL, PINI or PISY

**dbh\_neighbor** Neighbor tree diameter(cm).

**x\_neighbor** x coordinates of the neighbor tree within the plot, as measured from the plot center (m).

**y\_neighbor** y coordinates of the neighbor tree within the plot, as measured from the plot center (m).

**n\_neighbor** Correlative number identifying neighbor position within the plot.

**ID\_neighbor** Unique identifier for neighbor trees

**Source**

Aitor Ameztegui

**Examples**

```
## Not run:
  neighbors

## End(Not run)
```

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tree\_data

*Forest inventory data in Pyrenean forests*

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**Description**

Forest inventory data in Pyrenean forests

**Usage**

tree\_data

**Format**

A data frame with columns:

**plot** Plot identifier

**sps** Tree species, with 3 possible values: ABAL, PINI or PISY

**dbh** Tree diameter(cm).

**x** x coordinates of the tree within the plot, as measured from the plot center (m).

**y** y coordinates of the tree within the plot, as measured from the plot center (m).

**Source**

Aitor Ameztegui

**Examples**

```
## Not run:  
tree_data
```

```
## End(Not run)
```

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