Package 'morph'

December 10, 2021

Type Package

Title 3D Segmentation of Voxels into Morphologic Classes

Version 1.0.0

Date 2021-11-25

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Description Automatically segments a 3D array of voxels into mutually exclusive morphological elements. This package extends existing work for segmenting 2D binary raster data. A paper documenting this approach has been accepted for publication in the journal Landscape Ecology. Detailed references will be updated here once those are known.

License GPL-3

LazyData true

LazyDataCompression xz

Depends R (>= 4.1.0), rgl, reshape2, igraph, stringr

NeedsCompilation no

Repository CRAN

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Date/Publication 2021-12-10 15:10:02 UTC

R topics documented:

morph-package	*3D Segmentation of Voxels into Morphologic Classes*

Description

Automatically segments a 3D array of voxels into mutually exclusive morphological elements. This package extends existing work for segmenting 2D binary raster data. A paper documenting this approach has been accepted for publication in the journal Landscape Ecology. Detailed references will be updated here once those are known.

Details

The DESCRIPTION file:

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Title:	3D Segmentation of Voxels into Morphologic Classes
Version:	1.0.0
Date:	2021-11-25
Authors@R:	c(person("Tarmo K.", "Remmel", email = "remmelt@yorku.ca", role = c("aut", "cre"), comment = (
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                    function called by morph3d() and not intended
                    to be called on its own.
morph3dplot         A plot function that converts a 3D array of
                    voxels into an interactive rgl plot.
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```

```
                         plotting.
```

This package handles the segmentation of binary voxel data, provided as a numeric 3D array, into its constituent morphological classes. Each voxel is assigned to one of nine mutually exclusive morpholocal classes: outside, mass, skin, crumb, circuit, antenna, bond, void-volume, or void.

Author(s)

NA Maintainer: Tarmo K. Remmel <remmelt@yorku.ca>

References

Remmel, T.K. (Accepted December 2021). Extending morphological pattern segmentation to 3D voxels. Landscape Ecology.

See Also

See Also [melt](#)

Examples

```
# Need to provide some simple examples here.
```

---

arraytrim   *Trim excess white-space (0 planes) from a 3D binary array.*

Description

A helper function for reducing the size of 3D arrays if necessary. This reduction can improve memory utilization and speed processing, since voxels outside the feature of interest are eliminated.

Usage

```
arraytrim(VOLOBJ = NULL)
```

Arguments

VOLOBJ   This is a 3D binary (0,1) numeric array, which represent voxels. If there are outter margins that are all zeros, they will be trimmed off to reduce the size of the array.

Details

The function scans inward, starting at the outer margins, for planes that are all zeros. If they are, those planes will be trimmed at the end. Only planes of zeros that connect contiguously to the outer margins will be trimmed.

Value

The output is an array with the excess outter zero planes removed.

Note

It can happen that trimming reduces the resulting dimensions to be <3, and thus, prior to running morph3d(), ensure that your data still fits the requirements.

Author(s)

Tarmo K. Remmel

References

Remmel, T.K. 2021. (Unpuplished manuscript)

See Also

See Also morph3d, morph3dprep

Examples

```
LEdemoSmall <- arraytrim(LEdemo)
```

LEdemo   *Landscape Ecology Demo Data (3D Voxels)*

Description

This is a 3D numeric array with dimensions [10,10,10], representing 1000 voxels for demonstration purposes. The data was manually produced to ensure that all morphological classes are present, to allow demonstration and illustration within the Landscape Ecology paper in which the morph3d() functionality was introduced.

Usage

```
data("LEdemo")
```

Format

The format is: num [1:10, 1:10, 1:10] 1 1 0 0 0 0 0 0 0 0 ...

Details

This data can be used for testing, demonstrations, or for quickly getting the package up and running, before getting your own data into the proper format.

Source

This data was produced by the author of the package for demonstration purposes and was used in the paper referenced below as the example data.

References

Remmel, T.K. 2021. (Unpublished manuscript)

Examples

```
data(LEdemo)
str(LEdemo)
```

---

morph3d   *Performs a morphological segmentation of a binary 3D array*

Description

This is the extension of 2D morphological segmentation of binary pixels in a planar raster setting to the 3D domain of voxels. A 3D binary array with 1 (belonging to the feature of interest) and 0 (not belonging to the feature of interest) is the only input required for the mathematical morphological segmentation to proceed. The result is a list object containing the original input data, the categorical segmentation layer, and various summary outputs that may be necessary at later interpretation stages. The algorithm assigns voxels into mutually exclusive categories: outside, mass, skin, crumb, circuit, antenna, bond, void-volume, and void based on their relative positioning and connectivity within the feature of interest.

Usage

```
morph3d(DATACUBE = NULL, VERBOSE = FALSE, PLOT = FALSE, FINALPLOT = TRUE, PLOTIDS = FALSE)
```

Arguments

DATACUBE	This is the input 3D data array. The dimensions do not need to be equal, but the data must be binary (0,1) and be of numeric type.
VERBOSE	This is a Boolean flag that turns on | off additional feedback as the code is running. This is generally used for testing and debugging and can easily be set to FALSE with no concern over how the code runs.
PLOT	This is a Boolean flag that turns on | off 3D interactive environment plots for each mutually exclusive morphological class. If these plots are not explicitly required, set this to FALSE, as the plotting is the bottleneck that dramatically slows processing.
FINALPLOT	This is a Boolean flag that turns on | off the 3D interactive environment plot for the final voxel segmentation result. If this is set to FALSE, it can readily be plotted in the future, since the results are saved by the function to a compound list object and the plotting function is supplied with this package.

PLOTIDS   This is a Boolean flag that turns on | off the plotting of unique voxel IDS at the
                   centroids of each voxel during plotting. These can be very useful for identifying
                   specific voxels and associations, but can also clutter the view if they are not
                   expressly required.

Details

Each voxel can belong to only a single 3D morphological class. The concept expands the planar
morphological segmentation avaliable in the MSPA software package and establishes corresponding
terminology to distinguish the 3D case. The processessing logic is presented and a fully-functional
environment allows any binary 3D data to be processed with this engine.

Value

The function returns a LIST object with the following items:

OriginalData   This is the original input 3D data array of 0,1 values.

Graph   This is the network graph object in igraph format for the feature of interest.

VoxelIDs   This is a 3D array with the same dimensions as the input data and contains the
                   unique voxel ID value for each voxel.

ObjectID   If there are multiple disconnected components for the input feature of interest,
                   each component is assigned a unique object ID. This 3D array with the same
                   dimensions as the input data contains those unique object ID values for each
                   voxel.

Morphology   This is a 3D array with the same dimensions as the input data and is a categorical
                   voxel map identifying which morphological class each voxel belongs to. The
                   codes are: 1=outside, 2=mass, 3=skin, 4=crumb, 5=circuit, 6=antenna, 7=bond,
                   8=void-volume, and 9=void.

Cores   This is a 3D array with the same dimensions as the input data and contains the
                   codes for unique cores (of mass voxels) that may exist within the feature of
                   interest.

ExpCores   This is the same as Cores, but expanded outward to enlarge the volume repre-
                   sented by each core. This is used for internal processing but may be of use or
                   benefit to some, so it is also provided here.

Summary   This is a tabular summary of the morphological segmentation by class. The call
                   name, number of voxels, and the percentage of the total volume is summarized
                   for the actual data provided in the Morphology item.

Egg   This is a temporary output that is used for checking and debugging. It is likely
                   to be eliminated in the future.

Bgrnd   This 3D array identifies the voxels outside the feature of interest, but that are not
                   part of the voids internal to the structure itself.

VOIDvolume   This 3D array identifies the voxels that form the holes, gaps, or voids within the
                   structure.

Note

Current implementation consideres voxels as neighbours if they share a face only (orthogonal neighbours). Expansion to include diagonal neighbours, where voxels share an edge or a point, are being considered. The use of rgl provides functionality to produce interactive 3D plots that greatly facilitate visualization, but dramatically slow the processing as input volumes increase in size. Avoid plotting unless explicitly required. You are able to plot from the stored list object at anytime afterwards too, it is not necessary to plot during the segmentation call.

Author(s)

Tarmo K. Remmel

References

Remmel, T.K. (Accepted December 2021). Extending morphological pattern segmentation to 3D voxels. Landscape Ecology.

See Also

See Also morph3dplot, morph3dprep

Examples

```
# SET FINALPLOT=TRUE IF THE INTERACTIVE 3D PLOT IS DESIRED
# THAT CONTAINS THE FINAL SEGMENTATION CATEGORIES
# IF A PLOT FOR EACH CATEGORY IS REQUIRED, SET PLOT=TRUE
LEdemoOut <- morph3d(LEdemo, PLOT=FALSE, FINALPLOT=FALSE)
str(LEdemoOut)
```

---

morph3dlinks	*An internal function that computes the spatial neighbours for voxels. It is an internal function called by morph3d() and not intended to be called on its own.*

Description

An internal helper function to compute voxel neighbours in orthogonal 3D space and to return the information in data frame format back to morph3d(), the function that calls this function.

Usage

```
morph3dlinks(VOLOBJ = NULL, VOXELIDS = NULL, VERBOSE = FALSE)
```

Arguments

VOLOBJ	This is a 3D array that is larger in all dimensions, within which the actual data array is inset. This ensures that outer margins will be properly processed.
VOXELIDS	This is a 3D array of the unique voxel IDS, which are used to track individual voxels and their connectivity.
VERBOSE	This is a Boolean flag for turning on	off additional feedback during processing.

Details

This internal function simply makes the total length of the morph3d() function shorter.

Value

This function returns an intermediate data frame of voxel neighbours that is subsequently pared down as morph3d() continues.

Note

No additional notes at this time.

Author(s)

Tarmo K. Remmel

References

No references at this time.

See Also

See Also morph3d

Examples

```
# THIS IS AN INTERNAL FUNCITON AND USAGE EXAMPLES ARE NOT NECESSARY
```

---

morph3dplot	*A plot function that converts a 3D array of voxels into an interactive rgl plot.*

Description

This plot functionality can be used for any 3D array data that represent voxAels. This functionality is called directly by morph3d() but can be called independently by passing it 3D array data that has been processed by morph3dprep().

Usage

```
morph3dplot(data = NULL, CELLID = TRUE, LEGEND = FALSE, ORIGTRANSP = TRUE)
```

Arguments

data	This is the voxel data to be plotted and needs to be processed with morph3dprep() first.
CELLID	A Boolean flag used to control whether the unique voxel IDs are plotted or not.
LEGEND	A Boolean flag that determines whether a legend will be drawn on the ouput interactive plot or not. When this is set to TRUE, plotting is much slower.
ORIGTRANSP	A Boolean flag that is used to set the transparency of original binary input voxel data. It can be used to help produce better visualizations but is not an overly important argument for most.

Details

Output classes are coloured (with varying degrees of transparency to make classes easier to see) as follows. Mass = "green", Skin = "black", Crumb = "brown", Circuit = "orange", Antenna = "pink", Bond = "cornflowerblue", Void-volume = "navy", and Void = "seagreen".

Value

The output is an interactive 3D rgl plot of the voxels supplied as input. Morphological segmentations produced by morph3d() will always have elements drawn in consistent color for ease of interpretation.

Note

No further notes available at this time.

Author(s)

Tarmo K. Remmel

References

Remmel, T.K. 2021. (Unpuplished manuscript)

See Also

See Also morph3d, morph3dprep

Examples

```
LEdemoOut <- morph3d(DATACUBE = LEdemo, VERBOSE = FALSE, FINALPLOT = FALSE)
morph2plot <- morph3dprep(INCUBE=LEdemoOut$Morphology, ORIG=FALSE)
# PLOTTING IS TIME INTENSIVE
morph3dplot(data=morph2plot, CELLID=FALSE, LEGEND=FALSE, ORIGTRANSP=TRUE)
```

---

morph3dprep   *Prepare 3D voxel data for interactive 3D plotting.*

Description

Prepares 3D array data for plotting.

Usage

```
morph3dprep(INCUBE = NULL, ORIG = FALSE)
```

Arguments

INCUBE	This is the input 3D array of voxels.
ORIG	A Boolean flag to control whether the data is the original input binary data (TRUE), or some other morphological segmentation (FALSE).

Details

No additional details at this time.

Value

The output is...

Note

No additional notes at this time.

Author(s)

Tarmo K. Remmel

References

Remmel, T.K. 2021 (Unpublished manuscript).

See Also

See Also morph3d, morph3dplot

Examples

```
out <- morph3dprep(INCUBE = LEdemo, ORIG = FALSE)
print(out)
```

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