Package: clustree (via r-universe)

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Type Package

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Maintainer Luke Zappia <luke@lazappi.id.au>

Description Deciding what resolution to use can be a difficult question when approaching a clustering analysis. One way to approach this problem is to look at how samples move as the number of clusters increases. This package allows you to produce clustering trees, a visualisation for interrogating clusterings as resolution increases.

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`clustree-package` *Clustree*

Description

Deciding what resolution to use can be a difficult question when approaching a clustering analysis. One way to approach this problem is to look at how samples move as the number of clusters increases. This package allows you to produce clustering trees, a visualisation for interrogating clusterings as resolution increases.

`clustree` *Plot a clustering tree*

Description

Creates a plot of a clustering tree showing the relationship between clusterings at different resolutions.

Usage

```
clustree(x, ...)

## S3 method for class 'matrix'
clustree(
  x,
  prefix,
  suffix = NULL,
  metadata = NULL,
  count_filter = 0,
```

```
  prop_filter = 0.1,
  layout = c("tree", "sugiyama"),
  use_core_edges = TRUE,
  highlight_core = FALSE,
  node_colour = prefix,
  node_colour_aggr = NULL,
  node_size = "size",
  node_size_aggr = NULL,
  node_size_range = c(4, 15),
  node_alpha = 1,
  node_alpha_aggr = NULL,
  node_text_size = 3,
  scale_node_text = FALSE,
  node_text_colour = "black",
  node_text_angle = 0,
  node_label = NULL,
  node_label_aggr = NULL,
  node_label_size = 3,
  node_label_nudge = -0.2,
  edge_width = 1.5,
  edge_arrow = TRUE,
  edge_arrow_ends = c("last", "first", "both"),
  show_axis = FALSE,
  return = c("plot", "graph", "layout"),
  ...
)

## S3 method for class 'data.frame'
clustree(x, prefix, ...)

## S3 method for class 'SingleCellExperiment'
clustree(x, prefix, exprs = "counts", ...)

## S3 method for class 'seurat'
clustree(x, prefix = "res.", exprs = c("data", "raw.data", "scale.data"), ...)

## S3 method for class 'Seurat'
clustree(
  x,
  prefix = paste0(assay, "_snn_res."),
  exprs = c("data", "counts", "scale.data"),
  assay = NULL,
  ...
)
```

Arguments

x	object containing clustering data

...	extra parameters passed to other methods
prefix	string indicating columns containing clustering information
suffix	string at the end of column names containing clustering information
metadata	data.frame containing metadata on each sample that can be used as node aesthetics
count_filter	count threshold for filtering edges in the clustering graph
prop_filter	in proportion threshold for filtering edges in the clustering graph
layout	string specifying the "tree" or "sugiyama" layout, see igraph::layout_as_tree() and igraph::layout_with_sugiyama() for details
use_core_edges	logical, whether to only use core tree (edges with maximum in proportion for a node) when creating the graph layout, all (unfiltered) edges will still be displayed
highlight_core	logical, whether to increase the edge width of the core network to make it easier to see
node_colour	either a value indicating a colour to use for all nodes or the name of a metadata column to colour nodes by
node_colour_aggr	if node_colour is a column name than a string giving the name of a function to aggregate that column for samples in each cluster
node_size	either a numeric value giving the size of all nodes or the name of a metadata column to use for node sizes
node_size_aggr	if node_size is a column name than a string giving the name of a function to aggregate that column for samples in each cluster
node_size_range	numeric vector of length two giving the maximum and minimum point size for plotting nodes
node_alpha	either a numeric value giving the alpha of all nodes or the name of a metadata column to use for node transparency
node_alpha_aggr	if node_aggr is a column name than a string giving the name of a function to aggregate that column for samples in each cluster
node_text_size	numeric value giving the size of node text if scale_node_text is FALSE
scale_node_text	logical indicating whether to scale node text along with the node size
node_text_colour	colour value for node text (and label)
node_text_angle	the rotation of the node text
node_label	additional label to add to nodes
node_label_aggr	if node_label is a column name than a string giving the name of a function to aggregate that column for samples in each cluster

node_label_size
: numeric value giving the size of node label text

node_label_nudge
: numeric value giving nudge in y direction for node labels

edge_width
: numeric value giving the width of plotted edges

edge_arrow
: logical indicating whether to add an arrow to edges

edge_arrow_ends
: string indicating which ends of the line to draw arrow heads if edge_arrow is TRUE, one of "last", "first", or "both"

show_axis
: whether to show resolution axis

return
: string specifying what to return, either "plot" (a ggplot object), "graph" (a tbl_graph object) or "layout" (a ggraph layout object)

exprs
: source of gene expression information to use as node aesthetics, for SingleCellExperiment objects it must be a name in assayNames(x), for a seurat object it must be one of data, raw.data or scale.data and for a Seurat object it must be one of data, counts or scale.data

assay
: name of assay to pull expression and clustering data from for Seurat objects

Details

Data sources

Plotting a clustering tree requires information about which cluster each sample has been assigned to at different resolutions. This information can be supplied in various forms, as a matrix, data.frame or more specialised object. In all cases the object provided must contain numeric columns with the naming structure PXS where P is a prefix indicating that the column contains clustering information, X is a numeric value indicating the clustering resolution and S is any additional suffix to be removed. For SingleCellExperiment objects this information must be in the colData slot and for Seurat objects it must be in the meta.data slot. For all objects except matrices any additional columns can be used as aesthetics, for matrices an additional metadata data.frame can be supplied if required.

Filtering

Edges in the graph can be filtered by adjusting the count_filter and prop_filter parameters. The count_filter removes any edges that represent less than that number of samples, while the prop_filter removes edges that represent less than that proportion of cells in the node it points towards.

Node aesthetics

The aesthetics of the plotted nodes can be controlled in various ways. By default the colour indicates the clustering resolution, the size indicates the number of samples in that cluster and the transparency is set to 100%. Each of these can be set to a specific value or linked to a supplied metadata column. For a SingleCellExperiment or Seurat object the names of genes can also be used. If a metadata column is used than an aggregation function must also be supplied to combine the samples in each cluster. This function must take a vector of values and return a single value.

Layout

The clustering tree can be displayed using either the Reingold-Tilford tree layout algorithm or the Sugiyama layout algorithm for layered directed acyclic graphs. These layouts were selected

as the are the algorithms available in the igraph package designed for trees. The Reingold-Tilford algorithm places children below their parents while the Sugiyama places nodes in layers while trying to minimise the number of crossing edges. See igraph::layout_as_tree() and igraph::layout_with_sugiyama() for more details. When use_core_edges is TRUE (default) only the core tree of the maximum in proportion edges for each node are used for constructing the layout. This can often lead to more attractive layouts where the core tree is more visible.

Value

a ggplot object (default), a tbl_graph object or a ggraph layout object depending on the value of return

Examples

```
data(nba_clusts)
clustree(nba_clusts, prefix = "K")
```

---

clustree_overlay *Overlay a clustering tree*

Description

Creates a plot of a clustering tree overlaid on a scatter plot of individual samples.

Usage

```
clustree_overlay(x, ...)

## S3 method for class 'matrix'
clustree_overlay(
  x,
  prefix,
  metadata,
  x_value,
  y_value,
  suffix = NULL,
  count_filter = 0,
  prop_filter = 0.1,
  node_colour = prefix,
  node_colour_aggr = NULL,
  node_size = "size",
  node_size_aggr = NULL,
  node_size_range = c(4, 15),
  node_alpha = 1,
  node_alpha_aggr = NULL,
  edge_width = 1,
  use_colour = c("edges", "points"),
```

```
  alt_colour = "black",
  point_size = 3,
  point_alpha = 0.2,
  point_shape = 18,
  label_nodes = FALSE,
  label_size = 3,
  plot_sides = FALSE,
  side_point_jitter = 0.45,
  side_point_offset = 1,
  ...
)

## S3 method for class 'data.frame'
clustree_overlay(x, prefix, ...)

## S3 method for class 'SingleCellExperiment'
clustree_overlay(
  x,
  prefix,
  x_value,
  y_value,
  exprs = "counts",
  red_dim = NULL,
  ...
)

## S3 method for class 'seurat'
clustree_overlay(
  x,
  x_value,
  y_value,
  prefix = "res.",
  exprs = c("data", "raw.data", "scale.data"),
  red_dim = NULL,
  ...
)

## S3 method for class 'Seurat'
clustree_overlay(
  x,
  x_value,
  y_value,
  prefix = paste0(assay, "_snn_res."),
  exprs = c("data", "counts", "scale.data"),
  red_dim = NULL,
  assay = NULL,
  ...
)
```

Arguments

x	object containing clustering data
...	extra parameters passed to other methods
prefix	string indicating columns containing clustering information
metadata	data.frame containing metadata on each sample that can be used as node aesthetics
x_value	numeric metadata column to use as the x axis
y_value	numeric metadata column to use as the y axis
suffix	string at the end of column names containing clustering information
count_filter	count threshold for filtering edges in the clustering graph
prop_filter	in proportion threshold for filtering edges in the clustering graph
node_colour	either a value indicating a colour to use for all nodes or the name of a metadata column to colour nodes by
node_colour_aggr	if node_colour is a column name than a string giving the name of a function to aggregate that column for samples in each cluster
node_size	either a numeric value giving the size of all nodes or the name of a metadata column to use for node sizes
node_size_aggr	if node_size is a column name than a string giving the name of a function to aggregate that column for samples in each cluster
node_size_range	numeric vector of length two giving the maximum and minimum point size for plotting nodes
node_alpha	either a numeric value giving the alpha of all nodes or the name of a metadata column to use for node transparency
node_alpha_aggr	if node_aggr is a column name than a string giving the name of a function to aggregate that column for samples in each cluster
edge_width	numeric value giving the width of plotted edges
use_colour	one of "edges" or "points" specifying which element to apply the colour aesthetic to
alt_colour	colour value to be used for edges or points (whichever is NOT given by use_colour)
point_size	numeric value giving the size of sample points
point_alpha	numeric value giving the alpha of sample points
point_shape	numeric value giving the shape of sample points
label_nodes	logical value indicating whether to add labels to clustering graph nodes
label_size	numeric value giving the size of node labels is label_nodes is TRUE
plot_sides	logical value indicating whether to produce side on plots
side_point_jitter	numeric value giving the y-direction spread of points in side plots

`side_point_offset`
: numeric value giving the y-direction offset for points in side plots

`exprs`
: source of gene expression information to use as node aesthetics, for `SingleCellExperiment` objects it must be a name in `assayNames(x)`, for a `seurat` object it must be one of `data`, `raw.data` or `scale.data` and for a `Seurat` object it must be one of `data`, `counts` or `scale.data`

`red_dim`
: dimensionality reduction to use as a source for x_value and y_value

`assay`
: name of assay to pull expression and clustering data from for `Seurat` objects

Details

Data sources

Plotting a clustering tree requires information about which cluster each sample has been assigned to at different resolutions. This information can be supplied in various forms, as a matrix, data.frame or more specialised object. In all cases the object provided must contain numeric columns with the naming structure `PXS` where `P` is a prefix indicating that the column contains clustering information, `X` is a numeric value indicating the clustering resolution and `S` is any additional suffix to be removed. For `SingleCellExperiment` objects this information must be in the `colData` slot and for `Seurat` objects it must be in the `meta.data` slot. For all objects except matrices any additional columns can be used as aesthetics.

Filtering

Edges in the graph can be filtered by adjusting the `count_filter` and `prop_filter` parameters. The `count_filter` removes any edges that represent less than that number of samples, while the `prop_filter` removes edges that represent less than that proportion of cells in the node it points towards.

Node aesthetics

The aesthetics of the plotted nodes can be controlled in various ways. By default the colour indicates the clustering resolution, the size indicates the number of samples in that cluster and the transparency is set to 100%. Each of these can be set to a specific value or linked to a supplied metadata column. For a `SingleCellExperiment` or `Seurat` object the names of genes can also be used. If a metadata column is used than an aggregation function must also be supplied to combine the samples in each cluster. This function must take a vector of values and return a single value.

Colour aesthetic

The colour aesthetic can be applied to either edges or sample points by setting `use_colour`. If "edges" is selected edges will be coloured according to the clustering resolution they originate at. If "points" is selected they will be coloured according to the cluster they are assigned to at the highest resolution.

Dimensionality reductions

For `SingleCellExperiment` and `Seurat` objects precomputed dimensionality reductions can be used for x or y aesthetics. To do so `red_dim` must be set to the name of a dimensionality reduction in `reducedDimNames(x)` (for a `SingleCellExperiment`) or `x@dr` (for a `Seurat` object). `x_value` and `y_value` can then be set to `red_dimX` when `red_dim` matches the `red_dim` argument and `X` is the column of the dimensionality reduction to use.

Value

a ggplot object if plot_sides is FALSE or a list of ggplot objects if plot_sides is TRUE

Examples

```
data(nba_clusts)
clustree_overlay(nba_clusts, prefix = "K", x_value = "PC1", y_value = "PC2")
```

---

nba_clusts *Clustered NBA positions dataset*

Description

NBA positions dataset clustered using k-means with a range of values of k

Usage

```
nba_clusts
```

Format

nba_clusts is a data.frame containing the NBA positions dataset with additional columns holding k-means clusterings at different values of k and the first two principal components

- **Position** - Player position
- **TurnoverPct** - Turnover percentage
- **ReboundPct** - Rebound percentage
- **AssistPct** - Assist percentage
- **FieldGoalPct** - Field goal percentage
- **K1 - K5** - Results of k-means clustering
- **PC1** - First principal component
- **PC2** - Second principal component

Source

NBA positions downloaded from https://github.com/lazappi/nba_positions.

The source dataset is available from Kaggle at https://www.kaggle.com/drgilermo/nba-players-stats/data?select=Seasons_Stats.csv and was originally scraped from Basketball Reference.

See https://github.com/lazappi/clustree/blob/master/data-raw/nba_clusts.R for details of how clustering was performed.

sc_example *Simulated scRNA-seq dataset*

Description

A simulated scRNA-seq dataset generated using the splatter package and clustered using the SC3 and Seurat packages.

Usage

```
sc_example
```

Format

sc_example is a list holding a simulated scRNA-seq dataset. Items in the list included the simulated counts, normalised log counts, tSNE dimensionality reduction and cell assignments from SC3 and Seurat clustering.

Source

```
# Simulation
library("splatter") # Version 1.2.1

sim <- splatSimulate(batchCells = 200, nGenes = 10000,
                     group.prob = c(0.4, 0.2, 0.2, 0.15, 0.05),
                     de.prob = c(0.1, 0.2, 0.05, 0.1, 0.05),
                     method = "groups", seed = 1)
sim_counts <- counts(sim)[1:1000, ]

# SC3 Clustering
library("SC3") # Version 1.7.6
library("scater") # Version 1.6.2

sim_sc3 <- SingleCellExperiment(assays = list(counts = sim_counts))
rowData(sim_sc3)$feature_symbol <- rownames(sim_counts)
sim_sc3 <- normalise(sim_sc3)
sim_sc3 <- sc3(sim_sc3, ks = 1:8, biology = FALSE, n_cores = 1)
sim_sc3 <- runTSNE(sim_sc3)

# Seurat Clustering
library("Seurat") # Version 2.2.0

sim_seurat <- CreateSeuratObject(sim_counts)
sim_seurat <- NormalizeData(sim_seurat, display.progress = FALSE)
sim_seurat <- FindVariableGenes(sim_seurat, do.plot = FALSE,
                                display.progress = FALSE)
sim_seurat <- ScaleData(sim_seurat, display.progress = FALSE)
```

```
sim_seurat <- RunPCA(sim_seurat, do.print = FALSE)
sim_seurat <- FindClusters(sim_seurat, dims.use = 1:6,
                           resolution = seq(0, 1, 0.1),
                           print.output = FALSE)

sc_example <- list(counts = counts(sim_sc3),
                   logcounts = logcounts(sim_sc3),
                   tsne = reducedDim(sim_sc3),
                   sc3_clusters = as.data.frame(colData(sim_sc3)),
                   seurat_clusters = sim_seurat@meta.data)
```

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