Package 'langevitour'

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Description An HTML widget that randomly tours 2D projections of numerical data. A ran-

Title Langevin Tour

Version 0.5

	dom walk through projections of the data is shown. The user can manipulate the plot to use specified axes, or turn on Guided Tour mode to find an informative projection of the data. Groups within the data can be hidden or shown, as can particular axes. Known projections of interest can be added as ``extra axes" and also manipulated. The underlying method to produce the random walk and projection pursuit uses Langevin dynamics. The widget can be used from within R, or included in a self-contained Rmarkdown document, or used in a Shiny app.
URL	https://logarithmic.net/langevitour/
BugR	Reports https://github.com/pfh/langevitour/issues/
Impo	rts htmlwidgets, RANN, assertthat
Sugge	ests shiny, palmerpenguins, knitr, rmarkdown
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R to	opics documented:
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Description

Reduce noise in a high-dimensional dataset by averaging each point with its nearby neighbors.

Usage

```
knnDenoise(X, block = rep(1, nrow(X)), k = 30, steps = 2)
```

Arguments

X	A matrix of numeric data, or something that can be cast to a matrix. Each row represents a point.
block	Optional. A block for each row in X. A factor, or something that can be cast to a factor. Denoising will be performed independently within each block.
k	Number of nearest neighbors to find around each point (including itself).
steps	Number of steps to take along the directed k-nearest neighbor graph. steps=1 uses the k-nearest neighbors, steps=2 uses the k-nearest neighbors and their k-nearest neighbors, etc.

Details

knnDenoise first finds the k-nearest neighbors to each point (including the point itself). Then, for each point, the average is found of the points reachable in steps steps along the directed k-nearest neighbor graph.

```
library(palmerpenguins)

completePenguins <- na.omit(penguins[,c(1,3,4,5,6)])

# Dimensions need to be on comparable scales to apply knnDenoise scaled <- scale(completePenguins[,-1])

denoised <- knnDenoise(scaled)

langevitour(denoised, completePenguins$species, pointSize=2)</pre>
```

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langevitour Langevin Tour

Description

Make a Langevin Tour HTML widget, which can be used to explore high-dimensional numeric datasets.

Usage

```
langevitour(
 Χ,
 group = NULL,
 name = NULL,
 center = NULL,
  scale = NULL,
  extraAxes = NULL,
 lineFrom = NULL,
 lineTo = NULL,
  axisColors = NULL,
 levelColors = NULL,
  colorVariation = 0.3,
 pointSize = 1,
  subsample = NULL,
  state = NULL,
 width = NULL,
 height = NULL,
 elementId = NULL
)
```

Arguments

X	The data to plot. A matrix of numeric data, or something that can be cast to a matrix. Rows will be shown as points in the widget. Columns are the variables of your data.
group	A group for each row in X, will be used to color points. A factor, or something that can be cast to a factor.
name	A name for each row in X.
center	Center for each variable. If omitted, the column means will be used.
scale	Scale for each variable. Scale +/- center will be the range of guaranteed visible data. If omitted, a reasonable default will be chosen, equal for all variables. (The default is the largest singular value of the centered X times 2.5.)
extraAxes	A matrix with each column defining a projection of interest. The columns of X %*% extraAxes will be presented as extra "variables".
lineFrom	A vector of row numbers. Draw lines starting at these rows.

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lineTo A vector of row numbers. Draw lines ending at these rows.

axisColors Character vector. Colors for each variable and then each extra axis.

levelColors Character vector. Colors for each level of group.

colorVariation Number between 0 and 1. Individual points are given slightly different bright-

nesses. How strong should this effect be?

pointSize Point radius in pixels.

subsample For speed, randomly subsample down to this many rows.

state A JSON string, or an object that htmlwidgets will convert to the correct JSON.

Initial widget state settings. The state of a widget can be obtained by pressing the "?" button. I am not going to guarantee that states will be compatible between

versions of langevitour.

width Width of widget. height Height of widget.

elementId An element ID for the widget, see htmlwidgets::createWidget.

Details

To retain the original units on plot axes within the widget, use center and scale rather than altering X.

langevitour will by default not scale variables individually. If you want variables to be individually scaled, use something like scale=apply(X,2,sd)*4.

In Javascript, the langevitour object can be obtained using document.getElementById(elementId).langevitour. For example you could have a button that sets the state of a widget using document.getElementById(elementId).langevi

Value

An htmlwidget object.

```
library(palmerpenguins)

completePenguins <- na.omit(penguins[,c(1,3,4,5,6)])
scale <- apply(completePenguins[,-1], 2, sd)*4

langevitour(
    completePenguins[,-1],
    completePenguins$species,
    scale=scale, pointSize=2)</pre>
```

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langevitour-shiny

Shiny bindings for langevitour

Description

Output and render functions for using langevitour within Shiny applications and interactive Rmd documents.

Usage

```
langevitourOutput(outputId, width = "100%", height = "600px")
renderLangevitour(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

outputId output variable to read from

width, height Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended.

expr An expression that generates a langevitour, usually a block of code ending with a call to langevitour()

env The environment in which to evaluate expr.

quoted Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.

```
library(shiny)
library(palmerpenguins)
completePenguins <- na.omit(penguins[,c(1,3,4,5,6)])</pre>
scale <- apply(completePenguins[,-1], 2, sd)*4</pre>
ui <- fluidPage(</pre>
    sliderInput('zoom', 'Zoom', 0, min=-1, max=1, step=0.1),
    langevitourOutput('widget')
)
server <- function(input,output) {</pre>
    output$widget <- renderLangevitour({</pre>
        langevitour(
             completePenguins[,-1],
             completePenguins$species,
             scale=scale * 10^input$zoom, pointSize=2)
    })
}
```

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```
app <- shinyApp(ui, server)
# Use runApp(app) or runGadget(app) to run app.</pre>
```

zeiselPC

Principal components of scRNA-Seq of mouse brain cells

Description

Single-cell RNA-Seq gene expression of 2,816 mouse brain cells (Zeisel, 2015). The top 10 principal components were produced using the steps in the Bioconductor OSCA workflow.

Usage

```
data(zeiselPC)
```

Format

A data frame with 2,816 rows representing brain cells and 11 columns:

type Cell type.

PC1 Principal component score.

PC2 Principal component score.

PC3 Principal component score.

PC4 Principal component score.

PC5 Principal component score.

PC6 Principal component score.

PC7 Principal component score.

PC8 Principal component score.

PC9 Principal component score.

PC10 Principal component score.

References

Zeisel, A., Muñoz-Manchado, A. B., Codeluppi, S., Lönnerberg, P., La Manno, G., Juréus, A., Marques, S., Munguba, H., He, L., Betsholtz, C., Rolny, C., Castelo-Branco, G., Hjerling-Leffler, J., & Linnarsson, S. (2015). Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq. *Science*, 347(6226), 1138–1142. doi:10.1126/science.aaa1934

```
data(zeiselPC)
langevitour(zeiselPC[,-1], zeiselPC$type)
```

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