

Package ‘langevitour’

March 23, 2022

Title Langevin Tour

Version 0.2

Description An HTML widget that tours 2D projections of numerical data. A random walk through projections of the data is shown. The user can manipulate the plot to use specified axes, or turn on projection pursuit to find an informative projection of the data. Groups within the data can be turned off or on, as can particular axes. Extra axes, for example principal component axes, can be specified. The underlying method to produce the random walk and projection pursuit uses Langevin dynamics. The widget can be used from within R, or included for example in a self-contained Rmarkdown document.

URL <https://logarithmic.net/langevitour/>

BugReports <https://github.com/pfh/langevitour/issues/>

Imports htmlwidgets

Suggests shiny, GPArotation, tourr, liminal, geozoo, palmerpenguins, RANN, MASS, ggplot2, dplyr, tibble, knitr, rmarkdown, airway, limma, edgeR, EnsDb.Hsapiens.v86, AnnotationDbi

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Encoding UTF-8

RoxygenNote 7.1.2

VignetteBuilder knitr

Depends R (>= 2.10)

NeedsCompilation no

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R topics documented:

langevitour	2
langevitour-shiny	3
zeiselPC	4

langevitour	<i>Langevin Tour</i>
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Description

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

Usage

```
langevitour(
  X,
  group = NULL,
  name = NULL,
  center = NULL,
  scale = NULL,
  extraAxes = NULL,
  axisColors = NULL,
  pointSize = 1,
  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".
axisColors	Character vector. Colors for each variable and then each extra axis.
pointSize	Point radius in pixels.
width	Width of widget.
height	Height of widget.
elementId	An element ID for the widget, see <code>htmlwidgets::createWidget</code> .

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 this, use something like `scale=apply(X,2,sd)*4`.

Value

An `htmlwidget` object.

Examples

```
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)
```

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

<code>outputId</code>	output variable to read from
<code>width, height</code>	Must be a valid CSS unit (like <code>'100%'</code> , <code>'400px'</code> , <code>'auto'</code>) or a number, which will be coerced to a string and have <code>'px'</code> appended.
<code>expr</code>	An expression that generates a <code>langevitour</code> , usually a block of code ending with a call to <code>langevitour()</code>
<code>env</code>	The environment in which to evaluate <code>expr</code> .
<code>quoted</code>	Is <code>expr</code> a quoted expression (with <code>quote()</code>)? This is useful if you want to save an expression in a variable.

Examples

```
library(shiny)
library(palmerpenguins)

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

ui <- fluidPage(
  sliderInput('zoom', 'Zoom', 0, min=-1, max=1, step=0.1),
  langevitourOutput('widget')
)

server <- function(input,output) {
  output$widget <- renderLangevitour({
    langevitour(
      completePenguins[,-1],
      completePenguins$species,
      scale=scale * 10^input$zoom, pointSize=2)
  })
}

app <- shinyApp(ui, server)

# Use runApp(app) or runGadget(app) to run app.
```

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](https://doi.org/10.1126/science.aaa1934)

Examples

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

Index

* datasets

zeiselPC, 4

langevitour, 2

langevitour-shiny, 3

langevitourOutput (langevitour-shiny), 3

renderLangevitour (langevitour-shiny), 3

zeiselPC, 4