

Package ‘HPAStainR’

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Title Queries the Human Protein Atlas Staining Data for Multiple Proteins and Genes

Version 1.0.0.9000

Description This package is built around the HPAStainR function. The purpose of the HPAStainR function is to query the visual staining data in the Human Protein Atlas to return a table of staining ranked cell types. The function also has multiple arguments to personalize to output as well as include cancer data, csv readable names, modify the confidence levels of the results and more. The other functions exist exclusively to easily acquire the data required to run HPAStainR.

License GNU

Encoding UTF-8

LazyData true

Depends R (>= 3.1.0), tidyverse, shiny

RoxygenNote 7.1.0

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HPAStainR	<i>HPAStainR</i>
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Description

Uses a protein/gene list to query Human Protein Atlas (HPA) staining data.

Usage

```
HPAStainR(  
  gene_list,  
  hpa_dat,  
  cancer_dat,  
  cancer_analysis = c("normal", "cancer", "both"),
```

```

tissue_level = TRUE,
stringency = c("normal", "high", "low"),
scale_abundance = TRUE,
round_to = 2,
csv_names = TRUE,
stained_gene_data = TRUE,
tested_protein_column = TRUE,
percent_or_count = c("percent", "count", "both"),
drop_na_row = FALSE
)

```

Arguments

<code>gene_list</code>	A list of proteins or genes that you want to query the HPA staining data with.
<code>hpa_dat</code>	The data frame of normal HPA staining data data, required to run HPAStainR.
<code>cancer_dat</code>	The data frame of pathologic HPA staining data, required to run HPAStainR.
<code>cancer_analysis</code>	A character string indicating inclusion of cancer data in the result, must be one of "normal" (default), "cancer", or "both".
<code>tissue_level</code>	A boolean that determines whether tissue level data for the cell types are included. Default is TRUE
<code>stringency</code>	A character string indicating how stringent the confidence level of the staining findings have to be. Must be "normal" (default), "high", or "low".
<code>scale_abundance</code>	A boolean that determines whether you scale Staining Score based on the size of the gene list. Default is TRUE
<code>round_to</code>	A numeric that determines how many decimals in numeric outputs are desired. Default 2.
<code>csv_names</code>	A Boolean determining if you want names suited for a csv file/pipeline, or for presentation. Default is TRUE giving csv names.
<code>stained_gene_data</code>	A boolean determining if there is a list of which proteins stained, TRUE is default.
<code>tested_protein_column</code>	A boolean dsetermining if there is a column listing which proteins were tested, TRUE is default.
<code>percent_or_count</code>	A character string determining if percent of proteins stained, count of proteins stained, or both are shown for high, medium, and low staining. Must be "percent" (default), "count", or "both".
<code>drop_na_row</code>	A boolean that determines if cell types with no proteins tested are kept or dropped, default is FALSE.

Value

A tibble containing the results of HPAStainR.

Examples

```
HPA_out <- HPASTainR(c("PRSS1", "PNLIP", "CELA3A", "PRL"), hpa_dat, cancer_dat, "both", stringency = "high")

#Below will give you the results found on the shiny app website
#This examples also uses HPA_data_downloader ouput as an example

HPA_out <- HPASTainR(c("PRSS1", "PNLIP", "CELA3A", "PRL"), downloader_out$hpa_dat, downloader_out$cancer_dat,
```

HPA_data_downloader *HPA_data_downloader*

Description

Used to download required data for HPASTainR

Usage

```
HPA_data_downloader(
  tissue_type = c("both", "normal", "cancer"),
  save_file = T,
  save_location = ""
)
```

Arguments

tissue_type	A character string that determines which HPA data you want to download from the website. Has to be "both" (default), "normal", or "cancer".
save_file	A boolean determining if you want the HPA data downloaded permanently or temporarily. Default is TRUE, meaning the file will be saved in the given "save_location", default being the current working directory.
save_location	A character string indicating where you want the files to be saved if you are saving them. If the file(s) already exists in that location, those will be loaded instead of redownloading the files.

Value

List of dataframes or dataframe depending on tissue_type arguement. If tissue_type == "both" it will be a list of dataframes.

Examples

```
HPA_data <- HPA_data_downloader()
HPA_data$hpa_dat
HPA_data$cancer_dat

HPA_normal_data <- HPA_data_downloader("normal")
```

hpa_summary_maker	<i>hpa_summary_maker</i>
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Description

Used to generate a summary file used in the second tab of the Shiny app version of HPASTainR

Usage

```
hpa_summary_maker(hpa_dat)
```

Arguments

tissue_type	A character string that determines which HPA data you want to download from the website. Has to be "both" (default), "normal", or "cancer".
save_file	A boolean determining if you want the HPA data downloaded permanently or temporarily. Default is TRUE, meaning the file will be saved in the given "save_location", default being the current working directory.
save_location	A character string indicating where you want the files to be saved if you are saving them. If the file(s) already exists in that location, those will be loaded instead of re-downloading the files.

Value

A dataframe summarizing the amount of proteins tested to detected, used for the shiny app.

Examples

```
hpa_summary <- hpa_summary_maker(hpa_dat)
```

shiny_HPASTainR	<i>shiny_HPASTainR</i>
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Description

Runs HPASTainR as a the shiny app found at <https://32tim32.shinyapps.io/HPASTainR/>

Usage

```
shiny_HPASTainR(hpa_dat, cancer_dat, cell_type_data = NULL)
```

Arguments

hpa_dat	A required dataframe that has the normal tissue dataframe (see HPA_data_downloader).)
cancer_dat	A required dataframe that has the cancer tissue dataframe (see HPA_data_downloader).
cell_type_data	An optional dataframe that comes out of the hpa_summary_maker function, only needed if you want the second tab of HPASTainR, which shows the ratio of tested proteins to stained proteins, to be functional.

Value

A locally ran shiny app

Examples

```
shiny_HPASTainR(download_out$hpa_dat, download_out$cancer_dat, summary_out)
```

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