Shantropy: Computes Shannon entropy for gene expression data

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Introduction:

Computes Shannon entropy for gene expression across cell types or conditions to find cell type or condition specific gene expression patterns genomic regions.

Installation:

```
Install the package from Github.

devtools::install_github("nashchem/Shantropy")
```

Quick start:

Load the package into R session.

```
library(Shantropy)
```

The enrichmotifpairR package includes an example dataset called example_data.

```
data(example_data)
```

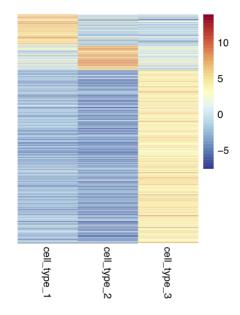
Compute cell type/condition specific expression.

Plot the cell type/condition specific expression data. Install/load the required packages for visualization.

```
library(pheatmap)
library(RColorBrewer)
```

Plotting version 1

path_to_fig <- '/Users/njayavel/Downloads/Shantropy/data/Shannon_entropy_based_cell_type_expression_hear
knitr::include_graphics(path_to_fig)</pre>



Plotting version 2

 ${\tt knitr::include_graphics('/Users/njayavel/Downloads/Shantropy/data/Shannon_entropy_based_cell_type_expression of the contraction of the contra$

