SpaceX

The goal of SpaceX is to provide shared and cluster specfic gene co-expression networks for spatial transcriptomics data.

Installation

This package requires a Fortran compiler in order to work. Here are the instructions:

- Windows: install the Rtools package that is appropriate for your version of R

- Mac: Go to this website and follow the instructions: (https://mac.R-project.org/tools/)

- Linux: From a terminal, do the following: `sudo apt install gcc`. That will bring in multiple compilers.

The package requires a dependency that is not available on CRAN. Install it with:

```
remotes::install_github("rdevito/MSFA")
```

You can install the released version of SpaceX from (https://github.com/SatwikAch/SpaceX) with:

```
devtools::install_github("SatwikAch/SpaceX")
```

```
library(SpaceX)
#> Loading required package: PQLseq

## Reading the Breast cancer data

## Spatial locations
head(BC_loc)

## Gene expression for data
head(BC_count)

## Data processing
G <-dim(BC_count)[2] ## number of genes
N <-dim(BC_count)[1] ## number of locations

## Application to SpaceX algorithm
BC_fit <- SpaceX(BC_count,BC_loc[,1:2],BC_loc[,3],sPMM=FALSE,Post_process = TRUE)

## Shared_network :: Shared co-expression matrix
## Cluster_network :: Cluster specific co-expression matrices
```

You can view the supplementary file at this link: https://bookdown.org/satwik91/SpaceX_supplementary/.