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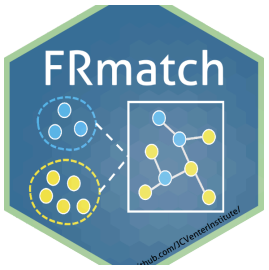
FR-Match: cell type matching for scRNAseq data



In 1 collection

DOI
https://dx.doi.org/10.17504/protocols.io.bmyfk7tn

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Human Cell Atlas Metho...

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OPEN ACCESS

DOI: https://dx.doi.org/10.17504/protocols.io.bmyfk7tn

External link: https://github.com/JCVenterInstitute/FRmatch

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Protocol status: Working
We use this protocol and it's working

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Abstract

FR-Match is a supervised cell phenotype matching strategy for cluster-to-cluster cell transcriptome integration across scRNAseq experiments.

An R package and Shiny application are provided at https://github.com/JCVenterInstitute/FRmatch.

Before start

Software

R programming language	NAME
The R Foundation	DEVELOPER
Comprehensive R Archive Network	REPOSITORY
https://cran.r-project.org/	SOURCE LINK

Require R Shiny package.

Launch Shiny app

1 Interactively explore and match scRNAseq cell type clusters with the seamless Shiny app. The Shiny app may serve as a quick start demo with pre-loaded datasets.

Command

new command name

```
runShiny()
```

Data preparation and exploration

2 Use the built-in data preparation function to create data objects with required and optional input data elements. Create data objects for experiment 1 (E1) and experiment 2 (E2)

Command

new command name

```
dat_E1 <- make_data_object()
dat_E2 <- make_data_object()
```

2.1 View comparative cell cluster sizes.

Command

new command name

```
plot_clusterSize(dat_E1, dat_E2)
```

2.2 View "barcode" plot for cluster of interest.

Command

new command name

```
plot_cluster_by_markers(dat_E1, cluster.name = "cluster_of_interest")
```

Run main algorithm

10m

3 Use wrapper function to perform bi-directional matching.

3.1 Map E1 to E2.

Command

new command name

```
rst12 <- FRmatch(sce.query = dat_E1, sce.ref = dat_E2)
```

3.2 Map E2 to E1.

Command

new command name

```
rst21 <- FRmatch(sce.query = dat_E2, sce.ref = dat_E1)
```

Combine and plot matching results

4 Combine the bi-directional matching results and plot.

Command

new command name

```
plot_bi_FRmatch(rst12, rst21)
```

Additional plots

5 Some optional plotting functions to help studying the matching results.

5.1 Plot one-directional matching results.

Command

new command name

```
plot_FRmatch(rst12)
```

Plot one-directional matching p-values.

Command

new command name

```
plot_FRmatch(rst12, type = "padj")
```

5.2 Minimum spanning tree (MST) plot. MST can be plotted by turning on the plot option in the test function.

Command

new command name

```
FR.test(samp1, samp2, plot.MST = TRUE)
```