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# FR-Match: cell type matching for scRNAseq data

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1 Works for me dx.doi.org/10.17504/protocols.io.bmyfk7tn

Human Cell Atlas Method Development Community

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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>.

## EXTERNAL LINK

<https://github.com/JCVenterInstitute/FRmatch>

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## KEYWORDS

single cell RNA sequencing, cell types, data integration

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BEFORE STARTING

**R programming language**  
**3.3.3 of later** [↗](#)  
[source](#) by The R Foundation

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.


**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)

**dat\_E1 <- make\_data\_object()**  
**dat\_E2 <- make\_data\_object()**

2.1 View comparative cell cluster sizes.

**plot\_clusterSize(dat\_E1, dat\_E2)**

2.2 View "barcode" plot for cluster of interest.

```
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.

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

3.2 Map E2 to E1.

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

Combine and plot matching results

4 Combine the bi-directional matching results and plot.

```
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.

```
plot_FRmatch(rst12)
```

Plot one-directional matching p-values.

```
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.



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