



Oct 02, 2020

## FR-Match: cell type matching for scRNAseq data

Yun Renee Zhang<sup>1</sup>, Brian Aevermann<sup>1</sup>, Richard Scheuermann<sup>1</sup>

<sup>1</sup>J. Craig Venter Institute

1

Works for me

dx.doi.org/10.17504/protocols.io.bmyfk7tn

Human Cell Atlas Method Development Community



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 <a href="https://github.com/JCVenterInstitute/FRmatch">https://github.com/JCVenterInstitute/FRmatch</a>.

**EXTERNAL LINK** 

https://github.com/JCVenterInstitute/FRmatch

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

https://doi.org/10.1101/2020.05.01.073445

DOI

dx.doi.org/10.17504/protocols.io.bmyfk7tn

EXTERNAL LINK

https://github.com/JCVenterInstitute/FRmatch

PROTOCOL CITATION

Yun Renee Zhang, Brian Aevermann, Richard Scheuermann 2020. FR-Match: cell type matching for scRNAseq data. **protocols.io** 

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

MANUSCRIPT CITATION please remember to cite the following publication along with this protocol

•

https://doi.org/10.1101/2020.05.01.073445

EXTERNAL LINK

https://github.com/JCVenterInstitute/FRmatch

**KEYWORDS** 

single cell RNA sequencing, cell types, data integration

LICENSE

This is an open access protocol distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Oct 02, 2020

LAST MODIFIED

Oct 02, 2020

mprotocols.io

10/02/2020

 $\textbf{Citation:} \ \ \text{Yun Renee Zhang, Brian Aevermann, Richard Scheuermann (10/02/2020)}. \ \ \text{FR-Match: cell type matching for scRNAseq data.} \\ \underline{\text{https://dx.doi.org/10.17504/protocols.io.bmyfk7tn}}$ 

42727

**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 <a href="https://github.com/JCVenterInstitute/FRmatch">https://github.com/JCVenterInstitute/FRmatch</a>.

**BEFORE STARTING** 



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.



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.



2.2 View "barcode" plot for cluster of interest.



Run main algorithm

10m

3 **P** 

Use wrapper function to perform bi-directional matching.

3.1 Map E1 to E2.



3.2 Map E2 to E1.



Combine and plot matching results

4 Combine the bi-directional matching results and plot.

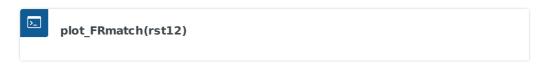


Additional plots

5

Some optional plotting functions to help studying the matching results.

5.1 Plot one-directional matching results.



Plot one-directional matching p-values.



 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)