

# Using the *SIMLR* package

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**Overview.** Single-cell RNA-seq technologies enable high throughput gene expression measurement of individual cells, and allow the discovery of heterogeneity within cell populations. Measurement of cell-to-cell gene expression similarity is critical to identification, visualization and analysis of cell populations. However, single-cell data introduce challenges to conventional measures of gene expression similarity because of the high level of noise, outliers and dropouts. We develop a novel similarity-learning framework, *SIMLR* (Single-cell Interpretation via Multi-kernel LeaRning), which learns an appropriate distance metric from the data for dimension reduction, clustering and visualization. *SIMLR* is capable of separating known subpopulations more accurately in single-cell data sets than do existing dimension reduction methods. Additionally, *SIMLR* demonstrates high sensitivity and accuracy on high-throughput peripheral blood mononuclear cells (PBMC) data sets generated by the GemCode single-cell technology from 10x Genomics.

*In this vignette, we give an overview of the package by presenting some of its main functions.*

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## 1 Changelog

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1.0.0 implements SIMLR and SIMLR feature ranking algorithms.

1.0.2 implements SIMLR large scale algorithms.

## 2 Algorithms and useful links

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Acronym	Extended name	Reference
SIMLR	Single-cell Interpretation via Multi-kernel LeaRning	<a href="#">Paper</a>

## 3 Using SIMLR

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We first load the data provided as an example in the package. The dataset BuettnerFlorian is used for an example of the standard SIMLR, while the dataset ZeiselAmit is used for an example of SIMLR large scale.

```
library(SIMLR)
data(BuettnerFlorian)
data(ZeiselAmit)
```

The external R package igraph is required for the computation of the normalized mutual information to assess the results of the clustering.

```
library(igraph)
```

We now run SIMLR as an example on an input dataset from Buettner, Florian, et al. "Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells." Nature biotechnology 33.2 (2015): 155-160. For this dataset we have a ground true of 3 cell populations, i.e., clusters.

## Using the *SIMLR* package

```
set.seed(11111)
example = SIMLR(X = BuettnerFlorian$in_X, c = BuettnerFlorian$n_clust, cores.ratio = 0)

## Computing the multiple Kernels.
## Performing network diffusion.
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Iteration: 6
## Iteration: 7
## Iteration: 8
## Iteration: 9
## Iteration: 10
## Iteration: 11
## Performing t-SNE.
## Epoch: Iteration # 100 error is: 0.1326426
## Epoch: Iteration # 200 error is: 0.08721104
## Epoch: Iteration # 300 error is: 0.05808032
## Epoch: Iteration # 400 error is: 0.05713627
## Epoch: Iteration # 500 error is: 0.0570977
## Epoch: Iteration # 600 error is: 0.0570602
## Epoch: Iteration # 700 error is: 0.05702496
## Epoch: Iteration # 800 error is: 0.05699161
## Epoch: Iteration # 900 error is: 0.05696026
## Epoch: Iteration # 1000 error is: 0.05693017
## Performing Kmeans.
## Performing t-SNE.
## Epoch: Iteration # 100 error is: 11.21592
## Epoch: Iteration # 200 error is: 0.6659411
## Epoch: Iteration # 300 error is: 0.5755609
## Epoch: Iteration # 400 error is: 0.3986313
## Epoch: Iteration # 500 error is: 0.4913843
## Epoch: Iteration # 600 error is: 0.3970208
## Epoch: Iteration # 700 error is: 0.3979712
## Epoch: Iteration # 800 error is: 0.3530334
## Epoch: Iteration # 900 error is: 0.3026329
## Epoch: Iteration # 1000 error is: 0.2887195
```

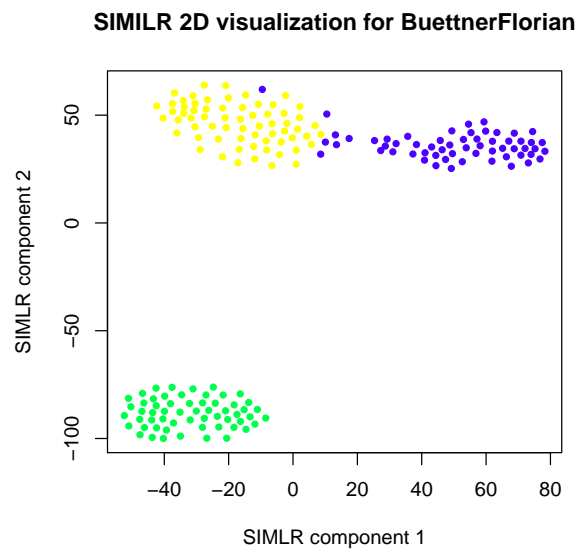
We now compute the normalized mutual information between the inferred clusters by SIMLR and the true ones. This measure with values in  $[0,1]$ , allows us to assess the performance of the clustering with higher values reflecting better performance.

```
nmi_1 = compare(BuettnerFlorian$true_labs[,1], example$y$cluster, method="nmi")
nmi_1
## [1] 0.888298
```

As a further understanding of the results, we now visualize the cell populations in a plot.

## Using the *SIMLR* package

```
plot(example$ydata,  
      col = c(topo.colors(BuettnerFlorian$n_clust))[BuettnerFlorian$true_labs[,1]],  
      xlab = "SIMLR component 1",  
      ylab = "SIMLR component 2",  
      pch = 20,  
      main="SIMLR 2D visualization for BuettnerFlorian")
```



**Figure 1:** Visualization of the 3 cell populations retrieved by SIMLR on the dataset by Florian, et al

We also run SIMLR feature ranking on the same inputs to get a rank of the key genes with the related pvalues.

```
set.seed(11111)  
ranks = SIMLR_Feature_Ranking(A=BuettnerFlorian$results$S,X=BuettnerFlorian$in_X)
```

```
head(ranks$pval)  
## [1] 2.201015e-125 2.531379e-90 5.632172e-77 6.719501e-76 4.444251e-72  
## [6] 8.822900e-69  
head(ranks$aggR)  
## [1] 5701 1689 7549 57 2653 8081
```

We finally show an example for SIMLR large scale on an input dataset being a reduced version of the dataset provided in Buettner, Zeisel, Amit, et al. "Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq." Science 347.6226 (2015): 1138-1142. For this dataset we have a ground true of 9 cell populations, i.e., clusters.

```
set.seed(11111)  
example_large_scale = SIMLR_Large_Scale(X = ZeiselAmit$in_X, c = ZeiselAmit$n_clust, kk = 10)  
  
## Performing fast PCA.  
## Performing k-nearest neighbour search.  
## Computing the multiple Kernels.  
## Performing the iterative procedure 5 times.
```

## Using the *SIMLR* package

```
## Iteration: 1
## Iteration: 2
## Iteration: 3
## Iteration: 4
## Iteration: 5
## Performing Kmeans.
## Performing t-SNE.
## The main loop will be now performed with a maximum of 300 iterations.
## Performing iteration 1.
## Performing iteration 2.
## Performing iteration 3.
## Performing iteration 4.
## Performing iteration 5.
## Performing iteration 6.
## Performing iteration 7.
## Performing iteration 8.
## Performing iteration 9.
## Performing iteration 10.
## Performing iteration 11.
## Performing iteration 12.
## Performing iteration 13.
## Performing iteration 14.
## Performing iteration 15.
## Performing iteration 16.
## Performing iteration 17.
## Performing iteration 18.
## Performing iteration 19.
## Performing iteration 20.
## Performing iteration 21.
## Performing iteration 22.
## Performing iteration 23.
## Performing iteration 24.
## Performing iteration 25.
## Performing iteration 26.
## Performing iteration 27.
## Performing iteration 28.
## Performing iteration 29.
## Performing iteration 30.
## Performing iteration 31.
## Performing iteration 32.
## Performing iteration 33.
## Performing iteration 34.
## Performing iteration 35.
## Performing iteration 36.
## Performing iteration 37.
## Performing iteration 38.
## Performing iteration 39.
## Performing iteration 40.
## Performing iteration 41.
## Performing iteration 42.
## Performing iteration 43.
```

## Using the *SIMLR* package

```
## Performing iteration 44.  
## Performing iteration 45.  
## Performing iteration 46.  
## Performing iteration 47.  
## Performing iteration 48.  
## Performing iteration 49.  
## Performing iteration 50.  
## Performing iteration 51.  
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## Performing iteration 89.  
## Performing iteration 90.  
## Performing iteration 91.  
## Performing iteration 92.  
## Performing iteration 93.  
## Performing iteration 94.
```

## Using the *SIMLR* package

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## Performing iteration 95.  
## Performing iteration 96.  
## Performing iteration 97.  
## Performing iteration 98.  
## Performing iteration 99.  
## Performing iteration 100.  
## Performing iteration 101.  
## Performing iteration 102.  
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## Performing iteration 144.  
## Performing iteration 145.
```

## Using the *SIMLR* package

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## Performing iteration 146.
## Performing iteration 147.
## Performing iteration 148.
## Performing iteration 149.
## Performing iteration 150.
## Performing iteration 151.
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## Performing iteration 153.
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## Performing iteration 191.
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## Performing iteration 193.
## Performing iteration 194.
## Performing iteration 195.
## Performing iteration 196.
```



## Using the *SIMLR* package

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## Performing iteration 197.  
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## Performing iteration 243.  
## Performing iteration 244.  
## Performing iteration 245.  
## Performing iteration 246.  
## Performing iteration 247.
```

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```
## Performing iteration 248.  
## Performing iteration 249.  
## Performing iteration 250.  
## Performing iteration 251.  
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## Performing iteration 291.  
## Performing iteration 292.  
## Performing iteration 293.  
## Performing iteration 294.  
## Performing iteration 295.  
## Performing iteration 296.  
## Performing iteration 297.  
## Performing iteration 298.
```

## Using the *SIMLR* package

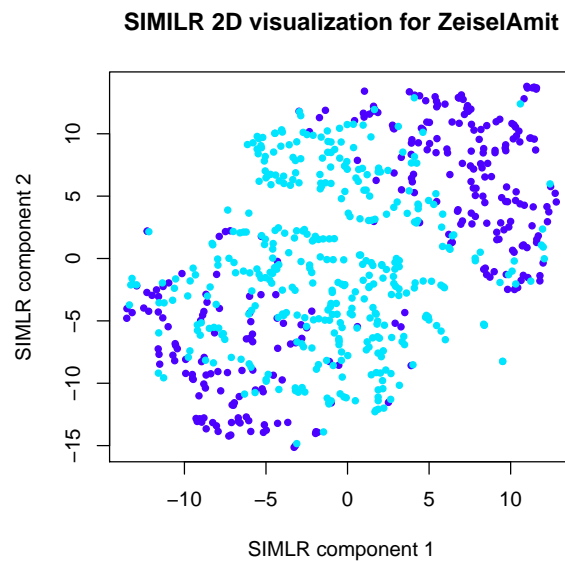
```
## Performing iteration 299.  
## Performing iteration 300.
```

We compute the normalized mutual information between the inferred clusters by SIMLR large scale and the true ones.

```
nmi_2 = compare(ZeiselAmit$true_labs[,1], example_large_scale$y$cluster, method="nmi")  
nmi_2  
## [1] 0.04158302
```

As a further understanding of the results, also in this case we visualize the cell populations in a plot.

```
plot(example_large_scale$ydata,  
      col = c(topo.colors(ZeiselAmit$n_clust))[ZeiselAmit$true_labs[,1]],  
      xlab = "SIMLR component 1",  
      ylab = "SIMLR component 2",  
      pch = 20,  
      main="SIMLR 2D visualization for ZeiselAmit")
```



**Figure 2:** Visualization of the 9 cell populations retrieved by SIMLR large scale on the dataset by Zeisel, Amit, et al

Now, as a final example, we also provide the results of two heuristics (see the original SIMLR paper) to estimate the number of clusters from data.

```
set.seed(53900)  
NUMC = 2:5  
res_example = SIMLR_Estimate_Number_of_Clusters(BuettnerFlorian$in_X,  
      NUMC = NUMC,  
      cores.ratio = 0)
```

Best number of clusters, K1 heuristic:

## Using the *SIMLR* package

```
NUMC[which.min(res_example$K1)]  
## [1] 2
```

K2 heuristic:

```
NUMC[which.min(res_example$K2)]  
## [1] 2
```

Results of the two heuristics:

```
res_example  
  
## $K1  
## [1] -63.04223 -19.49278 -23.77182 13.30109  
##  
## $K2  
## [1] -94.56335 -25.99037 -29.71477 15.96130
```

## 4 sessionInfo()

- R version 3.4.2 (2017-09-28), x86\_64-pc-linux-gnu
- Locale: LC\_CTYPE=en\_US.UTF-8, LC\_NUMERIC=C, LC\_TIME=en\_US.UTF-8, LC\_COLLATE=C, LC\_MONETARY=en\_US.UTF-8, LC\_MESSAGES=en\_US.UTF-8, LC\_PAPER=en\_US.UTF-8, LC\_NAME=C, LC\_ADDRESS=C, LC\_TELEPHONE=C, LC\_MEASUREMENT=en\_US.UTF-8, LC\_IDENTIFICATION=C
- Running under: Ubuntu 16.04.3 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.6-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: SIMLR 1.4.0, igraph 1.1.2, knitr 1.17
- Loaded via a namespace (and not attached): BiocStyle 2.6.0, Matrix 1.2-11, RSpectra 0.12-0, Rcpp 0.12.13, RcppAnnoy 0.0.10, backports 1.1.1, codetools 0.2-15, compiler 3.4.2, digest 0.6.12, evaluate 0.10.1, grid 3.4.2, highr 0.6, htmltools 0.3.6, lattice 0.20-35, magrittr 1.5, parallel 3.4.2, pkgconfig 2.0.1, pracma 2.0.7, quadprog 1.5-5, rmarkdown 1.6, rprojroot 1.2, stringi 1.1.5, stringr 1.2.0, tools 3.4.2, yaml 2.1.14