Gene-Relevance

immediate

April 27, 2020

Contents

1 Single Cell RNA-Sequencing data and gene relevance

Libraries

We need of course destiny, scran for preprocessing, and some tidyverse niceties.

```
[114]: library(conflicted)
       library(destiny)
       suppressPackageStartupMessages(library(scran))
       library(purrr)
       library(ggplot2)
```

Data

Let's use data from the scRNAseq[1] package. If necessary, install it via BiocManager::install('scRNAseq').

[1] Risso D, Cole M (2019). scRNAseq: A Collection of Public Single-Cell RNA-Seq Datasets.

```
[8]: # The parts of the help we're interested in
     help('scRNAseq-package', package = 'scRNAseq') %>% repr::repr_html()␣
       ↪%>%
         stringr::str_extract_all(stringr::regex('<p>The dataset.*?</p>',␣
       ↪dotall = TRUE)) %>% unlist() %>%
         paste(collapse = '') %>% IRdisplay::display_html()
```

379 cells seems sufficient to see something!

[136]:
```
data('allen', package = 'scRNAseq')
```

Preprocessing

We'll mostly stick to the scran vignette here. Let's add basic information to the data and choose what to work with.

As `scran` expects the raw counts in the `counts` assay, we rename the more accurate RSEM counts to `counts`:

[137]:
```
allen <- as(allen, 'SingleCellExperiment')
rowData(allen)$Symbol <- rownames(allen)
rowData(allen)$EntrezID <- AnnotationDbi::mapIds(org.Mm.eg.db::org.Mm.
  ↪eg.db, rownames(allen), 'ENTREZID', 'ALIAS')
rowData(allen)$Uniprot <- AnnotationDbi::mapIds(org.Mm.eg.db::org.Mm.
  ↪eg.db, rownames(allen), 'UNIPROT', 'ALIAS', multiVals = 'list')
assayNames(allen)[assayNames(allen) == 'rsem_counts'] <- 'counts'
isSpike(allen, 'ERCC') <- grepl('^ERCC-', rownames(allen))
allen
```

```
'select()' returned 1:many mapping between keys and columns

'select()' returned 1:many mapping between keys and columns
```

```
class: SingleCellExperiment
dim: 20908 379
metadata(2): SuppInfo which_qc
assays(4): tophat_counts cufflinks_fpkm counts rsem_tpm
rownames(20908): 0610007P14Rik 0610009B22Rik ... Zzef1 Zzz3
rowData names(3): Symbol EntrezID Uniprot
colnames(379): SRR2140028 SRR2140022 ... SRR2139341 SRR2139336
colData names(22): NREADS NALIGNED ... Animal.ID passes_qc_checks_s
reducedDimNames(0):
spikeNames(1): ERCC
```

Now we can use it to renormalize the data. We normalize the `counts` using the spike-in size factors and logarithmize them into `logcounts`.

[138]:
```
allen <- computeSpikeFactors(allen)
allen <- normalize(allen)
```

We also use the spike-ins to detect highly variable genes more accurately:

[139]:
```
decomp <- decomposeVar(allen, trendVar(allen, parametric = TRUE))
rowData(allen)$hvg_order <- order(decomp$bio, decreasing = TRUE)
```

We create a subset of the data containing only rasonably highly variable genes and no spike-ins:

```
[140]: allen_hvg <- subset(allen, hvg_order <= 5000L & !isSpike(allen))
```

Let's create a Diffusion map. For rapid results, people often create a PCA first, which can be stored in your `SingleCellExperiment` before creating the Diffusion map or simply created implicitly using `DiffusionMap(..., n_pcs = <number>)`.

However, even with many more principal components than necessary to get a nicely resolved Diffusion Map, the close spatial correspondence between diffusion components and genes are lost.

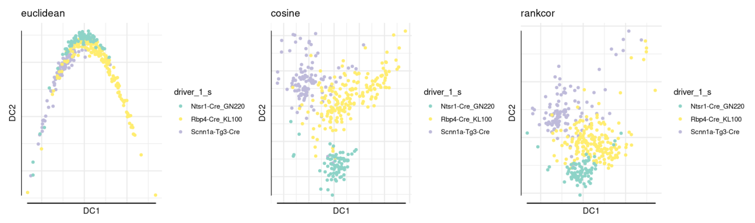
```
[75]: #reducedDim(allen_hvg, 'pca') <- irlba::prcomp_irlba(t(assay(allen,␣
        ↪'logcounts')), 50)$x
```

The chosen distance metric has big implications on your results, you should try at least cosine and rankcor.

```
[76]: set.seed(1)
      dms <- c('euclidean', 'cosine', 'rankcor') %>% #, 'l2'
          set_names() %>%
          map(~ DiffusionMap(allen_hvg, distance = ., knn_params =␣
        ↪list(method = 'covertree')))
```

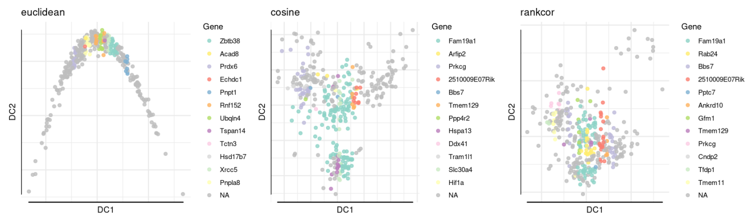
```
Warning message in DiffusionMap(allen_hvg, distance = ., knn_params =
list(method = "covertree")):
“You have 4972 genes. Consider passing e.g. n_pcs = 50 to speed up␣
  ↪computation.”
Warning message in DiffusionMap(allen_hvg, distance = ., knn_params =
list(method = "covertree")):
“You have 4972 genes. Consider passing e.g. n_pcs = 50 to speed up␣
  ↪computation.”
Warning message in DiffusionMap(allen_hvg, distance = ., knn_params =
list(method = "covertree")):
“You have 4972 genes. Consider passing e.g. n_pcs = 50 to speed up␣
  ↪computation.”
```

```
[77]: options(repr.plot.width = 14, repr.plot.height = 4)
      dms %>%
          imap(function(dm, dist) plot(dm, 1:2, col_by = 'driver_1_s') +␣
        ↪ggtitle(dist)) %>%
          cowplot::plot_grid(plotlist = ., nrow = 1)
```



[78]:
```
grs <- map(dms, gene_relevance)
```

[79]:
```
options(repr.plot.width = 14, repr.plot.height = 4)
gms <- imap(grs, function(gr, dist) plot(gr, iter_smooth = 0) +␣
  ↪ggtitle(dist))
cowplot::plot_grid(plotlist = gms, nrow = 1)
```



As you can see, despite the quite different embedding, the rankcor and Cosine diffusion Maps display a number of the same driving genes.

[116]:
```
gms[-1] %>% map(~ .$ids[1:10]) %>% purrr::reduce(intersect) %>%␣
  ↪cat(sep = ' ')
```

```
Fam19a1 Prkcg 2510009E07Rik Bbs7 Tmem129
```

[176]:
```
httr::GET('https://www.uniprot.org/uniprot/', query = list(
    columns = 'id,genes,comment(TISSUE SPECIFICITY)',
    format = 'tab',
    query = rowData(allen)$Uniprot[gms$cosine$ids[1:6]] %>% unlist()␣
  ↪%>% paste(collapse = ' or ')
)) %>% httr::content(type = 'text/tab-separated-values', encoding =␣
  ↪'utf-8', )
```

```
Parsed with column specification:
cols(
  Entry = col_character(),
  Gene names = col_character(),
  Tissue specificity = col_character()
)
```

A spec_tbl_df: 9 × 3	Entry <chr>	Gene names <chr>	Tissue specificity <chr>
	Q8K221	Arfip2	NA
	Q6GQU0	NA	NA
	Q7TPG8	Tafa1 Fam19a1	TISSUE SPECIFICITY: Expressed in the hippocampus and
	Q8K304	Tmem129	NA
	P63318	Prkcg Pkcc Pkcg Prkcc	TISSUE SPECIFICITY: Expressed in the cerebellum, cerebr
	Q8K2G4	Bbs7 Bbs2l1	NA
	Q2NKI4	Prkcg Prkcc	NA
	A0A1B0GSM3	Arfip2 mCG_19713	NA
	Q3UN66	Prkcg Prkcc mCG_18472	NA