Single Cell and Spatial Transcriptomics Defines the Cellular Architecture of the Antimicrobial Response Network in Human Leprosy Granulomas

Here we show the codes we used to make the plots in Figure 1

```
library(Seurat)
library(ggplot2)
library(scales)

# Load the data
load("all_cells_scRNA-seq_seurat_object.Rda")

# Random order of the cells in the UMAP plot
set.seed(1)
random_order = sample(colnames(allcells), ncol(allcells))

# Colors for each origin
my_color = brewer_pal(palette="RdBu")(10)

# Plot Figure 1a
DimPlot(allcells, label=TRUE, reduction="umap", group.by="celltype",
        pt.size=0.5, cells=random_order, label.size=4.3)
```
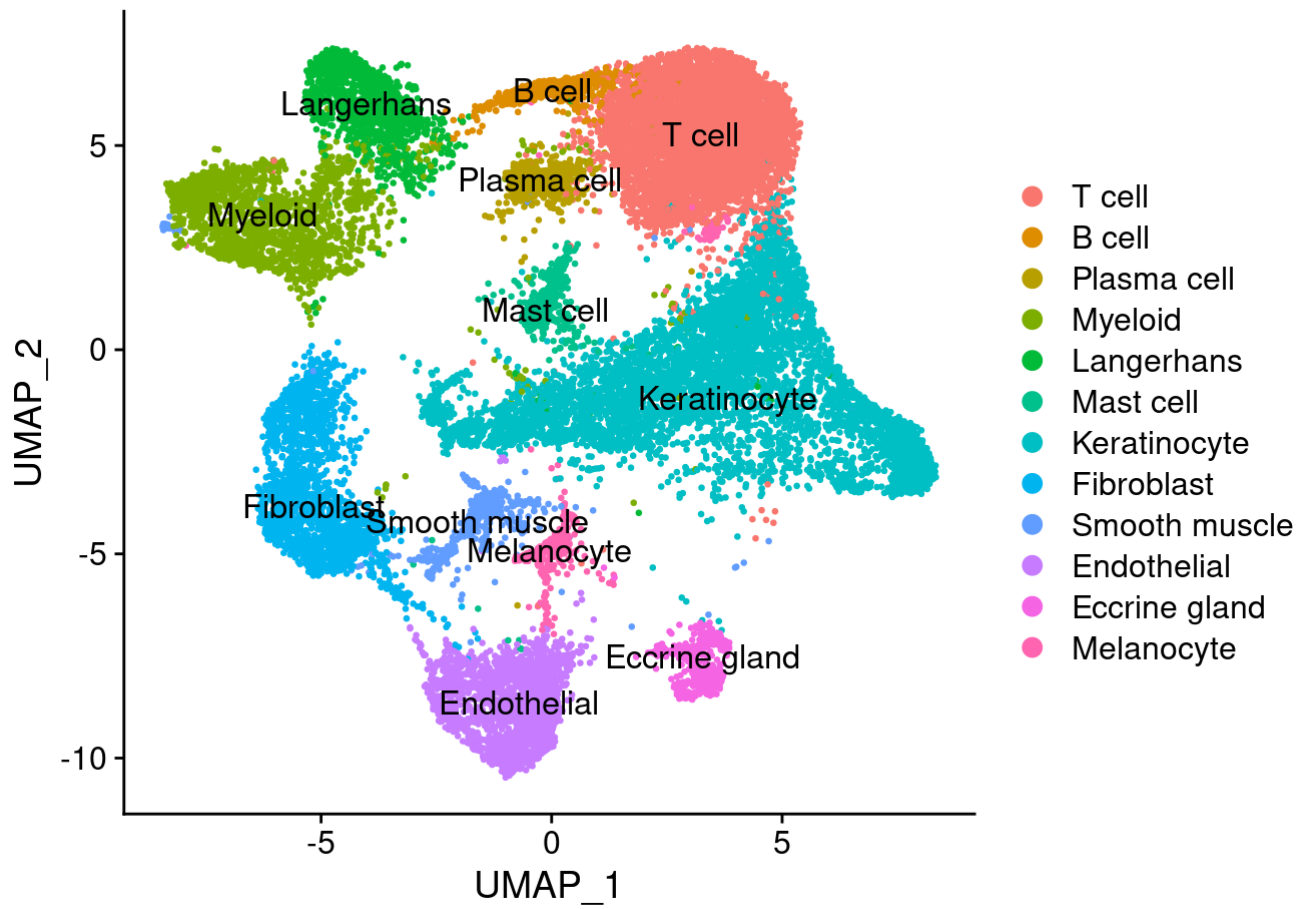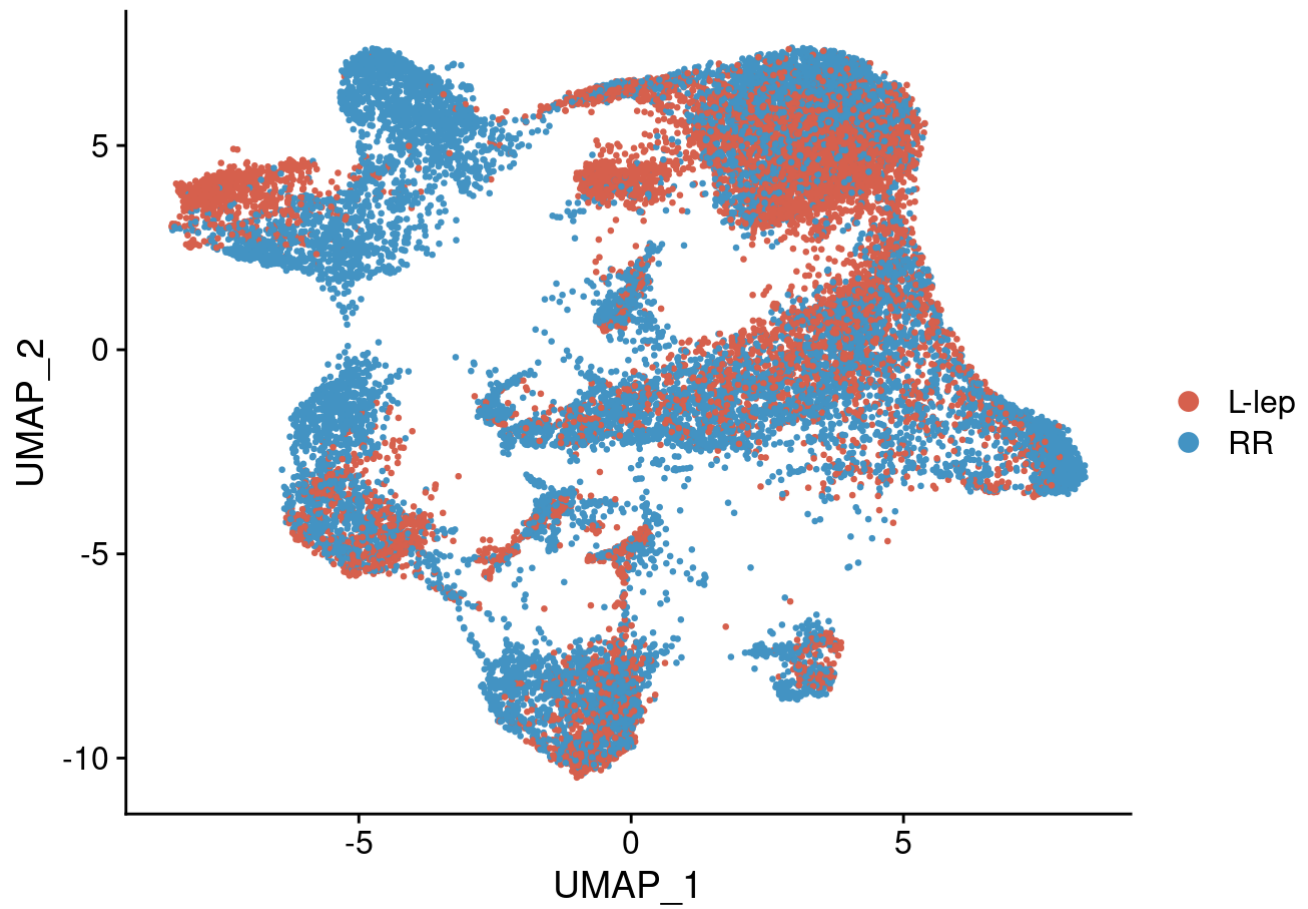
```
## Warning: Using `as.character()` on a quosure is deprecated as of rlang 0.3.0.
## Please use `as_label()` or `as_name()` instead.
## This warning is displayed once per session.
```

```
# Plot Figure 1b
DimPlot(allcells, label=FALSE, reduction="umap", group.by="CF",
        pt.size=0.5, cells=random_order, cols=my_color[c(3,8)])
```

```
# Select 200 cells for each cell type to plot the marker genes in the heatmap
table(allcells$celltype)
```

```
##
##         T cell         B cell    Plasma cell        Myeloid     Langerhans
##           5574            517            499           1947           1281
##      Mast cell   Keratinocyte      Fibroblast  Smooth muscle    Endothelial
##            451           5897           1876            533           1871
## Eccrine gland     Melanocyte
##            440            432
```

```
bars = c()
set.seed(1)
for (i in as.character(unique(allcells$celltype))){
  new_bars = colnames(allcells)[allcells$celltype == i]
  new_bars = new_bars[order(-allcells$nCount_RNA[new_bars])][1:200]
  new_bars = sample(new_bars)
  bars = c(bars, new_bars)
}

# Three signature genes for each cell type
genes = c("CD3D","CD3E","TRBC2","MS4A1","BANK1","CD79A","IGHG3","IGHG1","IGHG4",
          "LYZ","C1QC","CXCL8","CCL22","CD1A","CD207","TPSB2","CPA3","CTSG",
          "KRT10","KRT2","KRT1","C3","DCN","COL1A1","MYH11","ACTA2","TAGLN",
          "PECAM1","CDH5","AQP1","DCD","MUCL1","SCGB2A2","TYRP1","DCT","PMEL")

# Plot Figure 1c
heatmap_object = subset(allcells, cells=bars)
Idents(heatmap_object) = heatmap_object$celltype
heatmap_object = ScaleData(object=heatmap_object, features=rownames(heatmap_object))
```

```
## Centering and scaling data matrix
```
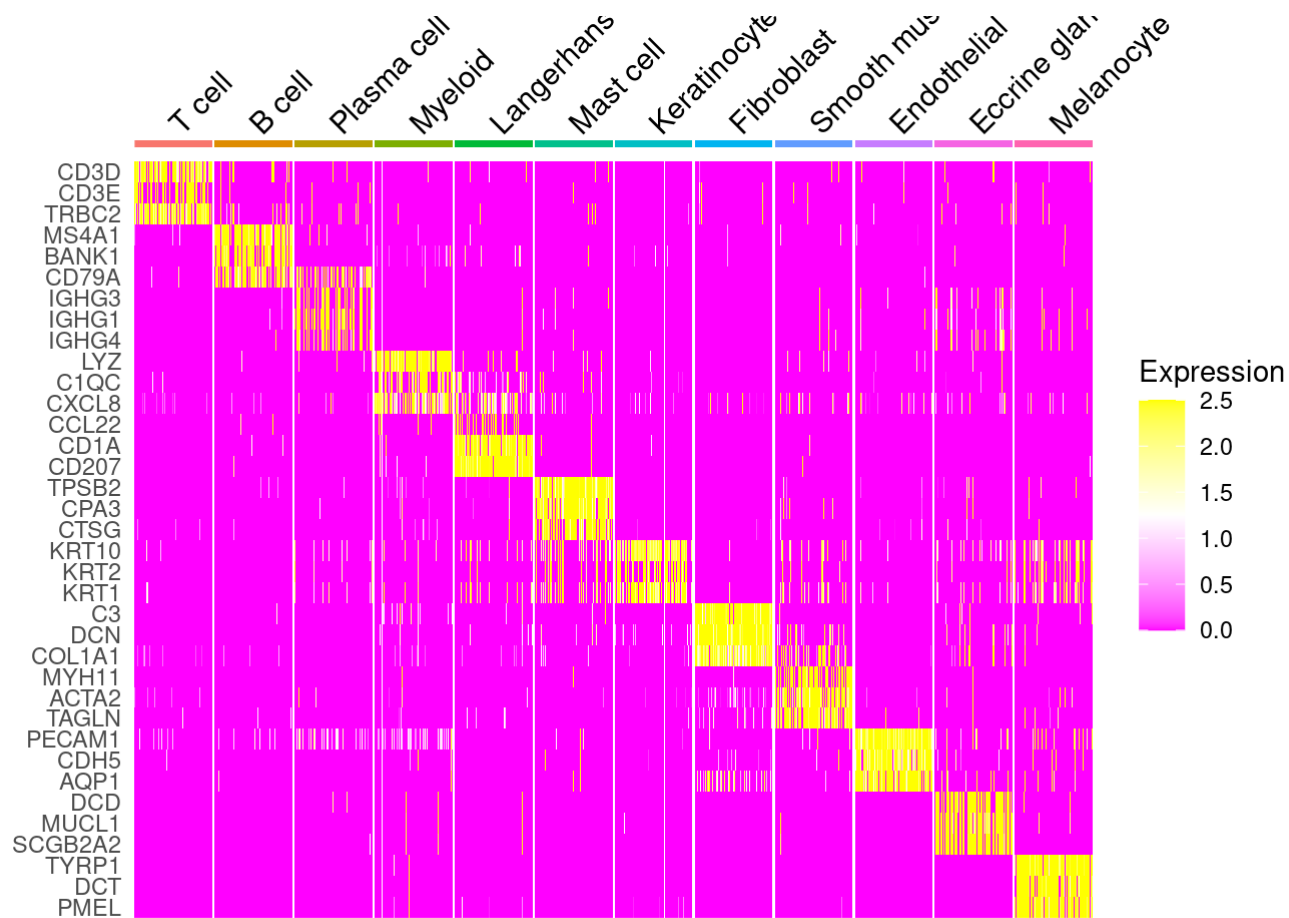
```
DoHeatmap(object=heatmap_object, features=genes, angle=45, size=4, raster=FALSE,
          cells=bars, disp.min=0, group.bar.height=0.01) +
  scale_fill_gradientn(colors=c("#FF00FF","white","#FFFF00"), na.value='white') +
  guides(color=FALSE)
```

```
## Scale for 'fill' is already present. Adding another scale for 'fill', which
## will replace the existing scale.
```

```r
# Count the number of cells for each cell types by each sample
orig = allcells$orig.ident
u_orig = sort(unique(orig))
celltype = as.character(allcells$celltype)
uct = sort(unique(celltype))
z = matrix(nrow=length(uct), ncol=length(u_orig))
rownames(z) = uct
colnames(z) = u_orig
for (i in 1:nrow(z)){
  for (j in 1:ncol(z)){
    z[i,j] = sum(orig[celltype==uct[i]] == u_orig[j])
  }
}

# Normalize by the total number of cells for each sample and then scale by each cell type
z = t(t(z) / rowSums(t(z)))
z = z / rowSums(z) * 100

# Plot Figure 1d
z1 = data.frame(ncells=as.vector(z), type=rep(rownames(z), ncol(z)), orig=rep(colnames(z), each=nrow(z)))
celltype_order = c("T cell","B cell","Plasma cell","Myeloid","Langerhans","Mast cell","Keratinocyte",
                   "Fibroblast","Smooth muscle","Endothelial","Eccrine gland","Melanocyte")
z1$type = factor(z1$type, levels=celltype_order)
z1$orig = gsub("[.]", "-", z1$orig)
my_color = brewer_pal(palette="RdBu")(10)
ggplot(z1, aes(x=type, y=ncells, fill=orig, group=orig)) +
  theme_classic() + geom_bar(stat="identity", width=0.7) +
  scale_fill_manual(values=my_color) +
  labs(x="", y="% Component of allcellss", fill=NULL) +
  theme(axis.text.x=element_text(angle=45, hjust=1, vjust=1, size=12))
```
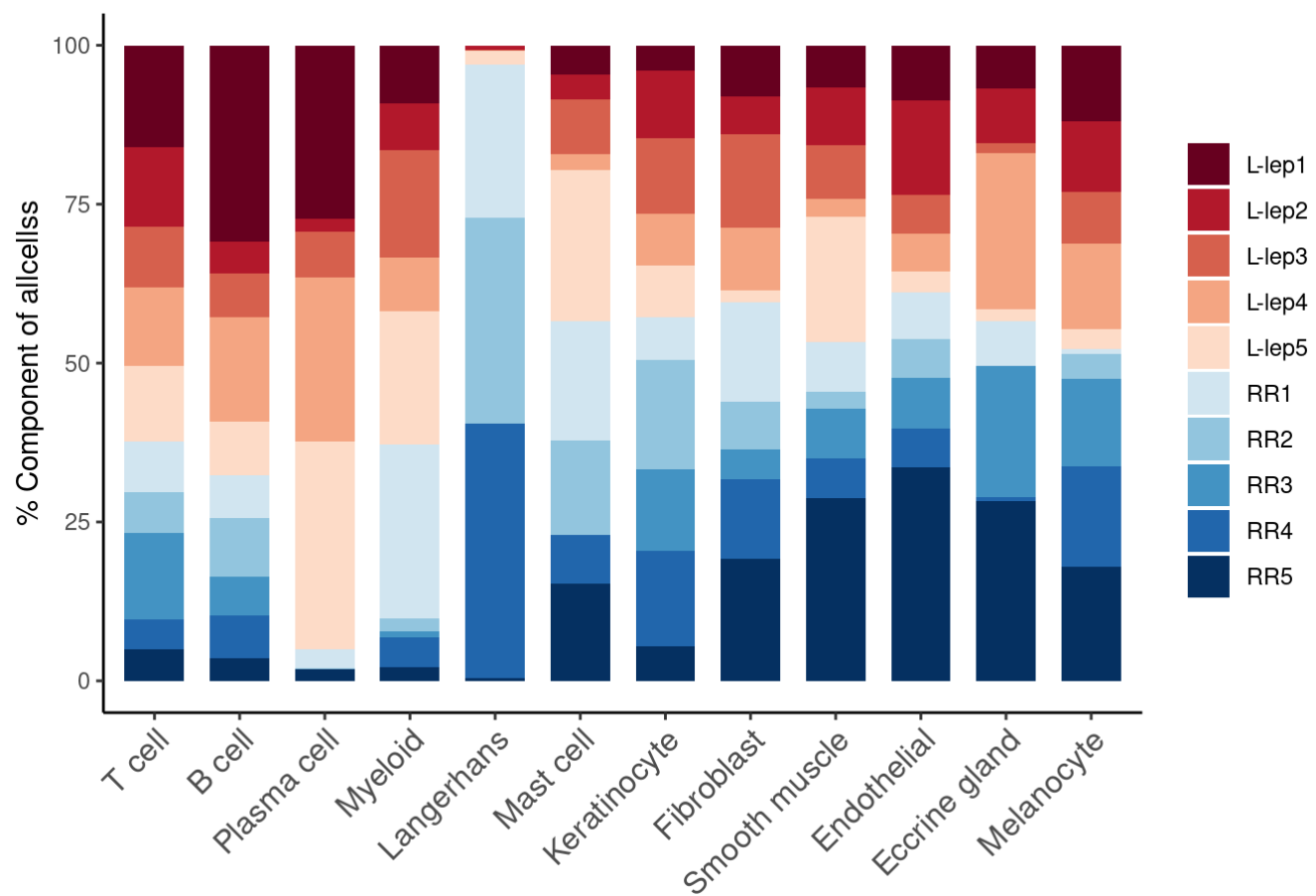
```
# Plot Figure 1e
VlnPlot(allcells, features=c("MLEP_nUMIs"), group.by="orig.ident", pt.size=0.1) +
  labs(y="log10 ( Mlep nUMIs )", title="MLEP nUMIs") + scale_fill_manual(values=my_colo
r) +
  labs(x=NULL) + guides(fill=FALSE)
```

MLEP nUMIs
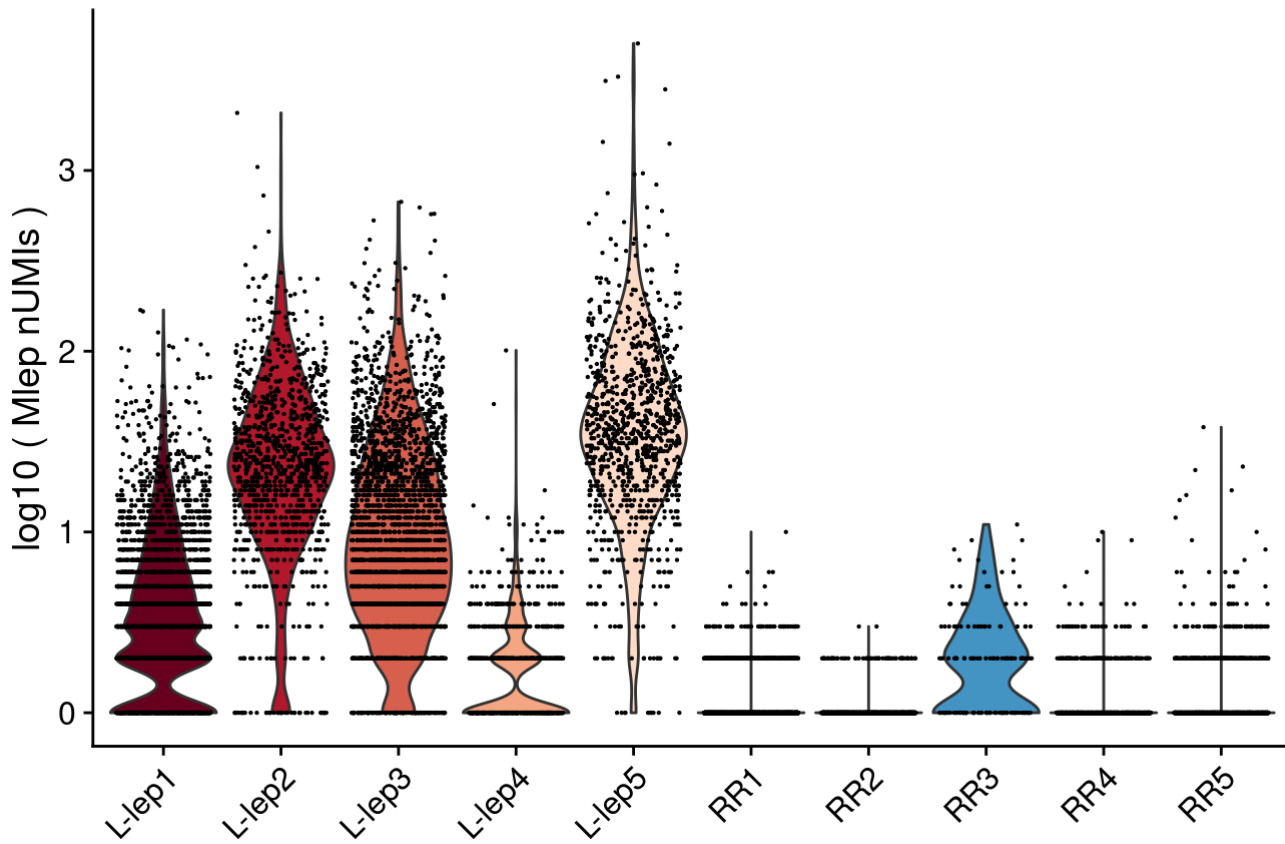
Session info

```
sessioninfo::session_info()
```

```
## Registered S3 method overwritten by 'cli':
##   method      from
##   print.boxx spatstat
```

```
## Warning in system("timedatectl", intern = TRUE): running command 'timedatectl'
## had status 1
```

```
## — Session info ─────────────────────────────────────────────────
##   setting  value
##   version  R version 3.6.0 (2019-04-26)
##   os       Red Hat Enterprise Linux
##   system   x86_64, linux-gnu
##   ui       X11
##   language (EN)
##   collate  en_US.UTF-8
##   ctype    en_US.UTF-8
##   tz       America/Los_Angeles
##   date     2021-03-08
##
## — Packages ──────────────────────────────────────────────────────
##   package        * version  date        lib source
##   abind            1.4-5     2016-07-21 [1] CRAN (R 3.6.0)
##   assertthat       0.2.1     2019-03-21 [1] CRAN (R 3.6.0)
##   bitops           1.0-6     2013-08-17 [2] CRAN (R 3.5.0)
##   caTools          1.18.0    2020-01-17 [1] CRAN (R 3.6.0)
##   cli              2.0.1     2020-01-08 [1] CRAN (R 3.6.0)
##   cluster          2.0.8     2019-04-05 [2] CRAN (R 3.6.0)
##   codetools        0.2-16    2018-12-24 [2] CRAN (R 3.6.0)
##   colorspace       1.4-1     2019-03-18 [1] CRAN (R 3.6.0)
##   cowplot          1.0.0     2019-07-11 [1] CRAN (R 3.6.0)
##   crayon           1.3.4     2017-09-16 [2] CRAN (R 3.5.0)
##   data.table       1.12.8    2019-12-09 [1] CRAN (R 3.6.0)
##   deldir           0.1-28    2020-07-15 [1] CRAN (R 3.6.0)
##   digest           0.6.23    2019-11-23 [1] CRAN (R 3.6.0)
##   dplyr            0.8.3     2019-07-04 [1] CRAN (R 3.6.0)
##   evaluate         0.14      2019-05-28 [1] CRAN (R 3.6.0)
##   fansi            0.4.1     2020-01-08 [1] CRAN (R 3.6.0)
##   farver           2.0.3     2020-01-16 [1] CRAN (R 3.6.0)
##   fastmap          1.0.1     2019-10-08 [1] CRAN (R 3.6.0)
##   fitdistrplus     1.0-14    2019-01-23 [2] CRAN (R 3.5.1)
##   future           1.16.0    2020-01-16 [1] CRAN (R 3.6.0)
##   future.apply     1.4.0     2020-01-07 [1] CRAN (R 3.6.0)
##   gdata            2.18.0    2017-06-06 [2] CRAN (R 3.5.0)
##   ggplot2        * 3.3.2     2020-06-19 [1] CRAN (R 3.6.0)
##   ggrepel          0.8.1     2019-05-07 [1] CRAN (R 3.6.0)
##   ggridges         0.5.2     2020-01-12 [1] CRAN (R 3.6.0)
##   globals          0.12.5    2019-12-07 [1] CRAN (R 3.6.0)
##   glue             1.4.2     2020-08-27 [1] CRAN (R 3.6.0)
##   goftest          1.2-2     2019-12-02 [1] CRAN (R 3.6.0)
##   gplots           3.0.3     2020-02-25 [1] CRAN (R 3.6.0)
##   gridExtra        2.3       2017-09-09 [2] CRAN (R 3.5.0)
##   gtable           0.3.0     2019-03-25 [1] CRAN (R 3.6.0)
##   gtools           3.8.1     2018-06-26 [2] CRAN (R 3.5.0)
##   htmltools        0.4.0     2019-10-04 [1] CRAN (R 3.6.0)
##   htmlwidgets      1.5.1     2019-10-08 [1] CRAN (R 3.6.0)
##   httpuv           1.5.2     2019-09-11 [1] CRAN (R 3.6.0)
##   httr             1.4.1     2019-08-05 [1] CRAN (R 3.6.0)
##   ica              1.0-2     2018-05-24 [2] CRAN (R 3.5.0)
##   igraph           1.2.4.2   2019-11-27 [1] CRAN (R 3.6.0)
##   irlba            2.3.3     2019-02-05 [2] CRAN (R 3.5.1)
```

```
##   jsonlite        1.7.1     2020-09-07 [2] CRAN (R 3.6.0)
##   KernSmooth      2.23-15   2015-06-29 [2] CRAN (R 3.6.0)
##   knitr           1.27      2020-01-16 [1] CRAN (R 3.6.0)
##   labeling        0.3       2014-08-23 [2] CRAN (R 3.5.0)
##   later           1.0.0     2019-10-04 [1] CRAN (R 3.6.0)
##   lattice         0.20-38   2018-11-04 [2] CRAN (R 3.6.0)
##   lazyeval        0.2.2     2019-03-15 [1] CRAN (R 3.6.0)
##   leiden          0.3.2     2020-01-18 [1] CRAN (R 3.6.0)
##   lifecycle       0.1.0     2019-08-01 [1] CRAN (R 3.6.0)
##   listenv         0.8.0     2019-12-05 [1] CRAN (R 3.6.0)
##   lmtest          0.9-37    2019-04-30 [1] CRAN (R 3.6.0)
##   lsei            1.2-0     2017-10-23 [2] CRAN (R 3.5.1)
##   magrittr        1.5       2014-11-22 [2] CRAN (R 3.5.0)
##   MASS            7.3-51.4  2019-03-31 [2] CRAN (R 3.6.0)
##   Matrix          1.2-17    2019-03-22 [2] CRAN (R 3.6.0)
##   matrixStats     0.55.0    2019-09-07 [1] CRAN (R 3.6.0)
##   mgcv            1.8-28    2019-03-21 [2] CRAN (R 3.6.0)
##   mime            0.8       2019-12-19 [1] CRAN (R 3.6.0)
##   miniUI          0.1.1.1   2018-05-18 [2] CRAN (R 3.5.1)
##   munsell         0.5.0     2018-06-12 [2] CRAN (R 3.5.0)
##   nlme            3.1-139   2019-04-09 [2] CRAN (R 3.6.0)
##   npsurv          0.4-0     2017-10-14 [2] CRAN (R 3.5.1)
##   patchwork       1.0.1     2020-06-22 [1] CRAN (R 3.6.0)
##   pbapply         1.4-2     2019-08-31 [1] CRAN (R 3.6.0)
##   pillar          1.4.3     2019-12-20 [1] CRAN (R 3.6.0)
##   pkgconfig       2.0.3     2019-09-22 [1] CRAN (R 3.6.0)
##   plotly          4.9.1     2019-11-07 [1] CRAN (R 3.6.0)
##   plyr            1.8.5     2019-12-10 [1] CRAN (R 3.6.0)
##   png             0.1-7     2013-12-03 [2] CRAN (R 3.5.0)
##   polyclip        1.10-0    2019-03-14 [1] CRAN (R 3.6.0)
##   promises        1.1.0     2019-10-04 [1] CRAN (R 3.6.0)
##   purrr           0.3.3     2019-10-18 [1] CRAN (R 3.6.0)
##   R6              2.4.1     2019-11-12 [1] CRAN (R 3.6.0)
##   RANN            2.6.1     2019-01-08 [2] CRAN (R 3.5.1)
##   RColorBrewer    1.1-2     2014-12-07 [2] CRAN (R 3.5.0)
##   Rcpp            1.0.3     2019-11-08 [1] CRAN (R 3.6.0)
##   RcppAnnoy       0.0.14    2019-11-12 [1] CRAN (R 3.6.0)
##   RcppParallel    4.4.4     2019-09-27 [1] CRAN (R 3.6.0)
##   reshape2        1.4.3     2017-12-11 [2] CRAN (R 3.5.0)
##   reticulate      1.14      2019-12-17 [1] CRAN (R 3.6.0)
##   rlang           0.4.8     2020-10-08 [1] CRAN (R 3.6.0)
##   rmarkdown       2.1       2020-01-20 [1] CRAN (R 3.6.0)
##   ROCR            1.0-7     2015-03-26 [2] CRAN (R 3.5.0)
##   rpart           4.1-15    2019-04-12 [2] CRAN (R 3.6.0)
##   rsvd            1.0.2     2019-07-29 [1] CRAN (R 3.6.0)
##   Rtsne           0.15      2018-11-10 [1] CRAN (R 3.6.0)
##   scales        * 1.1.0     2019-11-18 [1] CRAN (R 3.6.0)
##   sctransform     0.3       2020-09-20 [1] CRAN (R 3.6.0)
##   sessioninfo     1.1.1     2018-11-05 [1] CRAN (R 3.6.0)
##   Seurat        * 3.2.2     2020-09-26 [1] CRAN (R 3.6.0)
##   shiny           1.4.0     2019-10-10 [1] CRAN (R 3.6.0)
##   spatstat        1.64-1    2020-05-12 [1] CRAN (R 3.6.0)
##   spatstat.data   1.4-3     2020-01-26 [1] CRAN (R 3.6.0)
##   spatstat.utils  1.17-0    2020-02-07 [1] CRAN (R 3.6.0)
```

```
##   stringi        1.4.5     2020-01-11 [1] CRAN (R 3.6.0)
##   stringr        1.4.0     2019-02-10 [2] CRAN (R 3.5.1)
##   survival       2.44-1.1  2019-04-01 [2] CRAN (R 3.6.0)
##   tensor         1.5       2012-05-05 [1] CRAN (R 3.6.0)
##   tibble         2.1.3     2019-06-06 [1] CRAN (R 3.6.0)
##   tidyr          1.0.0     2019-09-11 [1] CRAN (R 3.6.0)
##   tidyselect     1.1.0     2020-05-11 [1] CRAN (R 3.6.0)
##   uwot           0.1.5     2019-12-04 [1] CRAN (R 3.6.0)
##   vctrs          0.3.6     2020-12-17 [1] CRAN (R 3.6.0)
##   viridisLite    0.3.0     2018-02-01 [2] CRAN (R 3.5.0)
##   withr          2.3.0     2020-09-22 [2] CRAN (R 3.6.0)
##   xfun           0.12      2020-01-13 [1] CRAN (R 3.6.0)
##   xtable         1.8-4     2019-04-21 [1] CRAN (R 3.6.0)
##   yaml           2.2.0     2018-07-25 [2] CRAN (R 3.5.0)
##   zoo            1.8-7     2020-01-10 [1] CRAN (R 3.6.0)
##
## [1] /data/home/mafeiyang/R/x86_64-redhat-linux-gnu-library/3.6
## [2] /usr/lib64/R/library
## [3] /usr/share/R/library
```