PBMC vs Tissue Figures

In [1]:
```
source('jupyterFunctions_perCellType.R')
```

In [2]:
```
data_prefix <- paste(sep='','../data/PBMCvsTissue/')
Tcell_PvT <- readRDS(paste(sep='',data_prefix,'Tcell_PBMCvsTissue_df.rds'))
Bcell_PvT <- readRDS(paste(sep='',data_prefix,'Bcell_PBMCvsTissue_df.rds'))
myeloid_PvT <- readRDS(paste(sep='',data_prefix,'myeloid_PBMCvsTissue_df.rds'))
```

In [3]:
```
tissue_color <- 'slateblue3'
PBMC_color <- 'brown3'
```

In [24]:
```
save_dir <- NA #'../output/' #or NA if don't want to save
```

T cell

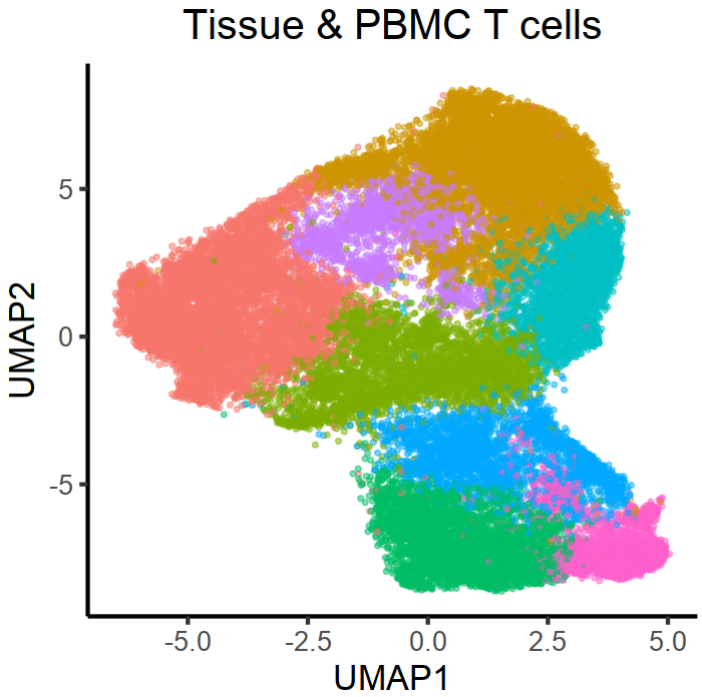
In [5]:
```
Tcell_res <- 'hres_0.40'
if(!(Tcell_res %in% colnames(Tcell_PvT))) stop('cluster resolution not in df')
```

In [6]:
```
Tcell_tissue_clusters <- sort(unique(Tcell_PvT[which(Tcell_PvT$bio_src=='tissue'),'bio_src_cellType']))
Tcell_PBMC_clusters <- sort(unique(Tcell_PvT[which(Tcell_PvT$bio_src=='PBMC'),'bio_src_cellType']))

Tcell_colors <- c(rep(tissue_color,length(Tcell_tissue_clusters)),rep(PBMC_color,length(Tcell_PBMC_clusters)))
names(Tcell_colors) <- c(Tcell_tissue_clusters,Tcell_PBMC_clusters)
```

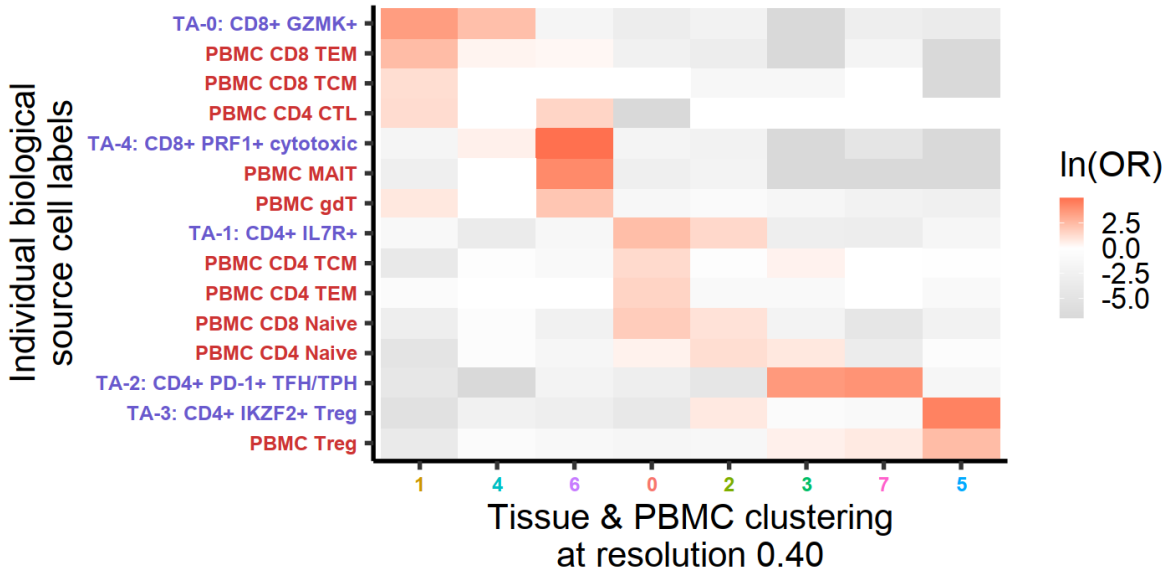
In [7]:
```
ll <- table(Tcell_PvT[which(Tcell_PvT$bio_src=='PBMC'),'bio_src_cellType'])
Tcell_tooSmall <- names(ll[ll<10])
```

In [8]:
```
Tcell_original_order <- c('TA-0: CD8+ GZMK+','PBMC CD8 TEM','PBMC CD8 TC
M','PBMC CD4 Proliferating','PBMC CD4 CTL',
                          'TA-4: CD8+ PRF1+ cytotoxic','PBMC MAIT','PBMC
gdT',
                          'TA-1: CD4+ IL7R+','PBMC CD4 TCM','PBMC CD4 TE
M','PBMC CD8 Naive','PBMC CD4 Naive',
                          'TA-2: CD4+ PD-1+ TFH/TPH',
                          'TA-3: CD4+ IKZF2+ Treg','PBMC Treg',
                          'PBMC dnT')
if(!all(Tcell_original_order %in% unique(Tcell_PvT$bio_src_cellType))) s
top('original order insufficient')

Tcell_PvT_order <- c(1,4,6,0,2,3,7,5)
if(!all(Tcell_PvT_order %in% unique(Tcell_PvT[,Tcell_res]))) stop('clust
er order insufficient')
```

In [9]:
```
#Fig S7a left

Tcell_cluster_colors <- hue_pal()(length(unique(Tcell_PvT[,Tcell_res])))
names(Tcell_cluster_colors) <- sort(unique(Tcell_PvT[,Tcell_res]))

options(repr.plot.height=6,repr.plot.width=6)
g <- ggplot(Tcell_PvT[which(!(Tcell_PvT$bio_src_cellType %in% Tcell_tooS
mall)),],
            aes_string(x='UMAP1',y='UMAP2',color=Tcell_res)) +
        geom_point(size=1,alpha=0.5) + theme_classic(base_size=20) + sca
le_color_manual(values=Tcell_cluster_colors) +
        theme(legend.position="none") +
        ggtitle('Tissue & PBMC T cells') + theme(plot.title = element_te
xt(hjust = 0.5))
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,'Tcell_PBMCvsTiss
ue_UMAP.png'),
                            plot=g,units='in',height=6,width=6,dpi=600)
```



In [10]:
```
#Fig 7a right

Tcell_fisher_df <- calc_OR(Tcell_PvT[which(!(Tcell_PvT$bio_src_cellType
%in% Tcell_tooSmall)),],
                           Tcell_res, 'bio_src_cellType')

g <- plot_OR(Tcell_fisher_df, Tcell_res, 'bio_src_cellType',
             paste('Tissue & PBMC clustering\nat resolution',str_split_f
ixed(Tcell_res,'_',2)[,2]),
             'Individual biological\nsource cell labels',
             Tcell_PvT_order, Tcell_original_order,clustColors=c(Tcell_c
olors,Tcell_cluster_colors))

options(repr.plot.height=6,repr.plot.width=12)
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,save_dir,'Tcell_P
BMCvsTissue_OR_heatmap.png'),
                           plot=g,units='in',height=6,width=12,dpi=600)
```



Myeloid

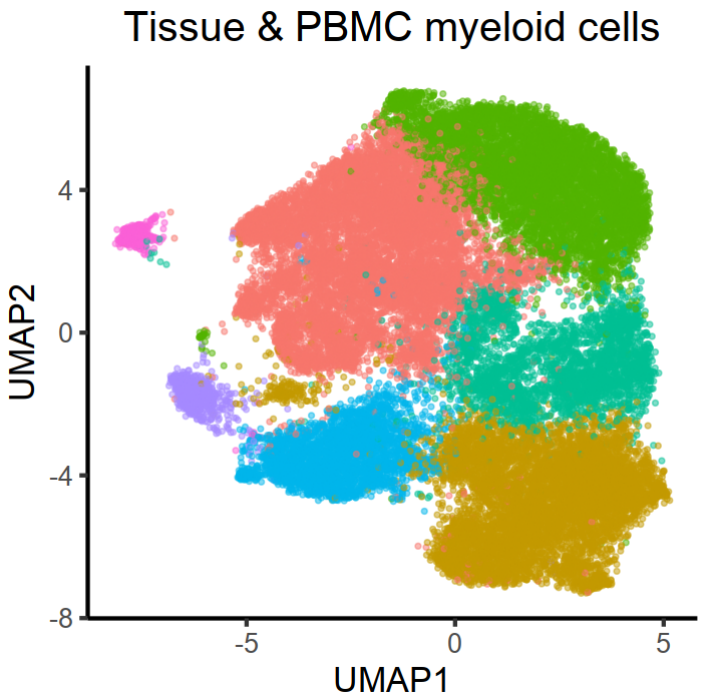
In [11]:
```
myeloid_res <- 'hres_0.20'
if(!(myeloid_res %in% colnames(myeloid_PvT))) stop('cluster resolution n
ot in df')
```

In [12]:
```
myeloid_tissue_clusters <- sort(unique(myeloid_PvT[which(myeloid_PvT$bio
_src=='tissue'),'bio_src_cellType']))
myeloid_PBMC_clusters <- sort(unique(myeloid_PvT[which(myeloid_PvT$bio_s
rc=='PBMC'),'bio_src_cellType']))

myeloid_colors <- c(rep(tissue_color,length(myeloid_tissue_clusters)),re
p(PBMC_color,length(myeloid_PBMC_clusters)))
names(myeloid_colors) <- c(myeloid_tissue_clusters,myeloid_PBMC_cluster
s)
```

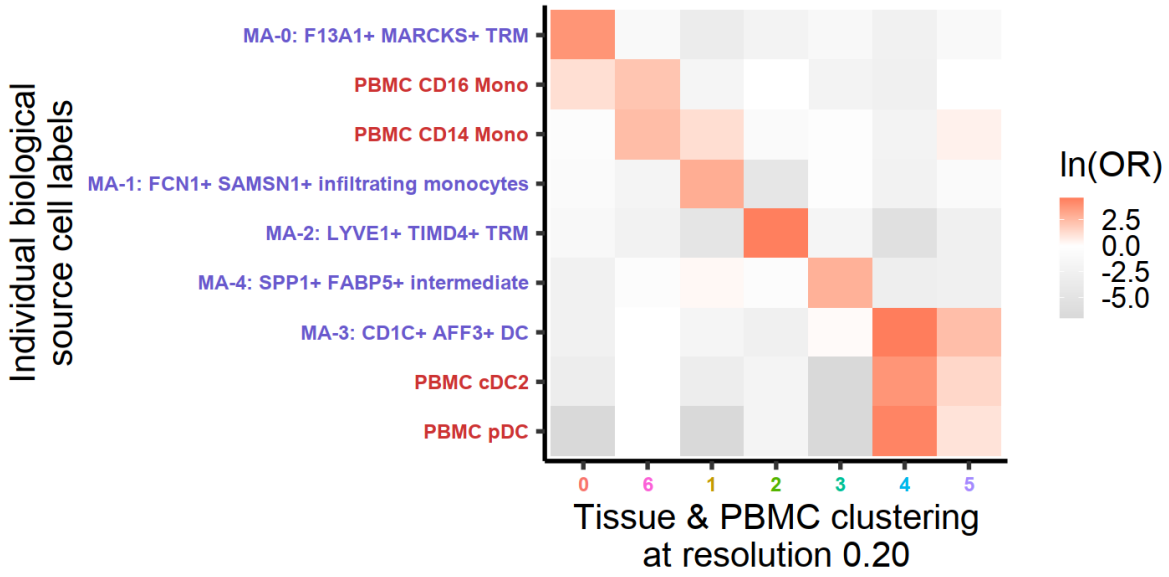
In [13]:
```
ll <- table(myeloid_PvT[which(myeloid_PvT$bio_src=='PBMC'),'bio_src_cell
Type'])
myeloid_tooSmall <- names(ll[ll<10])
```

In [14]:
```
myeloid_original_order <- c('MA-0: F13A1+ MARCKS+ TRM','PBMC CD16 Mon
o','PBMC CD14 Mono',
                            'MA-1: FCN1+ SAMSN1+ infiltrating monocyte
s',
                            'MA-2: LYVE1+ TIMD4+ TRM',
                            'MA-4: SPP1+ FABP5+ intermediate',
                            'MA-3: CD1C+ AFF3+ DC','PBMC cDC1','PBMC cDC
2','PBMC pDC')
if(!all(myeloid_original_order %in% unique(myeloid_PvT$bio_src_cellTyp
e))) stop('original order insufficient')

myeloid_PvT_order <- c(0,6,1,2,3,4,5)
if(!all(myeloid_PvT_order %in% unique(myeloid_PvT[,myeloid_res]))) stop
('cluster order insufficient')
```

In [15]:
```
#Fig S7b left

myeloid_cluster_colors <- hue_pal()(length(unique(myeloid_PvT[,myeloid_r
es])))
names(myeloid_cluster_colors) <- sort(unique(myeloid_PvT[,myeloid_res]))

options(repr.plot.height=6,repr.plot.width=6)
g <- ggplot(myeloid_PvT[which(!(myeloid_PvT$bio_src_cellType %in% myeloi
d_tooSmall)),],
            aes_string(x='UMAP1',y='UMAP2',color=myeloid_res)) +
        geom_point(size=1,alpha=0.5) + theme_classic(base_size=20) + sca
le_color_manual(values=myeloid_cluster_colors) +
        theme(legend.position="none") +
        ggtitle('Tissue & PBMC myeloid cells') + theme(plot.title = elem
ent_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,'myeloid_PBMCvsTi
ssue_UMAP.png'),
                            plot=g,units='in',height=6,width=6,dpi=600)
```



In [16]:
```
#Fig 7b right

myeloid_fisher_df <- calc_OR(myeloid_PvT[which(!(myeloid_PvT$bio_src_cel
lType %in% myeloid_tooSmall)),],
                             myeloid_res, 'bio_src_cellType')

g <- plot_OR(myeloid_fisher_df, myeloid_res, 'bio_src_cellType',
             paste('Tissue & PBMC clustering\nat resolution',str_split_f
ixed(myeloid_res,'_',2)[,2]),
'Individual biological\nsource cell labels',
             myeloid_PvT_order, myeloid_original_order,clustColors=c(mye
loid_colors,myeloid_cluster_colors))

options(repr.plot.height=6,repr.plot.width=12)
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,save_dir,'myeloid
_PBMCvsTissue_OR_heatmap.png'),
                             plot=g,units='in',height=6,width=12,dpi=600)
```



B cell

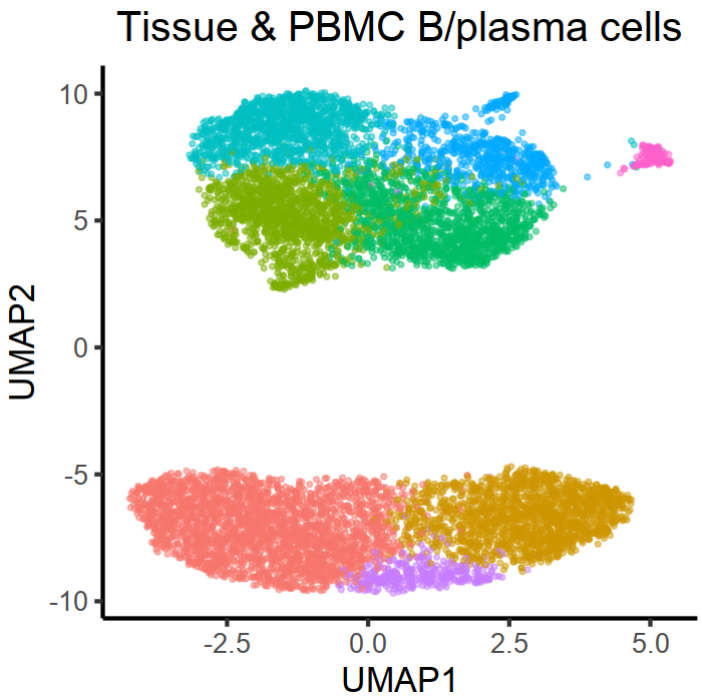
In [17]:
```
Bcell_res <- 'hres_0.60'
if(!(Bcell_res %in% colnames(Bcell_PvT))) stop('cluster resolution not i
n df')
```

In [18]:
```
Bcell_tissue_clusters <- sort(unique(Bcell_PvT[which(Bcell_PvT$bio_src=
='tissue'),'bio_src_cellType']))
Bcell_PBMC_clusters <- sort(unique(Bcell_PvT[which(Bcell_PvT$bio_src=='P
BMC'),'bio_src_cellType']))

Bcell_colors <- c(rep(tissue_color,length(Bcell_tissue_clusters)),rep(PB
MC_color,length(Bcell_PBMC_clusters)))
names(Bcell_colors) <- c(Bcell_tissue_clusters,Bcell_PBMC_clusters)
```

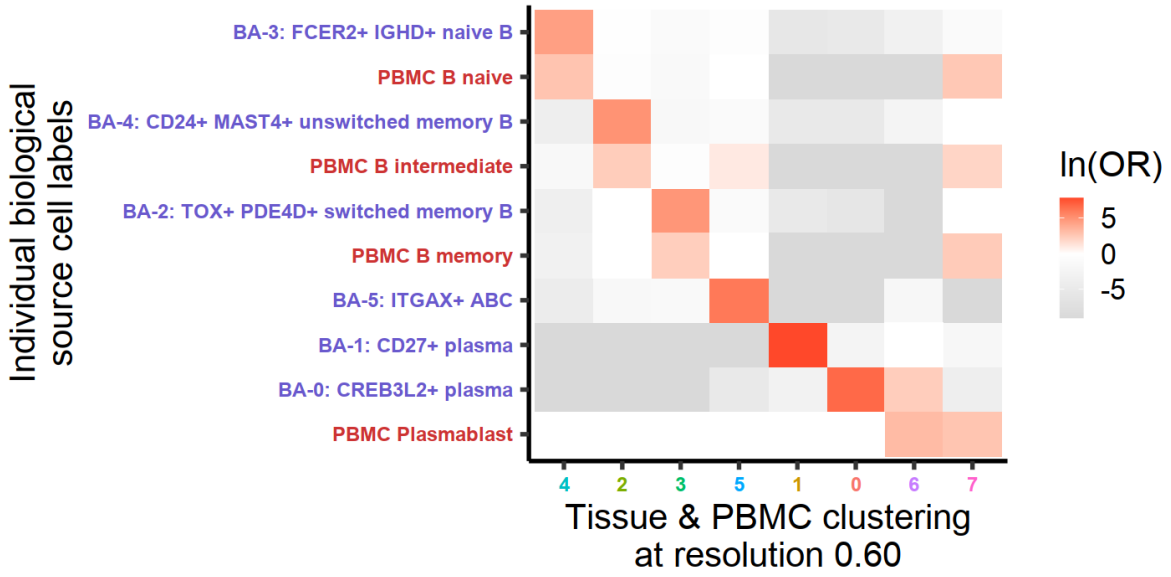
In [19]:
```
ll <- table(Bcell_PvT[which(Bcell_PvT$bio_src=='PBMC'),'bio_src_cellTyp
e'])
Bcell_tooSmall <- names(ll[ll<10])
```

In [20]:
```
Bcell_original_order <- c('BA-3: FCER2+ IGHD+ naive B','PBMC B naive',
                          'BA-4: CD24+ MAST4+ unswitched memory B','PBMC
B intermediate',
                          'BA-2: TOX+ PDE4D+ switched memory B','PBMC B
memory',
                          'BA-5: ITGAX+ ABC',
                          'BA-1: CD27+ plasma','BA-0: CREB3L2+ plasm
a','PBMC Plasmablast')
if(!all(Bcell_original_order %in% unique(Bcell_PvT$bio_src_cellType))) s
top('original order insufficient')

Bcell_PvT_order <- c(4,2,3,5,1,0,6,7)
if(!all(Bcell_PvT_order %in% unique(Bcell_PvT[,Bcell_res]))) stop('clust
er order insufficient')
```

In [21]:
```
#Fig S7c left

Bcell_cluster_colors <- hue_pal()(length(unique(Bcell_PvT[,Bcell_res])))
names(Bcell_cluster_colors) <- sort(unique(Bcell_PvT[,Bcell_res]))

options(repr.plot.height=6,repr.plot.width=6)
g <- ggplot(Bcell_PvT[which(!(Bcell_PvT$bio_src_cellType %in% Bcell_tooS
mall)),],
            aes_string(x='UMAP1',y='UMAP2',color=Bcell_res)) +
        geom_point(size=1,alpha=0.5) + theme_classic(base_size=20) + sca
le_color_manual(values=Bcell_cluster_colors) +
        theme(legend.position="none") +
        ggtitle('Tissue & PBMC B/plasma cells') + theme(plot.title = ele
ment_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,'Bcell_PBMCvsTiss
ue_UMAP.png'),
                            plot=g,units='in',height=6,width=6,dpi=600)
```



In [22]:
```
#Fig 7c right

Bcell_fisher_df <- calc_OR(Bcell_PvT[which(!(Bcell_PvT$bio_src_cellType
%in% Bcell_tooSmall)),],
                           Bcell_res, 'bio_src_cellType')

g <- plot_OR(Bcell_fisher_df, Bcell_res, 'bio_src_cellType',
             paste('Tissue & PBMC clustering\nat resolution',str_split_f
ixed(Bcell_res,'_',2)[,2]),
             'Individual biological\nsource cell labels',
             Bcell_PvT_order, Bcell_original_order,clustColors=c(Bcell_c
olors,Bcell_cluster_colors))

options(repr.plot.height=6,repr.plot.width=12)
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,save_dir,'Bcell_P
BMCvsTissue_OR_heatmap.png'),
                           plot=g,units='in',height=6,width=12,dpi=600)
```



Session Info

In [23]:
```
sessionInfo()
```

```
R version 3.6.1 (2019-07-05)
Platform: x86_64-conda_cos6-linux-gnu (64-bit)
Running under: Red Hat Enterprise Linux Server release 6.5 (Santiago)

Matrix products: default
BLAS/LAPACK: /PHShome/kew47/miniconda3/lib/R/lib/libRblas.so

locale:
[1] en_US.UTF-8

attached base packages:
[1] grid      stats     graphics  grDevices utils     datasets  methods
[8] base

other attached packages:
 [1] repr_1.0.1        gridExtra_2.3     scales_1.1.1      viridis_0.5.
1
 [5] viridisLite_0.3.0 ggrepel_0.8.2     ggrastr_0.2.3     ggplot2_3.3.
0
 [9] tidyr_1.0.3       stringr_1.4.0     ROCR_1.0-7        gplots_3.0.
1.1
[13] Rmisc_1.5.1       plyr_1.8.6        lattice_0.20-41   gtools_3.8.2
[17] Matrix_1.2-18

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.4.6         vipor_0.4.5          pillar_1.4.4
 [4] compiler_3.6.1       bitops_1.0-6         base64enc_0.1-3
 [7] tools_3.6.1          digest_0.6.25        uuid_0.1-2
[10] gtable_0.3.0         jsonlite_1.7.1       evaluate_0.14
[13] lifecycle_0.2.0      tibble_3.0.1         pkgconfig_2.0.3
[16] rlang_0.4.8          IRdisplay_0.7.0      IRkernel_1.0.2.9000
[19] beeswarm_0.2.3       withr_2.2.0          dplyr_1.0.2
[22] generics_0.0.2       vctrs_0.3.5          caTools_1.18.0
[25] tidyselect_1.1.0     glue_1.4.0           R6_2.4.1
[28] ggbeeswarm_0.6.0     gdata_2.18.0         pbdZMQ_0.3-3
[31] farver_2.0.3         purrr_0.3.4          magrittr_1.5
[34] htmltools_0.4.0      ellipsis_0.3.1       colorspace_1.4-1
[37] labeling_0.3         KernSmooth_2.23-15   stringi_1.4.6
[40] munsell_0.5.0        crayon_1.3.4         Cairo_1.5-10
```

In [ ]:
```

```