

MERFISH example

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MERFISH

[add description of data]

Load preprocessed data

```
col = MERFISH$col
pcs = MERFISH$pcs
vel = MERFISH$vel
```

Build VeloViz graph

```
curr = vel$current
proj = vel$projected
```

```
veloviz = buildVeloviz(
  curr = curr, proj = proj,
  normalize.depth = TRUE,
  use.ods.genes = TRUE,
  alpha = 0.05,
  pca = TRUE,
  nPCs = 2,
  center = TRUE,
  scale = TRUE,
  k = 50,
  similarity.threshold = 0,
  distance.weight = 0.01,
  distance.threshold = 0.9,
  weighted = TRUE,
  seed = 0,
  verbose = FALSE
)
```

```
## Warning in if (!class(curr) %in% c("dgCMatrx", "dgTMatrix")) {: the condition
## has length > 1 and only the first element will be used
```

```
## Warning in if (!class(proj) %in% c("dgCMatrx", "dgTMatrix")) {: the condition
## has length > 1 and only the first element will be used
```

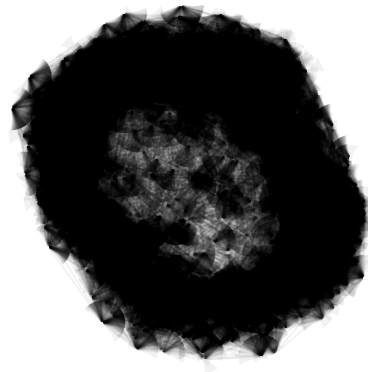
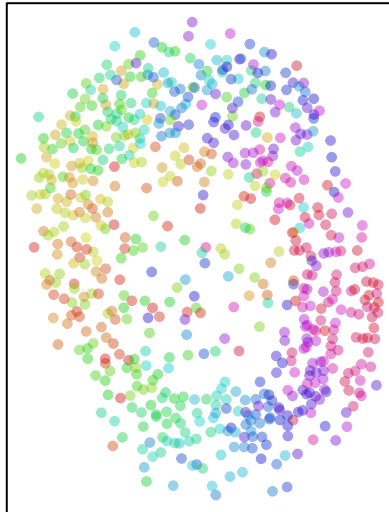
```
par(mfrow=c(1,2))
emb.veloviz = veloviz$fdg_coords
plotEmbedding(emb.veloviz, groups=col[rownames(emb.veloviz)], main='veloviz')

g = plotVeloviz(veloviz, clusters=col[rownames(emb.veloviz)], seed=0, verbose=TRUE)
```

```
## Warning in if (!is.na(clusters) & is.na(col)) {: the condition has length > 1
## and only the first element will be used
## Using provided clusters...
```

veloviz

C2



C1

Compare to other embeddings

```
par(mfrow = c(2,2))

#PCA
emb.pcs = MERFISH$pcs[,1:2]
plotEmbedding(emb.pcs, col=MERFISH$col, main='PCA')

#tSNE
set.seed(0)
emb.tsne = Rtsne::Rtsne(MERFISH$pcs[,1:5], perplexity = 100)$Y
rownames(emb.tsne) = rownames(MERFISH$pcs)
plotEmbedding(emb.tsne, col=MERFISH$col, main='tSNE',
              xlab = "t-SNE X", ylab = "t-SNE Y")

#UMAP
set.seed(0)
emb.umap = umap::umap(pcs[,1:5], min_dist = 0.3)$layout
rownames(emb.umap) = rownames(MERFISH$pcs)
plotEmbedding(emb.umap, col=MERFISH$col, main='UMAP',
              xlab = "UMAP X", ylab = "UMAP Y")

#veloviz
plotEmbedding(emb.veloviz, groups=col[rownames(emb.veloviz)], main='veloviz')
```

