AD_example

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Load required packages

```
library(DEGAS)
library(Rtsne)
```

```
## Warning: package 'Rtsne' was built under R version 4.0.2
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.0.2
```

Load data

```
scDat = read.csv('scDat.csv',row.names=1)
scLab = read.csv('scLab.csv',row.names=1)
patDat = read.csv('patDat.csv',row.names=1)
patLab = read.csv('patLab.csv',row.names=1)
```

Initialize DEGAS framework

```
path.data = ''
path.result = ''
initDEGAS()
tmpDir = paste0(path.result, 'tmp/')
```

Training DEGAS model

```
ccModel1 = runCCMTLBag(scDat,scLab,patDat,patLab,tmpDir,'ClassClass','DenseNet',3,5)
```

```
## 0
## 0
## 0
## 0
## 0
```

Predictions from DEGAS model

```
# Predicting patient outcome in cells
# ie, predicting AD association in individual cells
scpatPreds = predClassBag(ccModel1,scDat,'pat')
colnames(scpatPreds) = colnames(patLab)
```

Displaying single cells overlaid with AD impressions

```
# Set seed and run tSNE
set.seed(1)
scDat_tsne = Rtsne(scDat)
colnames(scDat_tsne$Y) = c('tSNE1','tSNE2')
# kNN smoothing of AD association
impressions_sc_smooth = knnSmooth(scpatPreds[,"AD"],scDat_tsne$Y)
# Conversion of AD association to correlation
impressions_sc_smooth_cor = toCorrCoeff(impressions_sc_smooth)
tmp = data.frame(tSNE1=scDat_tsne$Y[,"tSNE1"],tSNE2=scDat_tsne$Y[,"tSNE2"],Dis=impressions_sc_smooth_co
p = ggplot(tmp,aes(x=tSNE1,y=tSNE2,color=Dis,shape=CT))+ geom_point() + scale_color_gradient2(low = "bl
plot(p+labs(color='AD association',shape='Cell type') + theme(legend.title=element_text(size=rel(1)),le
```