# spatialExample

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```r
library(rgl)
library(projectR)
library(psych)
library(fields)
library(CoGAPS)
library(magick)
library(BiocParallel)

# Fix rgl crashing issue
Sys.setenv(LIBGL_ALWAYS_SOFTWARE=1)
```

# Overview

## Data Import

```r
# Read Raw data
raw.data = read.csv("dge_raw.txt",sep = "\t",header = F)
raw.data.genes = raw.data$V1
raw.data$V1 = NULL

print(grep("'",raw.data.genes,value = T,fixed = T))
```

```
## [1] "beta'COP" "PP2A-B'"
```

```r
raw.data.genes = gsub("'","",raw.data.genes,fixed = T)
raw.data = as.matrix(raw.data)
rownames(raw.data) = raw.data.genes

# Read Normalized data
normalized.data = read.csv("dge_normalized.txt", sep = "\t")

print(grep("'",rownames(normalized.data),value = T,fixed = T))
```

```
## [1] "beta'COP" "PP2A-B'"
```

```r
normalized.data.genes<-gsub("'","",rownames(normalized.data),fixed = T)
normalized.data <- as.matrix(normalized.data)
rownames(normalized.data) <- normalized.data.genes

# In situ data
insitu.matrix = read.csv("binarized_bdtnp.csv",check.names=F)
insitu.genes_orig <- colnames(insitu.matrix)

missingGenes = insitu.genes_orig[which(!insitu.genes_orig %in% normalized.data.genes)]
print(missingGenes)
```

```
## character(0)
```

```
insitu.genes = gsub(".","-",insitu.genes_orig,fixed = T)
insitu.genes = gsub("-spl-","(spl)",insitu.genes,fixed = T)
stopifnot(all(insitu.genes %in% raw.data.genes))
stopifnot(all(insitu.genes %in% normalized.data.genes))
insitu.matrix = as.matrix(insitu.matrix)
colnames(insitu.matrix) = insitu.genes
```

```
# Geometry data
geometry <- read.csv("geometry.txt",sep = " ")
geometry.inv<-geometry
geometry.inv$ycoord<--(geometry.inv$ycoord)
full.geometry<-rbind(geometry,geometry.inv)
xlim<-c(-max(abs(geometry)),max(abs(geometry)))
ylim<-xlim
zlim<-ylim

#Visualize the geometry
plot3d(full.geometry,xlim=xlim,ylim=ylim,zlim=zlim)
```

## CoGAPS on Gene expression data

```
#This can take few hours to run depending on the machine
nPat <- 20
runParams <- new("CogapsParams", nPatterns = nPat, seed = 123, nIterations = 50000)
dataCogaps <- CoGAPS(normalized.data, params = runParams, nThreads = 10)
```

## projectR on the cogapsResults

```
nPat <- 20
#importing the pre-computed cogaps result
dataCogaps <- readRDS('drosophilaNormalizedData20result2.rds')
projPosCgps <- projectR(t(insitu.matrix),loadings = dataCogaps, full = T)
```

```
## [1] "84 row names matched between data and loadings"
## [1] "Updated dimension of data: 84 3039"
```

## Visualize and save the patterns

Remove eval = FALSE to visualize all patterns

```
for(x in 1:nPat) {
      i <- x
      pp.plot <- c(projPosCgps[[1]][i, ], projPosCgps[[1]][i, ])
      par3d(windowRect = c(0, 50, 800, 800))

      plot3d(
            full.geometry,
            xlim = xlim,
            ylim = ylim,
            zlim = zlim,
            col = myColorRamp(palette = inferno(100), pp.plot),
            size = 10,
            box = F,
            axes = F,
            xlab = "",
            ylab = "",
            zlab = "",
            aspect = T
      )
      bgplot3d(suppressWarnings (
            image.plot(
                  legend.only = TRUE,
                  nlevel = 100,
                  zlim = c(min(pp.plot), max(pp.plot)),
                  legend.args = list(text = 'Projected pattern'),
                  col = inferno(100)
            )
      ))
      snapshot3d(
            filename = paste0(
                  "./plots/png/cpgs",
                  as.character(nPat),
                  "Pattern",
                  as.character(i),
                  ".png"
            ),
            fmt = "png"
      )
      movie3d(
            spin3d(axis = c(1, 1, 1), rpm = 5),
            duration = 10,
            movie = paste0("cgps", as.character(nPat), "Pattern", as.character(i)),
            dir = "./plots",
            convert = TRUE
      )
      while (rgl.cur() > 0) {
            rgl.close()
      }
}
```