PCA t-SNE.R

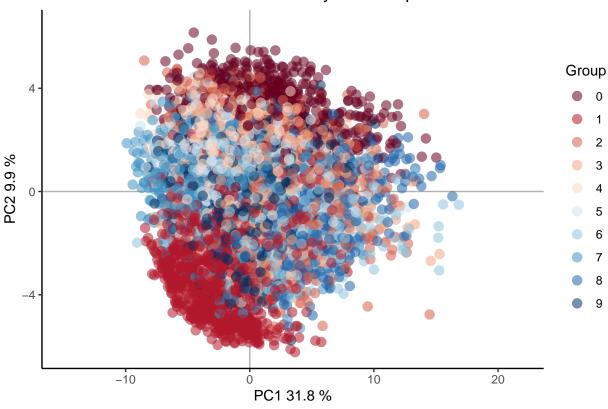
evegas

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```
# Principal Component Analysis (PCA) & t-SNE
# load libraries
library(ggplot2)
library(RColorBrewer)
library(Rtsne)
## Warning: package 'Rtsne' was built under R version 4.1.3
library(ggrepel)
# Load Data: enc_output.cifra & y_test_cifra
# from AE-MNIST.R script which do an autoencoder network
load("Encod_0123456789.RData")
# Load Data: enc_output.cifra & y_test_cifra
# from CAE-MNIST.R script which do an autoencoder network
# load("Conv_Encod_Flat_0123456789.RData")
# Change r objects names
data_to_project <- enc_output_cifra</pre>
v_labels <- as.factor(y_test_cifra)</pre>
n_v_labels <- nlevels(v_labels)</pre>
\#cifra \leftarrow as.factor(y\_test\_cifra)
# k is the number of images to project
k <- 8000 # nrow(data_to_project)
# Principal Component Analysis
# PCA function
```

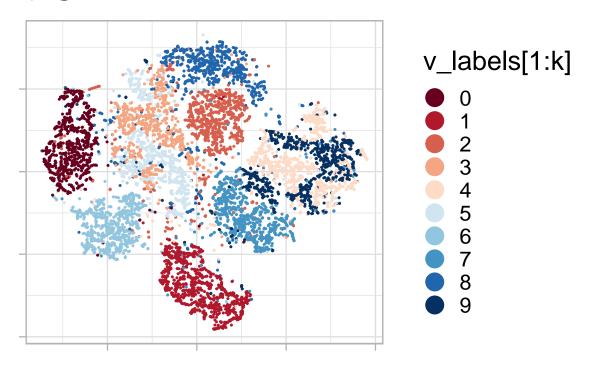
```
plotPCA3 <- function (datos, labels, factor, title, scale, colores, size = 2, glineas = 0.25) {
  data <- prcomp(datos , scale = scale)</pre>
  dataDf <- data.frame(data$x)</pre>
  Group <- factor</pre>
  loads <- round(data$sdev^2/sum(data$sdev^2)*100,1)</pre>
  # the graphic
  p1 <- ggplot(dataDf,aes(x=PC1, y=PC2)) +
    theme classic() +
    geom_hline(yintercept = 0, color = "gray70") +
    geom_vline(xintercept = 0, color = "gray70") +
    geom_point(aes(color = Group), alpha = 0.55, size = 3) +
    coord_cartesian(xlim = c(min(data$x[,1])-5,max(data$x[,1])+5)) +
    scale_fill_discrete(name = "")
  # the graphic with ggrepel
  p1 + geom_text_repel(aes(y = PC2 + 0.25, label = labels), segment.size = 0.25, size = size) +
    labs(x = c(paste("PC1", loads[1], "%")), y=c(paste("PC2", loads[2], "%"))) +
    ggtitle(paste("PCA based on", title, sep=" "))+
    theme(plot.title = element_text(hjust = 0.5)) +
    scale_color_manual(values=colores)
}
scale = FALSE
if (n_v_labels > 2) {
 colores <- brewer.pal(n = n_v_labels, name = "RdBu")</pre>
} else {
  colores <- c("red","blue")</pre>
plotPCA3(datos = data_to_project[1:k,],
         labels = rep("",k),
         factor = v_labels[1:k],
         scale = scale,
         title = paste ("last encode layer.", "# Samples:", k),
         colores = colores)
```

PCA based on last encode layer. # Samples: 8000



```
# t-SNE Representation
\# The next code of t-SNE reduction dimension is based on
# https://www.r-bloggers.com/playing-with-dimensions-from-clustering-pca-t-sne-to-carl-sagan/
## Rtsne function may take some minutes to complete...
set.seed(123456)
tsne_model_1 = Rtsne(data_to_project[1:k,],
                     check_duplicates=FALSE,
                     pca=TRUE,
                     perplexity=30,
                     theta=0.5,
                     dims=2)
## getting the two dimension matrix
d_tsne_1 = as.data.frame(tsne_model_1$Y)
\#str(d\_tsne\_1)
## plotting the results without clustering
ggplot(d_tsne_1, aes(x=V1, y=V2, colour=v_labels[1:k])) +
 geom_point(size=0.40) +
```

t-SNE



#+ scale_colour_brewer(palette = "RdBu") # create a custom color scale(>2 colours)