

[tbd]

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```
# Load R libraries

# Set working directory
setwd("/Users/davidfriesen/Desktop/OneDrive/USD/ADS-503-03-SU22/project")

# Expand output width and minimize exp notation
options(width = 110)
options(scipen = 100)
options(digits = 4)

# Set style defaults
knitr::opts_chunk$set(fig.width = 5.7, fig.height = (5.7 * .7))

#
gd_train_df <- read.table("/Users/davidfriesen/Desktop/OneDrive/USD/ADS-503-03-SU22/project/data/train_
gd_test_df <- read.table("/Users/davidfriesen/Desktop/OneDrive/USD/ADS-503-03-SU22/project/data/test_ge

## Warning in scan(file = file, what = what, sep = sep, quote = quote, dec = dec, : EOF within quoted s

#
str(gd_train_df); str(gd_test_df)

## 'data.frame': 11743 obs. of 1 variable:
## $ Patient.Id.Patient.Age.Genes.in.mothers.side.Inherited.from.father.Maternal.gene.Paternal.gene.Bl

## 'data.frame': 4590 obs. of 1 variable:
## $ Patient.Id.Patient.Age.Genes.in.mothers.side.Inherited.from.father.Maternal.gene.Paternal.gene.Bl

head(gd_train_df, 5); head(gd_test_df, 5)

##
## 1 PID0x6418,2,Yes,No,Yes,No,4.760603086,Richard,,Larre,,,Boston Specialty & Rehabilitation Hospital,
## 2
## 3
## 4
## 5

##
## 1 PID0x4175,6,No,Yes,No,No,4.981654852,Charles,,Kore,38,61,St. Elizabeths Hospital,"30 WARREN ST\nAL
## 2
## 3
## 4
## 5
```

```
summary(gd_train_df); summary(gd_test_df)
```

```
## Patient.Id.Patient.Age.Genes.in.mothers.side.Inherited.from.father.Maternal.gene.Paternal.gene.Blood
## Length:11743
## Class :character
## Mode :character

## Patient.Id.Patient.Age.Genes.in.mothers.side.Inherited.from.father.Maternal.gene.Paternal.gene.Blood
## Length:4590
## Class :character
## Mode :character
```