

Final Project Introduction

Group number 7

Members:

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Tasks:

data cleaning, summary of data, introduction - Truman

Organizing presentation/presenting - Truman, Minhaz, Vincent

Analyzing data/performing various test - Everyone (idea: each of us analyze different variables)

Putting everything together/conclusions - Navin, Bobak

Introduction

Breast cancer is a malignant cell growth in the breast. if it is left untreated the cancer can spread to other parts of the human body and it can be very deadly. there are generally two type of tumors non-cancerous and cancerous and the difference between the two is important, Benign tumor is non-cancerous and not dangerous on its own, but a malignant tumor, means the mass is cancerous.

summary of the data

```
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.2.1 --
## v ggplot2 3.1.0      v purrr  0.2.5
## v tibble  1.4.2      v dplyr  0.7.7
## v tidyr   0.8.2      v stringr 1.3.1
## v readr   1.1.1      v forcats 0.3.0

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

# preview of the data
mydata = read_csv("Project3-Data.csv")

## Parsed with column specification:
## cols(
##   .default = col_double(),
##   id = col_integer(),
##   diagnosis = col_character()
## )

## See spec(...) for full column specifications.
```

```
mydata
```

```
## # A tibble: 569 x 32
##       id diagnosis radius_mean texture_mean perimeter_mean area_mean
##   <int> <chr>          <dbl>         <dbl>         <dbl>         <dbl>
## 1 8.42e5 M             18.0          10.4          123.          1001
## 2 8.43e5 M             20.6          17.8          133.          1326
## 3 8.43e7 M             19.7          21.2          130           1203
## 4 8.43e7 M             11.4          20.4           77.6          386.
## 5 8.44e7 M             20.3          14.3          135.          1297
## 6 8.44e5 M             12.4          15.7           82.6          477.
## 7 8.44e5 M             18.2          20.0          120.          1040
## 8 8.45e7 M             13.7          20.8           90.2          578.
## 9 8.45e5 M             13           21.8           87.5          520.
## 10 8.45e7 M            12.5          24.0           84.0          476.
## # ... with 559 more rows, and 26 more variables: smoothness_mean <dbl>,
## # compactness_mean <dbl>, concavity_mean <dbl>, `concave
## # points_mean` <dbl>, symmetry_mean <dbl>, fractal_dimension_mean <dbl>,
## # radius_se <dbl>, texture_se <dbl>, perimeter_se <dbl>, area_se <dbl>,
## # smoothness_se <dbl>, compactness_se <dbl>, concavity_se <dbl>,
## # `concave points_se` <dbl>, symmetry_se <dbl>,
## # fractal_dimension_se <dbl>, radius_worst <dbl>, texture_worst <dbl>,
## # perimeter_worst <dbl>, area_worst <dbl>, smoothness_worst <dbl>,
## # compactness_worst <dbl>, concavity_worst <dbl>, `concave
## # points_worst` <dbl>, symmetry_worst <dbl>,
## # fractal_dimension_worst <dbl>
```

```
# number of variables we have
```

```
num_var = ncol(mydata) - 1
num_var
```

```
## [1] 31
```

```
# number of observation we have
```

```
num_obs = nrow(mydata)
num_obs
```

```
## [1] 569
```

```
# the number of each type of tumor
```

```
table(mydata$diagnosis)
```

```
##
```

```
##   B   M
```

```
## 357 212
```

```
# small summary of a few variables
```

```
summary(mydata$radius_mean)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  6.981 11.700 13.370 14.127 15.780 28.110
```

```
summary(mydata$texture_mean)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   9.71  16.17  18.84  19.29  21.80  39.28
```

```
summary(mydata$perimeter_mean)
```

```
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##  43.79   75.17   86.24   91.97  104.10  188.50
```

```
summary(mydata$perimeter_mean)
```

```
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##  43.79   75.17   86.24   91.97  104.10  188.50
```