Introduction to dplyr and ggplot2

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Explore dplyr

load dplyr and data

The dplyr package was designed to be efficient with large data but we will demonstrate the basic features with a smaller data set from package mlbench.

```
library(dplyr)
library(mlbench)
data("PimaIndiansDiabetes2")
```

tbl

A tbl "tibble" is a data frame with enhanced features. Now when we type the name at the console we get a neater display of our data, one page at a time.

```
df <- tbl_df(PimaIndiansDiabetes2)
rm(PimaIndiansDiabetes2)
df
```

```
## # A tibble: 768 x 9
##    pregnant glucose pressure triceps insulin  mass pedigree   age diabetes
##  *    <dbl>   <dbl>    <dbl>   <dbl>   <dbl> <dbl>    <dbl> <dbl> <fct>
##  1     6.00   148       72.0    35.0    NA    33.6    0.627  50.0 pos
##  2     1.00    85.0     66.0    29.0    NA    26.6    0.351  31.0 neg
##  3     8.00   183       64.0    NA      NA    23.3    0.672  32.0 pos
##  4     1.00    89.0     66.0    23.0    94.0  28.1    0.167  21.0 neg
##  5     0      137       40.0    35.0   168    43.1    2.29   33.0 pos
##  6     5.00   116       74.0    NA      NA    25.6    0.201  30.0 neg
##  7     3.00    78.0     50.0    32.0    88.0  31.0    0.248  26.0 pos
##  8    10.0    115       NA      NA      NA    35.3    0.134  29.0 neg
##  9     2.00   197       70.0    45.0   543    30.5    0.158  53.0 pos
## 10     8.00   125       96.0    NA      NA    NA      0.232  54.0 pos
## # ... with 758 more rows
```

glimpse

The glimpse function is similar to str but can handle bigger data more efficiently.

```
glimpse(df)
```

```
## Observations: 768
## Variables: 9
## $ pregnant <dbl> 6, 1, 8, 1, 0, 5, 3, 10, 2, 8, 4, 10, 10, 1, 5, 7, 0,...
## $ glucose  <dbl> 148, 85, 183, 89, 137, 116, 78, 115, 197, 125, 110, 1...
## $ pressure <dbl> 72, 66, 64, 66, 40, 74, 50, NA, 70, 96, 92, 74, 80, 6...
## $ triceps  <dbl> 35, 29, NA, 23, 35, NA, 32, NA, 45, NA, NA, NA, NA, 2...
## $ insulin  <dbl> NA, NA, NA, 94, 168, NA, 88, NA, 543, NA, NA, NA, NA,...
## $ mass     <dbl> 33.6, 26.6, 23.3, 28.1, 43.1, 25.6, 31.0, 35.3, 30.5,...
```

```
## $ pedigree <dbl> 0.627, 0.351, 0.672, 0.167, 2.288, 0.201, 0.248, 0.13...
## $ age      <dbl> 50, 31, 32, 21, 33, 30, 26, 29, 53, 54, 30, 34, 57, 5...
## $ diabetes <fct> pos, neg, pos, neg, pos, neg, pos, neg, pos, pos, neg...
```

5 functions of dplyr

- select - remove columns
- mutate - create new columns from the data
- filter - remove rows
- arrange - rearrange rows
- summarize or summarise - summary statistics

These functions do not change the original data but return a new object. The functions assume that the data is already "tidy" – observations in rows, features in columns.

select – used to select columns

Select a couple of columns to print. Notice it doesn't run off the screen, you get a screen's worth at a time.

```
print(select(df, diabetes, pregnant))
```

```
## # A tibble: 768 x 2
##    diabetes pregnant
##  * <fct>       <dbl>
##  1 pos          6.00
##  2 neg          1.00
##  3 pos          8.00
##  4 neg          1.00
##  5 pos          0
##  6 neg          5.00
##  7 pos          3.00
##  8 neg         10.0
##  9 pos          2.00
## 10 pos          8.00
## # ... with 758 more rows
```

mutate – used to add columns

Add a column that is a binary factor indicating if glucose is above average for the population.

```
mutate(df, glucose_high = as.factor(ifelse(glucose>mean(glucose, na.rm=TRUE), 1, 0)))
```

```
## # A tibble: 768 x 10
##    pregnant glucose pressure triceps insulin  mass pedigree   age diabetes
##       <dbl>   <dbl>    <dbl>   <dbl>   <dbl> <dbl>    <dbl> <dbl> <fct>
##  1     6.00   148       72.0    35.0    NA    33.6    0.627  50.0 pos
##  2     1.00    85.0     66.0    29.0    NA    26.6    0.351  31.0 neg
##  3     8.00   183       64.0    NA      NA    23.3    0.672  32.0 pos
##  4     1.00    89.0     66.0    23.0    94.0  28.1    0.167  21.0 neg
##  5     0      137       40.0    35.0   168    43.1    2.29   33.0 pos
##  6     5.00   116       74.0    NA      NA    25.6    0.201  30.0 neg
##  7     3.00    78.0     50.0    32.0    88.0  31.0    0.248  26.0 pos
##  8    10.0    115       NA      NA      NA    35.3    0.134  29.0 neg
##  9     2.00   197       70.0    45.0   543    30.5    0.158  53.0 pos
```

```
## 10     8.00   125       96.0    NA      NA    NA      0.232  54.0 pos
## # ... with 758 more rows, and 1 more variable: glucose_high <fct>
```

filter – used to remove rows

We replace df with a df that filtered out rows with NAs in the glucose or mass columns.

```
df <- filter(df, !is.na(glucose), !is.na(mass))
glimpse(df)
```

```
## Observations: 752
## Variables: 9
## $ pregnant <dbl> 6, 1, 8, 1, 0, 5, 3, 10, 2, 4, 10, 10, 1, 5, 7, 0, 7,...
## $ glucose  <dbl> 148, 85, 183, 89, 137, 116, 78, 115, 197, 110, 168, 1...
## $ pressure <dbl> 72, 66, 64, 66, 40, 74, 50, NA, 70, 92, 74, 80, 60, 7...
## $ triceps  <dbl> 35, 29, NA, 23, 35, NA, 32, NA, 45, NA, NA, NA, 23, 1...
## $ insulin  <dbl> NA, NA, NA, 94, 168, NA, 88, NA, 543, NA, NA, NA, 846...
## $ mass     <dbl> 33.6, 26.6, 23.3, 28.1, 43.1, 25.6, 31.0, 35.3, 30.5,...
## $ pedigree <dbl> 0.627, 0.351, 0.672, 0.167, 2.288, 0.201, 0.248, 0.13...
## $ age      <dbl> 50, 31, 32, 21, 33, 30, 26, 29, 53, 30, 34, 57, 59, 5...
## $ diabetes <fct> pos, neg, pos, neg, pos, neg, pos, neg, pos, neg, pos...
```

arrange – arrange rows based on content

Arrange rows based on bmi as stored in the mass column.

```
arrange(df, mass)  # ascending order
```

```
## # A tibble: 752 x 9
##    pregnant glucose pressure triceps insulin  mass pedigree   age diabetes
##       <dbl>   <dbl>    <dbl>   <dbl>   <dbl> <dbl>    <dbl> <dbl> <fct>
##  1     1.00    83.0     68.0    NA      NA    18.2    0.624  27.0 neg
##  2     1.00    97.0     70.0    15.0    NA    18.2    0.147  21.0 neg
##  3     1.00    97.0     64.0    19.0    82.0  18.2    0.299  21.0 neg
##  4     0      104       76.0    NA      NA    18.4    0.582  27.0 neg
##  5     1.00    80.0     55.0    NA      NA    19.1    0.258  21.0 neg
##  6     3.00    99.0     80.0    11.0    64.0  19.3    0.284  30.0 neg
##  7     1.00   103       80.0    11.0    82.0  19.4    0.491  22.0 neg
##  8     1.00    92.0     62.0    25.0    41.0  19.5    0.482  25.0 neg
##  9     1.00   100       74.0    12.0    46.0  19.5    0.149  28.0 neg
## 10     1.00    95.0     66.0    13.0    38.0  19.6    0.334  25.0 neg
## # ... with 742 more rows
```

```
arrange(df, desc(mass)) # descending order
```

```
## # A tibble: 752 x 9
##    pregnant glucose pressure triceps insulin  mass pedigree   age diabetes
##       <dbl>   <dbl>    <dbl>   <dbl>   <dbl> <dbl>    <dbl> <dbl> <fct>
##  1     0      129      110      46.0   130    67.1    0.319  26.0 pos
##  2     0      180       78.0    63.0    14.0  59.4    2.42   25.0 pos
##  3     3.00   123      100      35.0   240    57.3    0.880  22.0 neg
##  4     1.00    88.0     30.0    42.0    99.0  55.0    0.496  26.0 pos
##  5     0      162       76.0    56.0   100    53.2    0.759  25.0 pos
##  6     5.00   115       98.0    NA      NA    52.9    0.209  28.0 pos
##  7    11.0    135       NA      NA      NA    52.3    0.578  40.0 pos
```

```
##  8     0      165       90.0    33.0   680    52.3    0.427  23.0 neg
##  9     7.00   152       88.0    44.0    NA    50.0    0.337  36.0 pos
## 10     1.00   122       90.0    51.0   220    49.7    0.325  31.0 pos
## # ... with 742 more rows
```

summarize - a more powerful summary

Get summary statistics on mass.

```
summarize(df, min=min(mass), max=max(mass), sd(mass))
```

```
## # A tibble: 1 x 3
##     min   max `sd(mass)`
##   <dbl> <dbl>      <dbl>
## 1  18.2  67.1       6.93
```

```
summarize(df, n_diabetic = sum(diabetes=="pos"), n_not_diabetic = sum(diabetes=="neg"))
```

```
## # A tibble: 1 x 2
##   n_diabetic n_not_diabetic
##        <int>          <int>
## 1        264            488
```

pipes - work similar to unix pipes

Pipes make code easier to read and let you make several commands in one neat group of lines instead of nesting functions in the typical R fashion. The pipe operator %>% comes from package magrittr but dplyr automatically loads it.

```
df %>%
  group_by(diabetes) %>%
  summarize(n_diabetic = n())
```

```
## # A tibble: 2 x 2
##   diabetes n_diabetic
##   <fct>         <int>
## 1 neg             488
## 2 pos             264
```

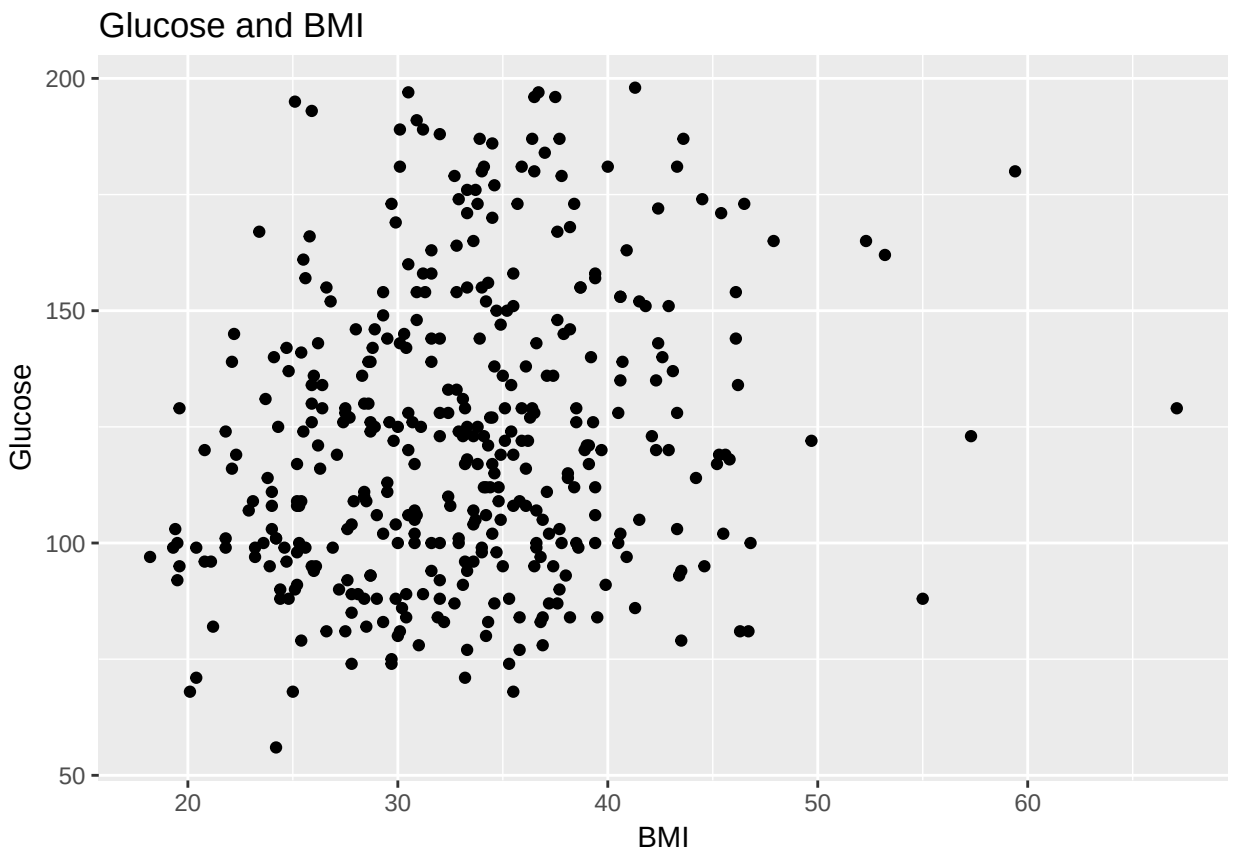
Explore ggplot2

Hadley Wickham developed ggplot2 in 2005, inspired by a grammar of graphics developed by Leland Wildinson in 1999. The ggplot2 functions are much more powerful than standard R graphs but also slower.

We have a short example below showing important components of building a ggplot. First we specify the data, then the aesthetics which are how the data is represented, followed by the geometry and finally labels.

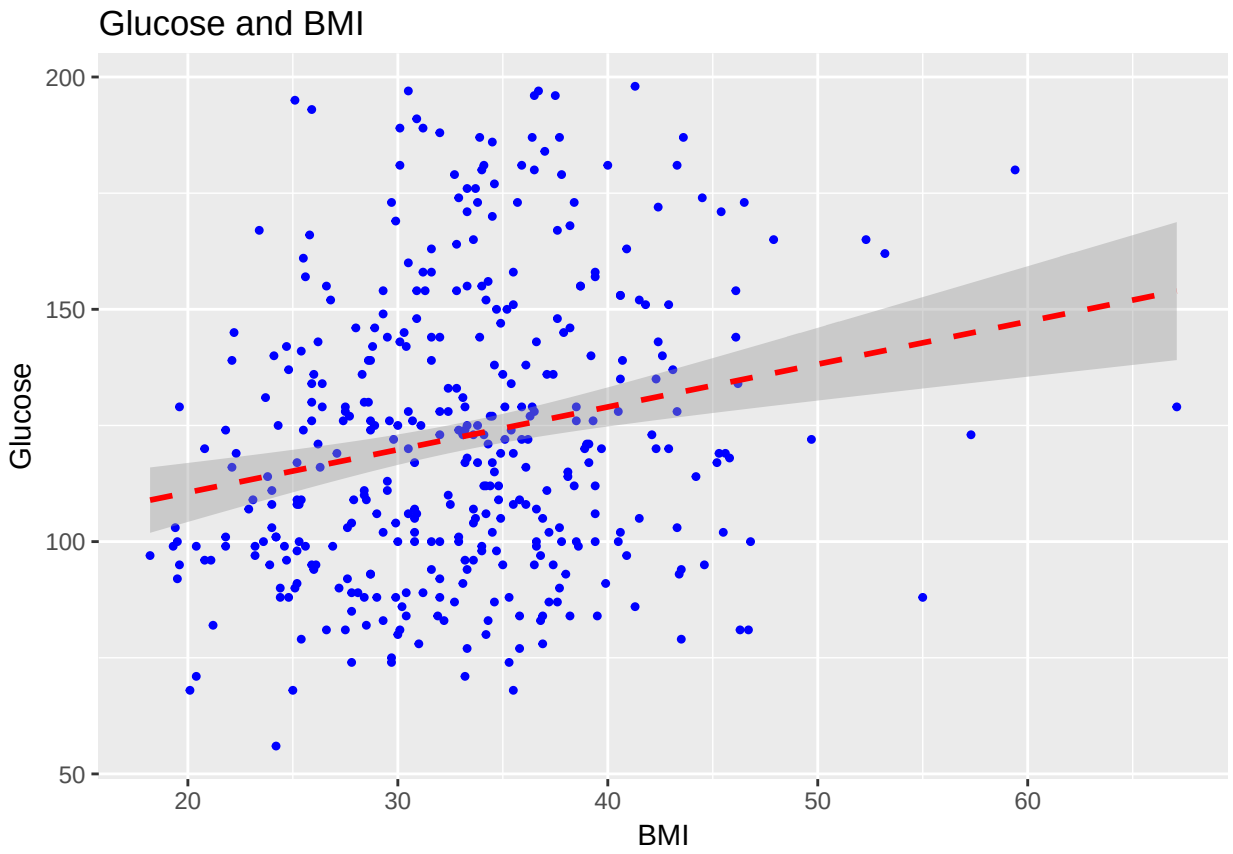
```
library(ggplot2)
# load data
library(mlbench)
data("PimaIndiansDiabetes2")
df <- PimaIndiansDiabetes2[complete.cases(PimaIndiansDiabetes2[]),]

ggplot(df, aes(x=mass, y=glucose)) +
```

```
  geom_point() +
  labs(title="Glucose and BMI", x="BMI", y="Glucose")
```



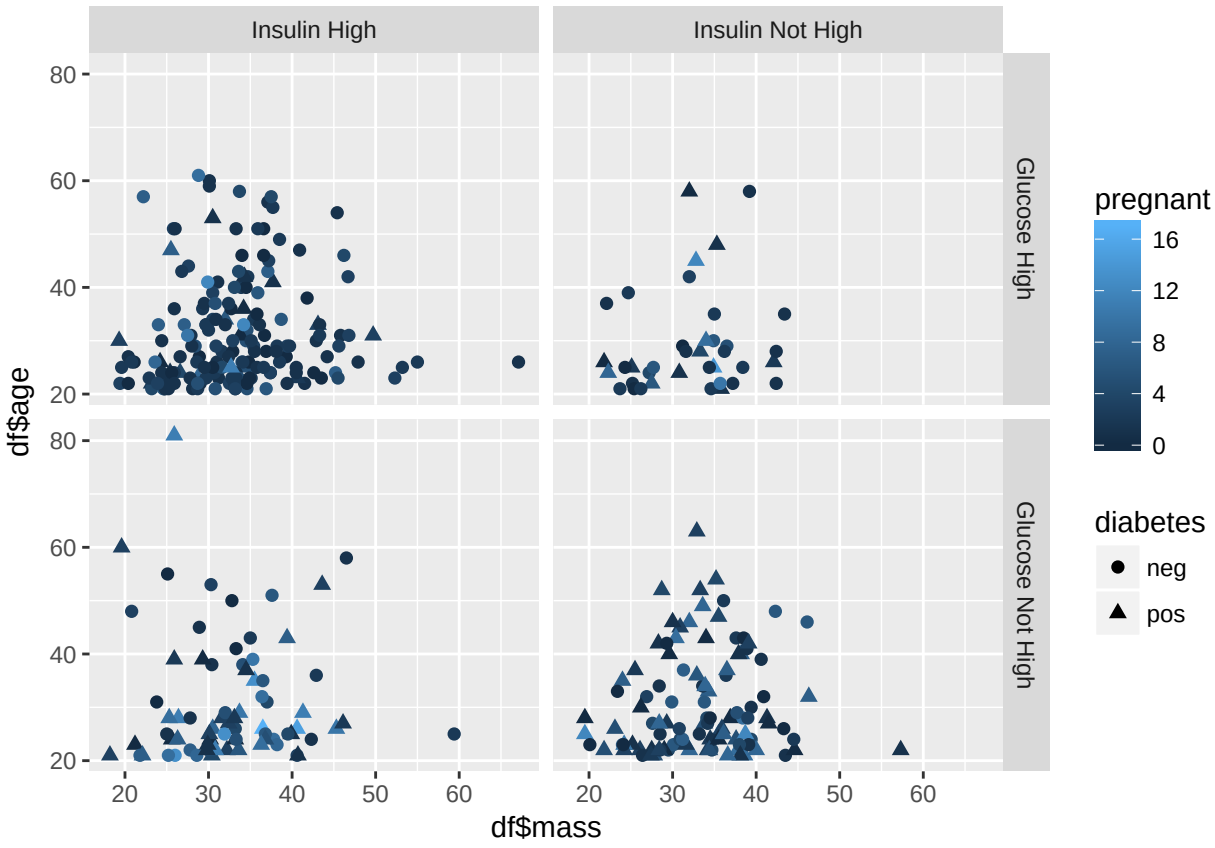
Next we add some color and a smoothing line which helps us see a trend in the data. By default the smoothing line has a shadow around it which specifies the 95

```
ggplot(df, aes(x=mass, y=glucose)) +
  geom_point(pch=20, color='blue', size=1.5) +
  geom_smooth(method='lm', color='red', linetype=2) +
  labs(title="Glucose and BMI", x="BMI", y="Glucose")
```



facet_grid

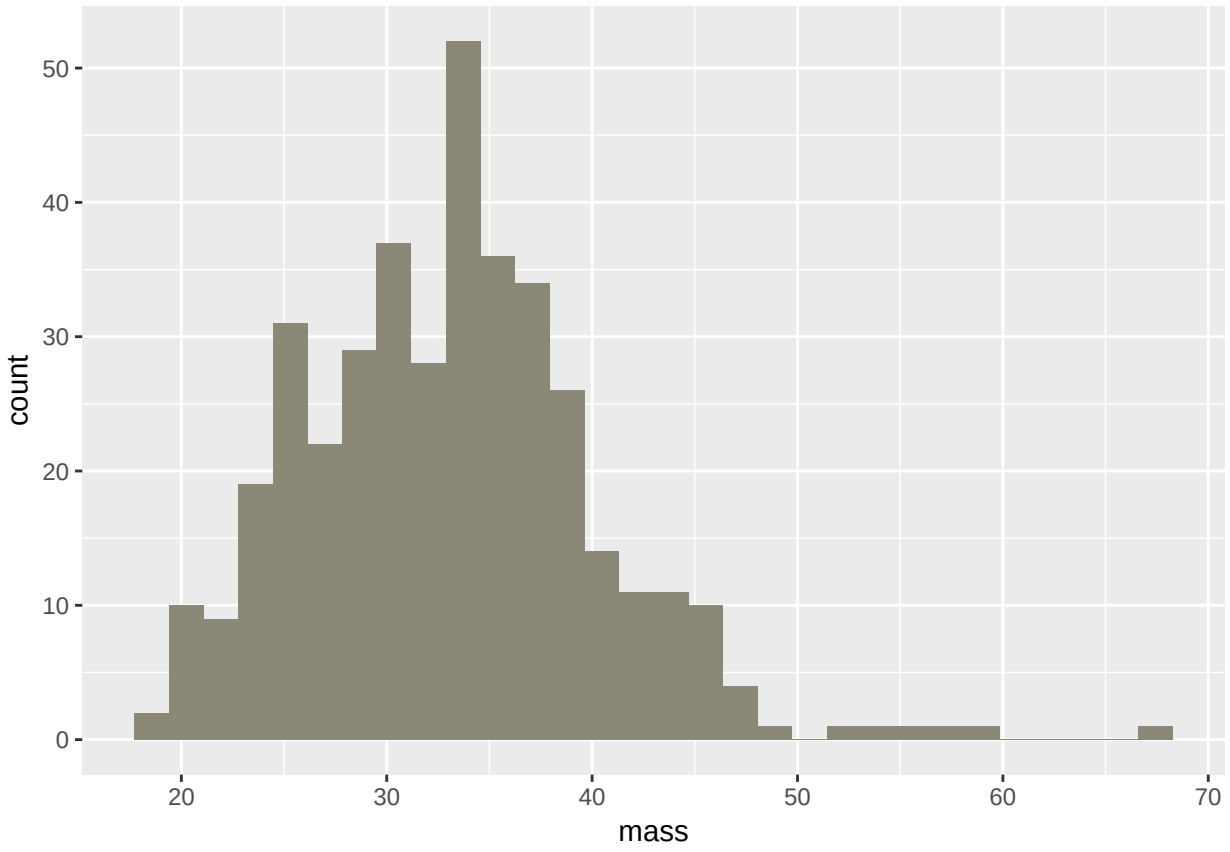
```
df$glucose_high <- factor(ifelse(df$glucose>mean(df$glucose, na.rm=TRUE), 1, 0),
                          levels=c(0,1), labels=c("Glucose High","Glucose Not High"))
df$insulin_high <- factor(ifelse(df$insulin>mean(df$insulin, na.rm=TRUE), 1, 0),
                          levels=c(0,1), labels=c("Insulin High","Insulin Not High"))

ggplot(df,
  aes(x=df$mass, y=df$age, shape=diabetes, col=pregnant)) +
  geom_point(size=2) +
  facet_grid(df$glucose_high~df$insulin_high)
```



histogram

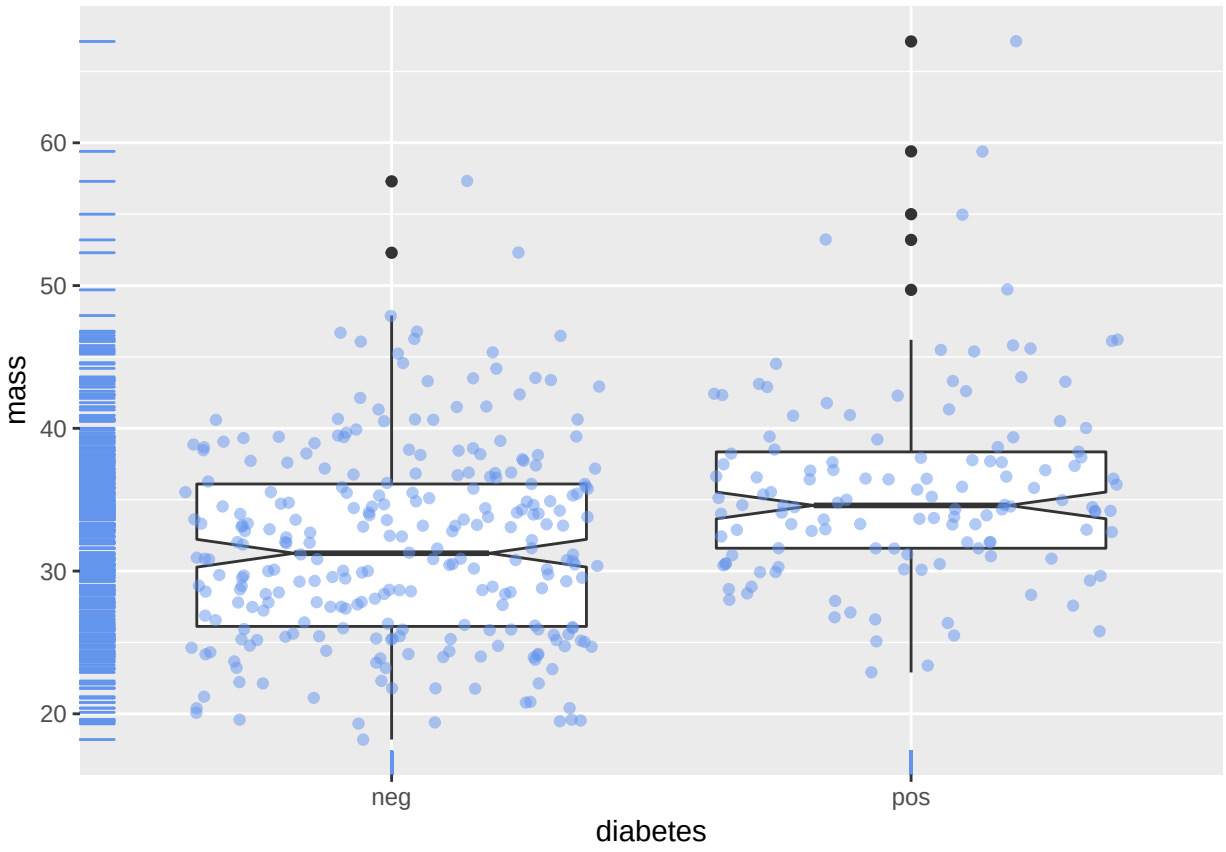
```
ggplot(df, aes(x=mass)) +
  geom_histogram(fill="cornsilk4")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



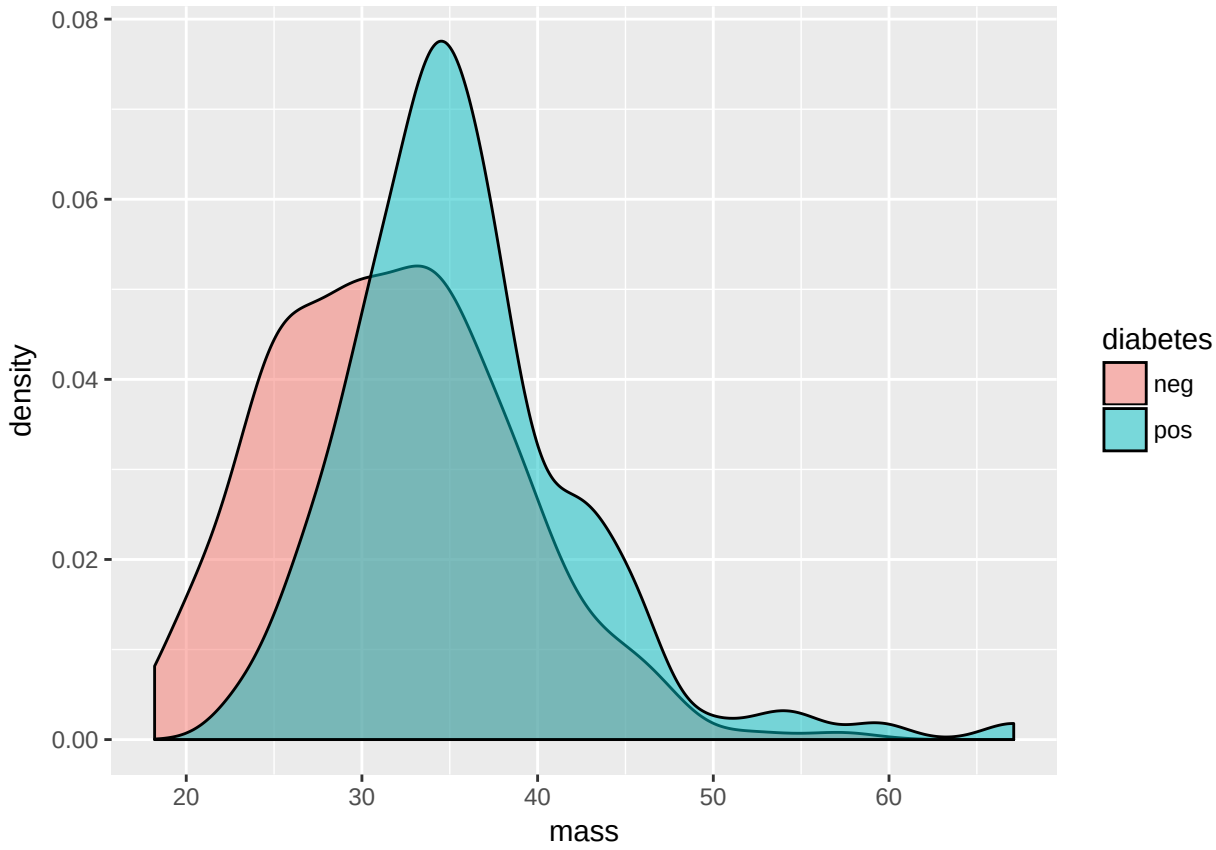
boxplot and rug

```
ggplot(df, aes(x=diabetes, y=mass)) +
  geom_boxplot(notch=TRUE) +
  geom_point(position="jitter", color="cornflowerblue", alpha=.5) +
  geom_rug(color="cornflowerblue")
```



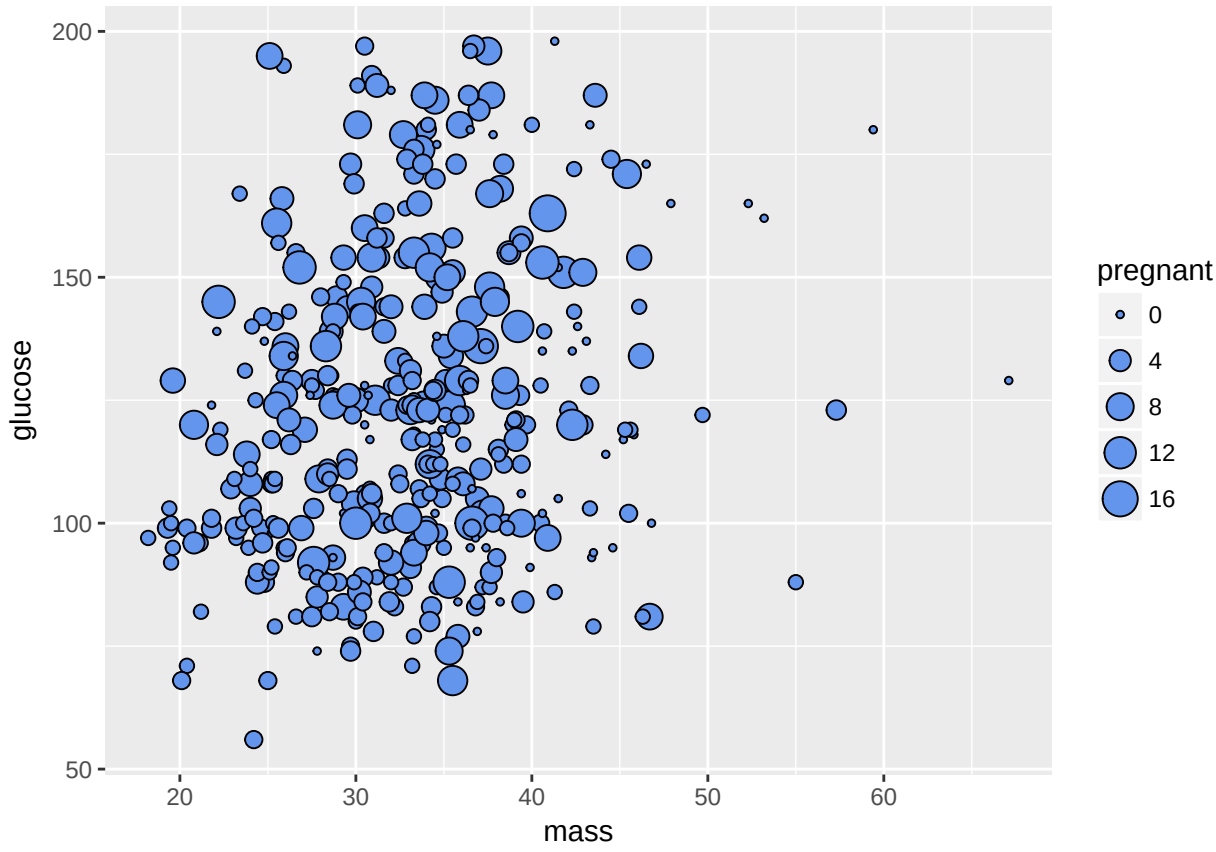
density plot

```
ggplot(df, aes(x=mass, fill=diabetes)) +
  geom_density(alpha=0.5)
```



bubble chart

```
ggplot(df,
       aes(x=mass, y=glucose, size=pregnant)) +
  geom_point(shape=21, fill="cornflowerblue")
```



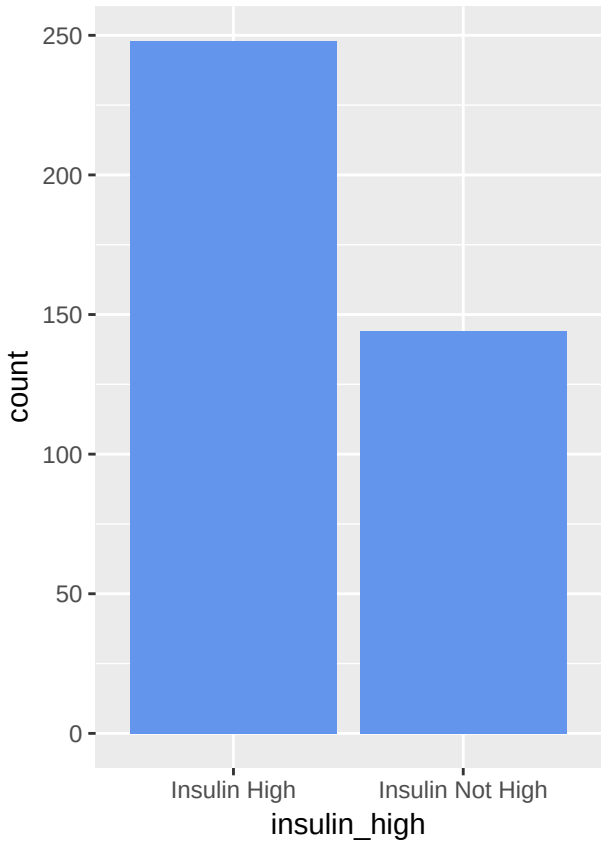
grid

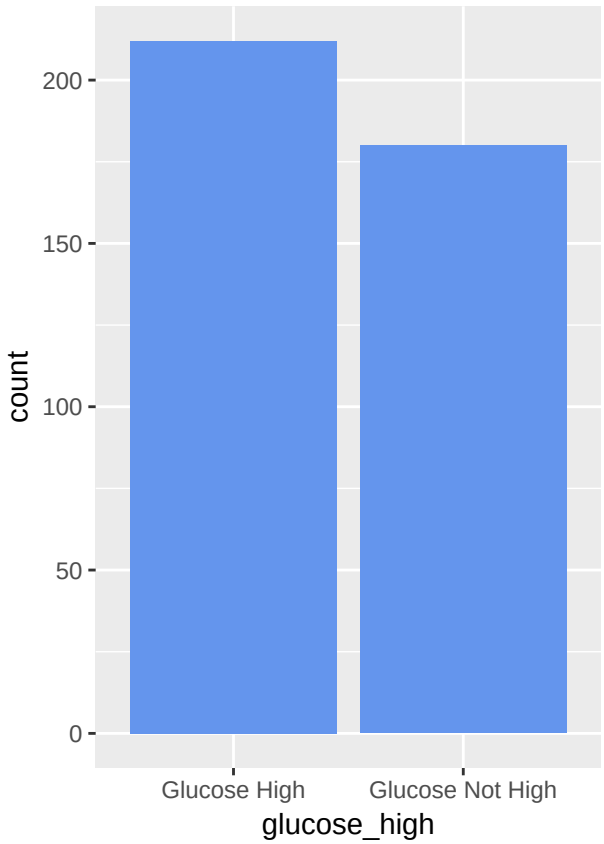
```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
p1 <- ggplot(df, aes(x=insulin_high)) + geom_bar(fill="cornflowerblue")
p2 <- ggplot(df, aes(x=glucose_high)) + geom_bar(fill="cornflowerblue")
grid.arrange(p1, p2, ncol=2)
```


250
200
150
100
50
0
count
Insulin High
Insulin Not High
insulin_high


200
150
100
50
0
count
Glucose High
Glucose Not High
glucose_high