

Graphics and Data Visualization in R

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Overview

Graphics in R

- Powerful environment for visualizing scientific data
- Integrated graphics and statistics infrastructure
- Publication quality graphics
- Fully programmable
- Highly reproducible
- Full LaTeX, Sweave, knitr and R Markdown support.
- Vast number of R packages with graphics utilities

Documentation on Graphics in R

- General
 - Graphics Task Page
 - R Graph Gallery
 - R Graphical Manual
 - Paul Murrell’s book R (Grid) Graphics
- Interactive graphics
 - `rggobi` (GGobi)
 - `iplots`
 - Open GL (`rgl`)

Graphics Environments

- Viewing and saving graphics in R
 - On-screen graphics
 - postscript, pdf, svg
 - jpeg/png/wmf/tiff/...
- Four major graphics environments
 - Low-level infrastructure
 - * R Base Graphics (low- and high-level)
 - * `grid`: Manual, Book
 - High-level infrastructure
 - * `lattice`: Manual, Intro, Book
 - * `ggplot2`: Manual, Intro, Book

Base Graphics

Overview

- Important high-level plotting functions
 - `plot`: generic x-y plotting
 - `barplot`: bar plots
 - `boxplot`: box-and-whisker plot
 - `hist`: histograms
 - `pie`: pie charts
 - `dotchart`: cleveland dot plots
 - `image`, `heatmap`, `contour`, `persp`: functions to generate image-like plots
 - `qqnorm`, `qqline`, `qqplot`: distribution comparison plots
 - `pairs`, `coplot`: display of multivariate data
- Help on these functions
 - `?myfct`
 - `?plot`
 - `?par`

Preferred Input Data Objects

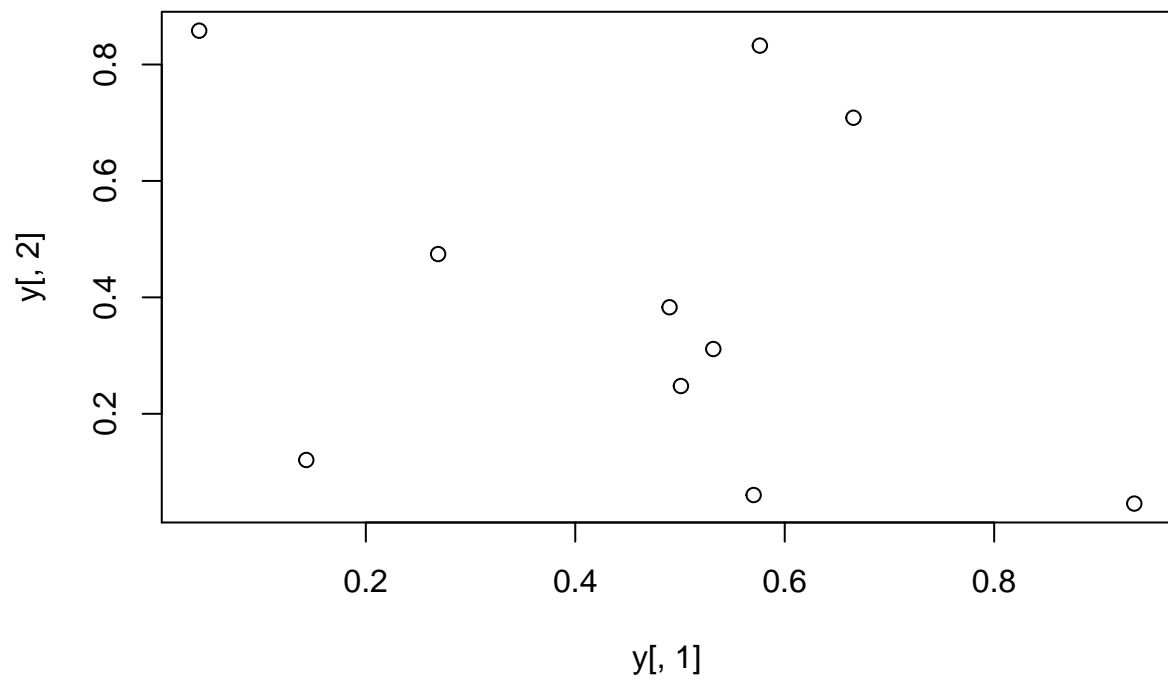
- Matrices and data frames
- Vectors
- Named vectors

Scatter Plots

Basic scatter plots

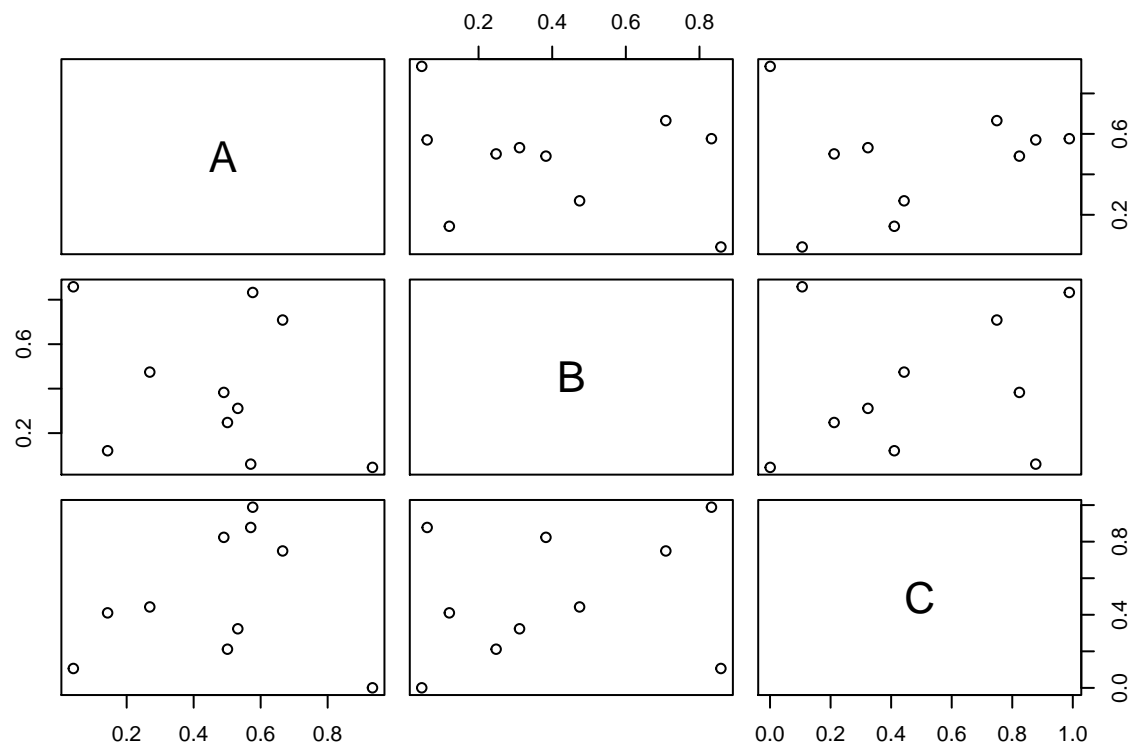
Sample data set for subsequent plots

```
set.seed(1410)
y <- matrix(runif(30), ncol=3, dimnames=list(letters[1:10], LETTERS[1:3]))
plot(y[,1], y[,2])
```



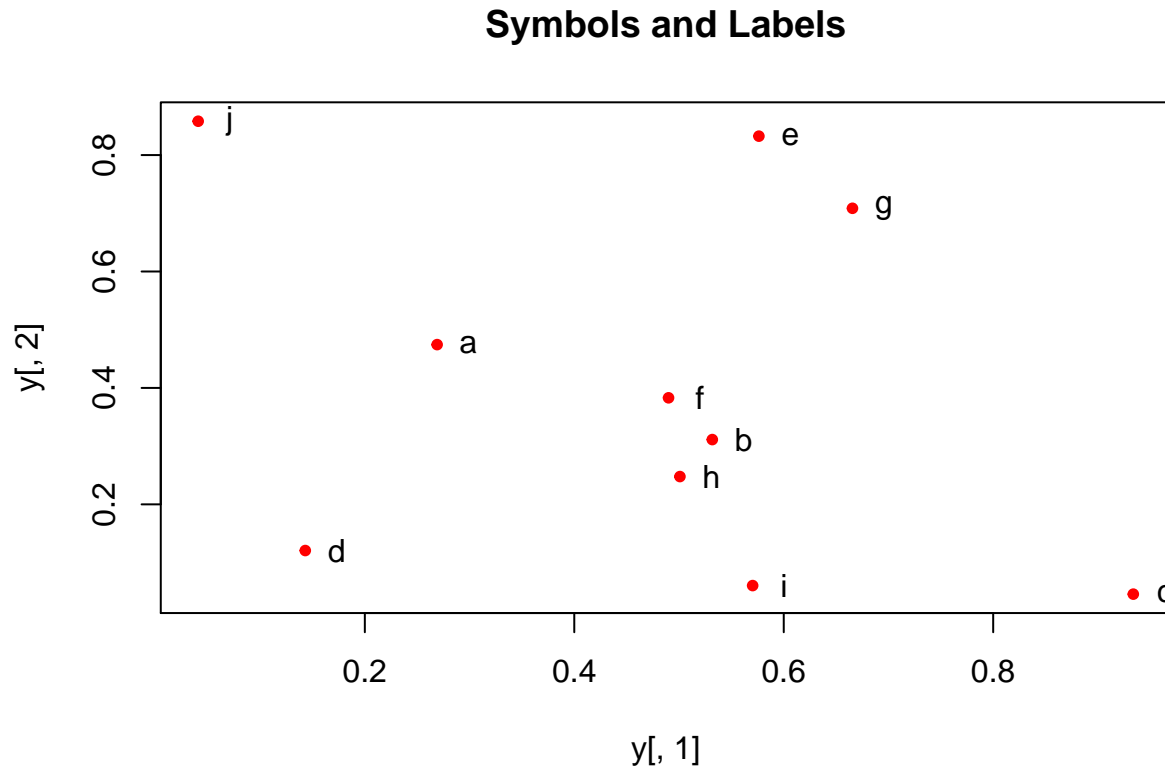
All pairs

```
pairs(y)
```



Plot labels

```
plot(y[,1], y[,2], pch=20, col="red", main="Symbols and Labels")
text(y[,1]+0.03, y[,2], rownames(y))
```



More examples

Print instead of symbols the row names

```
plot(y[,1], y[,2], type="n", main="Plot of Labels")
text(y[,1], y[,2], rownames(y))
```

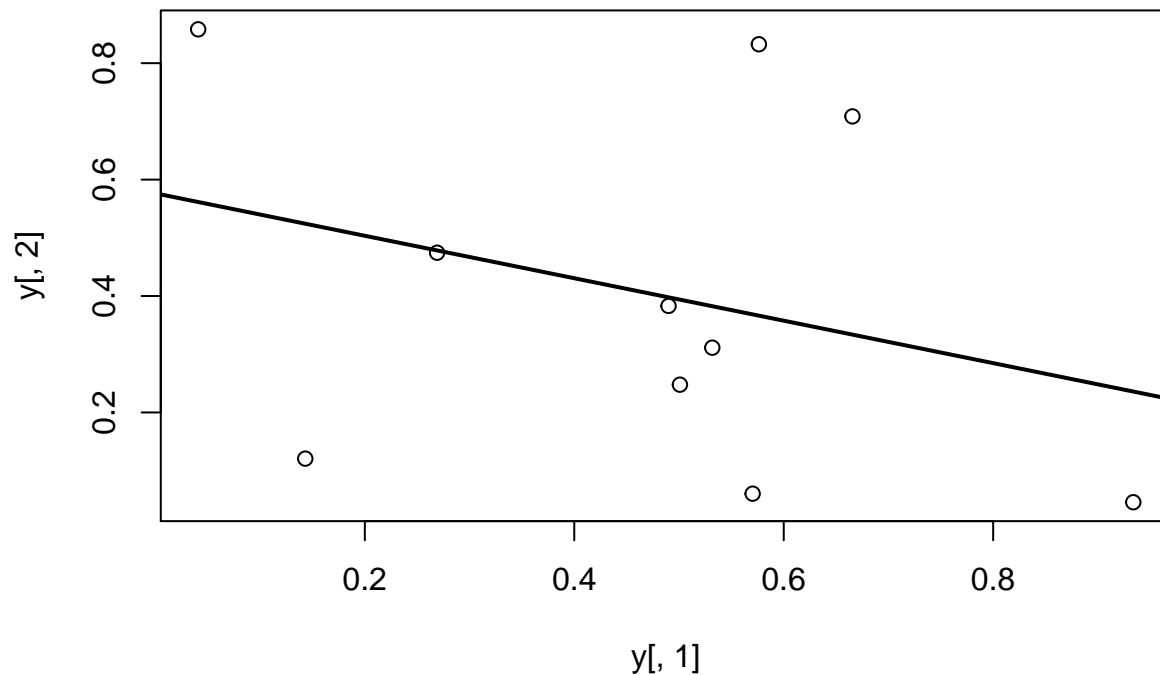
Usage of important plotting parameters

```
grid(5, 5, lwd = 2)
op <- par(mar=c(8,8,8,8), bg="lightblue")
plot(y[,1], y[,2], type="p", col="red", cex.lab=1.2, cex.axis=1.2,
      cex.main=1.2, cex.sub=1, lwd=4, pch=20, xlab="x label",
      ylab="y label", main="My Main", sub="My Sub")
par(op)
```

Important arguments} - **mar**: specifies the margin sizes around the plotting area in order: **c(bottom, left, top, right)** - **col**: color of symbols - **pch**: type of symbols, samples: **example(points)** - **lwd**: size of symbols - **cex.***: control font sizes - For details see **?par**

Add a regression line to a plot

```
plot(y[,1], y[,2])
myline <- lm(y[,2]~y[,1]); abline(myline, lwd=2)
```



```
summary(myline)
```

```
##
## Call:
## lm(formula = y[, 2] ~ y[, 1])
##
## Residuals:
```

| | Min | 1Q | Median | 3Q | Max |
|--|----------|----------|----------|---------|---------|
| | -0.40357 | -0.17912 | -0.04299 | 0.22147 | 0.46623 |

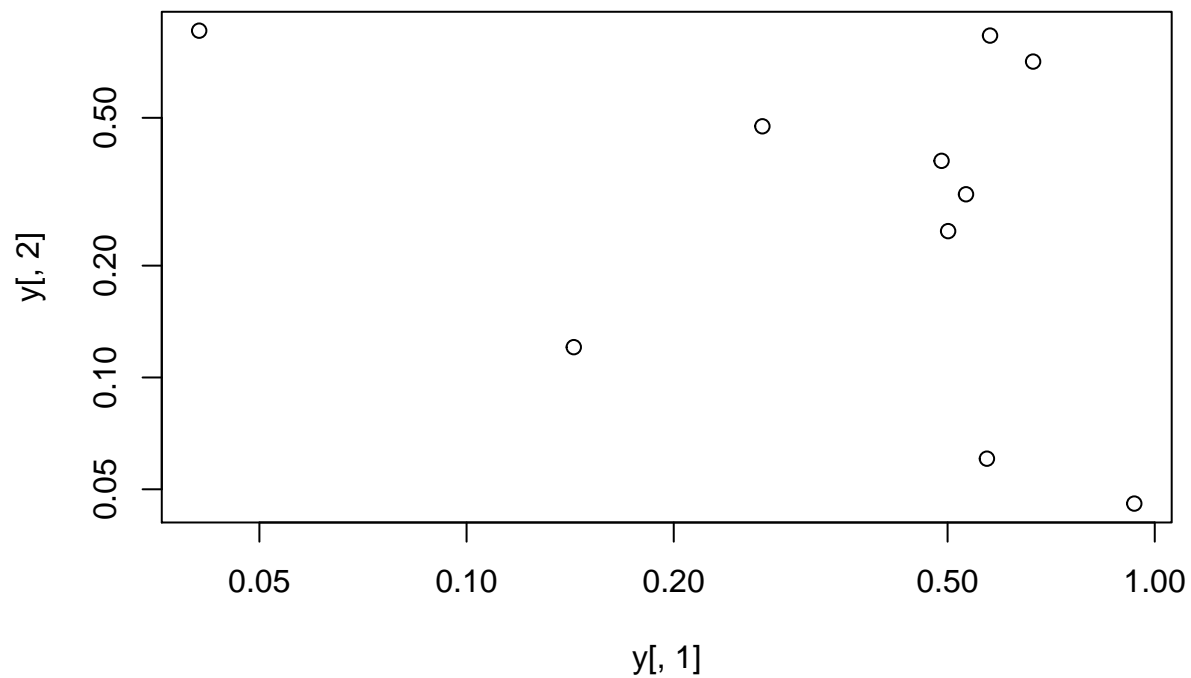
```
##
## Coefficients:
```

| | Estimate | Std. Error | t value | Pr(> t) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 0.5764 | 0.2110 | 2.732 | 0.0258 * |
| y[, 1] | -0.3647 | 0.3959 | -0.921 | 0.3839 |

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3095 on 8 degrees of freedom
## Multiple R-squared:  0.09589,    Adjusted R-squared:  -0.01712
## F-statistic: 0.8485 on 1 and 8 DF,  p-value: 0.3839
```

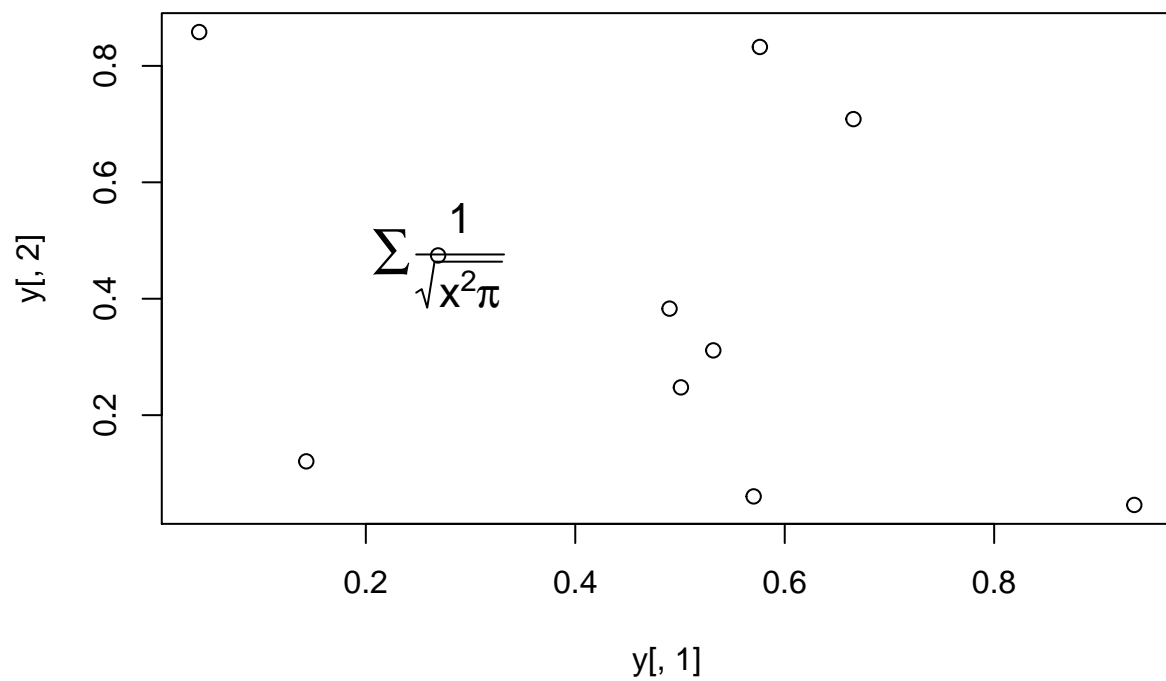
Same plot as above, but on log scale

```
plot(y[,1], y[,2], log="xy")
```



Add a mathematical expression to a plot

```
plot(y[,1], y[,2]); text(y[1,1], y[1,2],
  expression(sum(frac(1,sqrt(x^2*pi)))), cex=1.3)
```



Exercise 1

- **Task 1:** Generate scatter plot for first two columns in `iris` data frame and color dots by its `Species` column.

- **Task 2:** Use the `xlim/ylim` arguments to set limits on the x- and y-axes so that all data points are restricted to the left bottom quadrant of the plot.

Structure of iris data set:

```
class(iris)
```

```
## [1] "data.frame"
```

```
iris[1:4,]
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
## 4         4.6         3.1         1.5         0.2   setosa
```

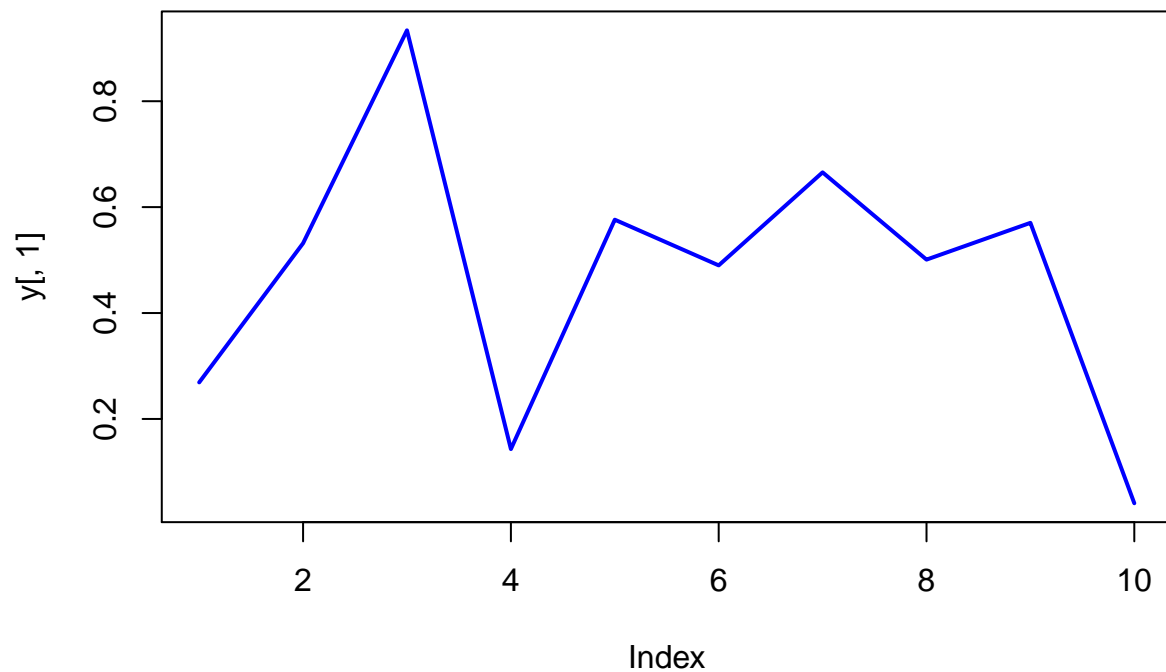
```
table(iris$Species)
```

```
##
##   setosa versicolor  virginica
##     50         50         50
```

Line Plots

Single Data Set

```
plot(y[,1], type="l", lwd=2, col="blue")
```



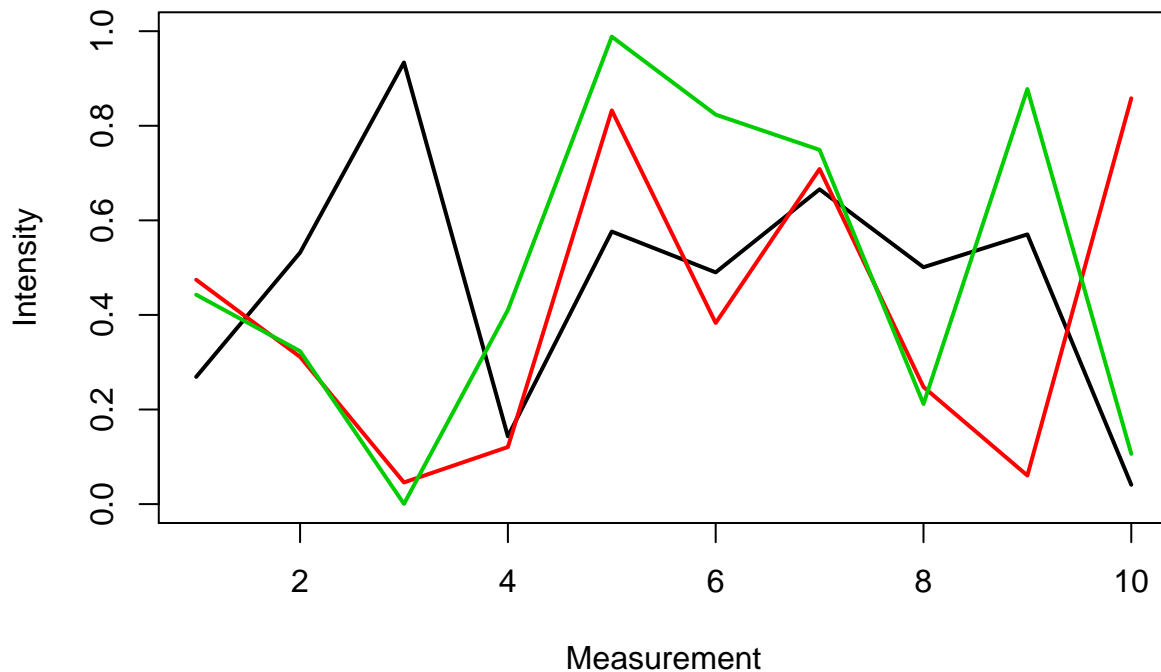
Many Data Sets

Plots line graph for all columns in data frame `y`. The `split.screen` function is used in this example in a for loop to overlay several line graphs in the same plot.

```
split.screen(c(1,1))
```

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

```
plot(y[,1], ylim=c(0,1), xlab="Measurement", ylab="Intensity", type="l", lwd=2, col=1)
for(i in 2:length(y[,])) {
  screen(1, new=FALSE)
  plot(y[,i], ylim=c(0,1), type="l", lwd=2, col=i, xaxt="n", yaxt="n", ylab="",
       xlab="", main="", bty="n")
}
```

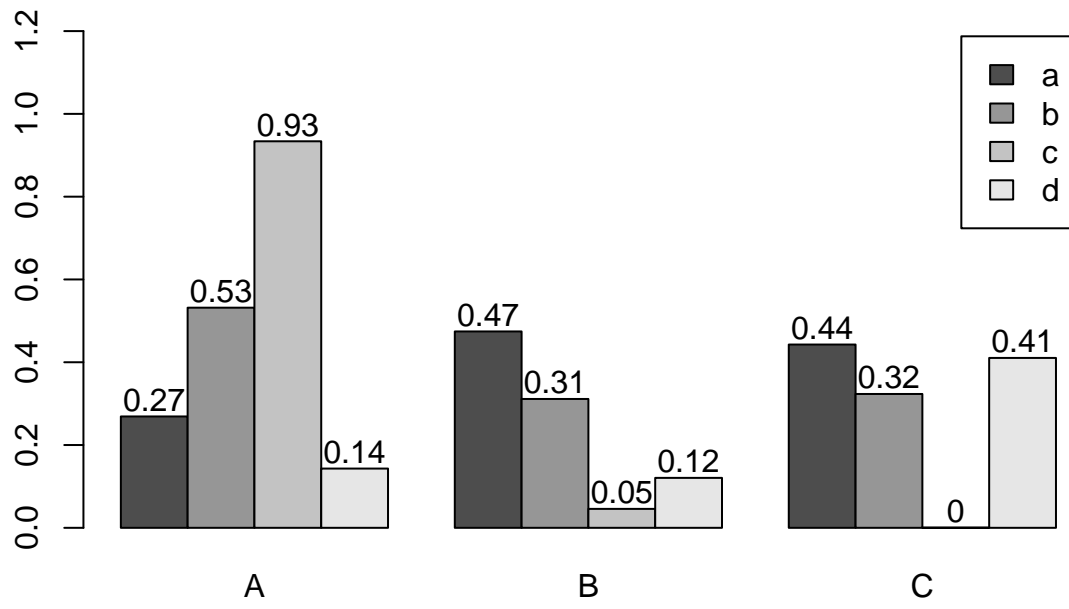


```
close.screen(all=TRUE)
```

Bar Plots

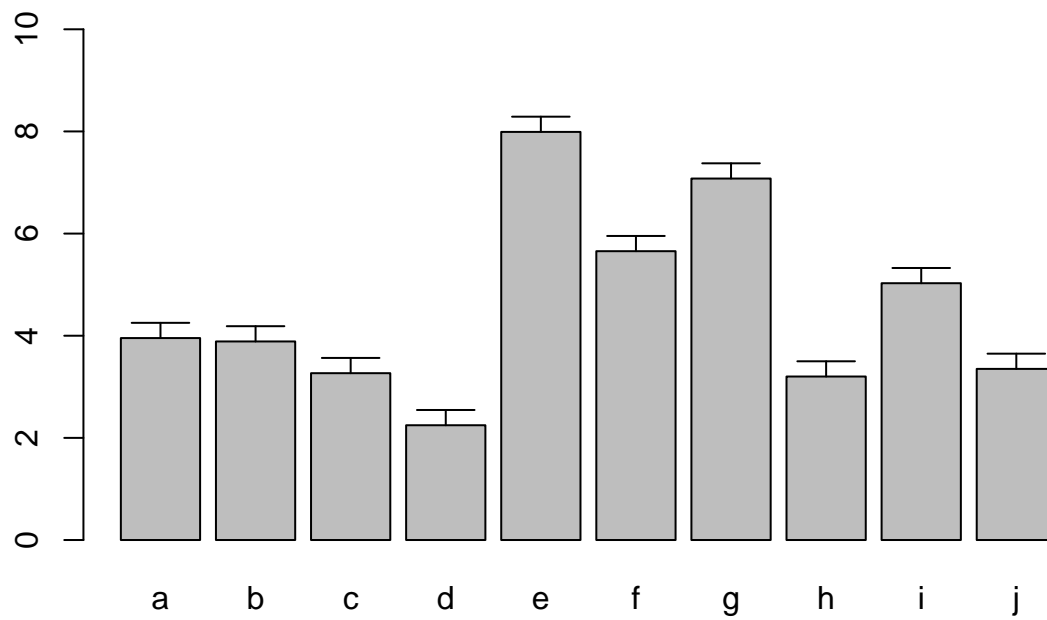
Basics

```
barplot(y[1:4,], ylim=c(0, max(y[1:4,])+0.3), beside=TRUE,
        legend=letters[1:4])
text(labels=round(as.vector(as.matrix(y[1:4,])),2), x=seq(1.5, 13, by=1)
     +sort(rep(c(0,1,2), 4)), y=as.vector(as.matrix(y[1:4,]))+0.04)
```

Error bars

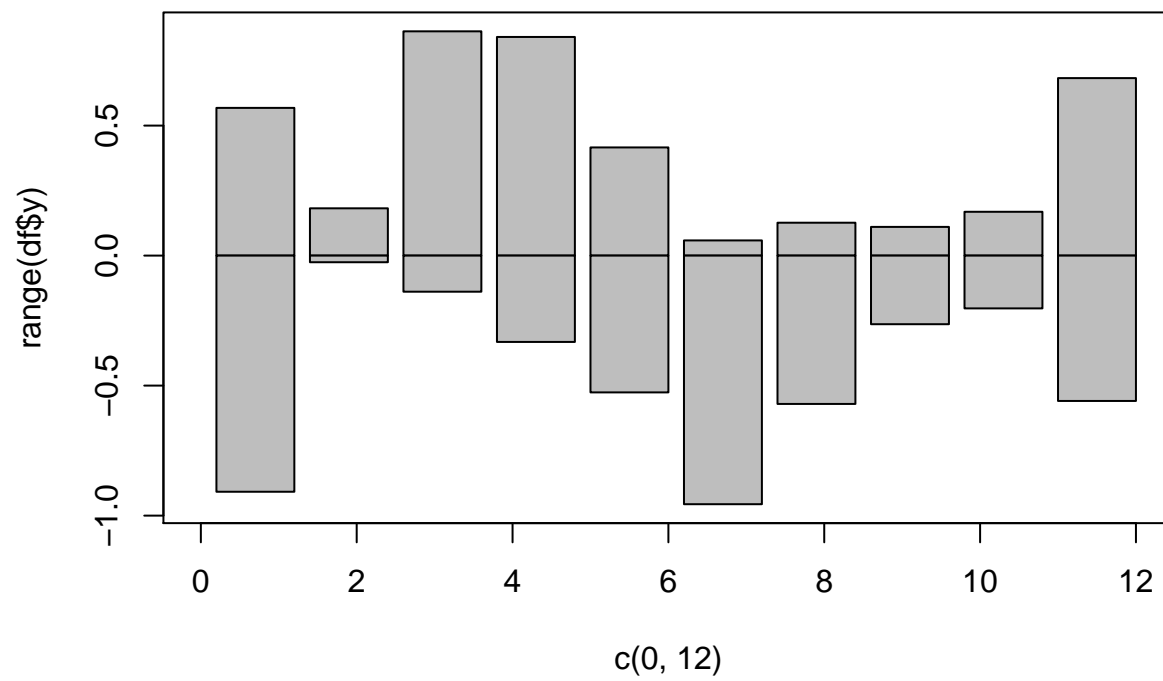
```
bar <- barplot(m <- rowMeans(y) * 10, ylim=c(0, 10))
stdev <- sd(t(y))
arrows(bar, m, bar, m + stdev, length=0.15, angle = 90)
```



Mirrored bar plot

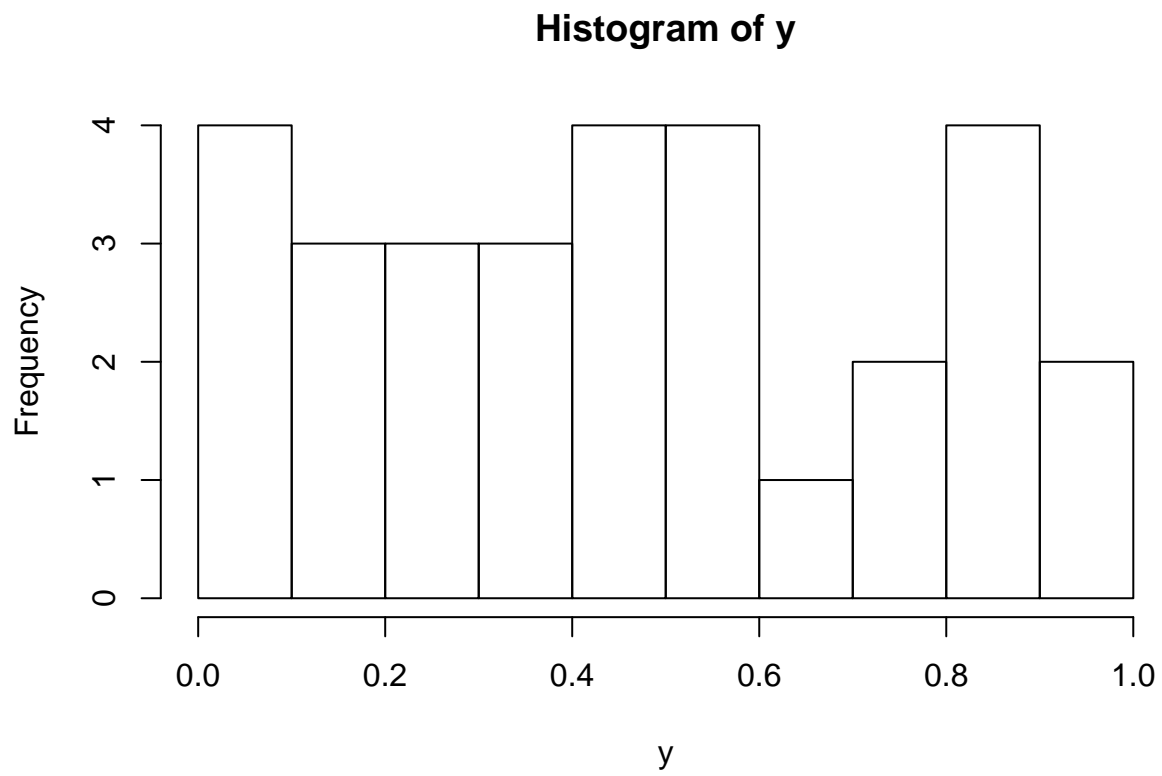
```
df <- data.frame(group = rep(c("Above", "Below"), each=10), x = rep(1:10, 2), y = c(runif(10, 0, 1), runif(10, 0, 1)))
plot(c(0,12), range(df$y), type = "n")
```

```
barplot(height = df$y[df$group == "Above"], add = TRUE, axes = FALSE)
barplot(height = df$y[df$group == "Below"], add = TRUE, axes = FALSE)
```



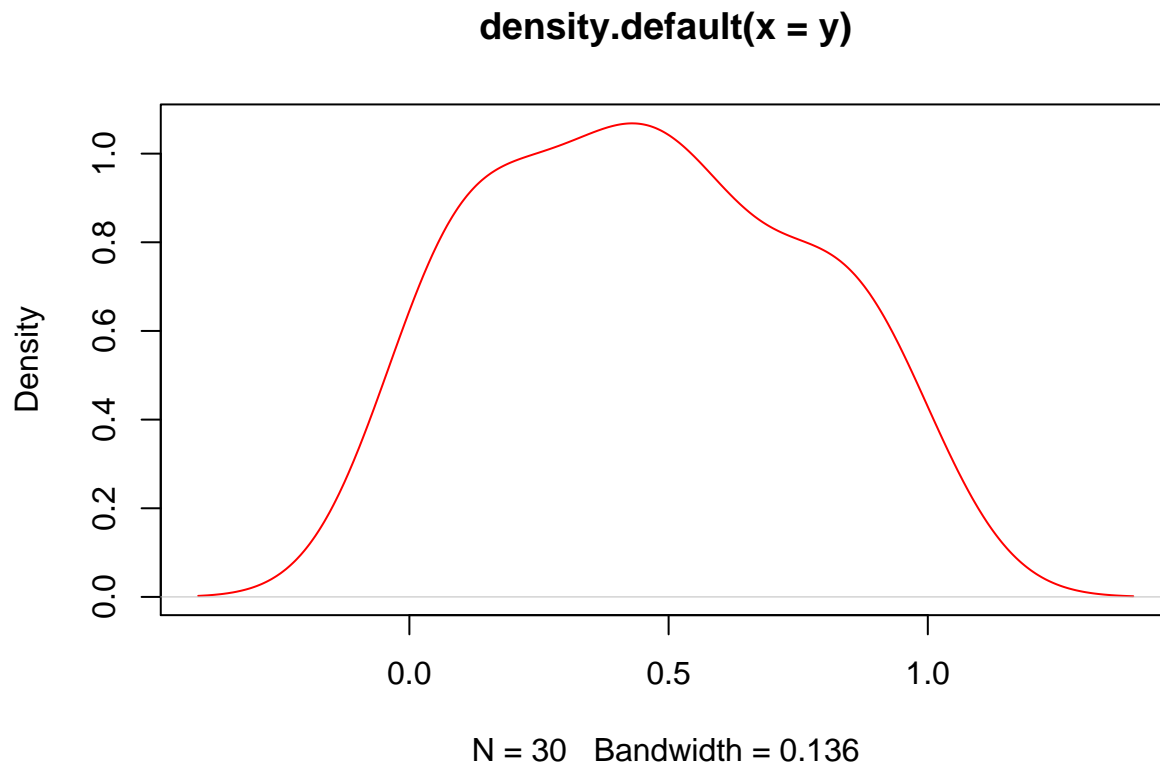
Histograms

```
hist(y, freq=TRUE, breaks=10)
```



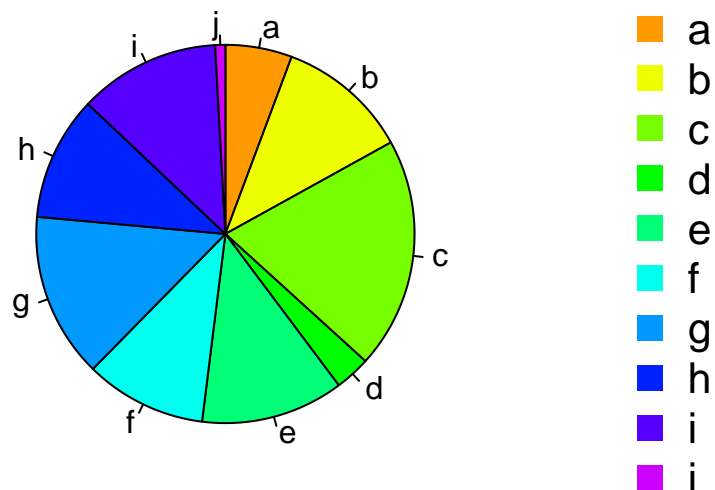
Density Plots}

```
plot(density(y), col="red")
```



Pie Charts

```
pie(y[,1], col=rainbow(length(y[,1]), start=0.1, end=0.8), clockwise=TRUE)
legend("topright", legend=row.names(y), cex=1.3, bty="n", pch=15, pt.cex=1.8,
col=rainbow(length(y[,1]), start=0.1, end=0.8), ncol=1)
```



Color Selection Utilities

Default color palette and how to change it

```
palette()
```

```
## [1] "black" "red" "green3" "blue" "cyan" "magenta" "yellow" "gray"
```

```
palette(rainbow(5, start=0.1, end=0.2))
```

```
palette()
```

```
## [1] "#FF9900" "#FFBF00" "#FFE600" "#F2FF00" "#CCFF00"
```

```
palette("default")
```

The `gray` function allows to select any type of gray shades by providing values from 0 to 1

```
gray(seq(0.1, 1, by= 0.2))
```

```
## [1] "#1A1A1A" "#4D4D4D" "#808080" "#B3B3B3" "#E6E6E6"
```

Color gradients with `colorpanel` function from `gplots` library

```
library(gplots)
```

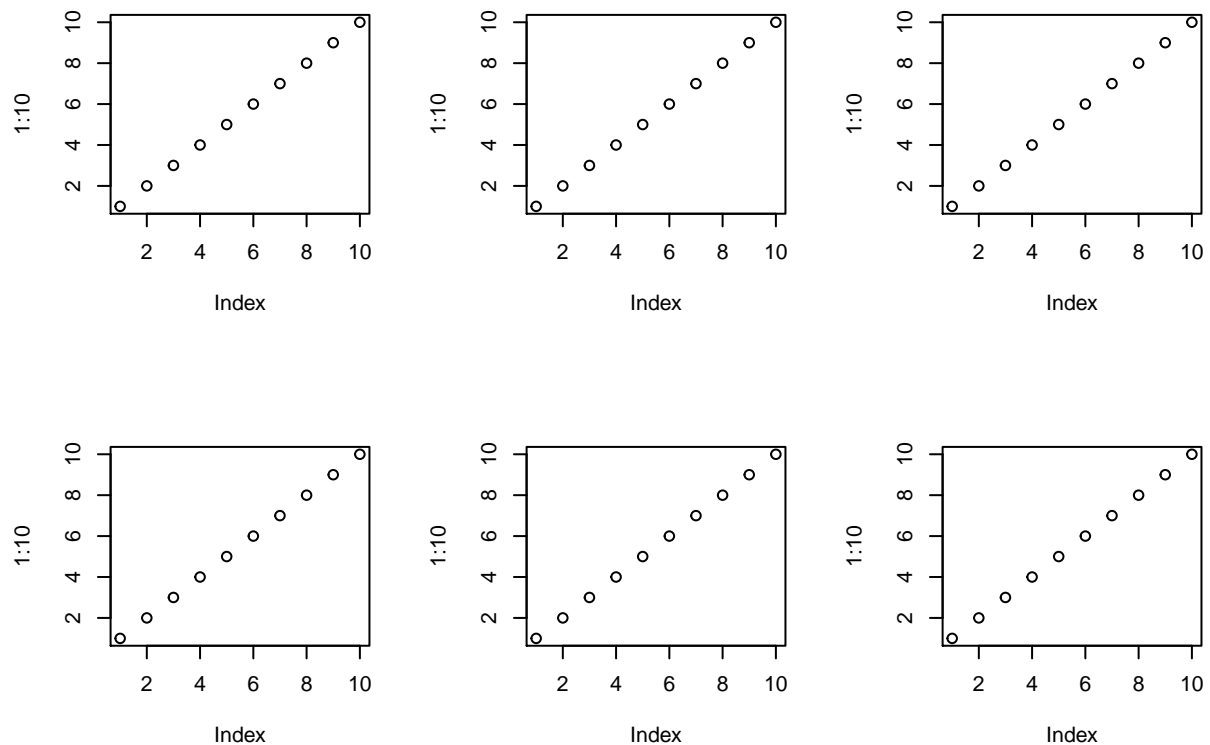
```
colorpanel(5, "darkblue", "yellow", "white")
```

Much more on colors in R see Earl Glynn's color chart

Arranging Several Plots on Single Page

With `par(mfrow=c(nrow,ncol))` one can define how several plots are arranged next to each other.

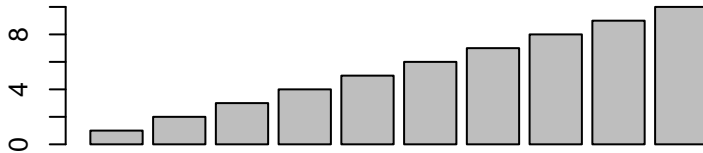
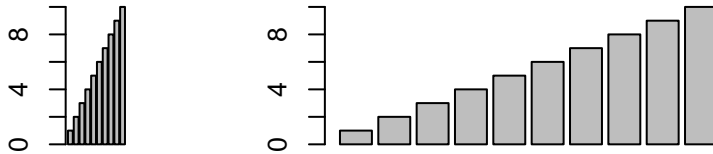
```
par(mfrow=c(2,3)); for(i in 1:6) { plot(1:10) }
```



Arranging Plots with Variable Width

The `layout` function allows to divide the plotting device into variable numbers of rows and columns with the column-widths and the row-heights specified in the respective arguments.

```
nf <- layout(matrix(c(1,2,3,3), 2, 2, byrow=TRUE), c(3,7), c(5,5),
                  respect=TRUE)
# layout.show(nf)
for(i in 1:3) { barplot(1:10) }
```



Saving Graphics to Files

After the `pdf()` command all graphs are redirected to file `test.pdf`. Works for all common formats similarly: jpeg, png, ps, tiff, ...

```
pdf("test.pdf"); plot(1:10, 1:10); dev.off()
```

Generates Scalable Vector Graphics (SVG) files that can be edited in vector graphics programs, such as Inkscape.

```
svg("test.svg"); plot(1:10, 1:10); dev.off()
```

Exercise 2

Bar plots

- **Task 1:** Calculate the mean values for the `Species` components of the first four columns in the `iris` data set. Organize the results in a matrix where the row names are the unique values from the `iris Species` column and the column names are the same as in the first four `iris` columns.
- **Task 2:** Generate two bar plots: one with stacked bars and one with horizontally arranged bars.

Structure of iris data set:

```
class(iris)
```

```
## [1] "data.frame"
```

```
iris[1:4,]
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
## 4         4.6         3.1         1.5         0.2   setosa
```

```
table(iris$Species)
```

```
##
##      setosa versicolor  virginica
##       50         50         50
```

Grid Graphics

- What is `grid`?
 - Low-level graphics system
 - Highly flexible and controllable system
 - Does not provide high-level functions
 - Intended as development environment for custom plotting functions
 - Pre-installed on new R distributions
- Documentation and Help
 - Manual
 - Book

lattice Graphics

- What is `lattice`?
 - High-level graphics system
 - Developed by Deepayan Sarkar
 - Implements Trellis graphics system from S-Plus
 - Simplifies high-level plotting tasks: arranging complex graphical features
 - Syntax similar to R's base graphics
- Documentation and Help
 - Manual
 - Intro
 - Book

Open a list of all functions available in the lattice package

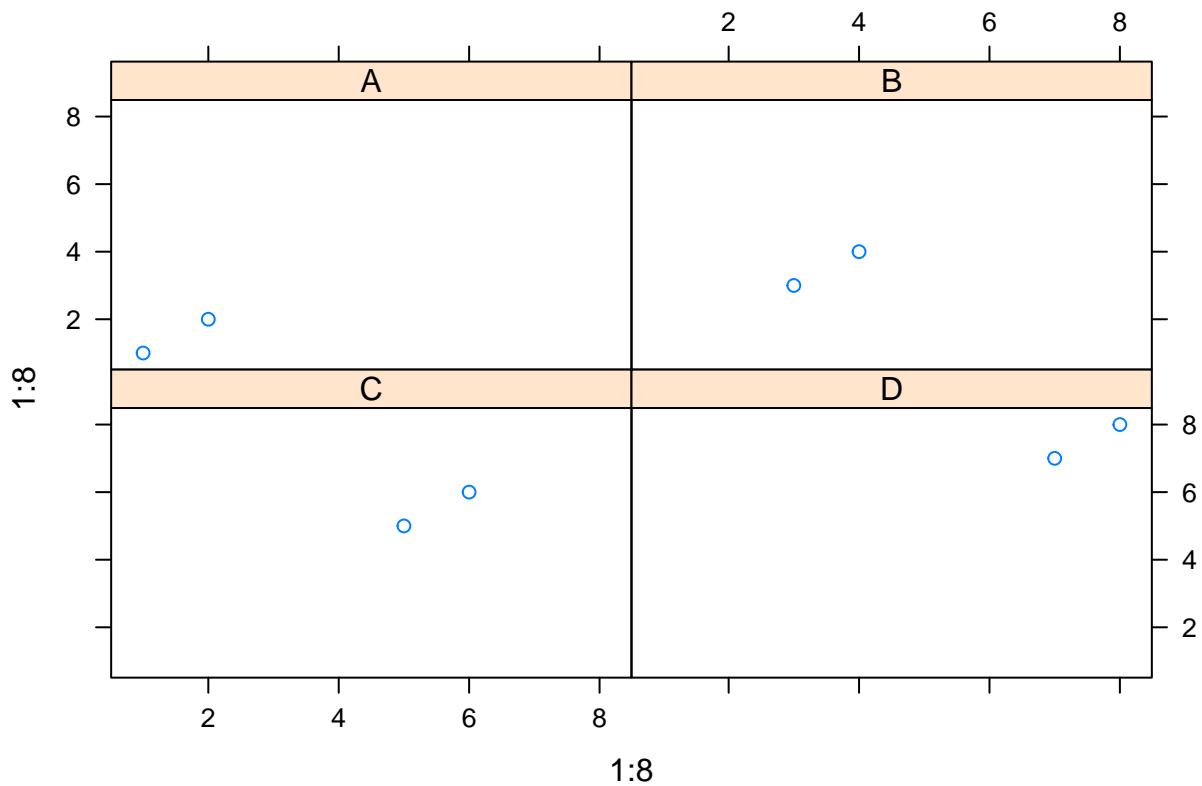
```
library(help=lattice)
```

Accessing and changing global parameters:

```
?lattice.options  
?trellis.device
```

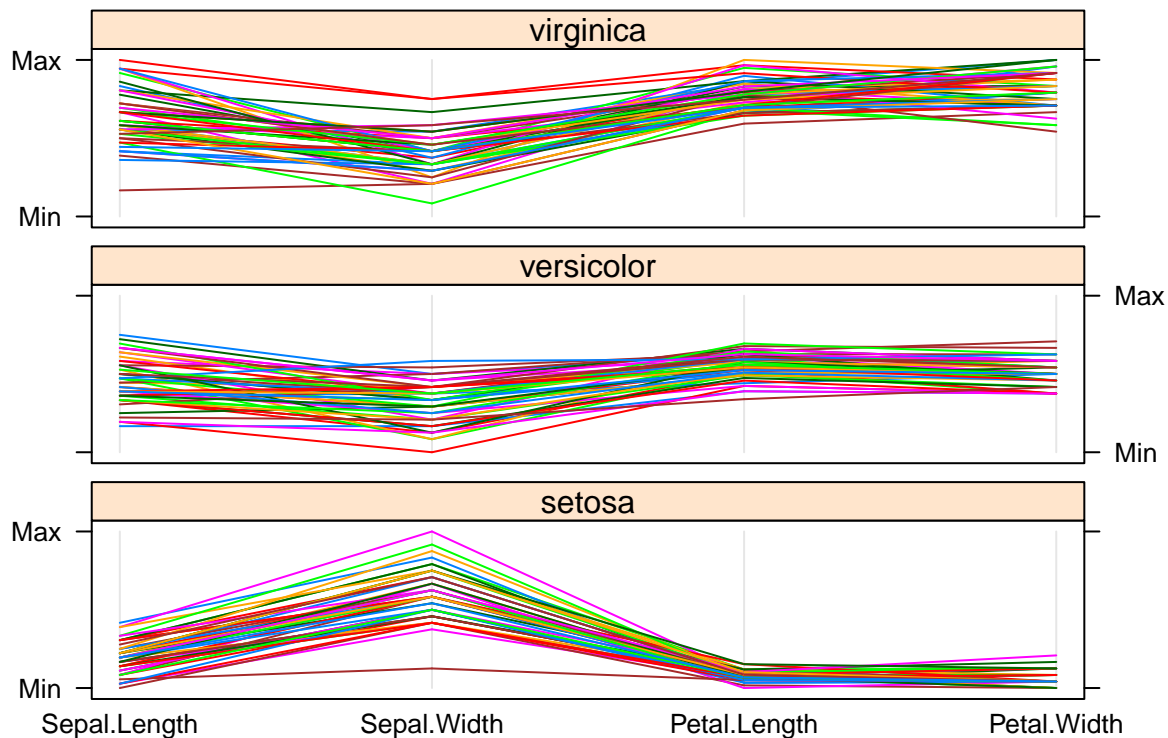
Scatter Plot Sample

```
library(lattice)  
p1 <- xyplot(1:8 ~ 1:8 | rep(LETTERS[1:4], each=2), as.table=TRUE)  
plot(p1)
```



Line Plot Sample

```
library(lattice)  
p2 <- parallelplot(~iris[1:4] | Species, iris, horizontal.axis = FALSE,  
  layout = c(1, 3, 1))  
plot(p2)
```

ggplot2 Graphics

- What is `ggplot2`?
 - High-level graphics system
 - Implements grammar of graphics from Leland Wilkinson
 - Streamlines many graphics workflows for complex plots
 - Syntax centered around main `ggplot` function
 - Simpler `qplot` function provides many shortcuts
- Documentation and Help
 - Manual
 - Intro
 - Book
 - Cookbook for R

ggplot2 Usage

- `ggplot` function accepts two arguments
 - Data set to be plotted
 - Aesthetic mappings provided by `aes` function
- Additional parameters such as geometric objects (*e.g.* points, lines, bars) are passed on by appending them with `+` as separator.
- List of available `geom_*` functions see [here](#)
- Settings of plotting theme can be accessed with the command `theme_get()` and its settings can be changed with `theme()`.
- Preferred input data object

- `qplot`: `data.frame` (support for `vector`, `matrix`, ...)
- `ggplot`: `data.frame`
- Packages with convenience utilities to create expected inputs
 - `plyr`
 - `reshape`

qplot Function

The syntax of `qplot` is similar as R's basic `plot` function

- Arguments
 - `x`: x-coordinates (*e.g.* `col1`)
 - `y`: y-coordinates (*e.g.* `col2`)
 - `data`: data frame with corresponding column names
 - `xlim`, `ylim`: *e.g.* `xlim=c(0,10)`
 - `log`: *e.g.* `log="x"` or `log="xy"`
 - `main`: main title; see `?plotmath` for mathematical formula
 - `xlab`, `ylab`: labels for the x- and y-axes
 - `color`, `shape`, `size`
 - ...: many arguments accepted by `plot` function

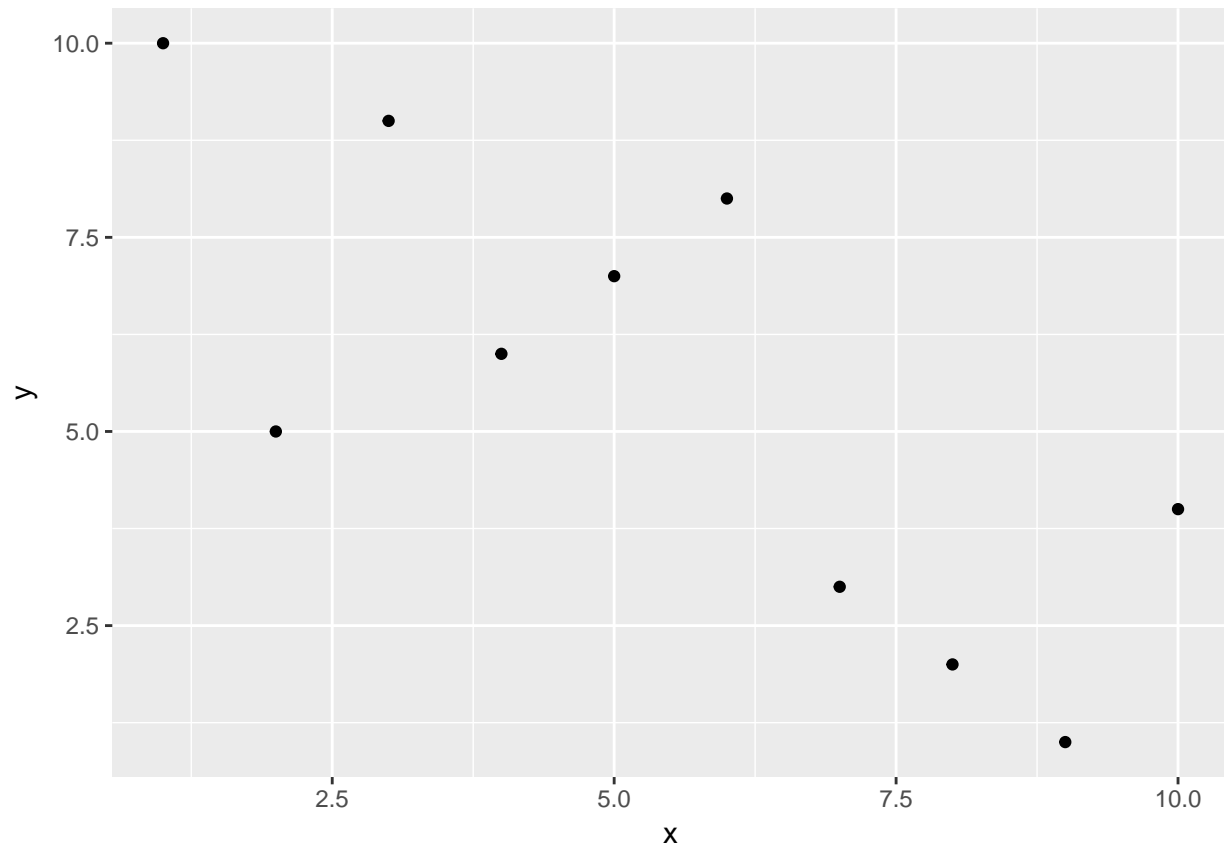
qplot: scatter plot basics

Create sample data

```
library(ggplot2)
x <- sample(1:10, 10); y <- sample(1:10, 10); cat <- rep(c("A", "B"), 5)
```

Simple scatter plot

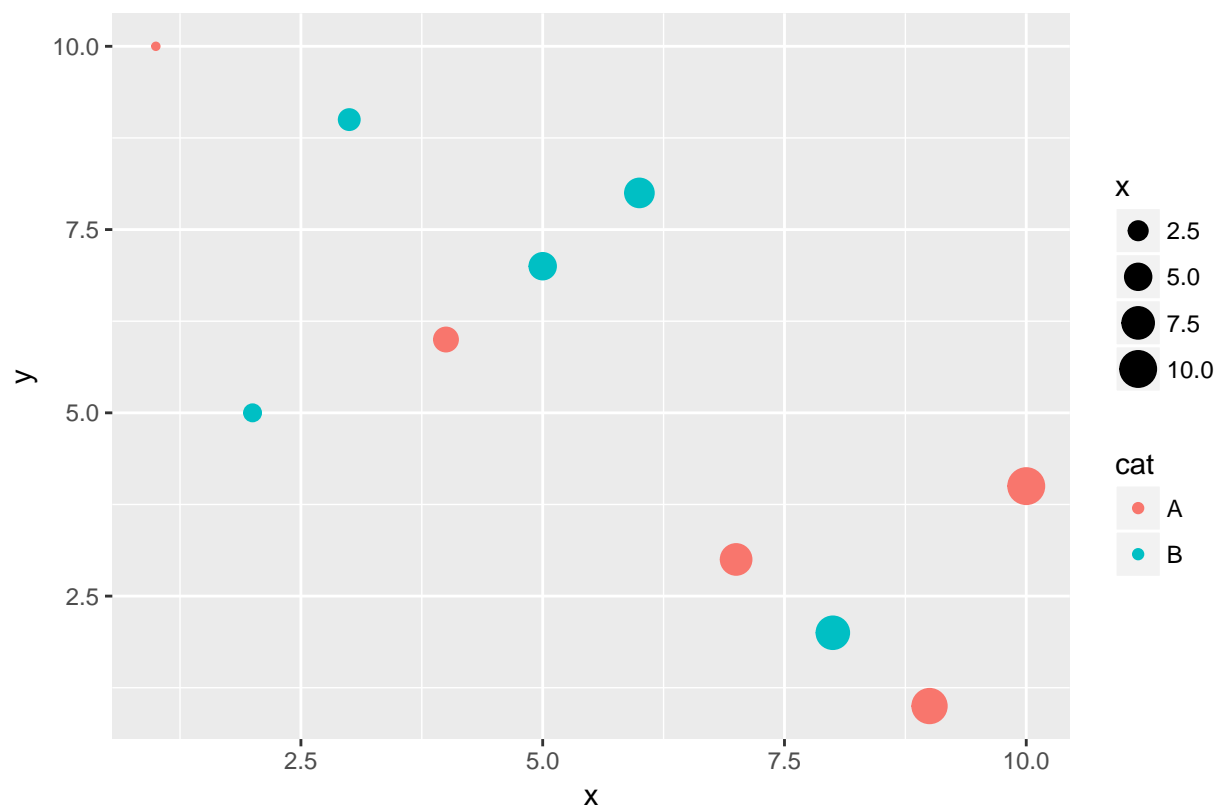
```
qplot(x, y, geom="point")
```



Prints dots with different sizes and colors

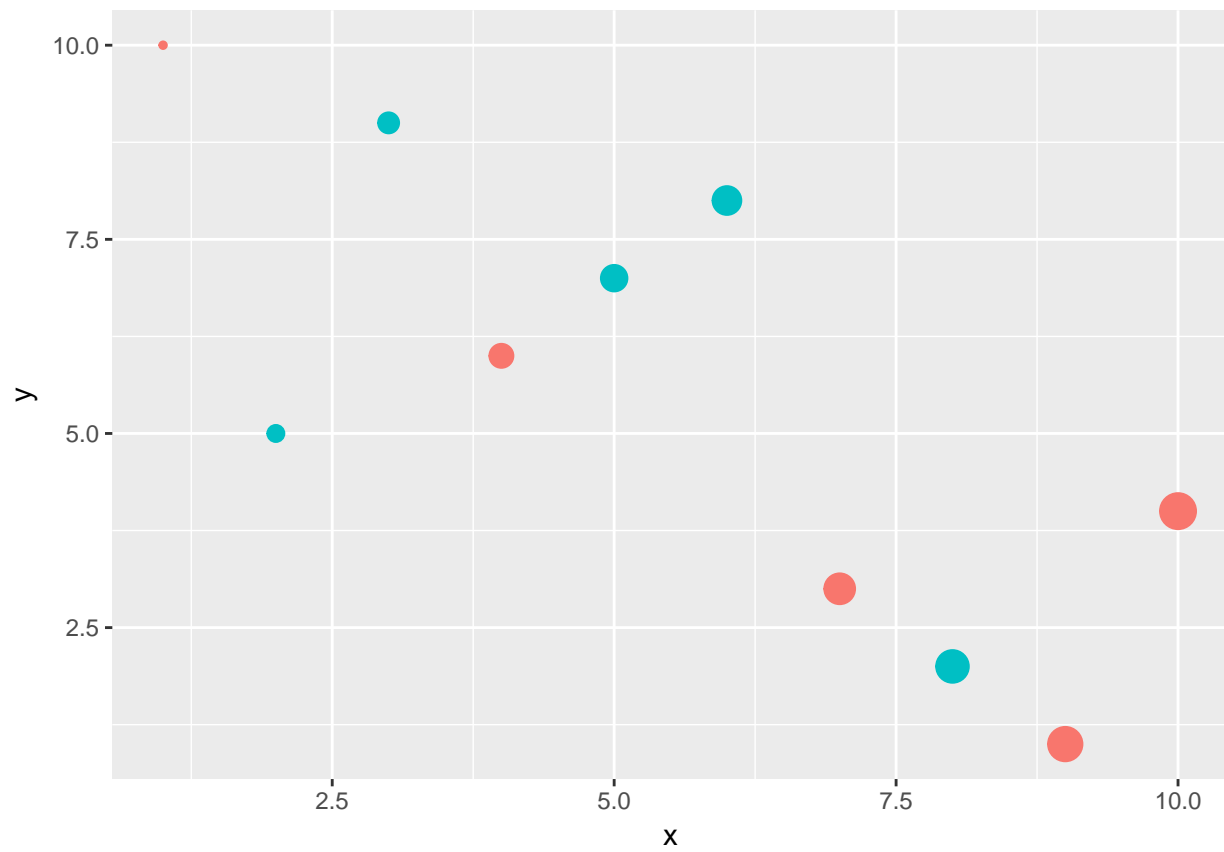
```
qplot(x, y, geom="point", size=x, color=cat,  
      main="Dot Size and Color Relative to Some Values")
```

Dot Size and Color Relative to Some Values



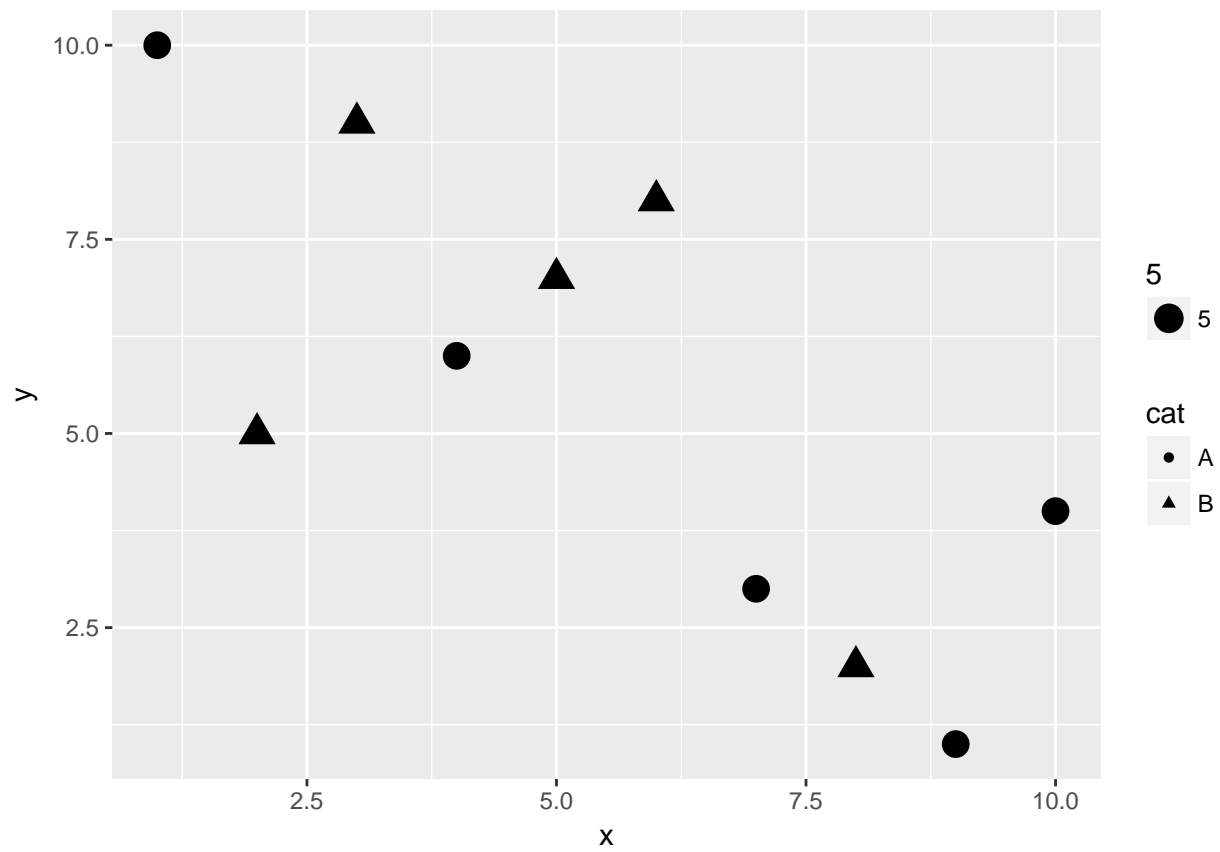
Drops legend

```
qplot(x, y, geom="point", size=x, color=cat) +  
  theme(legend.position = "none")
```



Plot different shapes

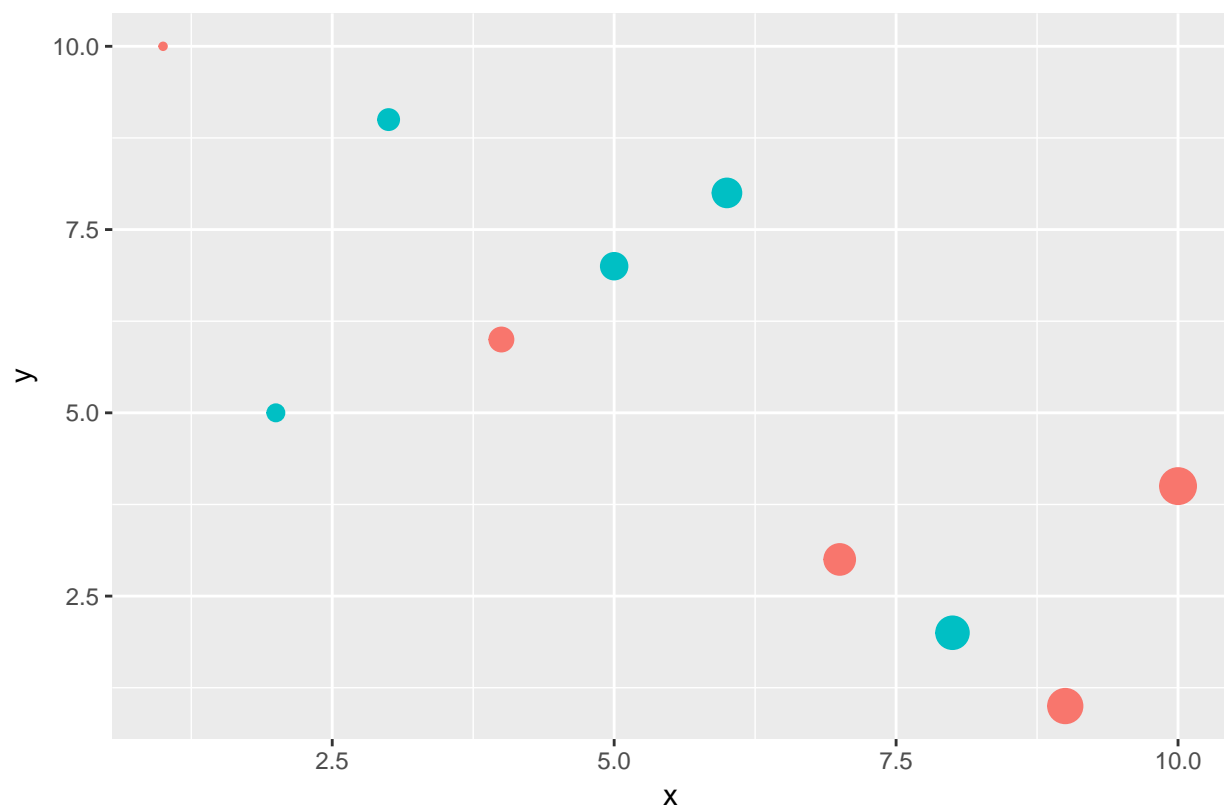
```
qplot(x, y, geom="point", size=5, shape=cat)
```



Colored groups

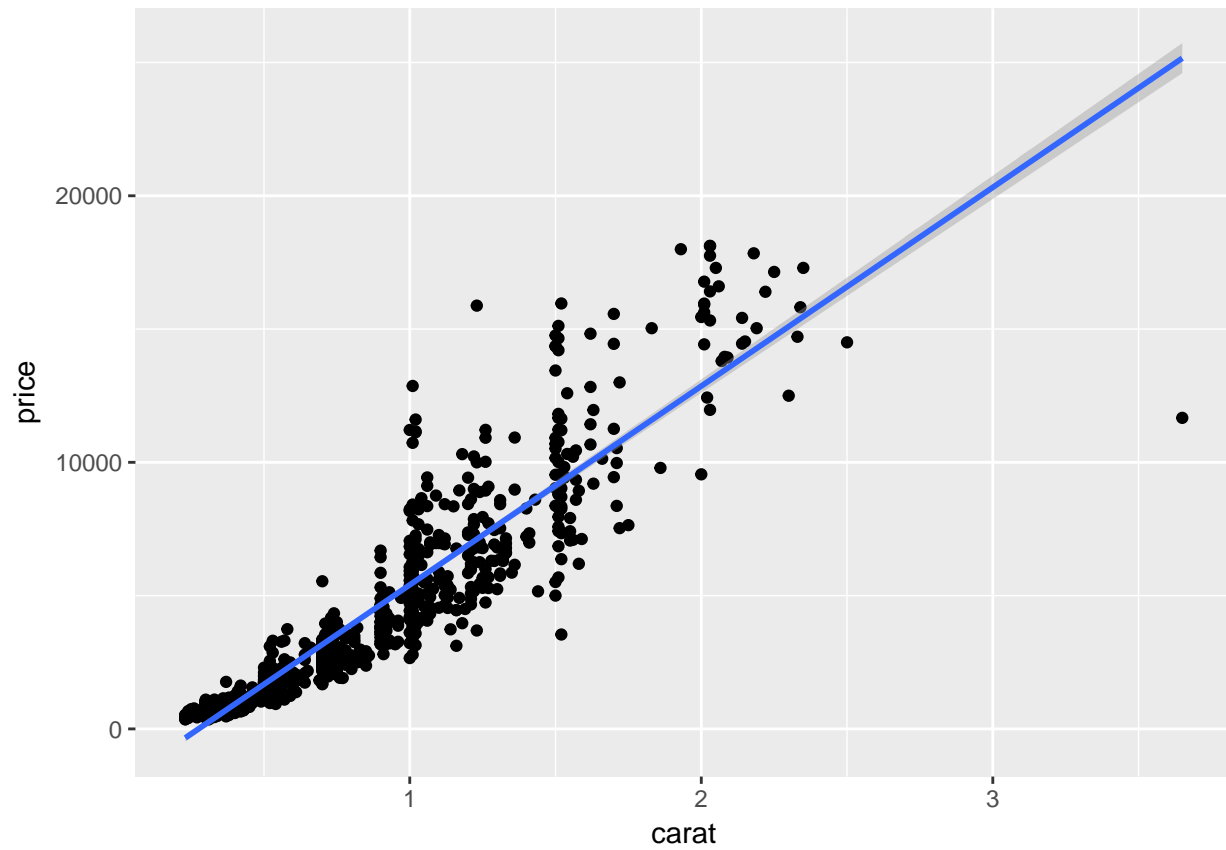
```
p <- qplot(x, y, geom="point", size=x, color=cat,  
           main="Dot Size and Color Relative to Some Values") +  
  theme(legend.position = "none")  
print(p)
```

Dot Size and Color Relative to Some Values



Regression line

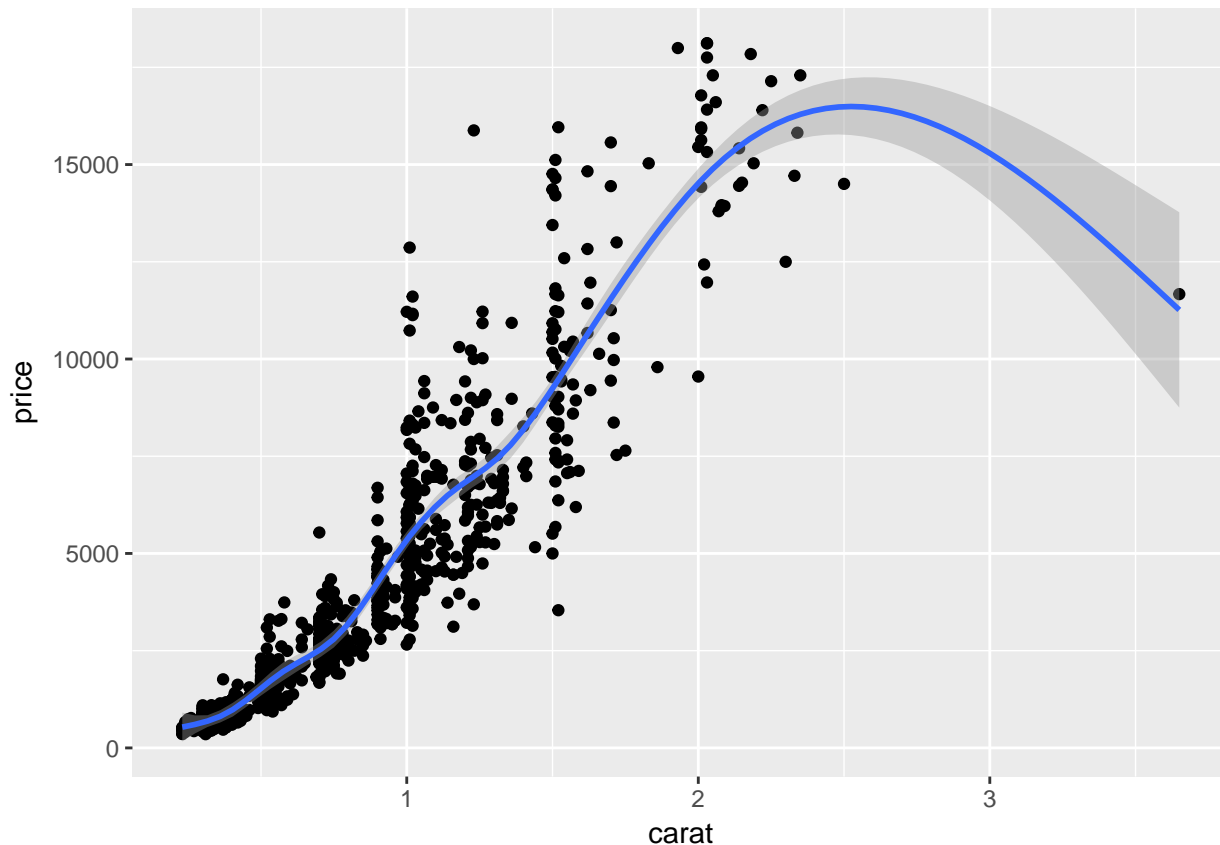
```
set.seed(1410)
dsmall <- diamonds[sample(nrow(diamonds), 1000), ]
p <- qplot(carat, price, data = dsmall) +
  geom_smooth(method="lm")
print(p)
```



Local regression curve (loess)

```
p <- qplot(carat, price, data=dsmall, geom=c("point", "smooth"))  
print(p) # Setting se=FALSE removes error shade
```

```
## `geom_smooth()` using method = 'gam'
```

ggplot Function

- More important than `qplot` to access full functionality of `ggplot2`
- Main arguments
 - data set, usually a `data.frame`
 - aesthetic mappings provided by `aes` function
- General `ggplot` syntax
 - `ggplot(data, aes(...)) + geom() + ... + stat() + ...`
- Layer specifications
 - `geom(mapping, data, ..., geom, position)`
 - `stat(mapping, data, ..., stat, position)`
- Additional components
 - `scales`
 - `coordinates`
 - `facet`
- `aes()` mappings can be passed on to all components (`ggplot`, `geom`, etc.). Effects are global when passed on to `ggplot()` and local for other components.
 - `x`, `y`
 - `color`: grouping vector (factor)
 - `group`: grouping vector (factor)

Changing Plotting Themes in ggplot

- Theme settings can be accessed with `theme_get()`
- Their settings can be changed with `theme()`

Example how to change background color to white

```
... + theme(panel.background=element_rect(fill = "white", colour = "black"))
```

Storing ggplot Specifications

Plots and layers can be stored in variables

```
p <- ggplot(dsmall, aes(carat, price)) + geom_point()
p # or print(p)
```

Returns information about data and aesthetic mappings followed by each layer

```
summary(p)
```

Print dots with different sizes and colors

```
bestfit <- geom_smooth(methodw = "lm", se = F, color = alpha("steelblue", 0.5), size = 2)
p + bestfit # Plot with custom regression line
```

Syntax to pass on other data sets

```
p %+% diamonds[sample(nrow(diamonds), 100),]
```

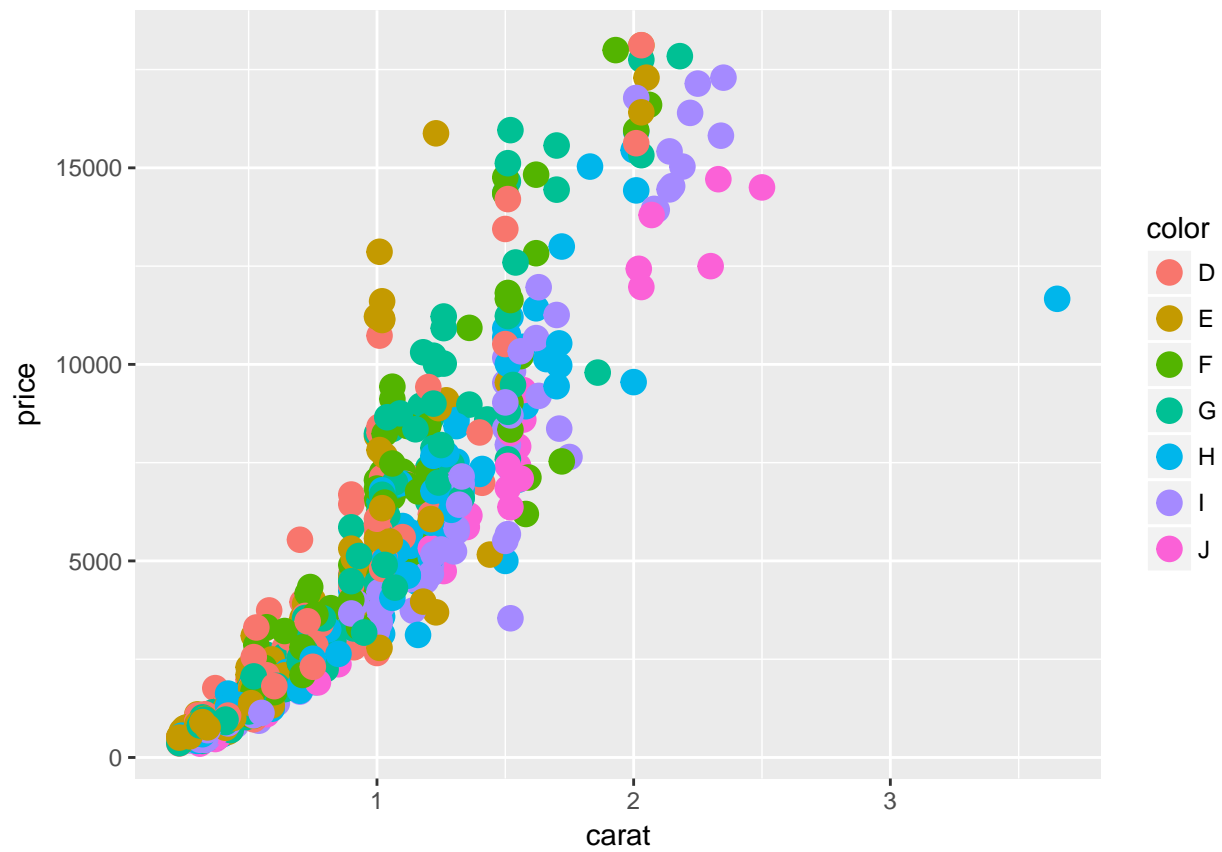
Saves plot stored in variable `p` to file

```
ggsave(p, file="myplot.pdf")
```

ggplot: scatter plots

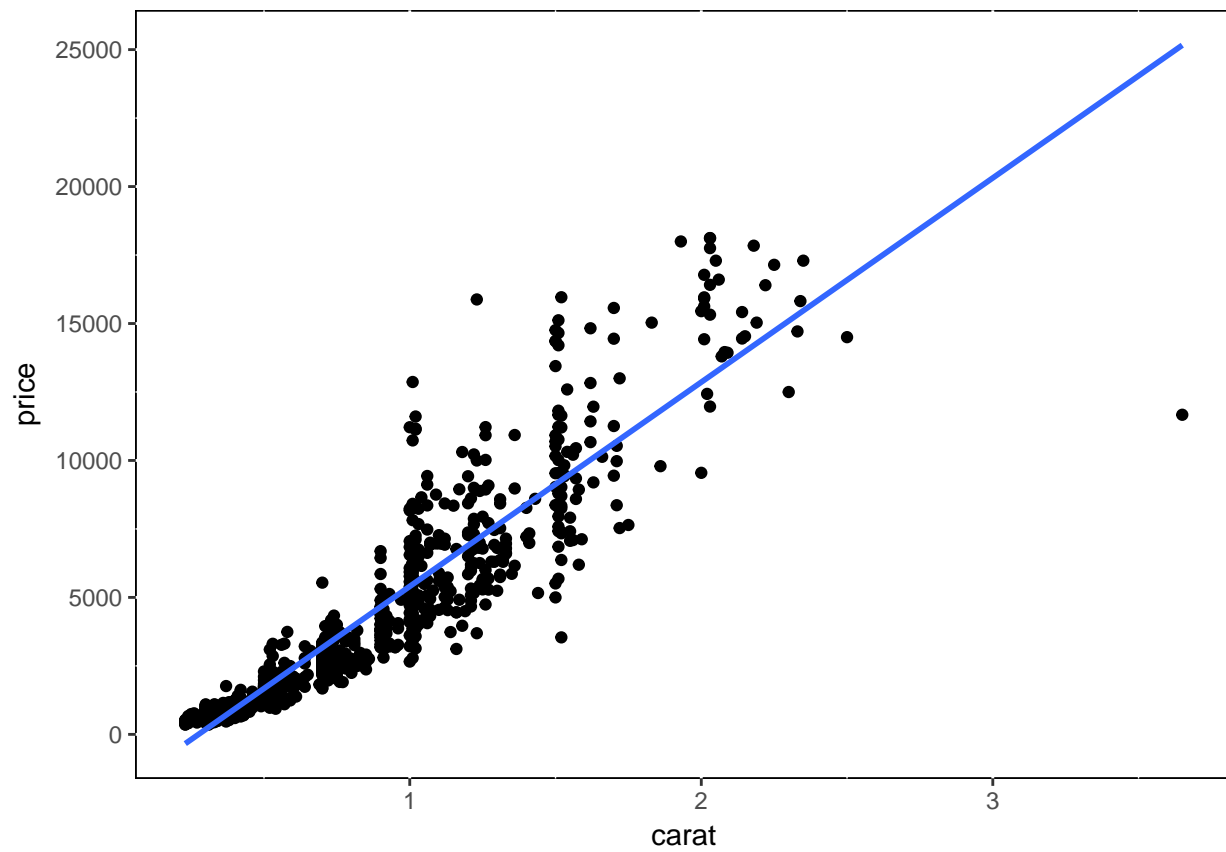
Basic example

```
p <- ggplot(dsmall, aes(carat, price, color=color)) +
  geom_point(size=4)
print(p)
```



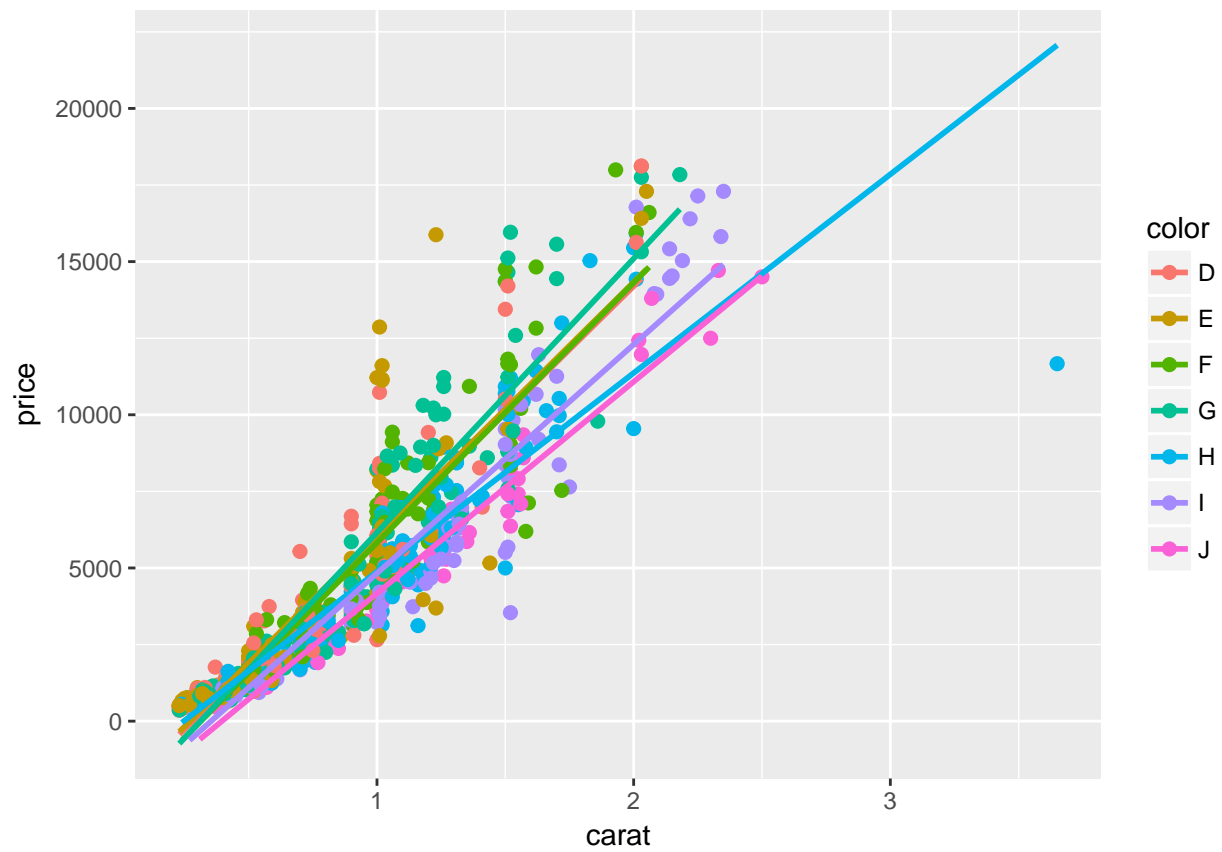
Regression line

```
p <- ggplot(dsmall, aes(carat, price)) + geom_point() +  
  geom_smooth(method="lm", se=FALSE) +  
  theme(panel.background=element_rect(fill = "white", colour = "black"))  
print(p)
```



Several regression lines

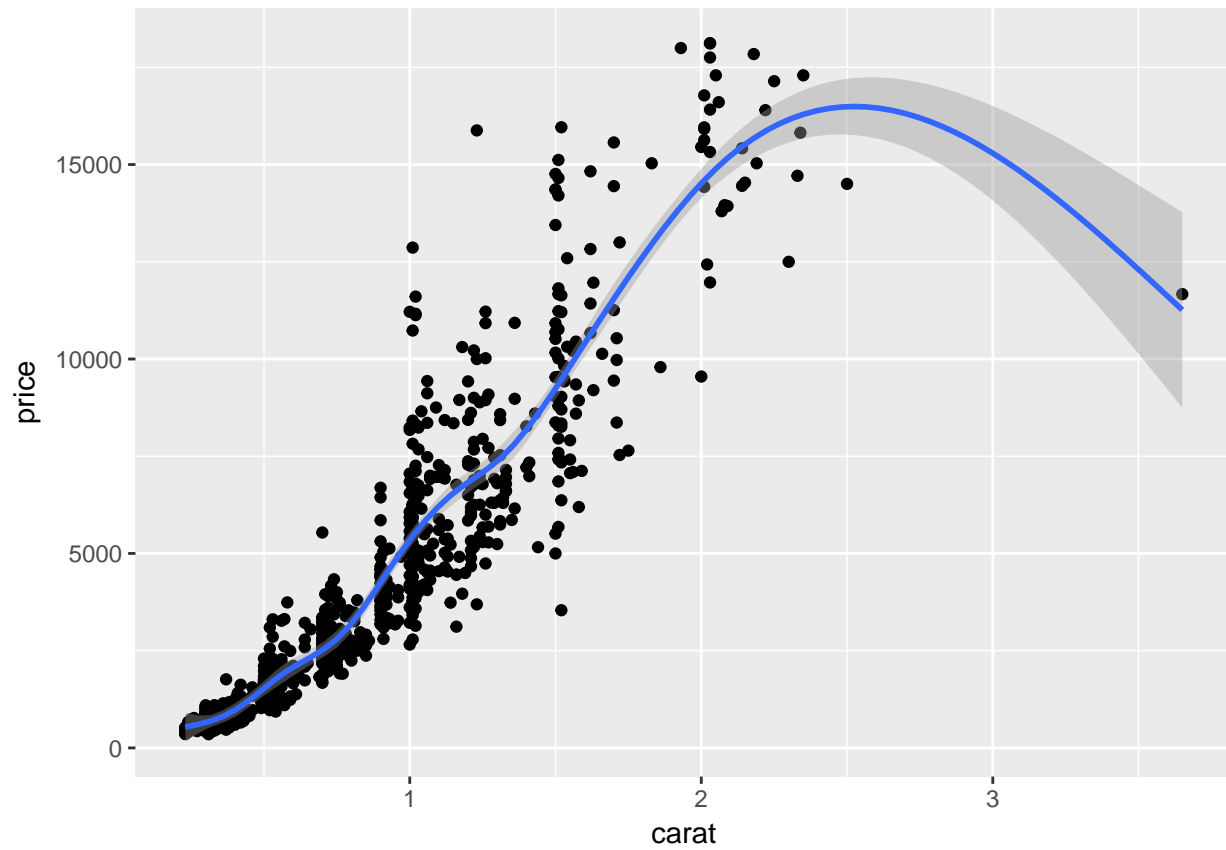
```
p <- ggplot(dsmall, aes(carat, price, group=color)) +  
  geom_point(aes(color=color), size=2) +  
  geom_smooth(aes(color=color), method = "lm", se=FALSE)  
print(p)
```



Local regression curve (loess)

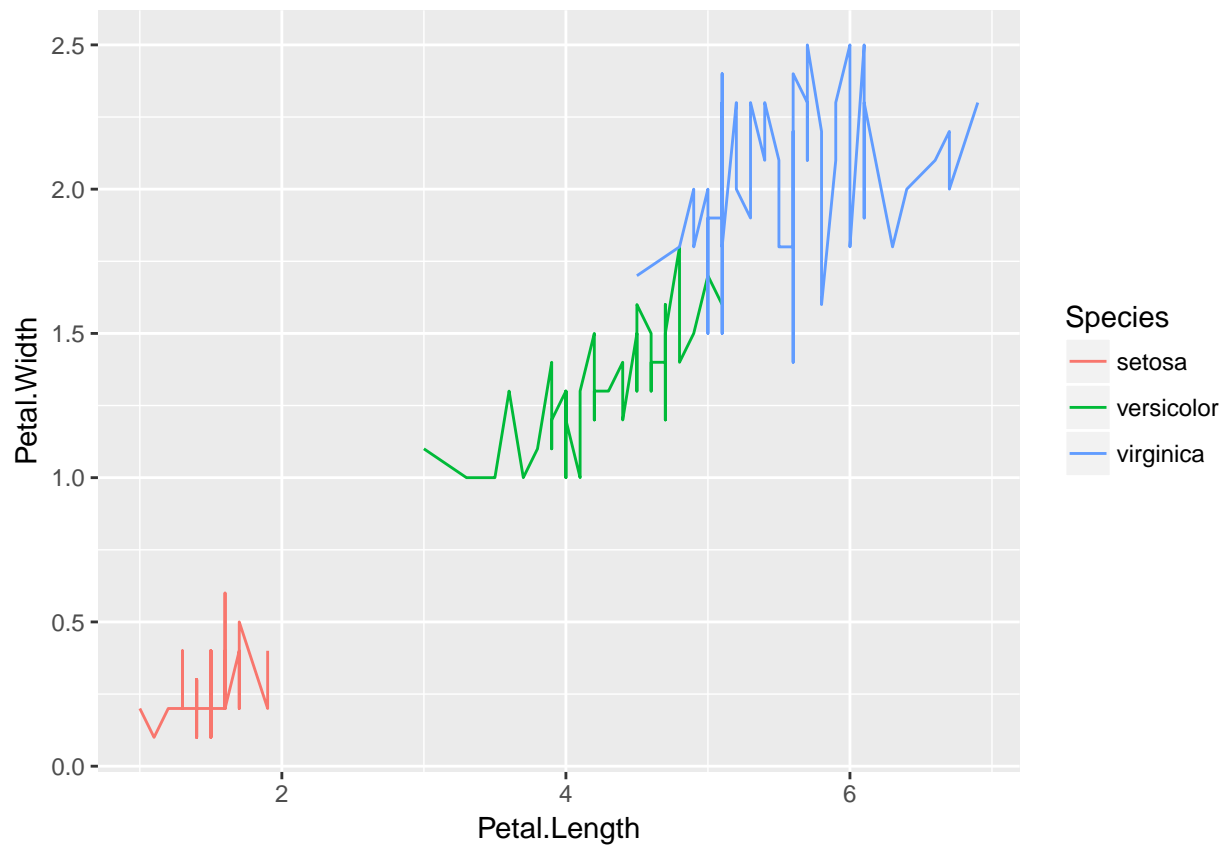
```
p <- ggplot(dsmall, aes(carat, price)) + geom_point() + geom_smooth()
print(p) # Setting se=FALSE removes error shade
```

```
## `geom_smooth()` using method = 'gam'
```



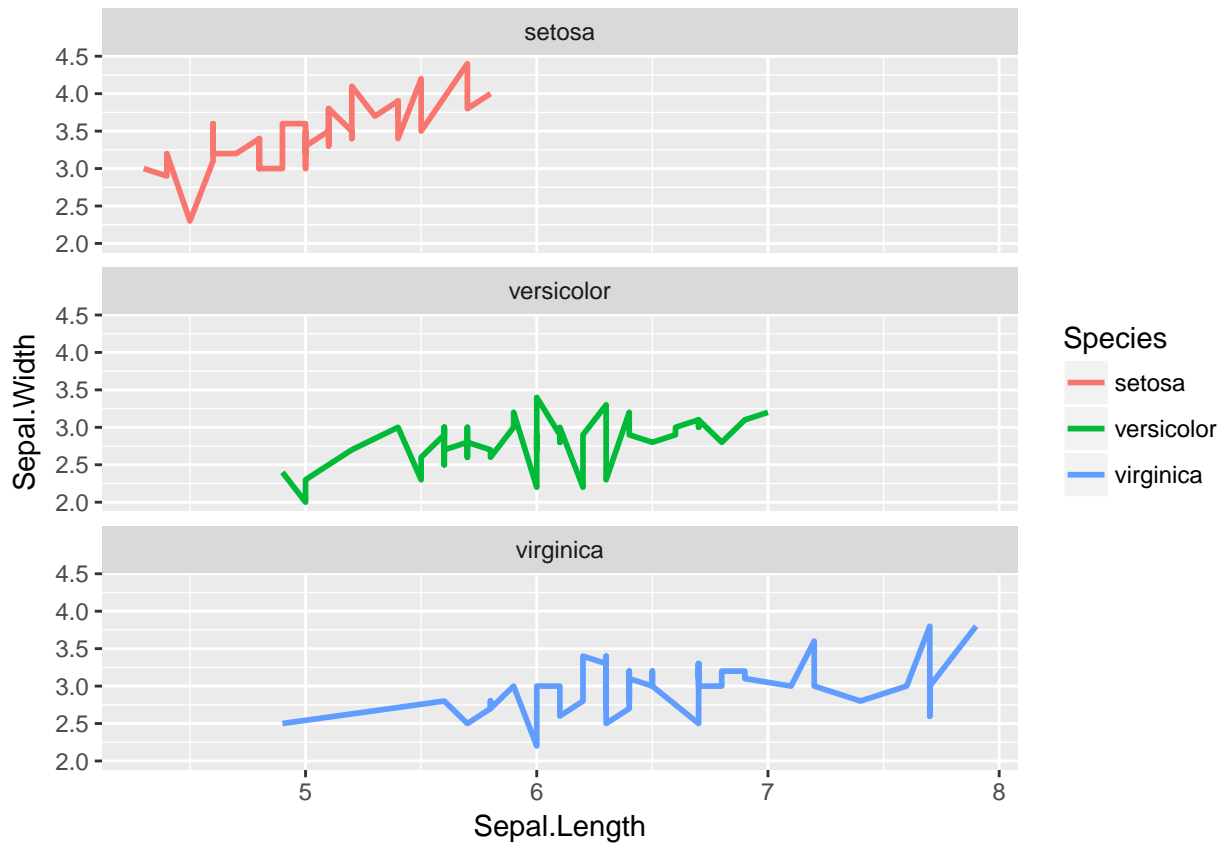
ggplot: line plot

```
p <- ggplot(iris, aes(Petal.Length, Petal.Width, group=Species,  
                      color=Species)) + geom_line()  
print(p)
```



Faceting

```
p <- ggplot(iris, aes(Sepal.Length, Sepal.Width)) +  
  geom_line(aes(color=Species), size=1) +  
  facet_wrap(~Species, ncol=1)  
print(p)
```



Exercise 3

Scatter plots with `ggplot2`

- **Task 1:** Generate scatter plot for first two columns in `iris` data frame and color dots by its `Species` column.
- **Task 2:** Use the `xlim` and `ylim` arguments to set limits on the x- and y-axes so that all data points are restricted to the left bottom quadrant of the plot.
- **Task 3:** Generate corresponding line plot with faceting show individual data sets in separate plots.

Structure of `iris` data set

```
class(iris)
```

```
## [1] "data.frame"
```

```
iris[1:4,]
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
## 4         4.6         3.1         1.5         0.2   setosa
```



```
table(iris$Species)
```

```
##  
##      setosa versicolor  virginica  
##         50         50         50
```

Bar plots

Sample Set: the following transforms the `iris` data set into a `ggplot2`-friendly format.

Calculate mean values for aggregates given by `Species` column in `iris` data set

```
iris_mean <- aggregate(iris[,1:4], by=list(Species=iris$Species), FUN=mean)
```

Calculate standard deviations for aggregates given by `Species` column in `iris` data set

```
iris_sd <- aggregate(iris[,1:4], by=list(Species=iris$Species), FUN=sd)
```

Reformat `iris_mean` with `melt`

```
library(reshape2) # Defines melt function  
df_mean <- melt(iris_mean, id.vars=c("Species"), variable.name = "Samples", value.name="Values")
```

Reformat `iris_sd` with `melt`

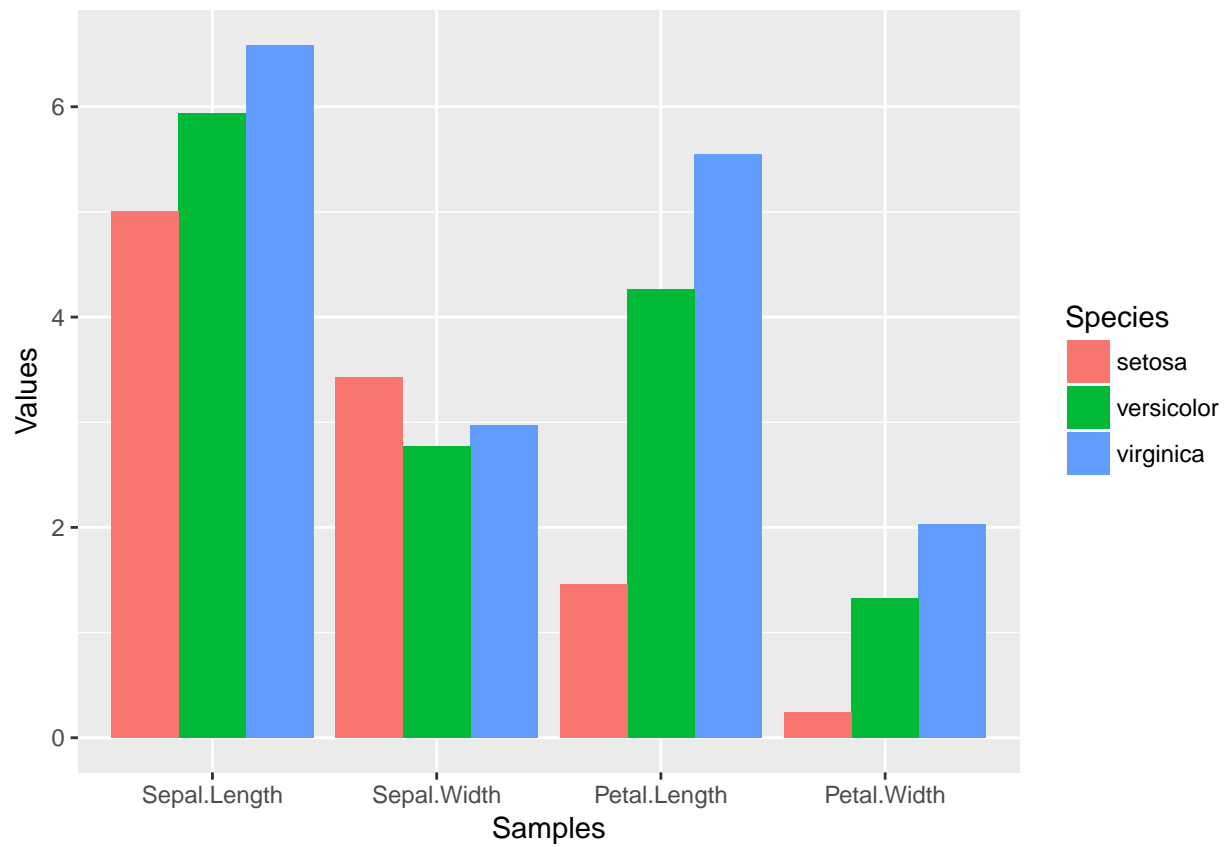
```
df_sd <- melt(iris_sd, id.vars=c("Species"), variable.name = "Samples", value.name="Values")
```

Define standard deviation limits

```
limits <- aes(ymax = df_mean[, "Values"] + df_sd[, "Values"], ymin=df_mean[, "Values"] - df_sd[, "Values"])
```

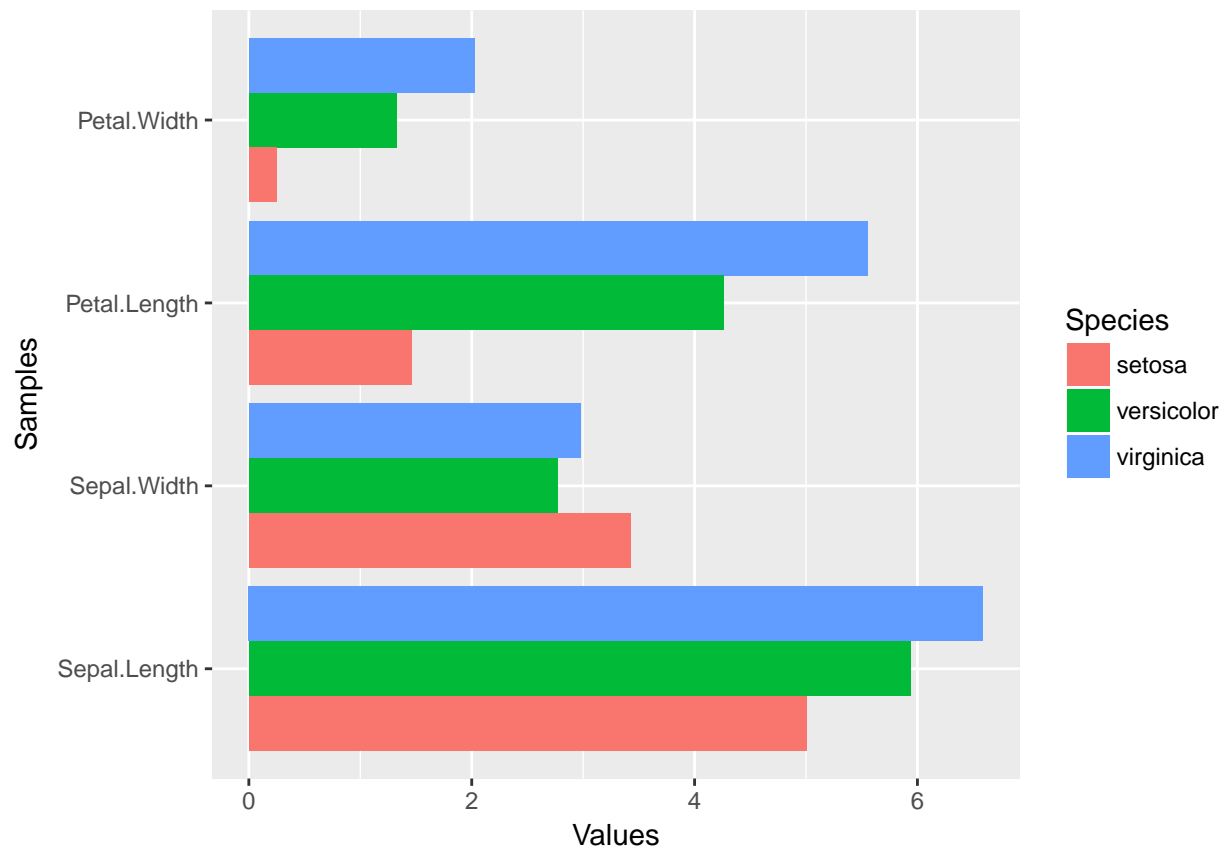
Verical orientation

```
p <- ggplot(df_mean, aes(Samples, Values, fill = Species)) +  
  geom_bar(position="dodge", stat="identity")  
print(p)
```



Horizontal orientation

```
p <- ggplot(df_mean, aes(Samples, Values, fill = Species)) +  
  geom_bar(position="dodge", stat="identity") + coord_flip() +  
  theme(axis.text.y=element_text(angle=0, hjust=1))  
print(p)
```

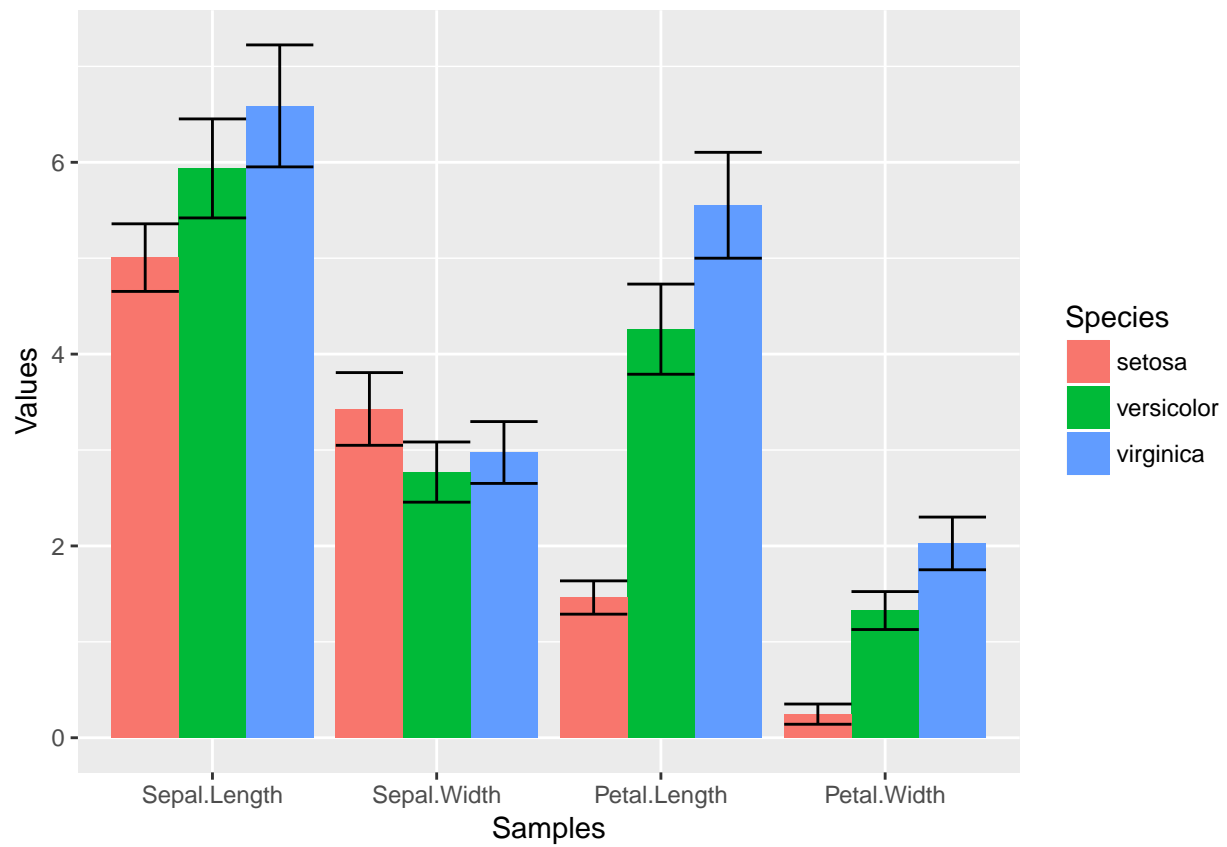


Faceting

```
p <- ggplot(df_mean, aes(Samples, Values)) + geom_bar(aes(fill = Species), stat="identity") +
  facet_wrap(~Species, ncol=1)
print(p)
```

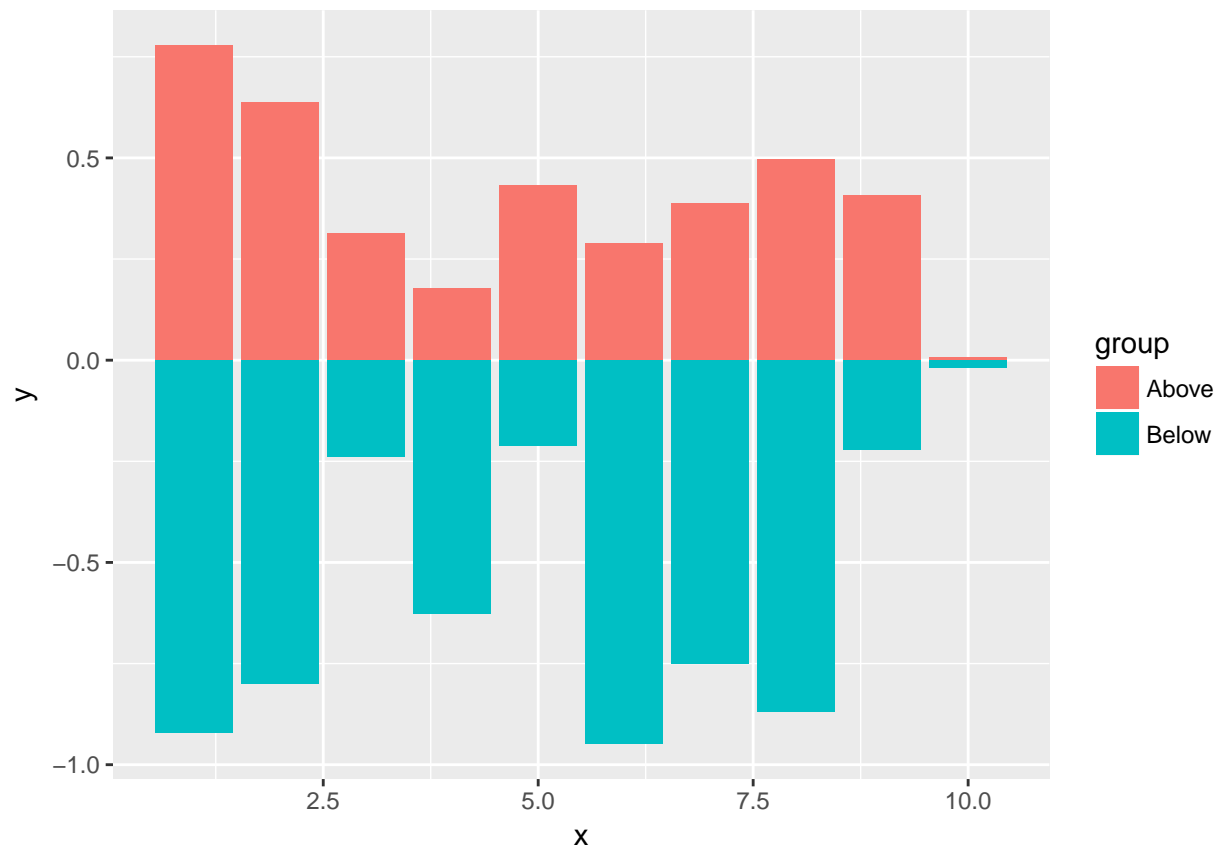
Error bars

```
p <- ggplot(df_mean, aes(Samples, Values, fill = Species)) +
  geom_bar(position="dodge", stat="identity") + geom_errorbar(limits, position="dodge")
print(p)
```



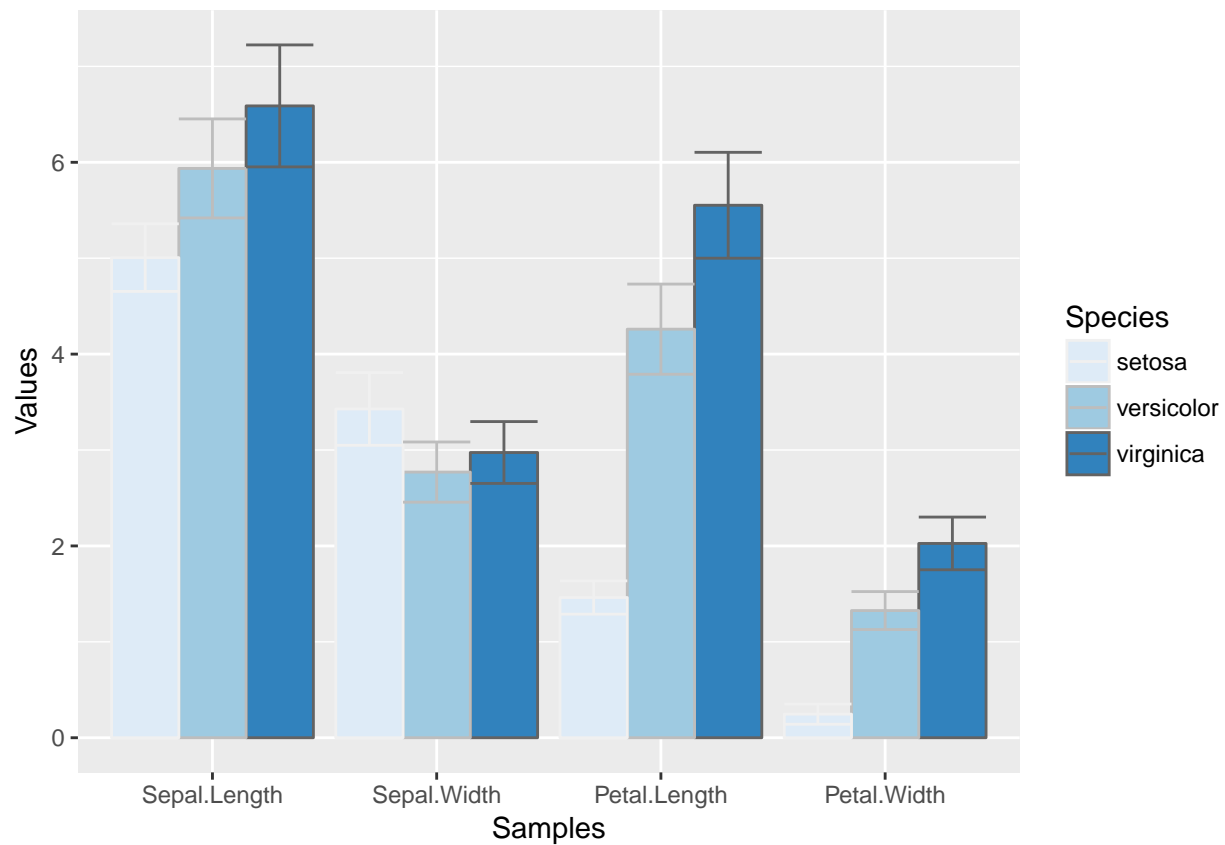
Mirrored

```
df <- data.frame(group = rep(c("Above", "Below"), each=10), x = rep(1:10, 2), y = c(runif(10, 0, 1), runif(10, 0, 1)))
p <- ggplot(df, aes(x=x, y=y, fill=group)) +
  geom_bar(stat="identity", position="identity")
print(p)
```



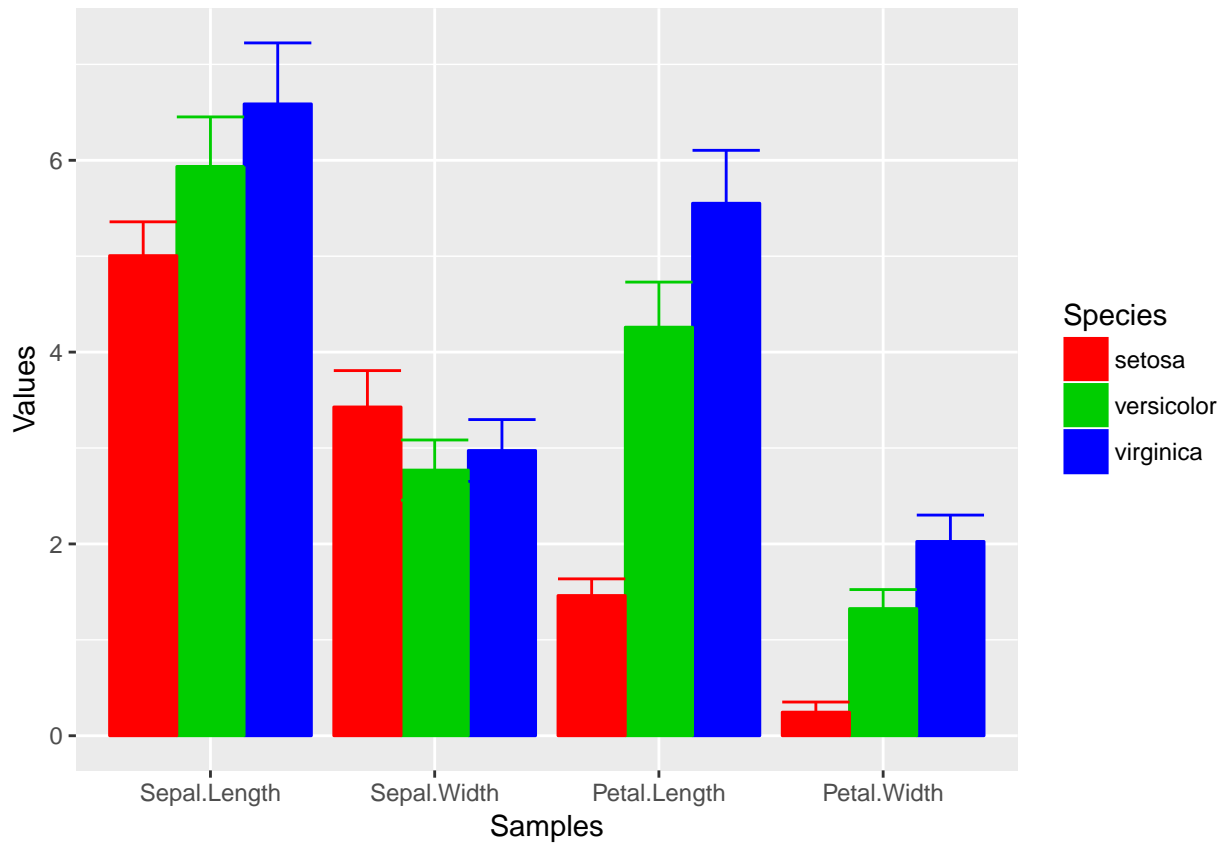
Changing Color Settings

```
library(RColorBrewer)
# display.brewer.all()
p <- ggplot(df_mean, aes(Samples, Values, fill=Species, color=Species)) +
  geom_bar(position="dodge", stat="identity") + geom_errorbar(limits, position="dodge") +
  scale_fill_brewer(palette="Blues") + scale_color_brewer(palette = "Greys")
print(p)
```



Using standard colors

```
p <- ggplot(df_mean, aes(Samples, Values, fill=Species, color=Species)) +
  geom_bar(position="dodge", stat="identity") + geom_errorbar(limits, position="dodge") +
  scale_fill_manual(values=c("red", "green3", "blue")) +
  scale_color_manual(values=c("red", "green3", "blue"))
print(p)
```



Exercise 4

Bar plots

- **Task 1:** Calculate the mean values for the `Species` components of the first four columns in the `iris` data set. Use the `melt` function from the `reshape2` package to bring the data into the expected format for `ggplot`.
- **Task 2:** Generate two bar plots: one with stacked bars and one with horizontally arranged bars.

Structure of iris data set

```
class(iris)
```

```
## [1] "data.frame"
```

```
iris[1:4,]
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
## 4         4.6         3.1         1.5         0.2   setosa
```

```
table(iris$Species)
```

```
##
##      setosa versicolor  virginica
##         50         50         50
```

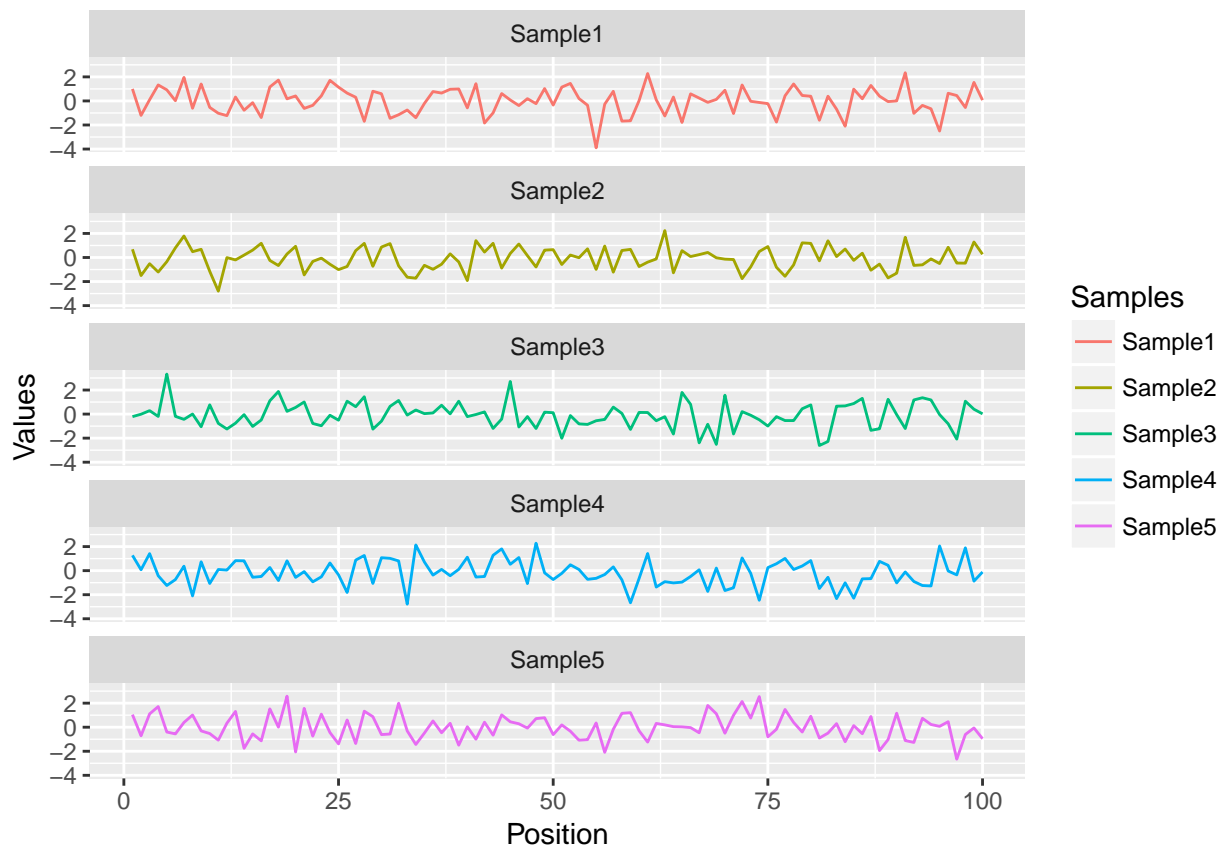
Data reformatting example

Here for line plot

```
y <- matrix(rnorm(500), 100, 5, dimnames=list(paste("g", 1:100, sep=""), paste("Sample", 1:5, sep="")))
y <- data.frame(Position=1:length(y[,1]), y)
y[1:4, ] # First rows of input format expected by melt()
```

```
##      Position  Sample1  Sample2  Sample3  Sample4  Sample5
## g1          1  1.0002088  0.6850199 -0.21324932  1.27195056  1.0479301
## g2          2 -1.2024596 -1.5004962 -0.01111579  0.07584497 -0.7100662
## g3          3  0.1023678 -0.5153367  0.28564390  1.41522878  1.1084695
## g4          4  1.3294248 -1.2084007 -0.19581898 -0.42361768  1.7139697
```

```
df <- melt(y, id.vars=c("Position"), variable.name = "Samples", value.name="Values")
p <- ggplot(df, aes(Position, Values)) + geom_line(aes(color=Samples)) + facet_wrap(~Samples, ncol=1)
print(p)
```

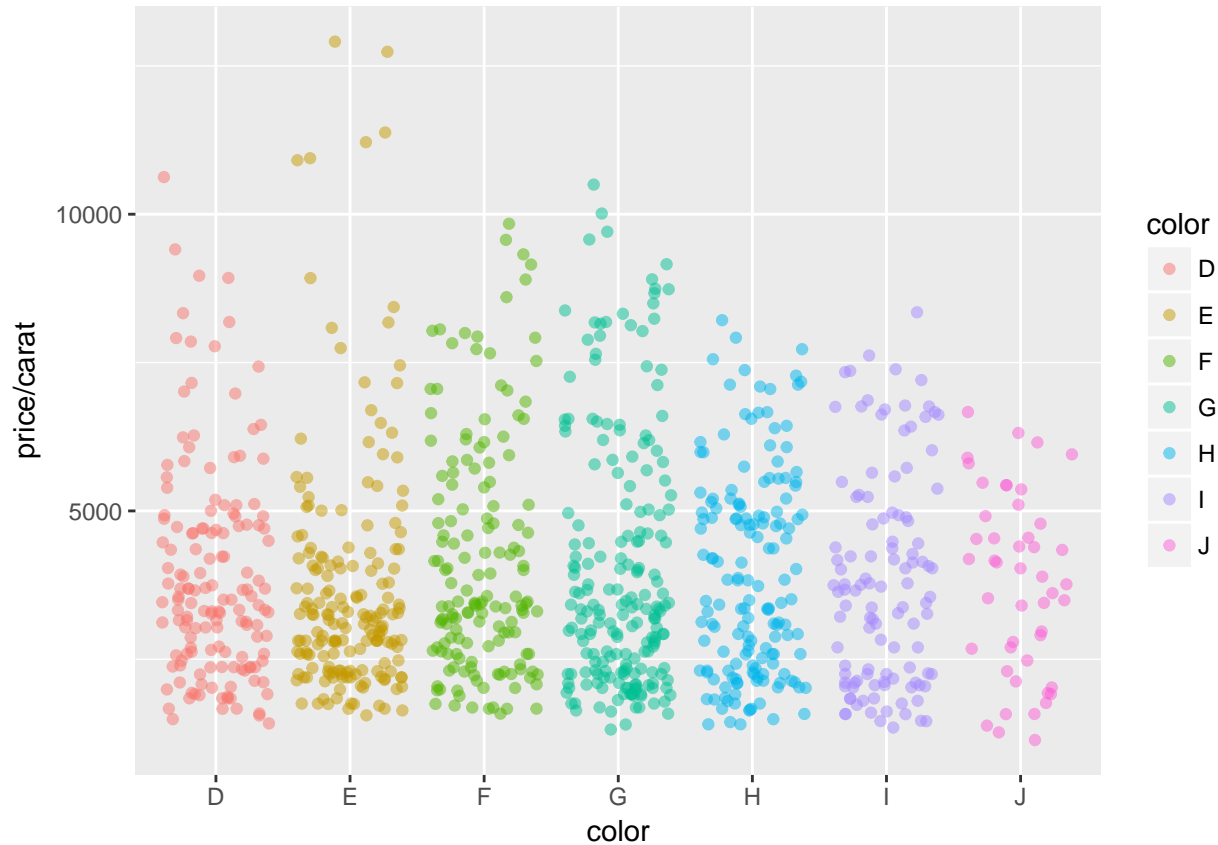


Same data can be represented in box plot as follows


```
ggplot(df, aes(Samples, Values, fill=Samples)) + geom_boxplot()
```

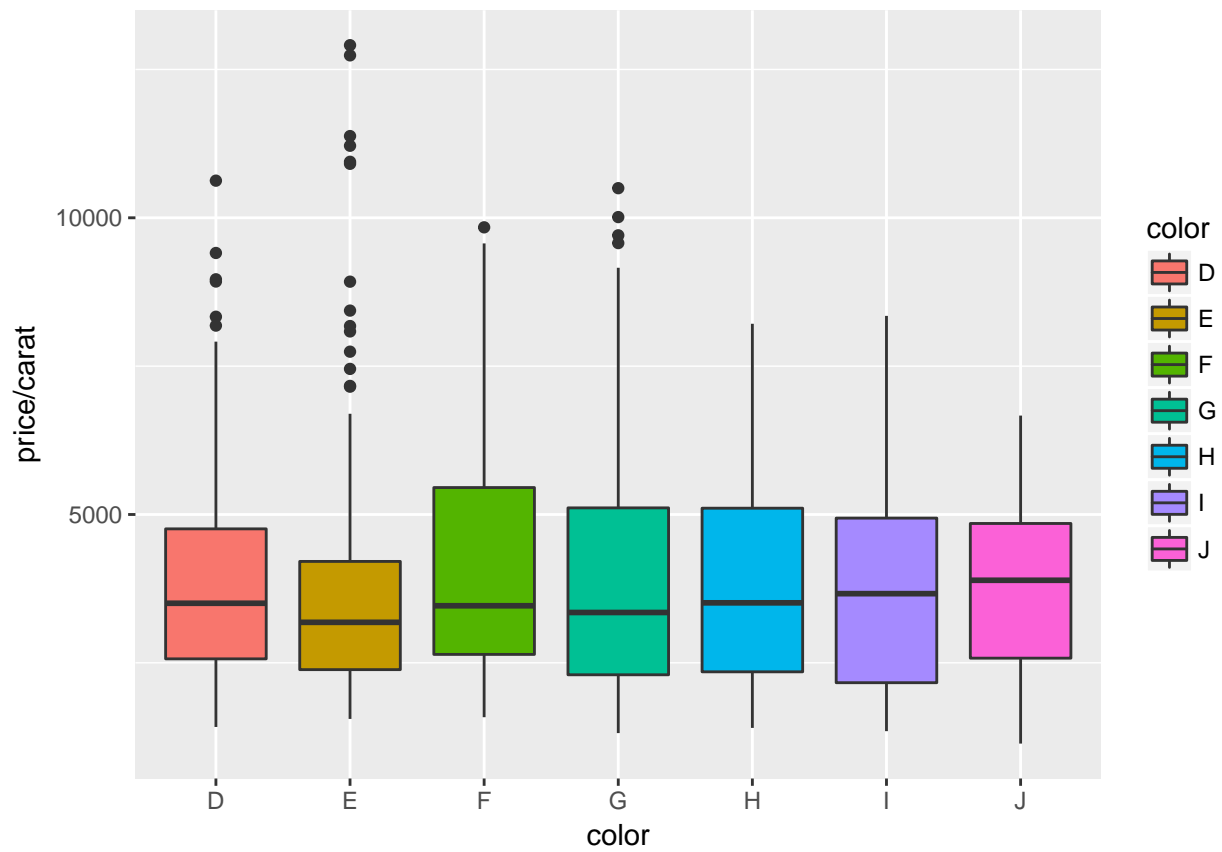
Jitter Plots

```
p <- ggplot(dsmall, aes(color, price/carat)) +  
  geom_jitter(alpha = I(1 / 2), aes(color=color))  
print(p)
```



Box plots

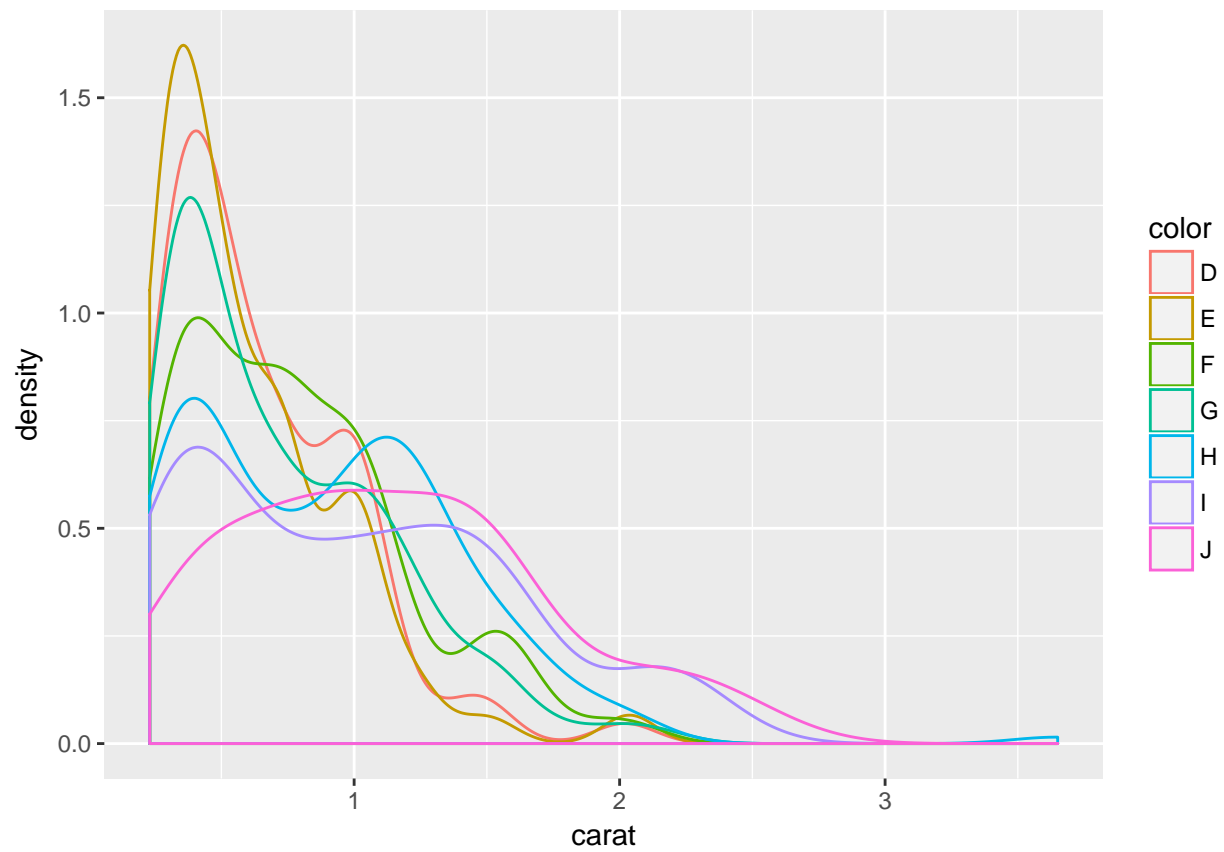
```
p <- ggplot(dsmall, aes(color, price/carat, fill=color)) + geom_boxplot()  
print(p)
```



Density plots

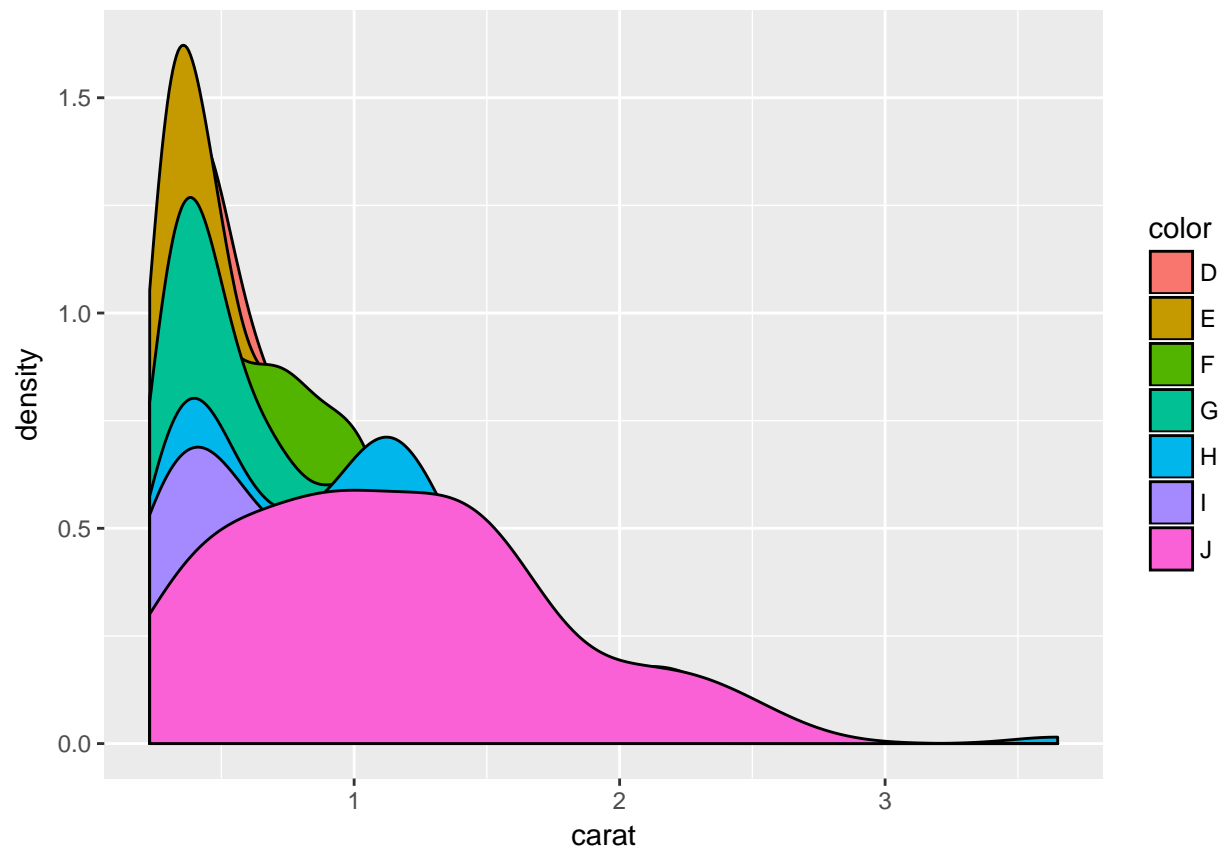
Line coloring

```
p <- ggplot(dsmall, aes(carat)) + geom_density(aes(color = color))  
print(p)
```



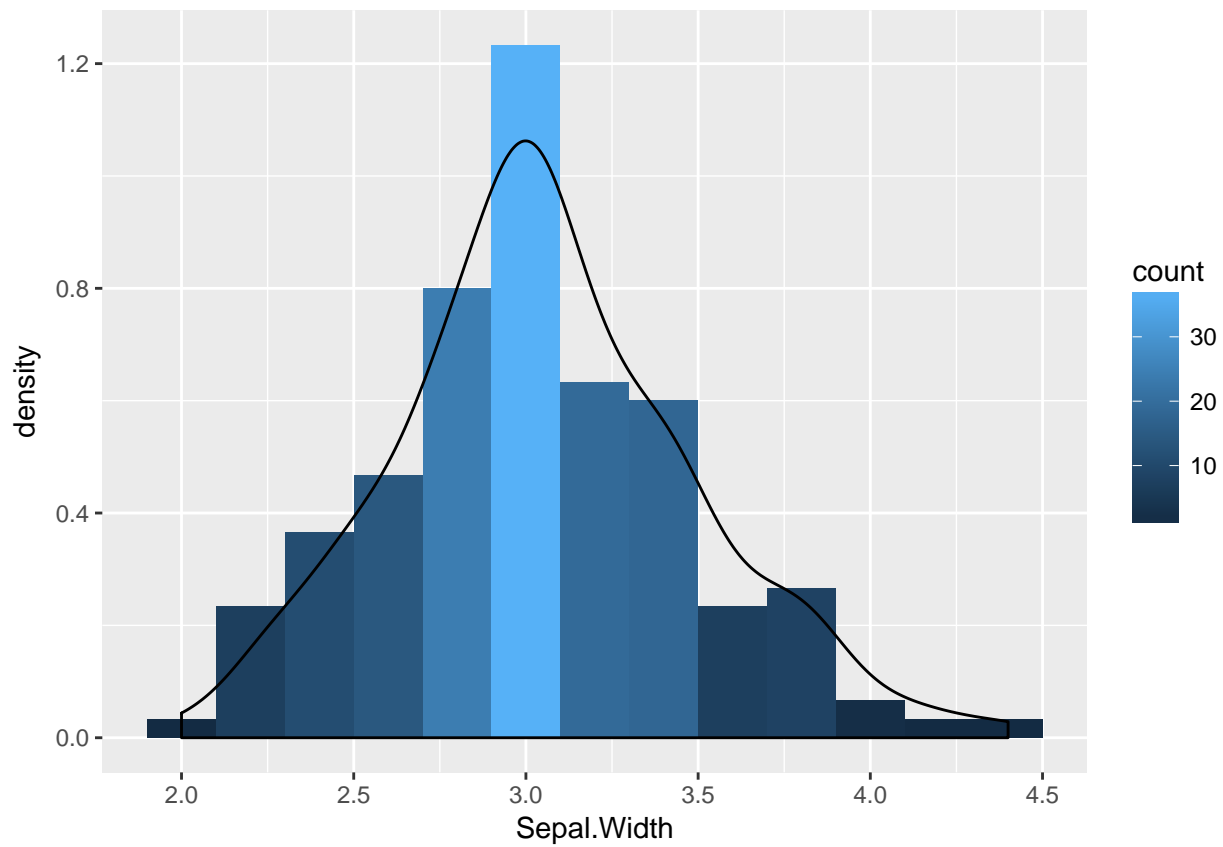
Area coloring

```
p <- ggplot(dsmall, aes(carat)) + geom_density(aes(fill = color))
print(p)
```



Histograms

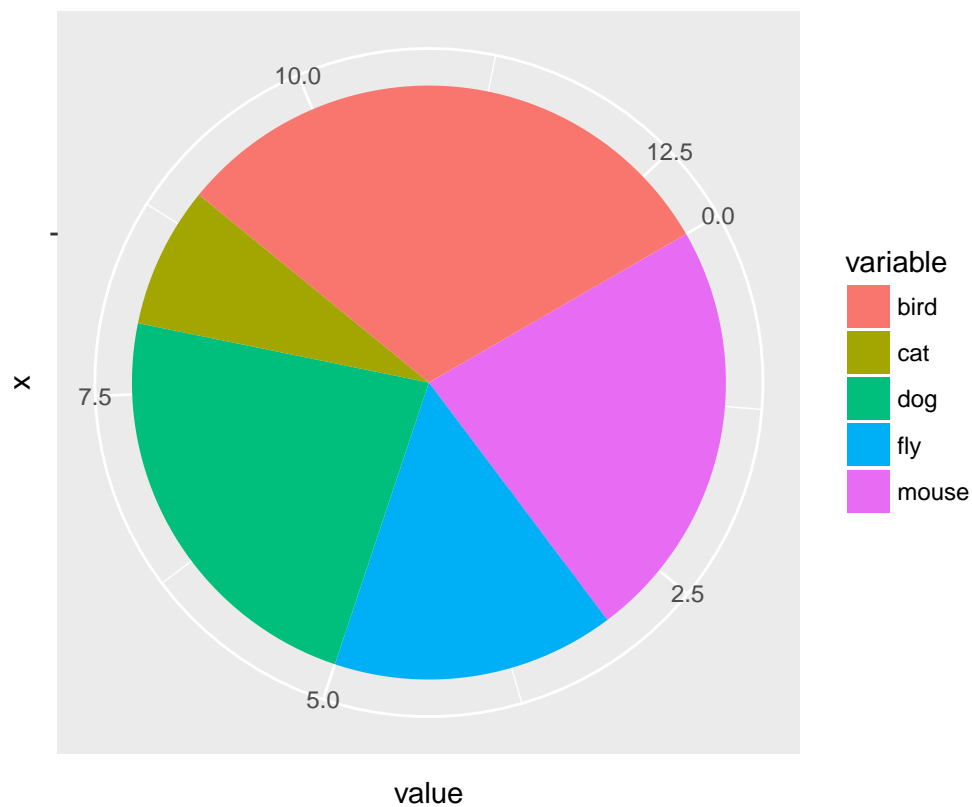
```
p <- ggplot(iris, aes(x=Sepal.Width)) + geom_histogram(aes(y = ..density..,  
  fill = ..count..), binwidth=0.2) + geom_density()  
print(p)
```



Pie Chart

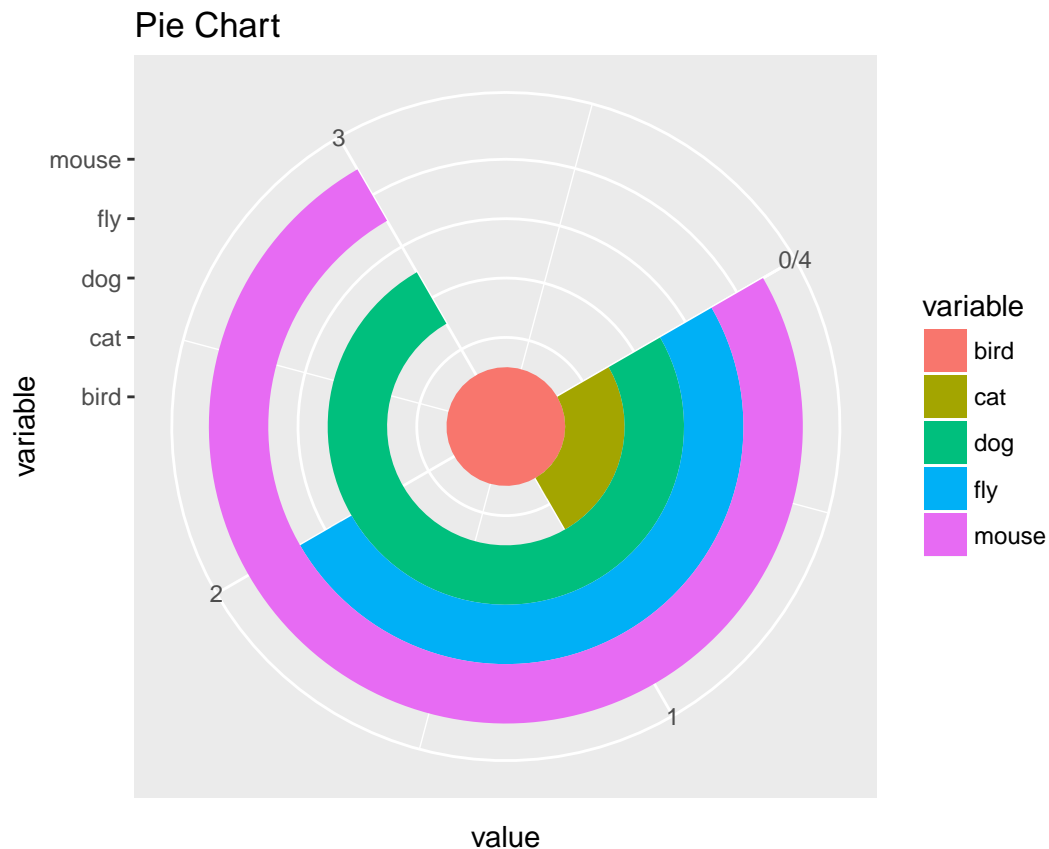
```
df <- data.frame(variable=rep(c("cat", "mouse", "dog", "bird", "fly")),
                  value=c(1,3,3,4,2))
p <- ggplot(df, aes(x = "", y = value, fill = variable)) +
  geom_bar(width = 1, stat="identity") +
  coord_polar("y", start=pi / 3) + ggtitle("Pie Chart")
print(p)
```

Pie Chart



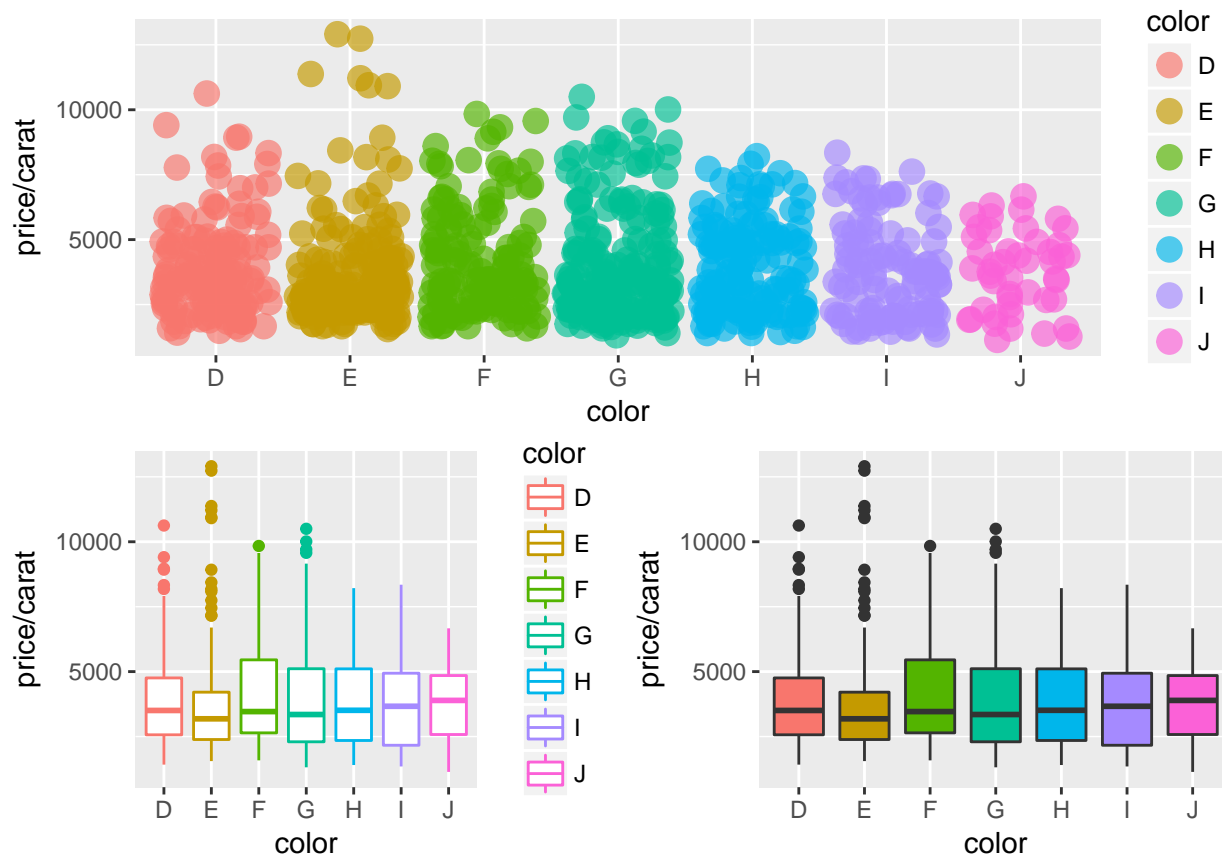
Wind Rose Pie Chart

```
p <- ggplot(df, aes(x = variable, y = value, fill = variable)) +  
  geom_bar(width = 1, stat="identity") + coord_polar("y", start=pi / 3) +  
  ggtitle("Pie Chart")  
print(p)
```



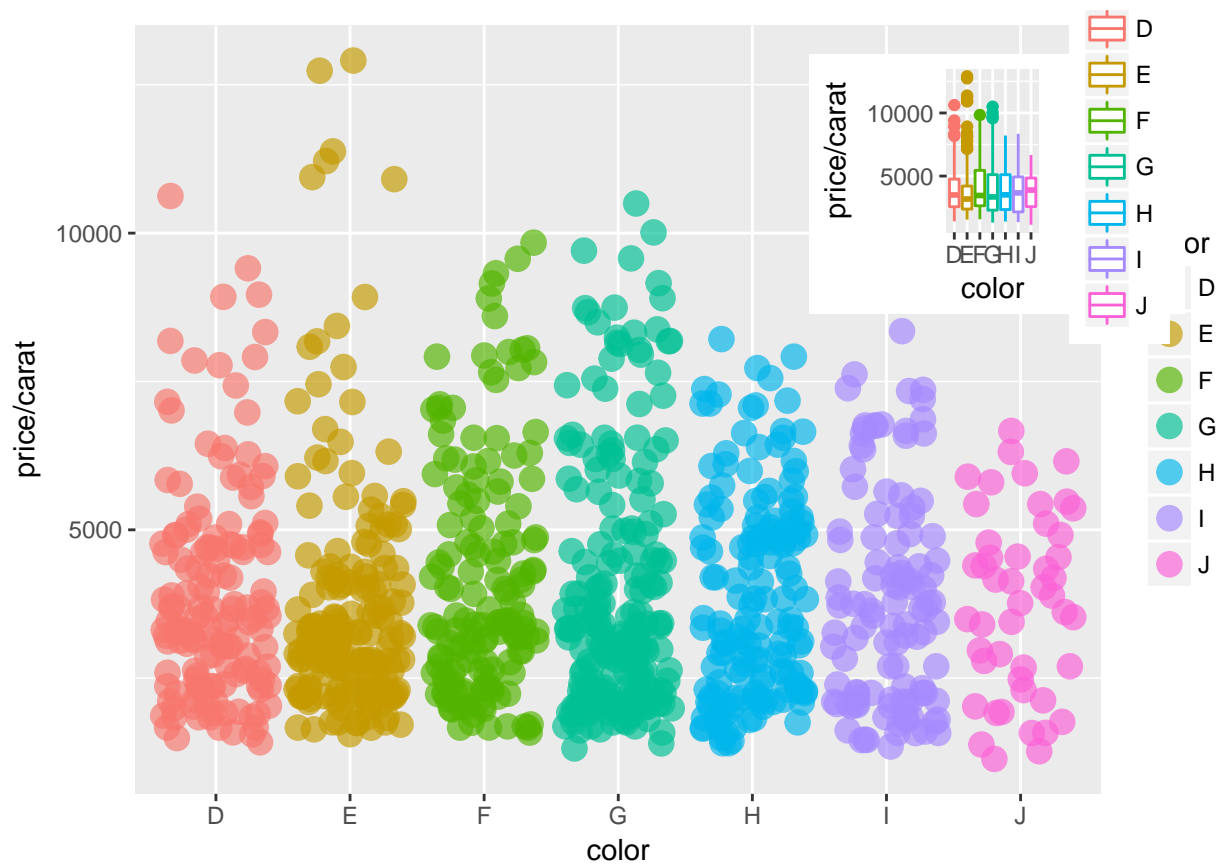
Arranging Graphics on Page

```
library(grid)
a <- ggplot(dsmall, aes(color, price/carat)) + geom_jitter(size=4, alpha = I(1 / 1.5), aes(color=color))
b <- ggplot(dsmall, aes(color, price/carat, color=color)) + geom_boxplot()
c <- ggplot(dsmall, aes(color, price/carat, fill=color)) + geom_boxplot() + theme(legend.position = "none")
grid.newpage() # Open a new page on grid device
pushViewport(viewport(layout = grid.layout(2, 2))) # Assign to device viewport with 2 by 2 grid layout
print(a, vp = viewport(layout.pos.row = 1, layout.pos.col = 1:2))
print(b, vp = viewport(layout.pos.row = 2, layout.pos.col = 1))
print(c, vp = viewport(layout.pos.row = 2, layout.pos.col = 2, width=0.3, height=0.3, x=0.8, y=0.8))
```



Inserting Graphics into Plots

```
library(grid)
print(a)
print(b, vp=viewport(width=0.3, height=0.3, x=0.8, y=0.8))
```

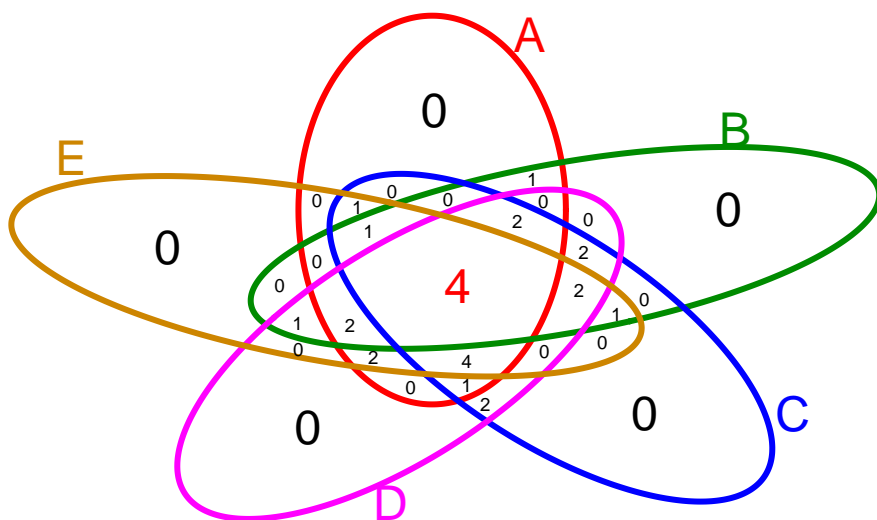



Specialty Graphics

Venn Diagrams

```
source("http://faculty.ucr.edu/~tgirke/Documents/R_BioCond/My_R_Scripts/overLapper.R")
setlist5 <- list(A=sample(letters, 18), B=sample(letters, 16), C=sample(letters, 20), D=sample(letters,
OLlist5 <- overLapper(setlist=setlist5, sep="_", type="vennsets")
counts <- sapply(OLlist5$Venn_List, length)
vennPlot(counts=counts, ccol=c(rep(1,30),2), lcex=1.5, ccex=c(rep(1.5,5), rep(0.6,25),1.5))
```

Venn Diagram



Unique objects: All = 26; S1 = 18; S2 = 16; S3 = 20; S4 = 22; S5 = 18

Compound Structures

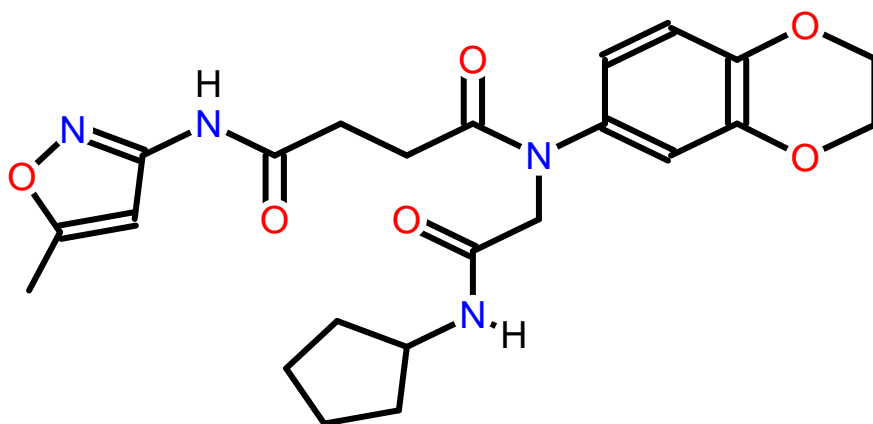
Plots depictions of small molecules with ChemmineR package

```
library(ChemmineR)
```

```
## Loading required package: methods
```

```
data(sdfsamples)  
plot(sdfsamples[1], print=FALSE)
```

CMP1



ROC Plots

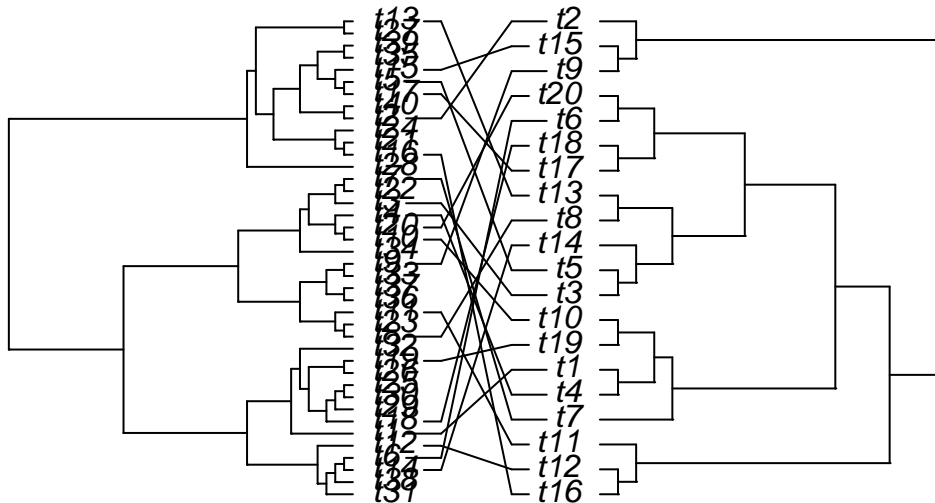
A variety of libraries are available for plotting receiver operating characteristic (ROC) curves in R:

- ROCR
- ROC
- pROC
- ggplot2

Trees

The **ape** package provides many useful utilities for phylogenetic analysis and tree plotting. Another useful package for plotting trees is **ggtree**. The following example plots two trees face to face with links to identical leaf labels.

```
library(ape)
tree1 <- rtree(40)
tree2 <- rtree(20)
association <- cbind(tree2$tip.label, tree2$tip.label)
cophyloplot(tree1, tree2, assoc = association,
             length.line = 4, space = 28, gap = 3)
```



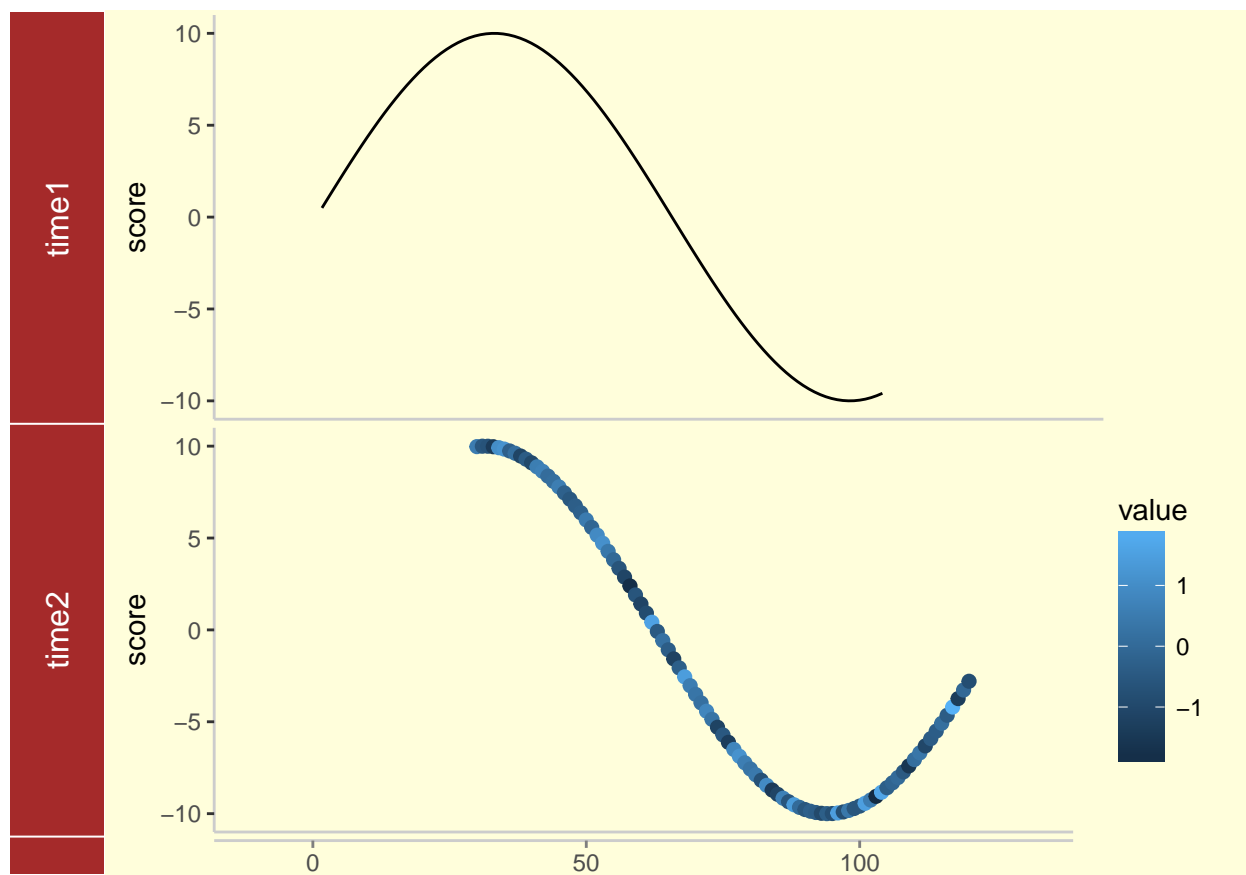
Genome Graphics

ggbio

- What is **ggbio**?
 - A programmable genome browser environment
- Genome browser concepts
 - A genome browser is a visualization tool for plotting different types of genomic data in separate tracks along chromosomes.
 - The **ggbio** package (Yin, Cook, and Lawrence 2012) facilitates plotting of complex genome data objects, such as read alignments (SAM/BAM), genomic context/annotation information (gff/txdb), variant calls (VCF/BCF), and more. To easily compare these data sets, it extends the faceting facility of **ggplot2** to genome browser-like tracks.
 - Most of the core object types for handling genomic data with R/Bioconductor are supported: **GRanges**, **GAlignments**, **VCF**, etc. For more details, see Table 1.1 of the **ggbio** vignette here.
 - **ggbio**'s convenience plotting function is **autoplot**. For more customizable plots, one can use the generic **ggplot** function.
 - Apart from the standard **ggplot2** plotting components, **ggbio** defines several new components useful for genomic data visualization. A detailed list is given in Table 1.2 of the vignette here.
 - Useful web sites:
 - * **ggbio** manual
 - * **ggbio** functions
 - * **autoplot** demo

Tracks: aligning plots along chromosomes

```
library(ggbio)
df1 <- data.frame(time = 1:100, score = sin((1:100)/20)*10)
p1 <- qplot(data = df1, x = time, y = score, geom = "line")
df2 <- data.frame(time = 30:120, score = sin((30:120)/20)*10, value = rnorm(120-30 +1))
p2 <- ggplot(data = df2, aes(x = time, y = score)) + geom_line() + geom_point(size = 2, aes(color = value))
tracks(time1 = p1, time2 = p2) + xlim(1, 40) + theme_tracks_sunset()
```



Plotting genomic ranges

GRanges objects are essential for storing alignment or annotation ranges in R/Bioconductor. The following creates a sample **GRanges** object and plots its content.

```
library(GenomicRanges)
```

```
## Loading required package: stats4
```

```
## Loading required package: S4Vectors
```

```
##
```

```
## Attaching package: 'S4Vectors'
```

```
## The following object is masked from 'package:ChemmineR':
```

```
##
```

```
## fold
```

```
## The following object is masked from 'package:base':
```

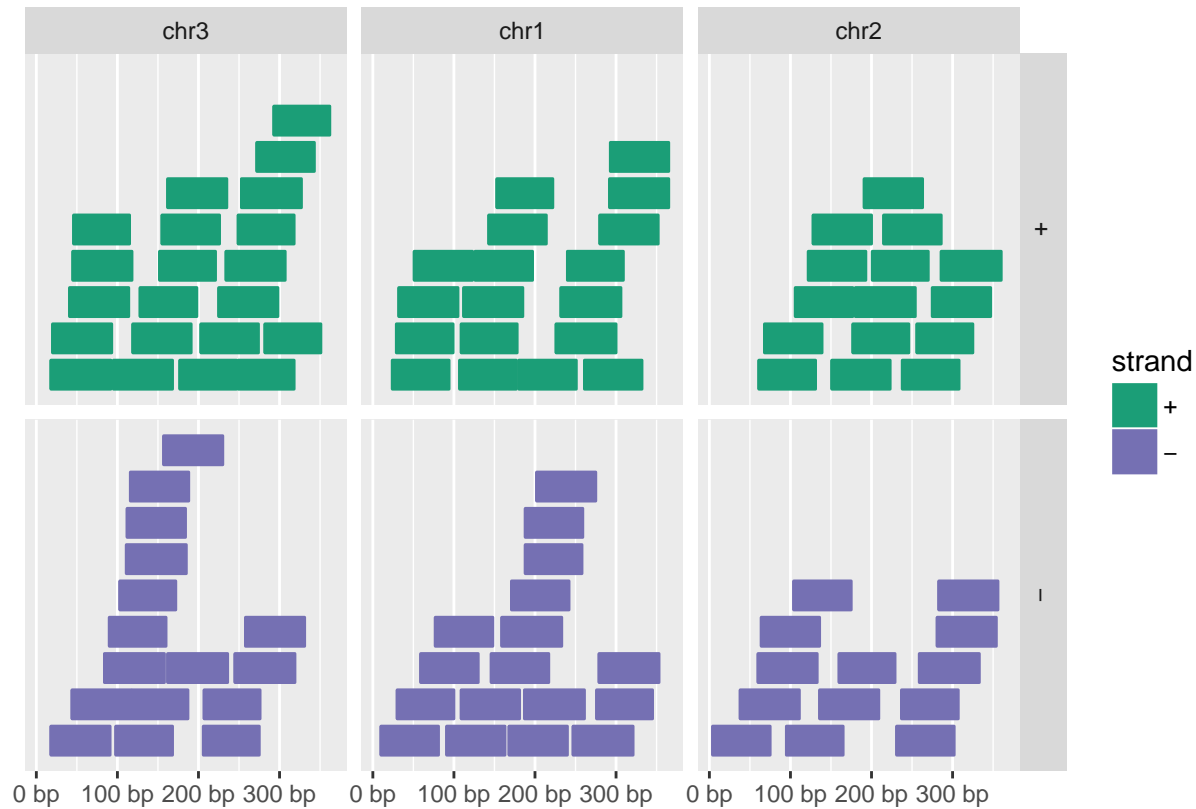
```
##
```

```
## expand.grid
```

```
## Loading required package: IRanges
```

```
## Loading required package: GenomeInfoDb
```

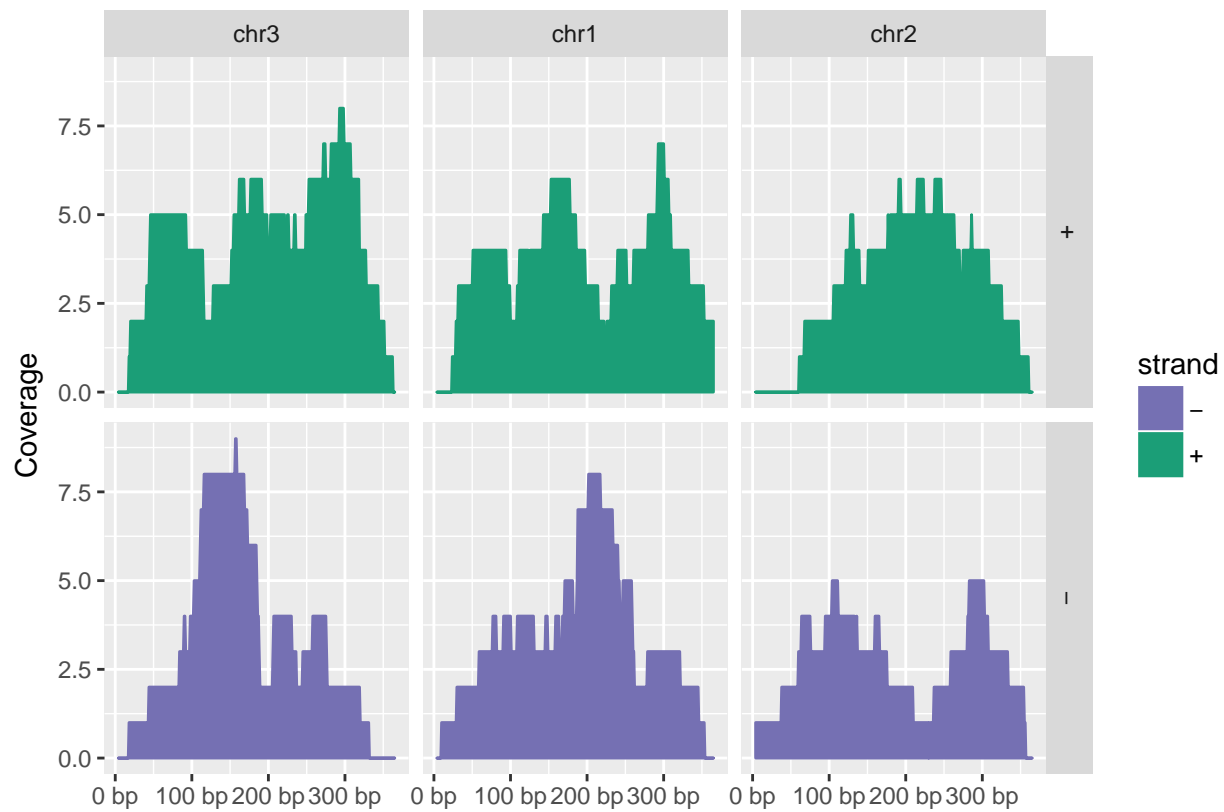
```
set.seed(1); N <- 100; gr <- GRanges(seqnames = sample(c("chr1", "chr2", "chr3"), size = N, replace = T),
autoplot(gr, aes(color = strand, fill = strand), facets = strand ~ seqnames)
```



Plotting coverage

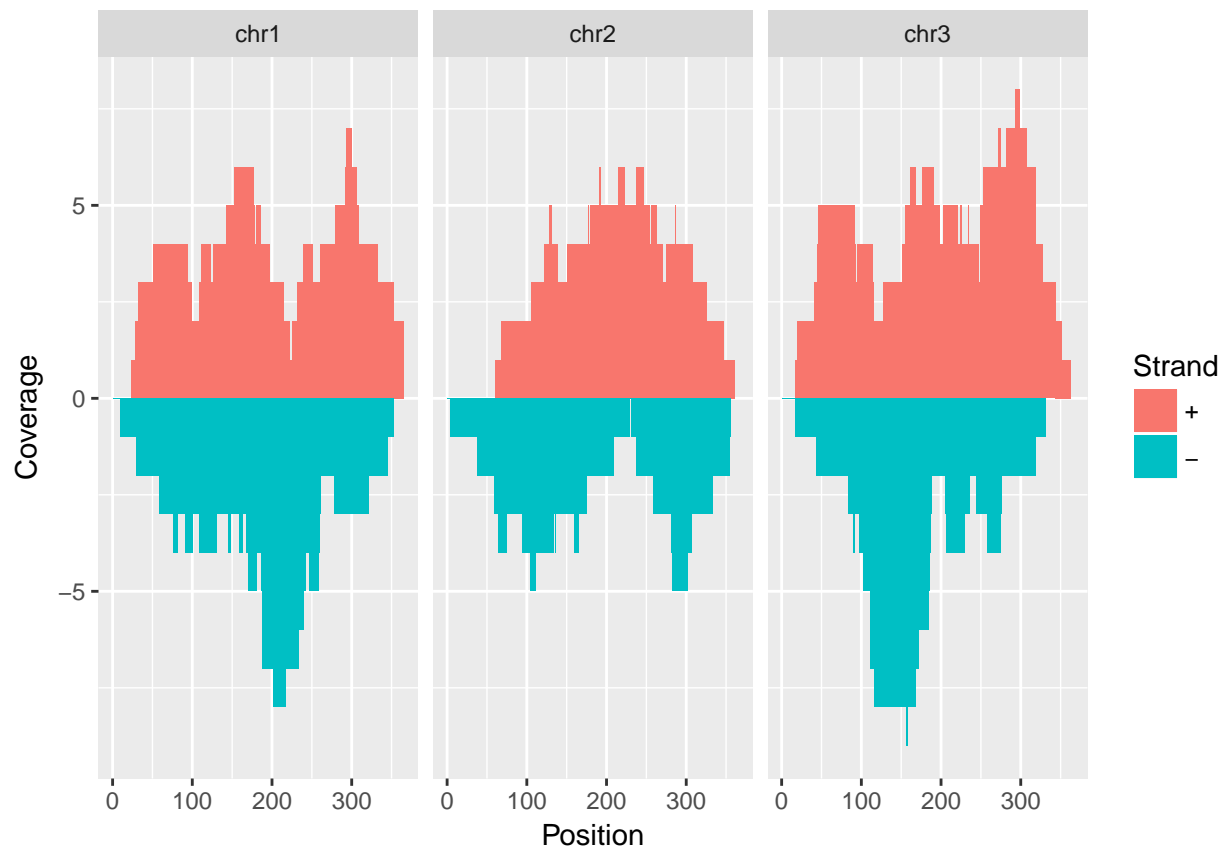
```
autoplot(gr, aes(color = strand, fill = strand), facets = strand ~ seqnames, stat = "coverage")
```

```
## Scale for 'x' is already present. Adding another scale for 'x', which will replace the existing
## scale.
```



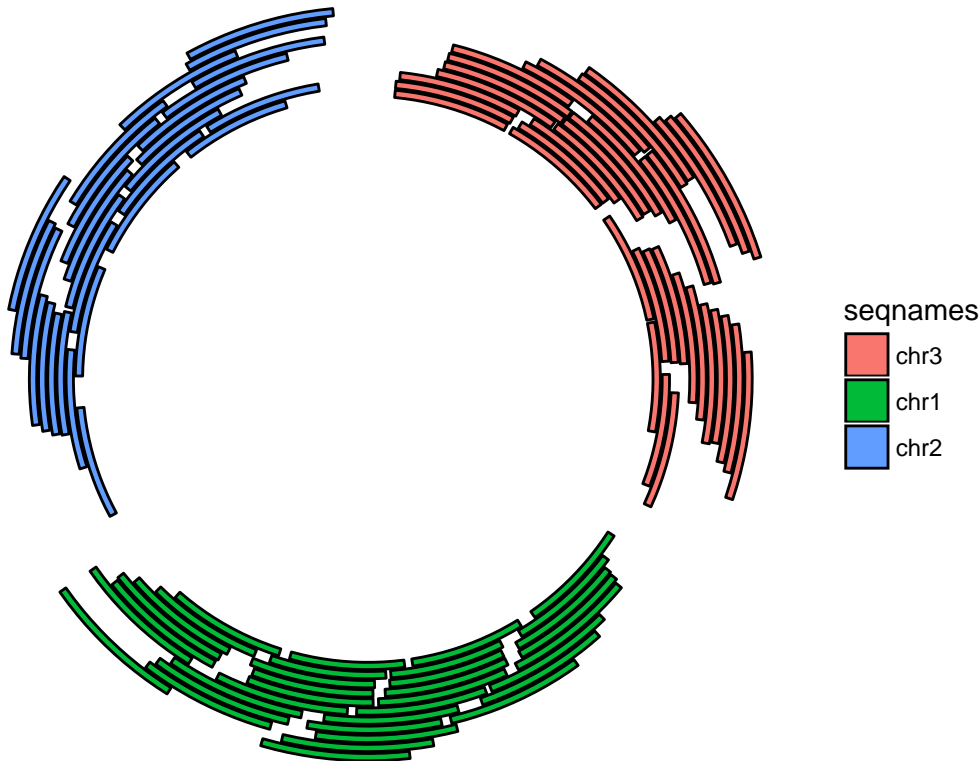
Mirrored coverage

```
pos <- sapply(coverage(gr[strand(gr)=="+"]), as.numeric)
pos <- data.frame(Chr=rep(names(pos), sapply(pos, length)), Strand=rep("+", length(unlist(pos))), Position=rep(1:length(pos), sapply(pos, length)))
neg <- sapply(coverage(gr[strand(gr)=="-"]), as.numeric)
neg <- data.frame(Chr=rep(names(neg), sapply(neg, length)), Strand=rep("-", length(unlist(neg))), Position=rep(1:length(neg), sapply(neg, length)))
covdf <- rbind(pos, neg)
p <- ggplot(covdf, aes(Position, Coverage, fill=Strand)) +
  geom_bar(stat="identity", position="identity") + facet_wrap(~Chr)
p
```



Circular genome plots

```
ggplot(gr) + layout_circle(aes(fill = seqnames), geom = "rect")
```

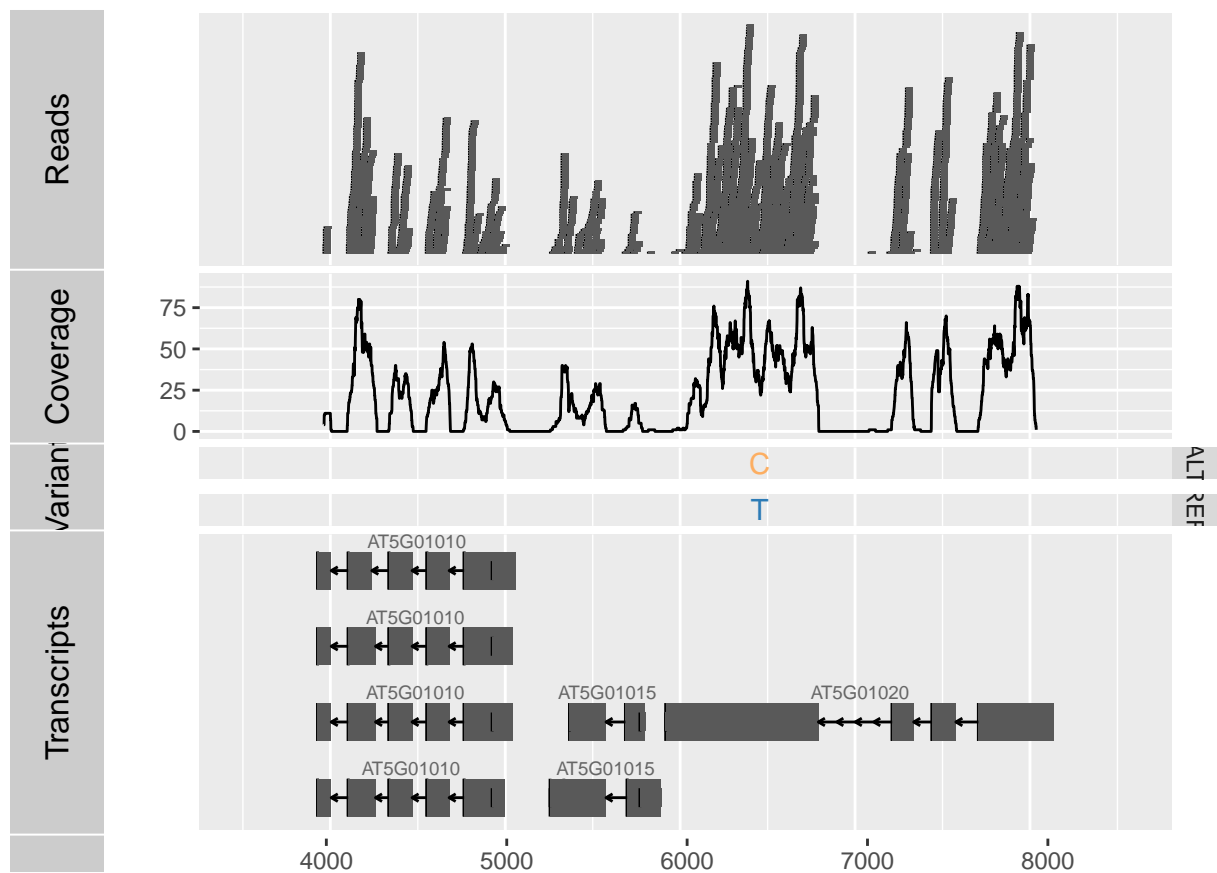
More complex circular example

```
seqlengths(gr) <- c(400, 500, 700)
values(gr)$to.gr <- gr[sample(1:length(gr), size = length(gr))]
idx <- sample(1:length(gr), size = 50)
gr <- gr[idx]
ggplot() + layout_circle(gr, geom = "ideo", fill = "gray70", radius = 7, trackWidth = 3) +
  layout_circle(gr, geom = "bar", radius = 10, trackWidth = 4,
    aes(fill = score, y = score)) +
  layout_circle(gr, geom = "point", color = "red", radius = 14,
    trackWidth = 3, grid = TRUE, aes(y = score)) +
  layout_circle(gr, geom = "link", linked.to = "to.gr", radius = 6, trackWidth = 1)
```

Alignments and variants

To make the following example work, please download and unpack this data archive containing GFF, BAM and VCF sample files.

```
library(rtracklayer); library(GenomicFeatures); library(Rsamtools); library(GenomicAlignments); library(GenomicAlignments)
ga <- readGAlignments("./data/SRR064167.fastq.bam", use.names=TRUE, param=ScanBamParam(which=GRanges("Chr5")))
p1 <- autoplot(ga, geom = "rect")
p2 <- autoplot(ga, geom = "line", stat = "coverage")
vcf <- readVcf(file="data/varianttools_gnsap.vcf", genome="ATH1")
p3 <- autoplot(vcf[seqnames(vcf)=="Chr5"], type = "fixed") + xlim(4000, 8000) + theme(legend.position = "bottom")
txdb <- makeTxDbFromGFF(file="./data/TAIR10_GFF3_trunc.gff", format="gff3")
p4 <- autoplot(txdb, which=GRanges("Chr5", IRanges(4000, 8000)), names.expr = "gene_id")
tracks(Reads=p1, Coverage=p2, Variant=p3, Transcripts=p4, heights = c(0.3, 0.2, 0.1, 0.35)) + ylab("")
```



Additional examples

See autoplot demo [here](#)

Additional genome graphics

- Gviz
- RCircos (Zhang, Meltzer, and Davis 2013)
- Genome Graphs
- genoPlotR

Genome Browser: IGV

View genome data in IGV

- Download and open IGV
- Select in menu in top left corner *A. thaliana* (TAIR10)
- Upload the following indexed/sorted Bam files with File -> Load from URL...

http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rnaseq/results/SRR064

http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rnaseq/results/SRR064

http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rnaseq/results/SRR064

http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rnaseq/results/SRR064

- To view area of interest, enter its coordinates Chr1:49,457-51,457 in position menu on top.

Create symbolic links

For viewing BAM files in IGV as part of `systemPipeR` workflows.

- `systemPipeR`: utilities for building NGS analysis pipelines

```
library("systemPipeR")
symLink2bam(sysargs=args, htmldir=c("~/html/", "somedir/"),
            urlbase="http://myserver.edu/~username/",
            urlfile="IGVurl.txt")
```

Controlling IGV from R

Note this may not work on all systems.

```
library(SRadb)
startIGV("lm")
sock <- IGVsocket()
session <- IGVsession(files=myurls,
                      sessionFile="session.xml",
                      genome="A. thaliana (TAIR10)")
IGVload(sock, session)
IGVgoto(sock, 'Chr1:45296-47019')
```

References

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