Graphics and Data Visualization in R

Data Analysis in Genome Biology
GEN242

Thomas Girke

May 21, 2015

Outline

Graphics in R

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

Documentation on Graphics in R

General

- Graphics Task Page Link
- R Graph Gallery Link
- R Graphical Manual Link
- Paul Murrell's book R (Grid) Graphics Link

Interactive graphics

- rggobi (GGobi) Link
- iplots Link
- Open GL (rgl) Link

Graphics Environments

Viewing and saving graphics in R

- On-screen graphics
- postscript, pdf, svg
- jpeg/png/wmf/tiff/...

Four major graphic environments

- Low-level infrastructure
  - R Base Graphics (low- and high-level)
  - *grid*: Manual Link, Book Link
- High-level infrastructure
  - *lattice:* Manual Link, Intro Link, Book Link
  - *ggplot2:* Manual Link, Intro Link, Book Link

Outline

Outline

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 multivariant data

Help on these functions

- `?myfct`
- `?plot`
- `?par`

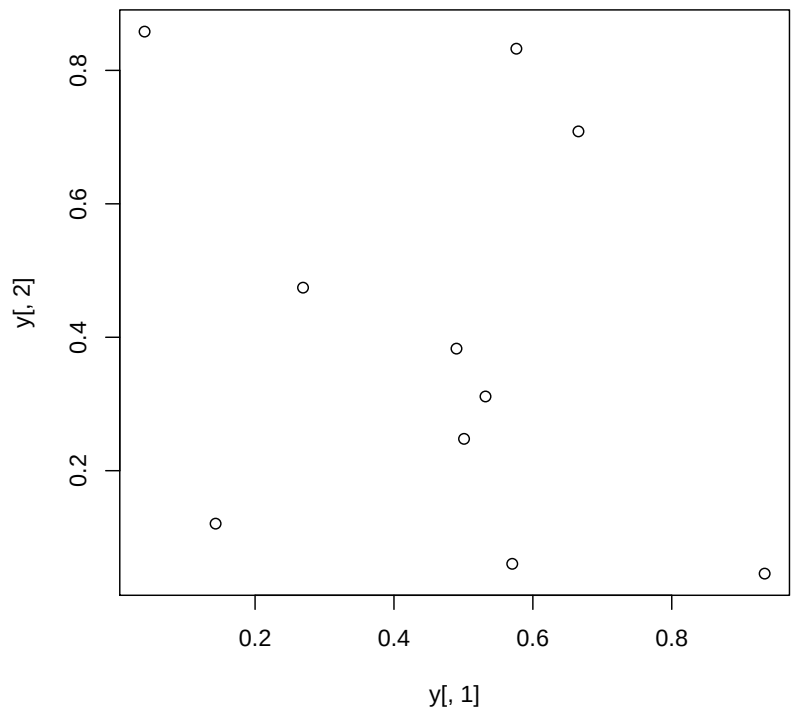
Base Graphics: Preferred Input Data Objects

- Matrices and data frames
- Vectors
- Named vectors

Scatter Plot: very basic

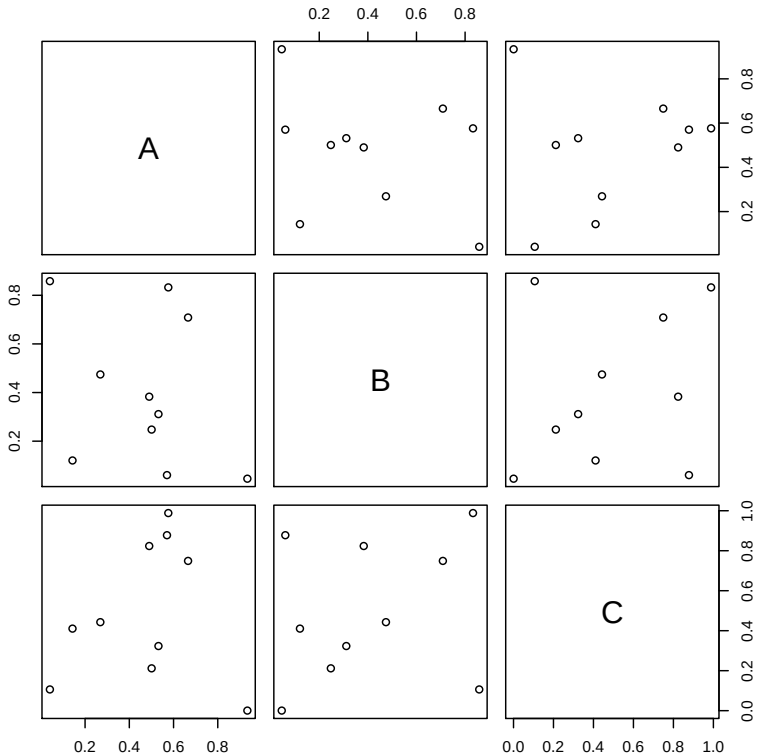
Sample data set for subsequent plots

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

> plot(y[,1], y[,2])
```



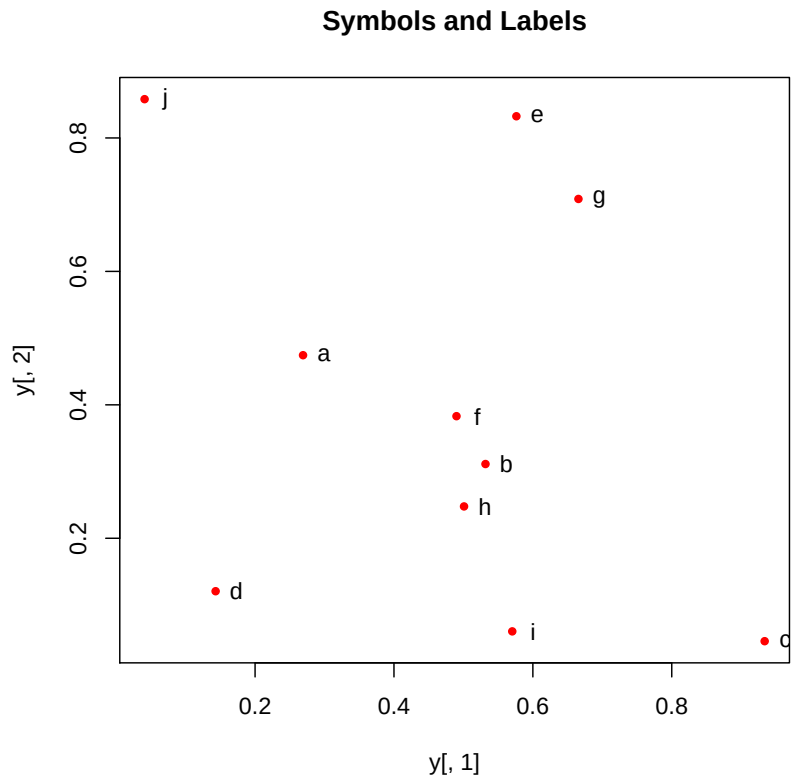
Scatter Plot: all pairs

```
> pairs(y)
```



Scatter Plot: with labels

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



Scatter Plots: 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`

Scatter Plots: more examples

Add a regression line to a plot

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

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: Scatter Plots

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

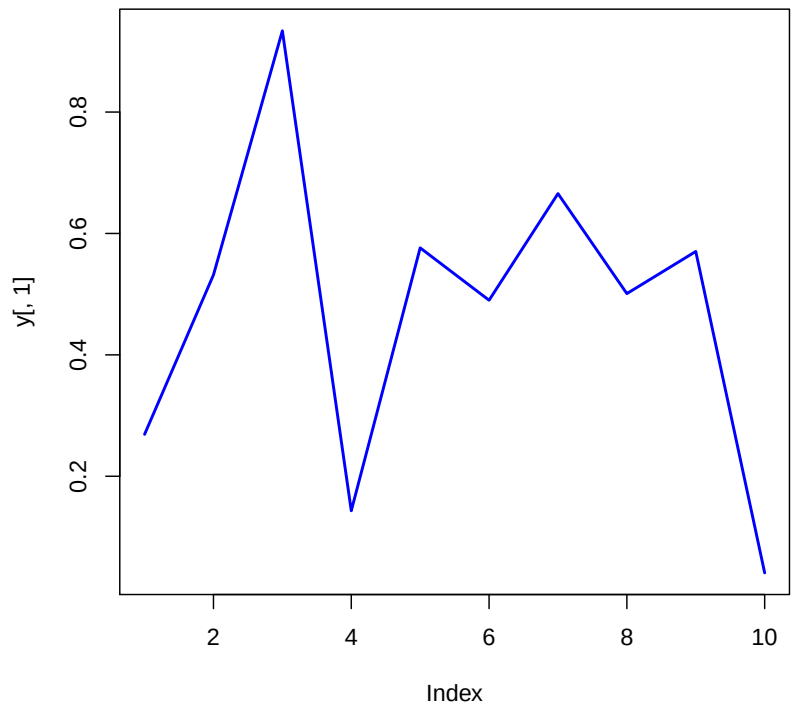
Task 2 Use the `xlim/ylim` arguments to set limits on the x- and y-axes so that all data points are restricted to the left bottom quadrant of the plot.

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
```

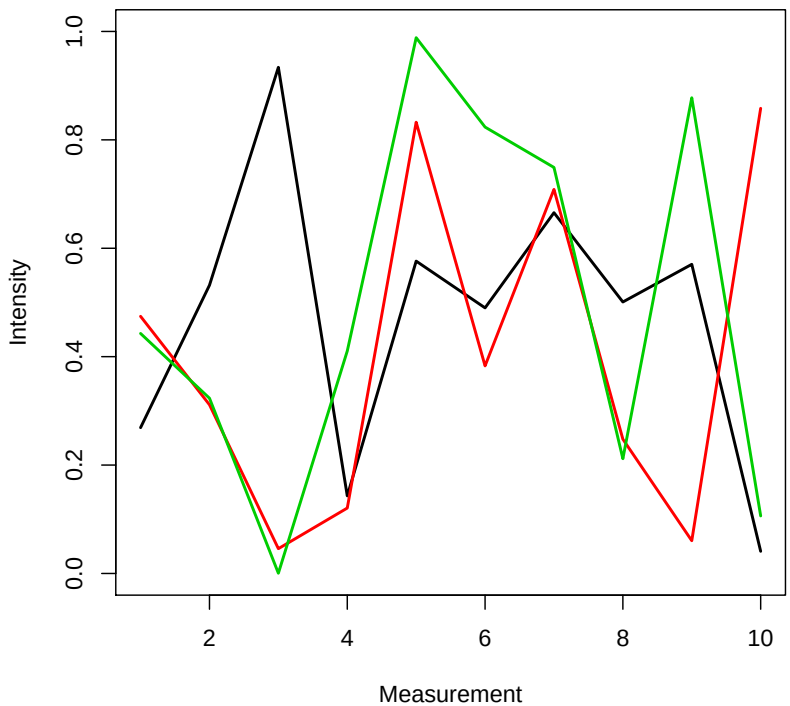
Line Plot: Single Data Set

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



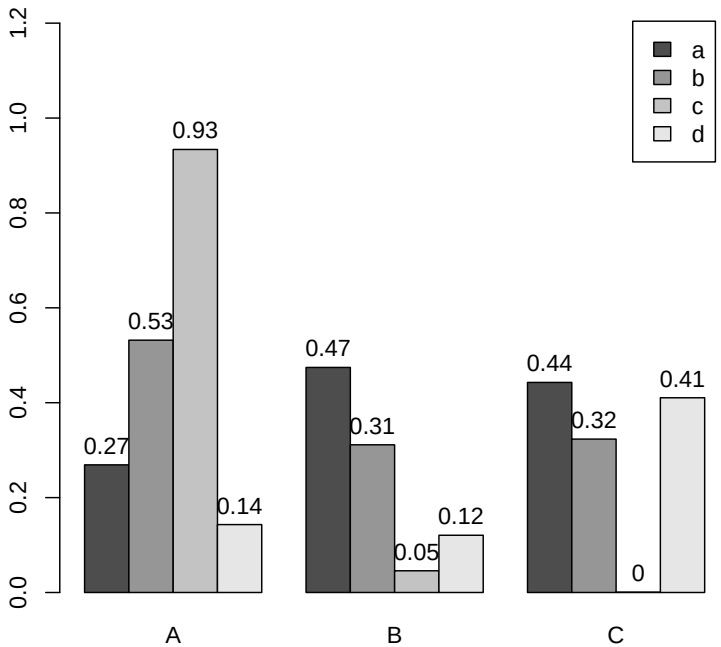
Line Plots: Many Data Sets

```
> 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[1,])) {
+         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)
```



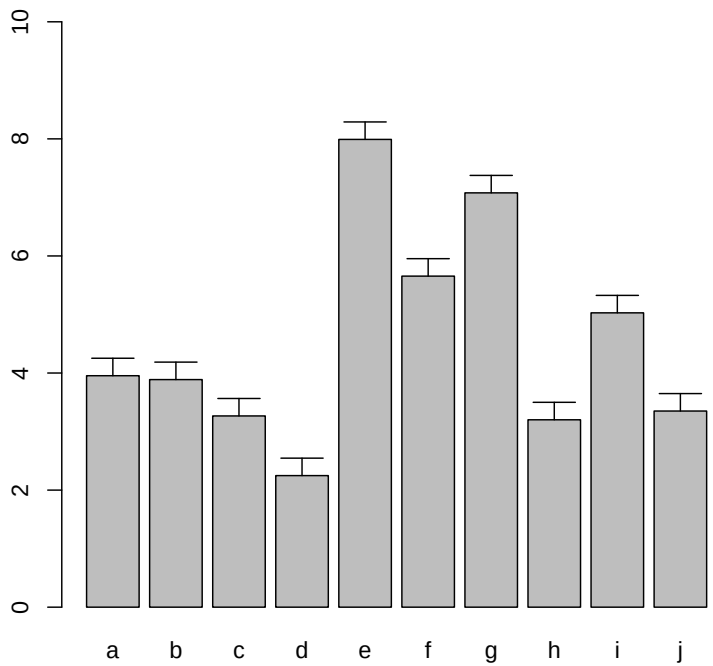
Bar Plot Basics

```
> 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)
```



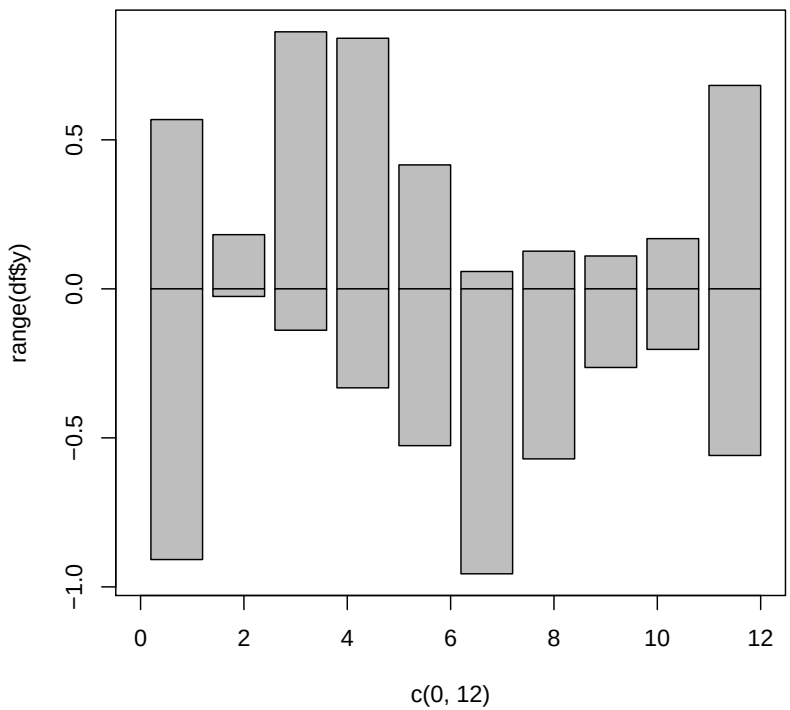
Bar Plots with Error Bars

```
> 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)
```



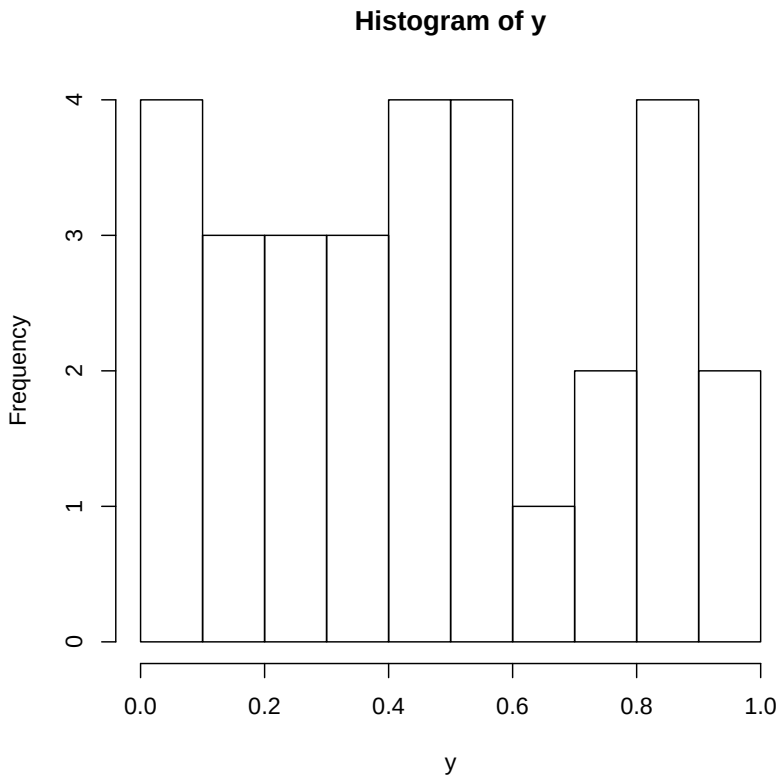
Mirrored Bar Plots

```
> df <- data.frame(group = rep(c("Above", "Below"), each=10), x = rep(1:10, 2),
> 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)
```



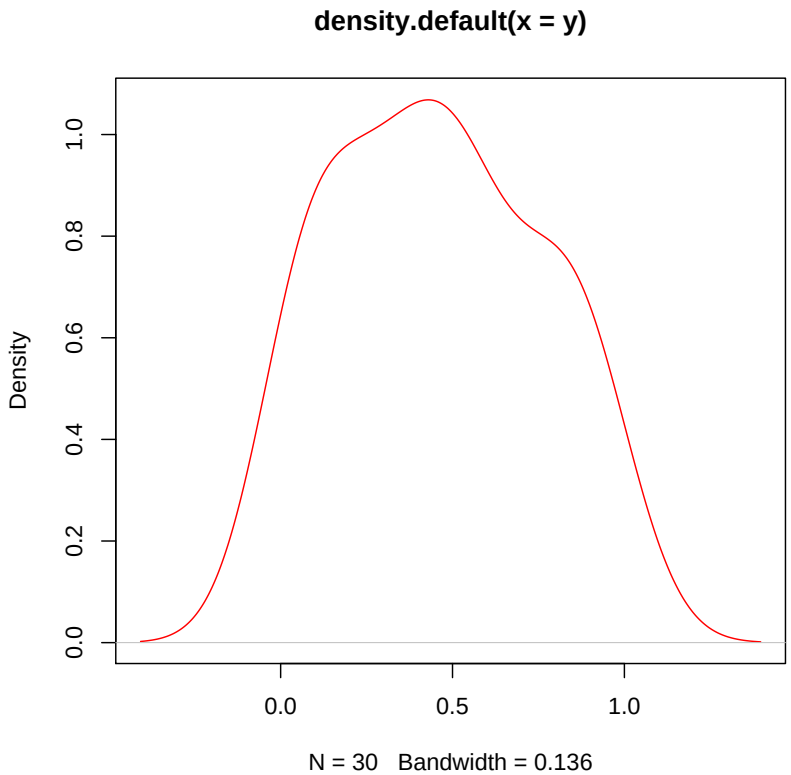
Histograms

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



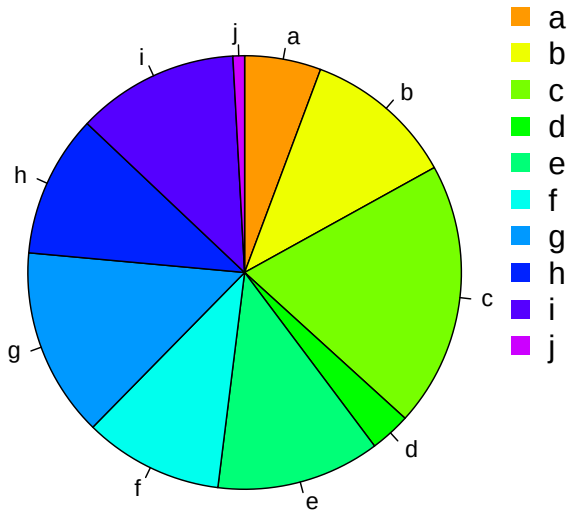
Density Plots

```
> 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

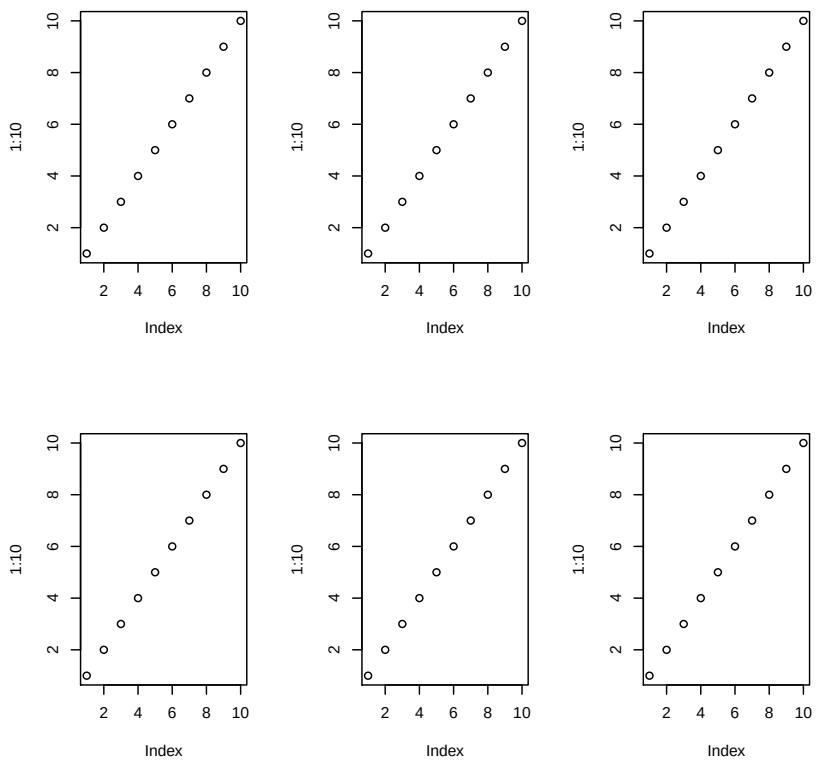
```
> library(gplots)
> colorpanel(5, "darkblue", "yellow", "white")
```

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

Arranging Several Plots on Single Page

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

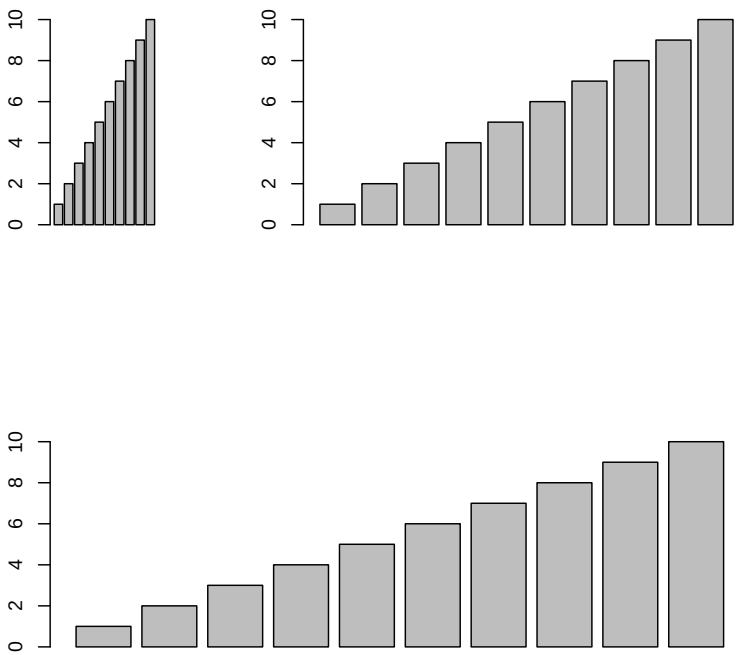
```
> par(mfrow=c(2,3)); for(i in 1:6) { plot(1:10) }
```



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
```

Outline

grid Graphics Environment

- 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 Link
  - Book Link

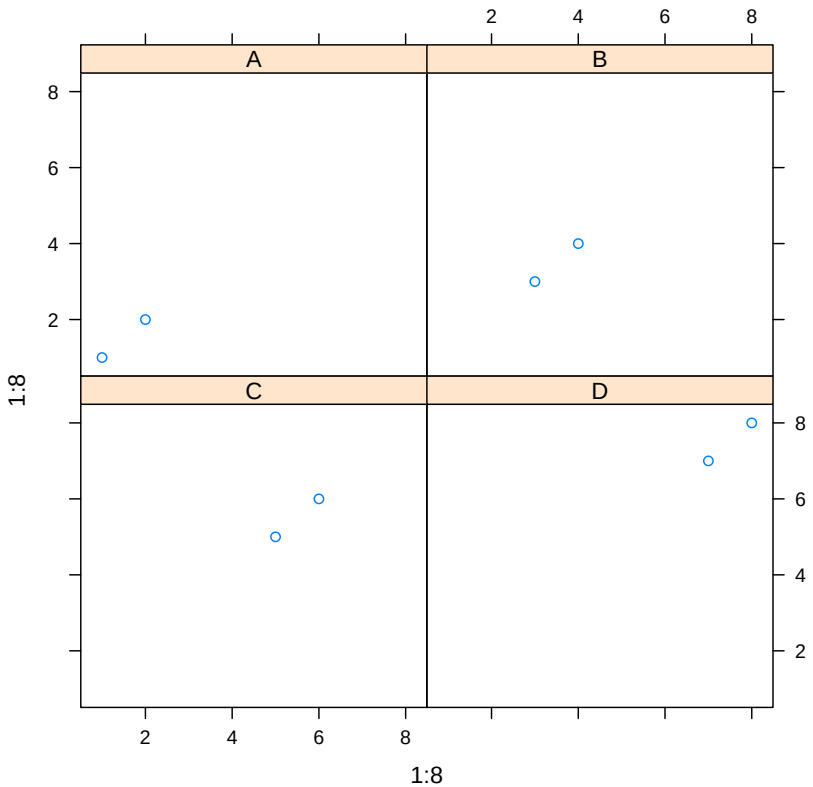
Outline

lattice Environment

- 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 Link
  - Intro Link
  - Book Link
  - `library(help=lattice)` opens a list of all functions available in the lattice package
  - Accessing and changing global parameters: `?lattice.options` and `?trellis.device`

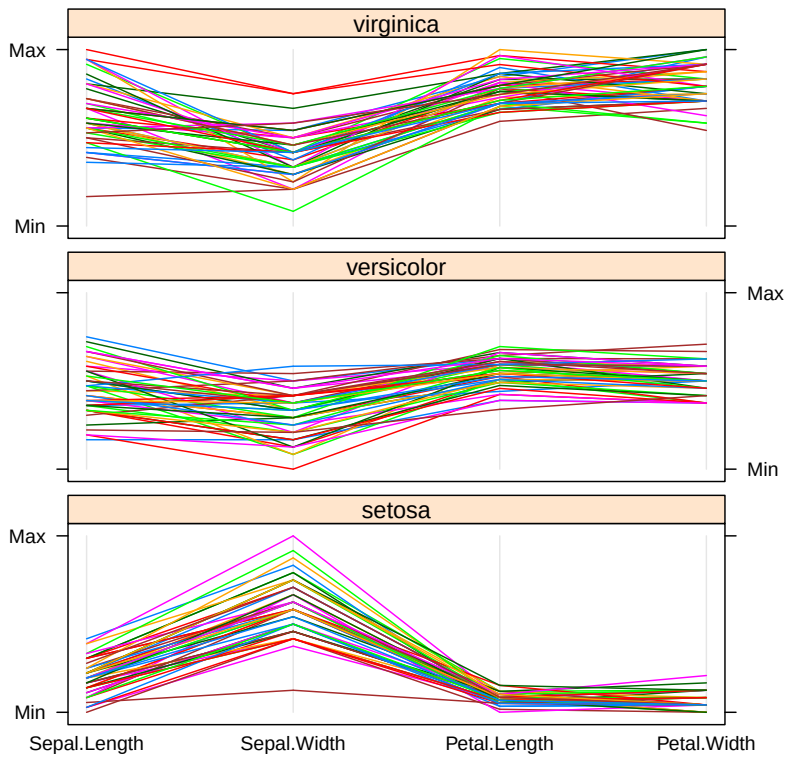
Scatter Plot Sample

```
> 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)
```



Outline

ggplot2 Environment

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

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: Link
- 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

- `qplot` syntax is similar to 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 Plots

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")
```

Drops legend

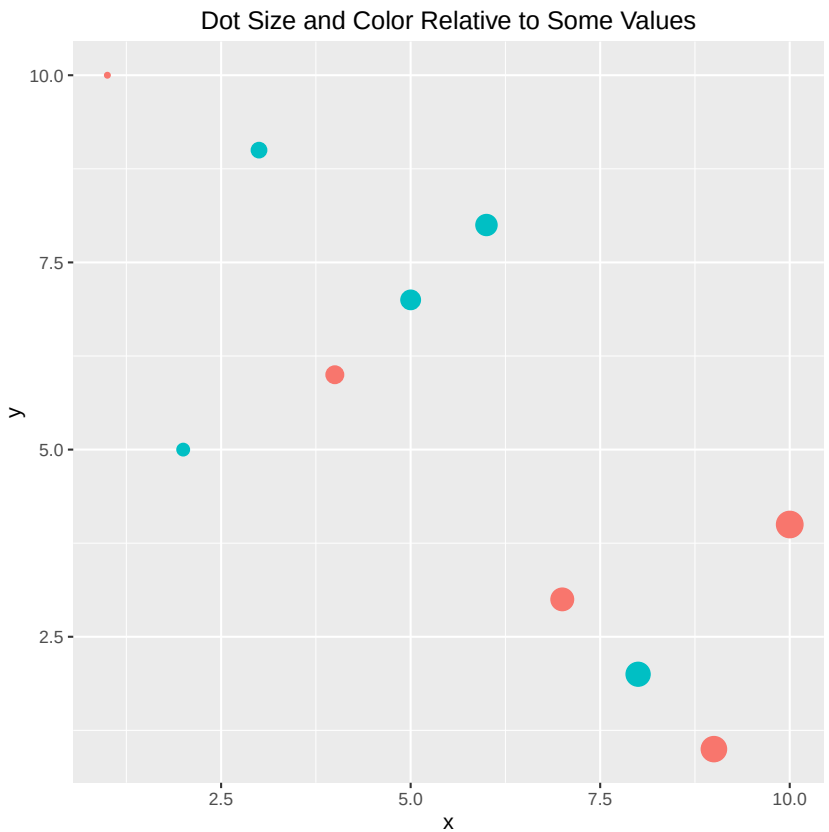
```
> qplot(x, y, geom="point", size=x, color=cat) +
+       theme(legend.position = "none")
```

Plot different shapes

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

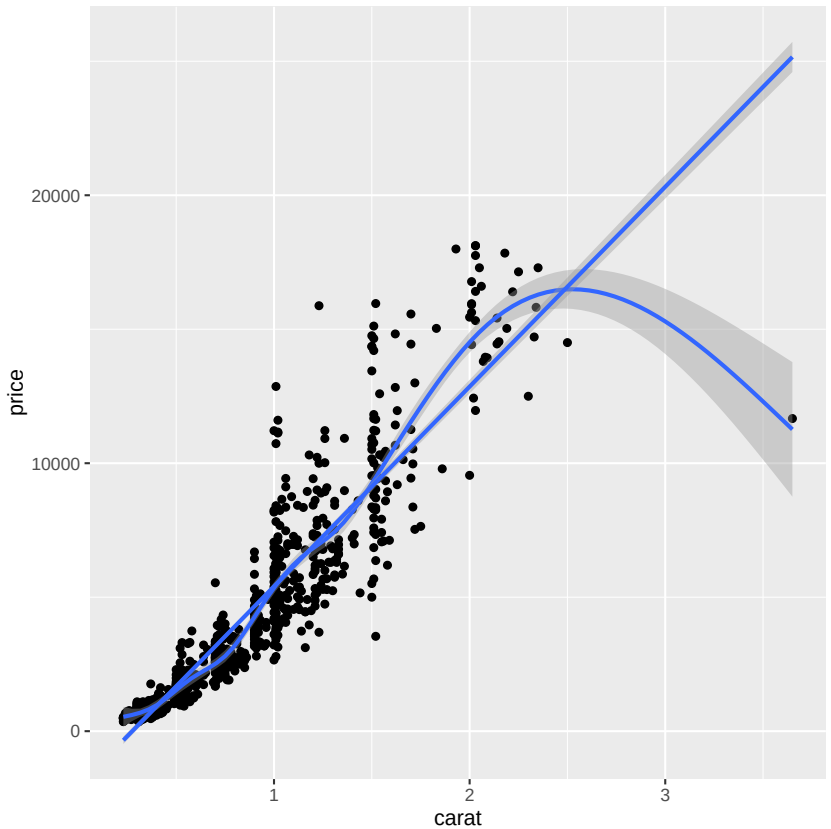
qplot: Scatter Plot with qplot

```
> 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)
```



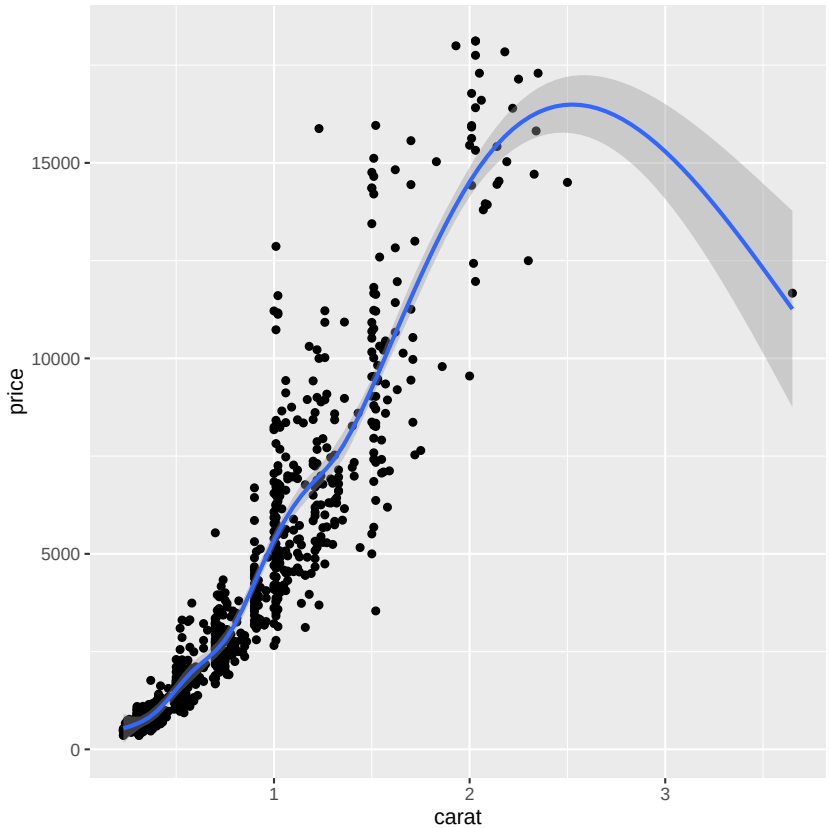
qplot: Scatter Plot with Regression Line

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



qplot: Scatter Plot with Local Regression Curve (loess)

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



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 with ggplot

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

Prints dots with different sizes and colors

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

Syntax to pass on other data sets

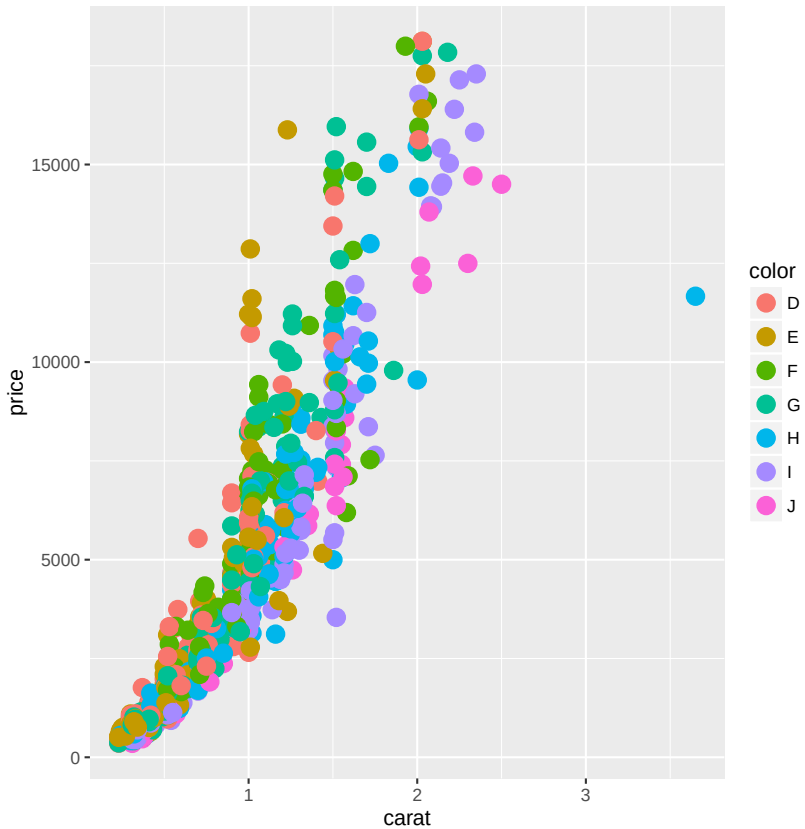
```
> p %+% diamonds[sample(nrow(diamonds), 100),]
```

Saves plot stored in variable p to file

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

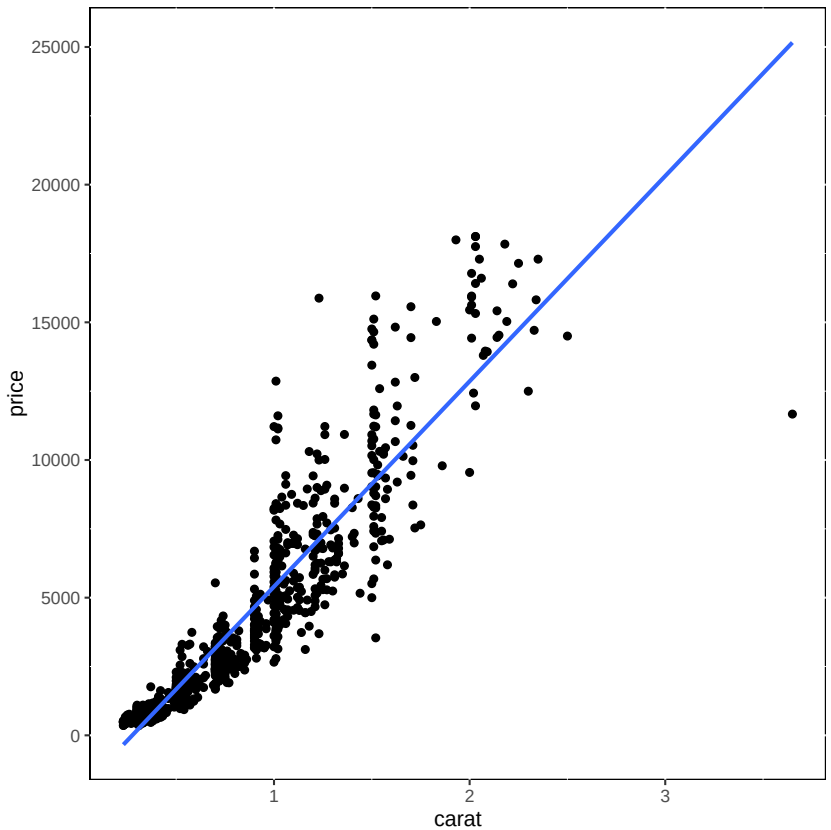
ggplot: Scatter Plot

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



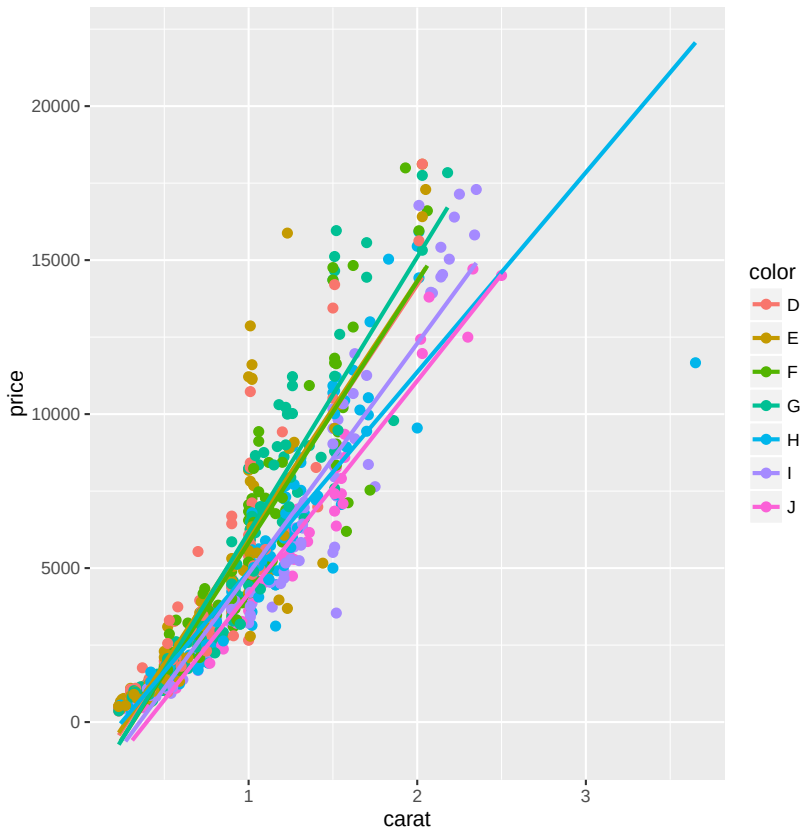
ggplot: Scatter Plot with Regression Line

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



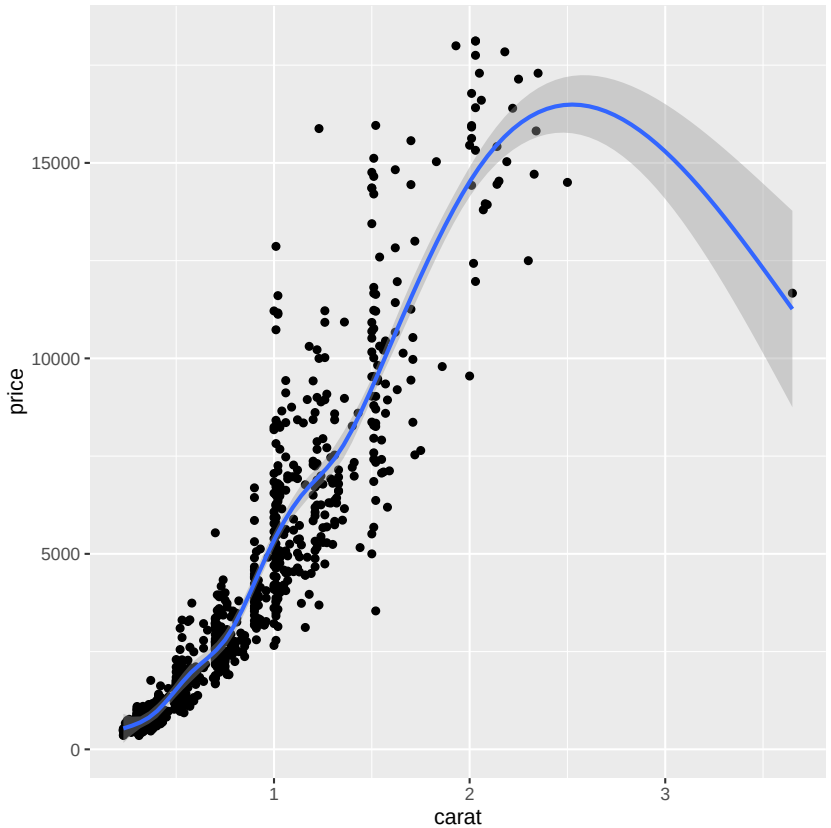
ggplot: Scatter Plot with Several Regression Lines

```
> 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)
```



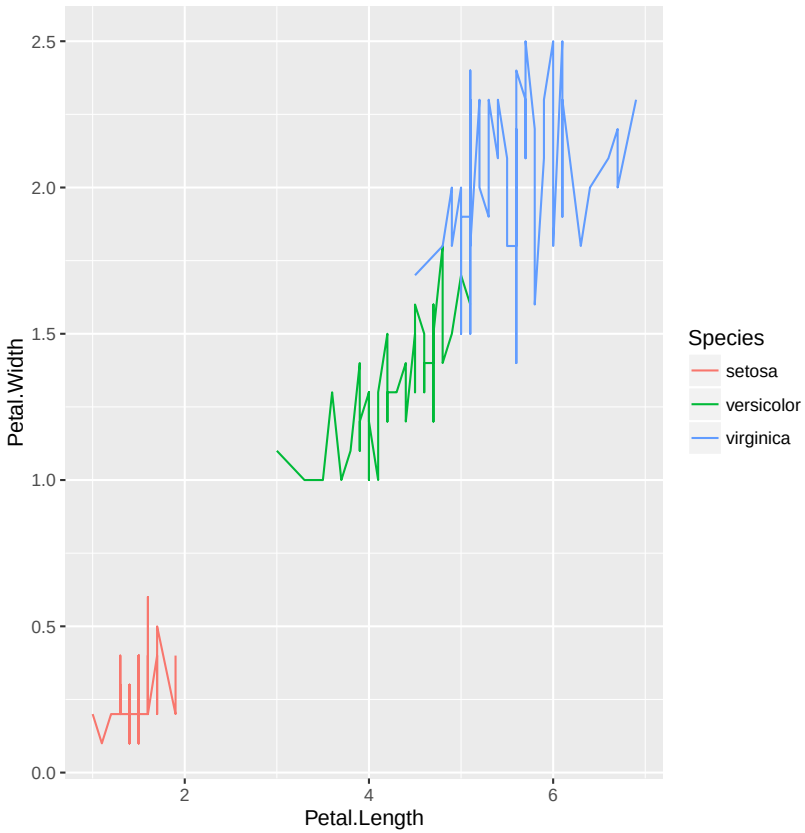
ggplot: Scatter Plot with Local Regression Curve (loess)

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



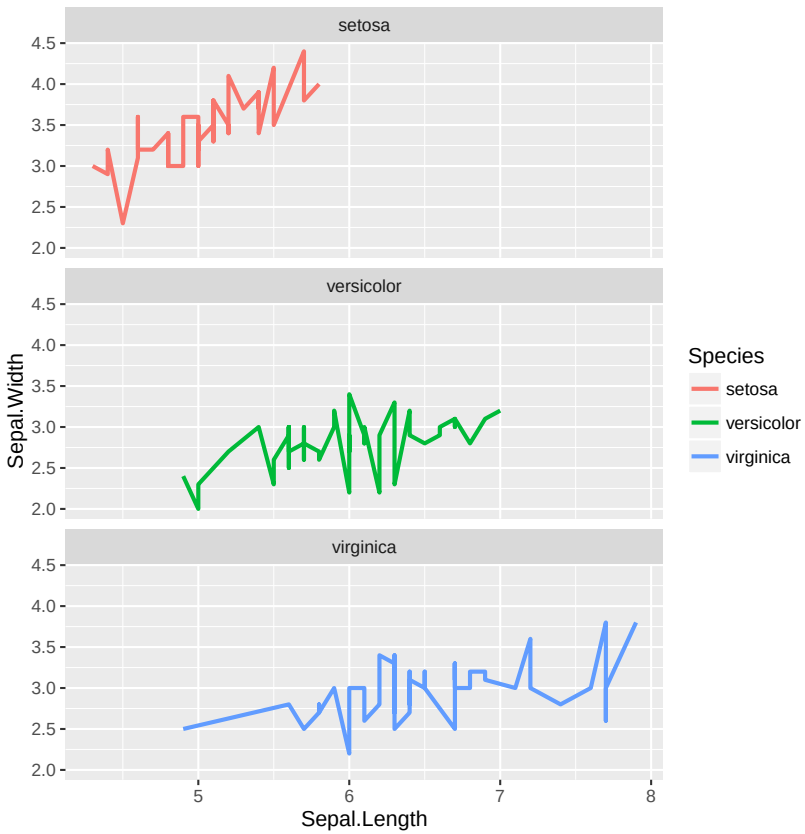
ggplot: Line Plot

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



ggplot: 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

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` functionss 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 saparate 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
```

ggplot: 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)
```

Convert iris_mean with melt

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

Convert iris_sd with melt

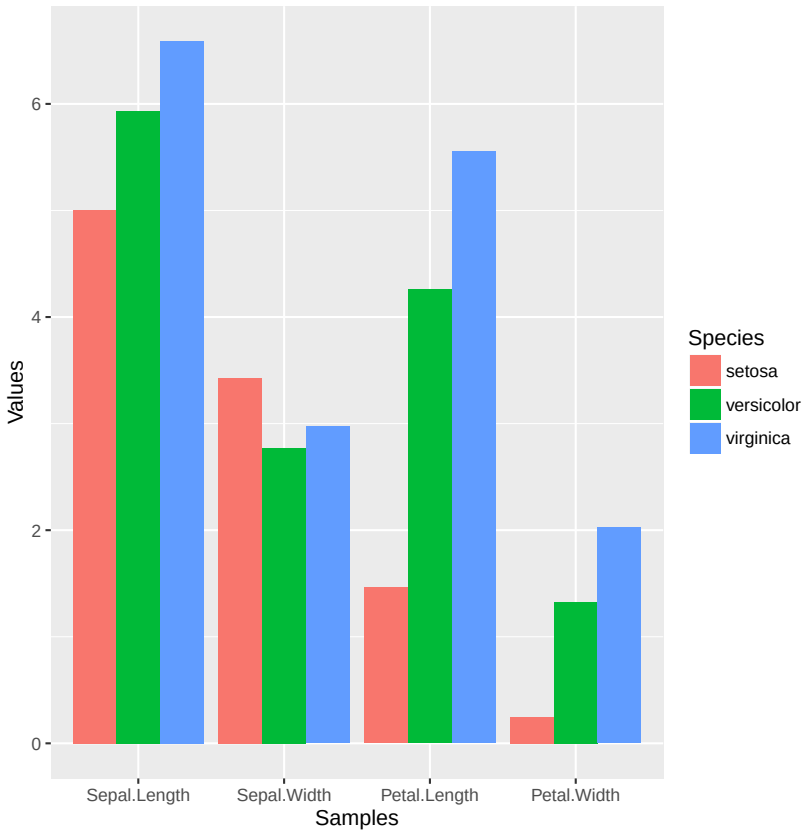
```
> df_sd <- melt(iris_sd, id.vars=c("Species"), variable.name = "Samples", value.name
```

Define standard deviation limits

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

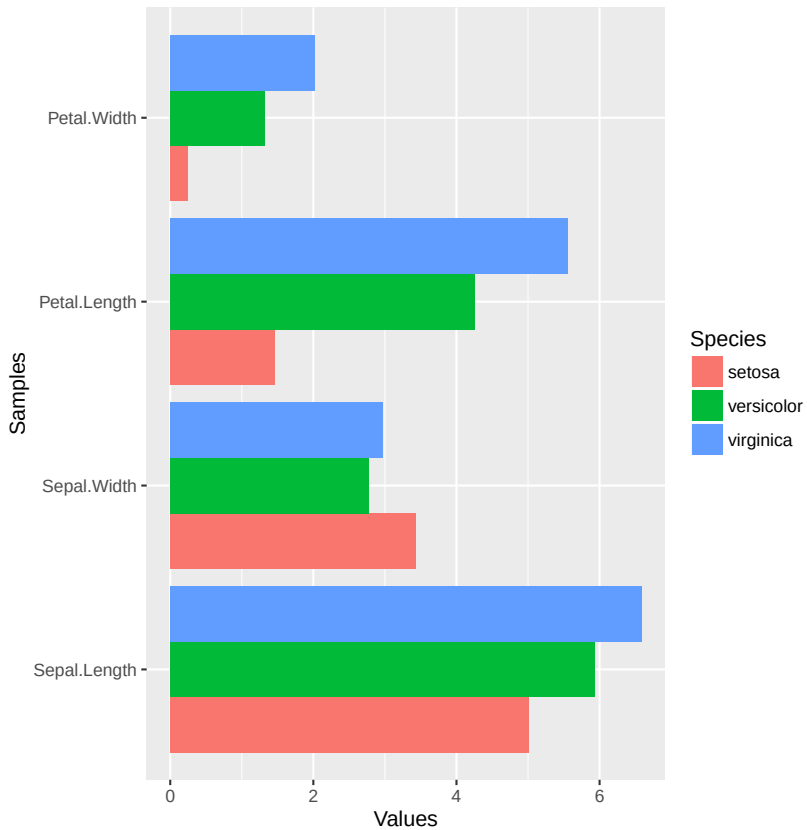
ggplot: Bar Plot

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



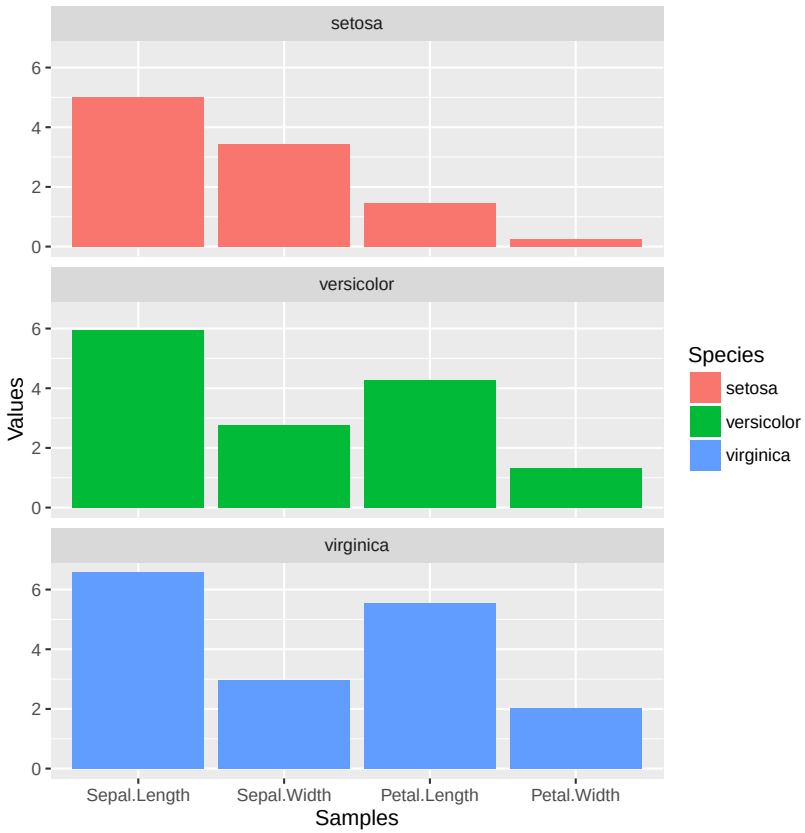
ggplot: Bar Plot Sideways

```
> 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)
```



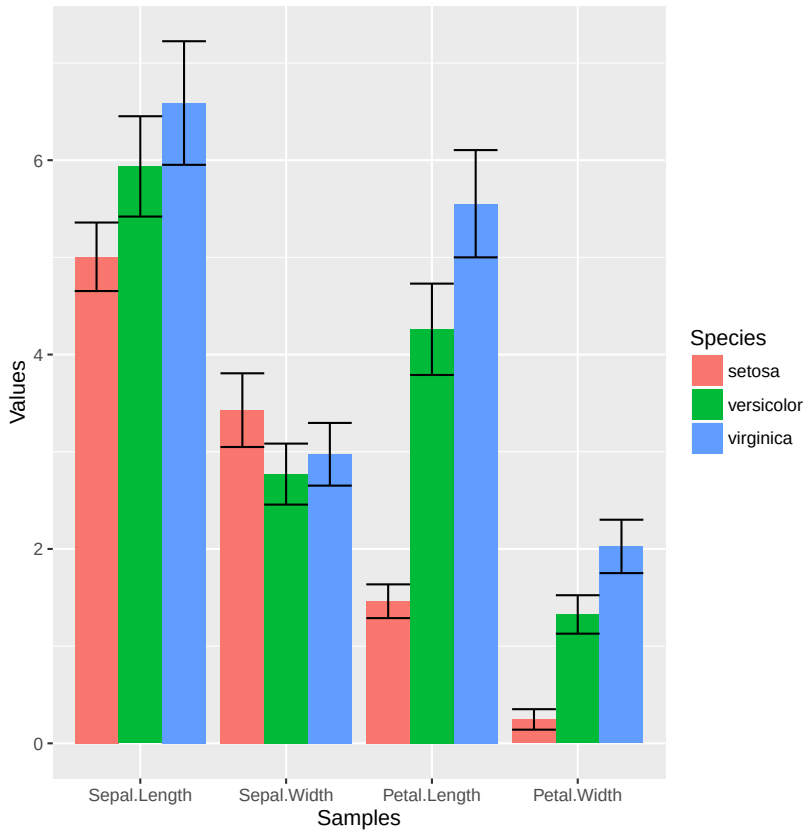
ggplot: Bar Plot with Faceting

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



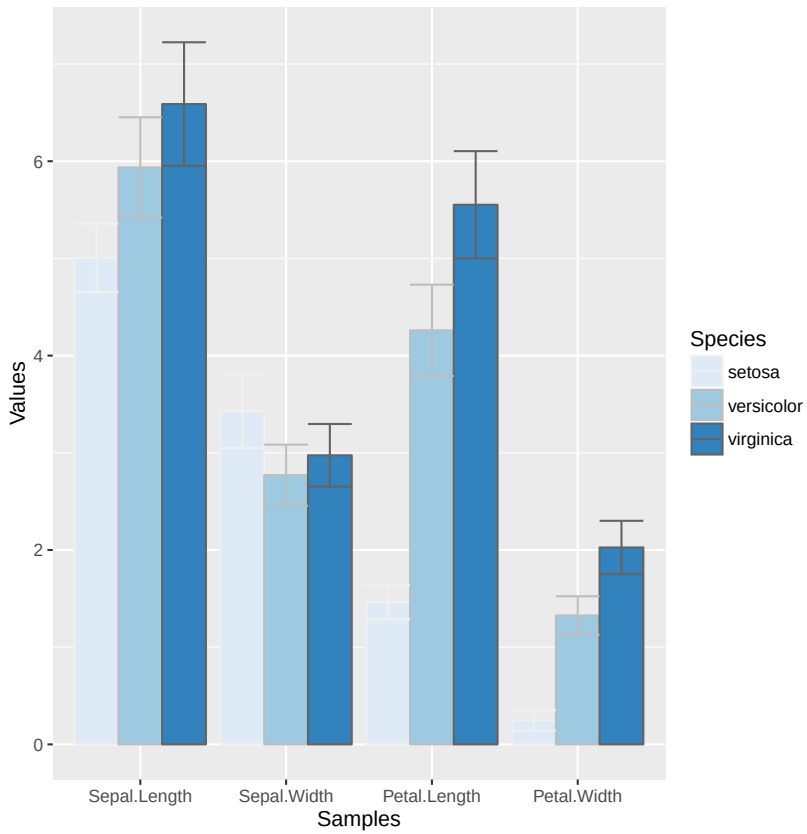
ggplot: Bar Plot with Error Bars

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



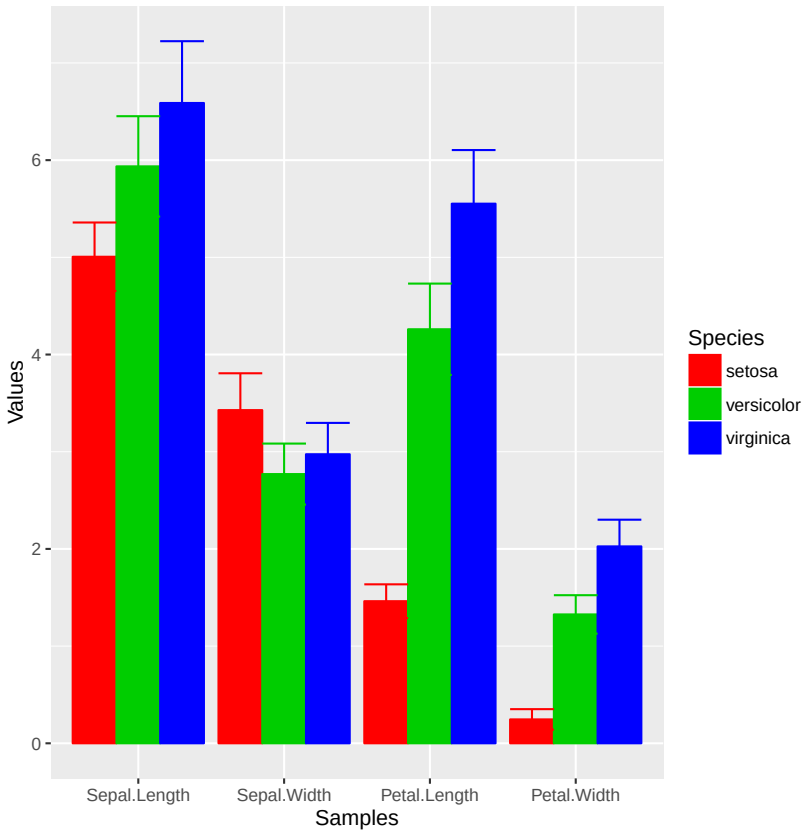
ggplot: Changing Color Settings

```
> 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)
```



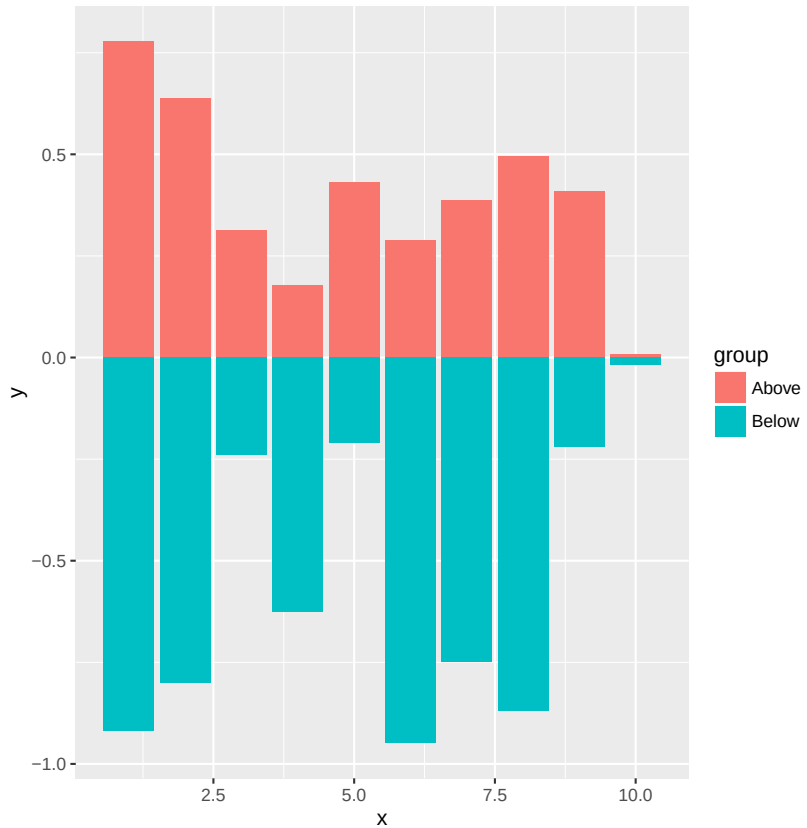
ggplot: Using Standard Colors

```
> 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)
```



ggplot: Mirrored Bar Plots

```
> df <- data.frame(group = rep(c("Above", "Below"), each=10), x = rep(1:10, 2), y = c(runif(10, 0, 1), runi
> p <- ggplot(df, aes(x=x, y=y, fill=group)) +
+             geom_bar(stat="identity", position="identity")
> 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 results into the expected format for `ggplot`.

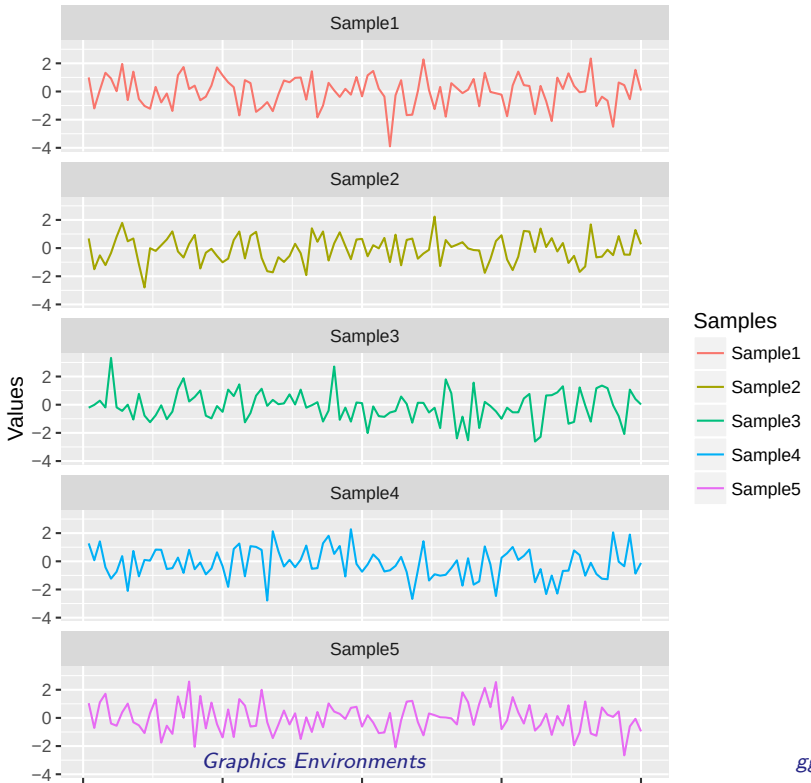
Task 2 Generate two bar plots: one with stacked bars and one with horizontally arranged bars.

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
```

ggplot: Data Reformatting Example 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)
> ## Represent same data in box plot
> ## ggplot(df, aes(Samples, Values, fill=Samples)) + geom_boxplot()
```

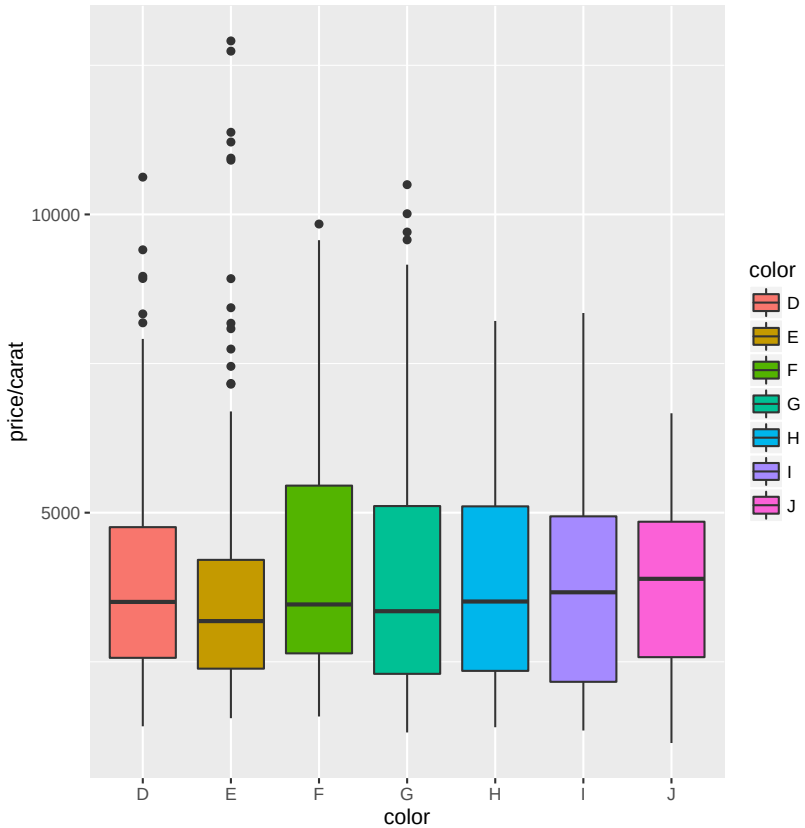


ggplot: Jitter Plots

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

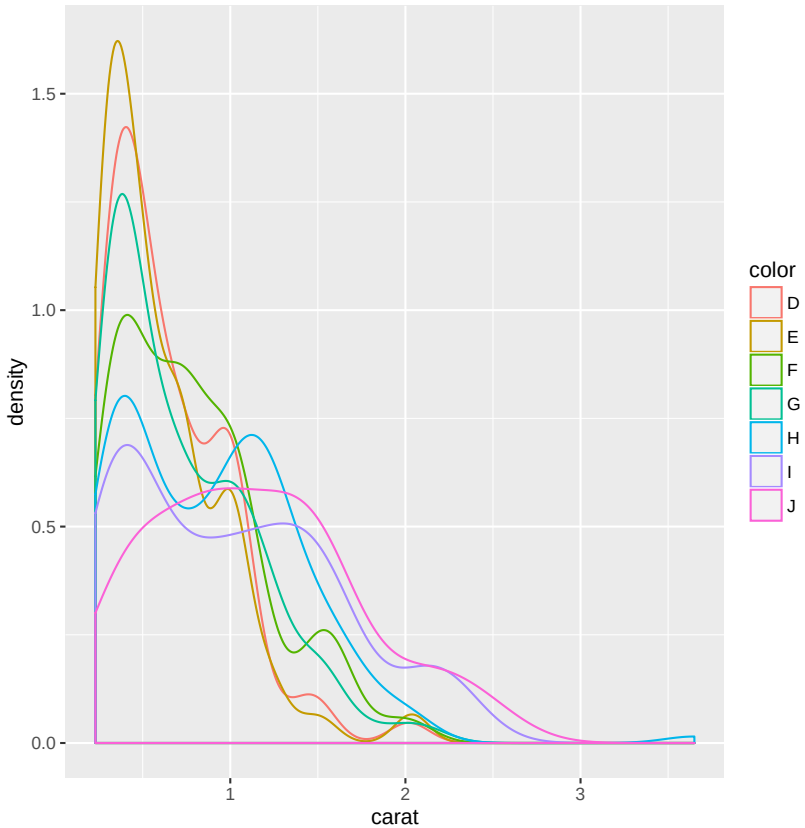
ggplot: Box Plots

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



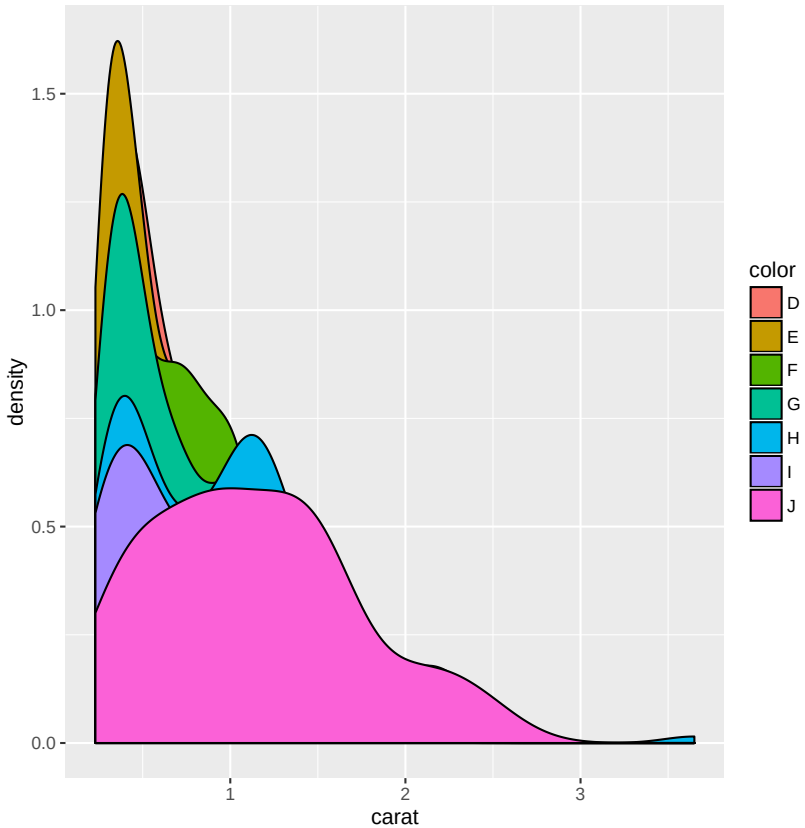
ggplot: Density Plot with Line Coloring

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



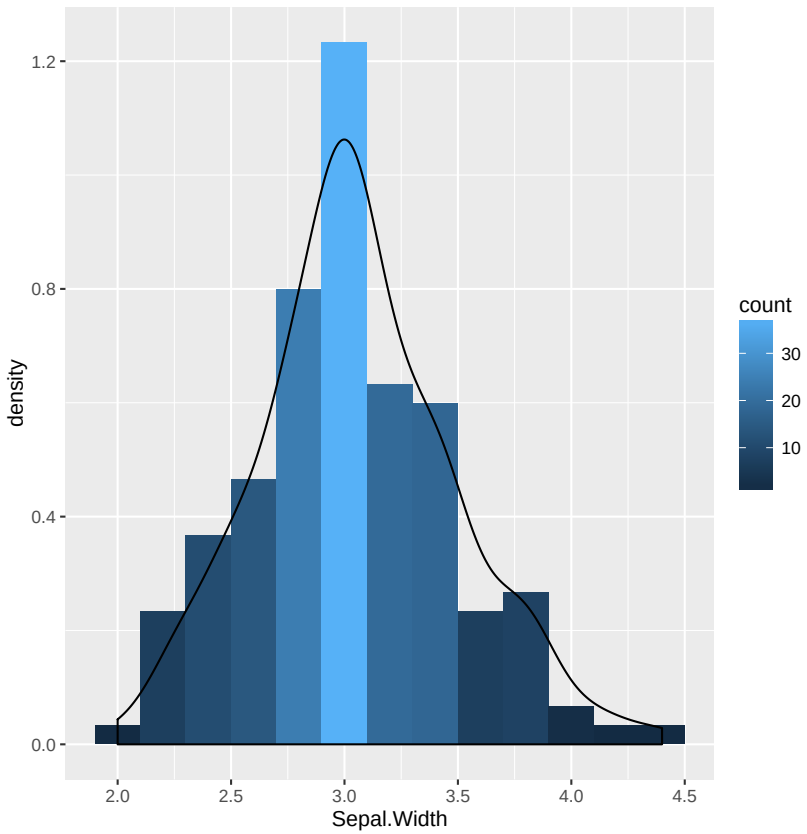
ggplot: Density Plot with Area Coloring

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



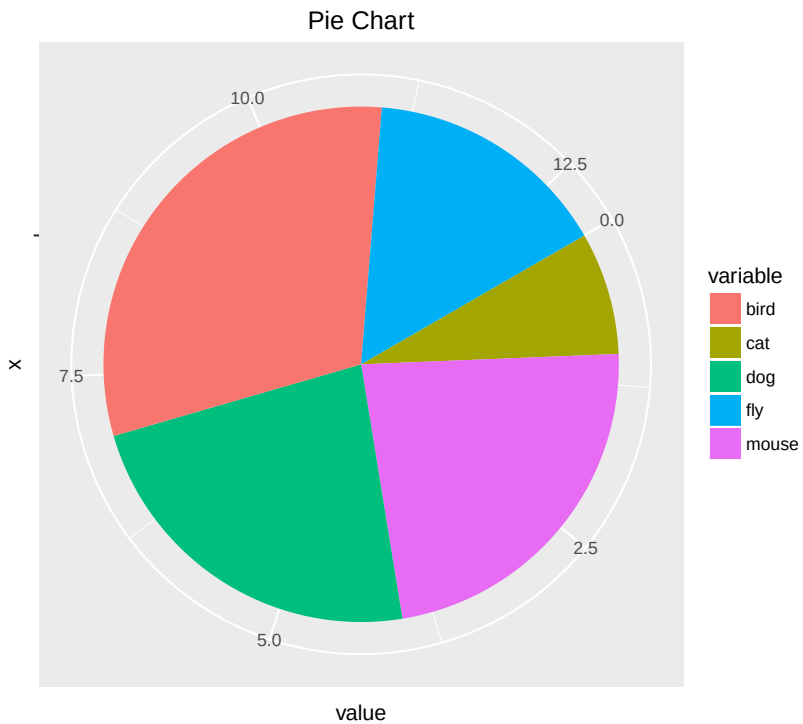
ggplot: Histograms

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



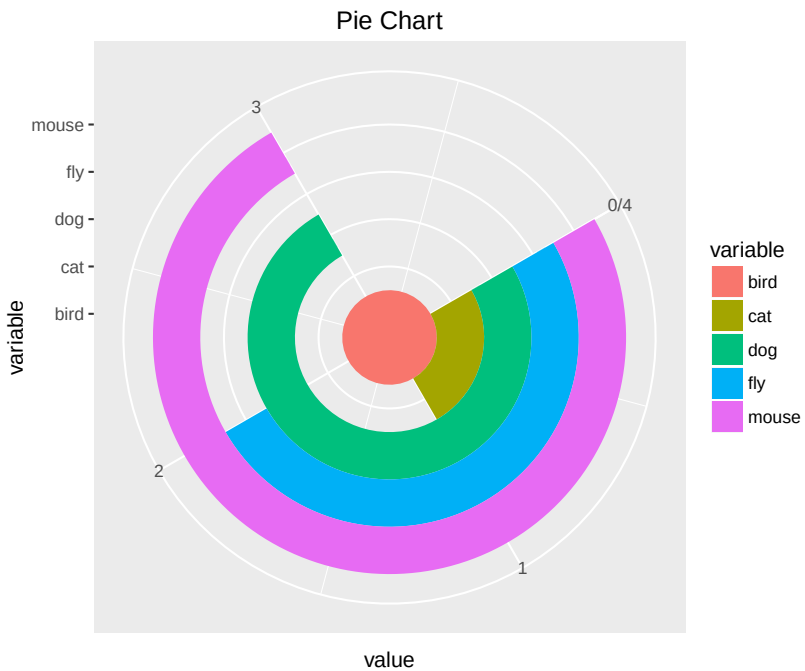
ggplot: Pie Chart

```
> 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)
```



ggplot: Wind Rose Pie Chart

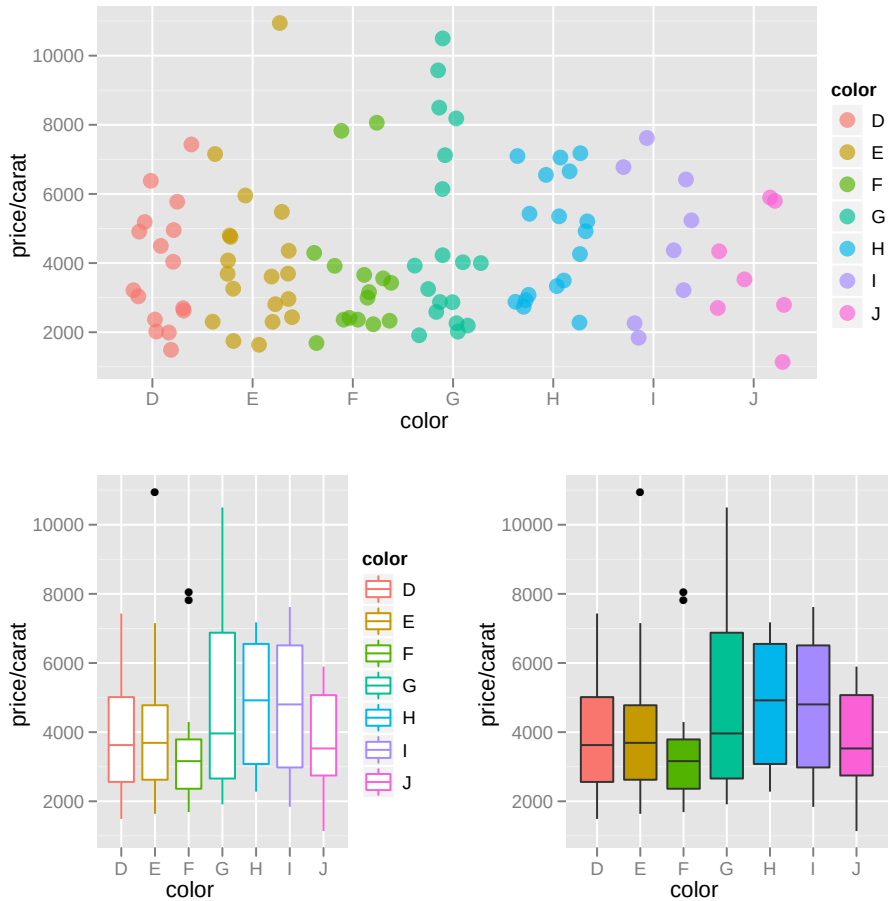
```
> p <- ggplot(df, aes(x = variable, y = value, fill = variable)) +
+         geom_bar(width = 1, stat="identity") + coord_polar("y", start=pi / 3) +
+         ggtitle("Pie Chart")
> print(p)
```



ggplot: Arranging Graphics on One Page

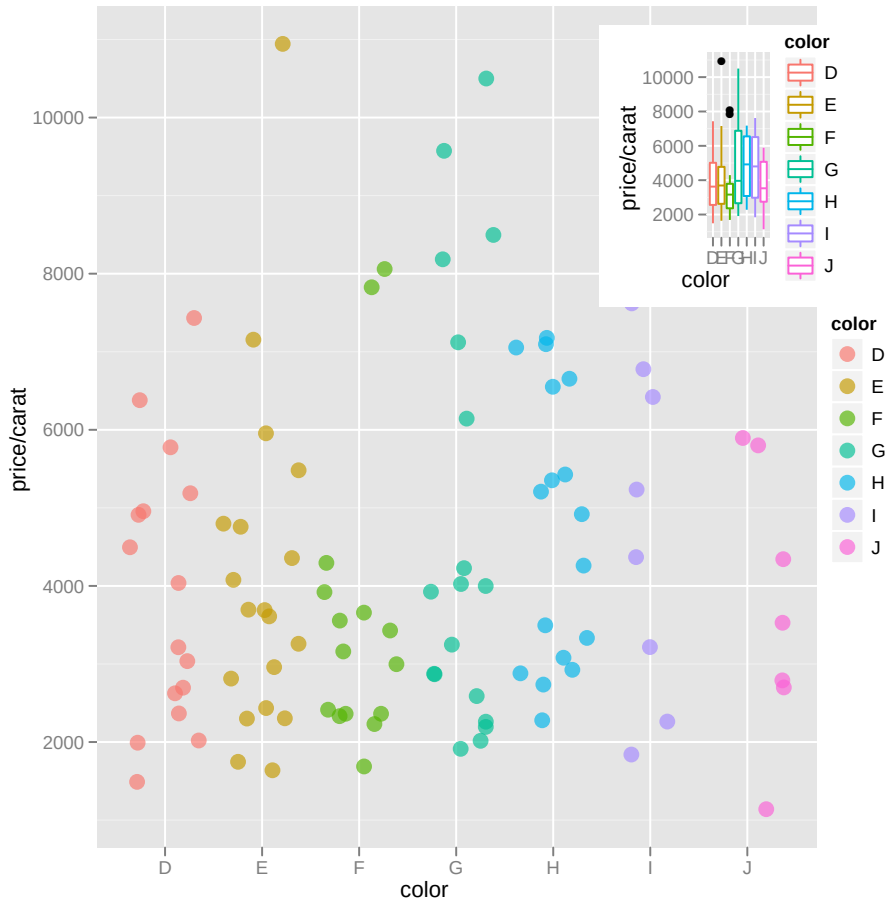
```
> library(grid)
> a <- ggplot(dsmall, aes(color, price/carat)) + geom_jitter(size=4, alpha = I(1 / 1.5), aes(color=color))
> b <- ggplot(dsmall, aes(color, price/carat, color=color)) + geom_boxplot()
> c <- ggplot(dsmall, aes(color, price/carat, fill=color)) + geom_boxplot() + theme(legend.position = "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))
```

ggplot: Arranging Graphics on One Page



ggplot: Inserting Graphics into Plots

```
> # pdf("insert.pdf")
> print(a)
> print(b, vp=viewport(width=0.3, height=0.3, x=0.8, y=0.8))
> # dev.off()
```



Outline

Venn Diagrams (Code)

```
> 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, 2
> OLlist5 <- overLapper(setlist=setlist5, sep="_", type="vennsets")
> counts <- sapply(OLlist5$Venn_List, length)
> # pdf("venn.pdf")
> vennPlot(counts=counts, ccol=c(rep(1,30),2), lcex=1.5, ccex=c(rep(1.5,5), rep(0.6,25),1.5))
> # dev.off()
```

Venn Diagram (Plot)

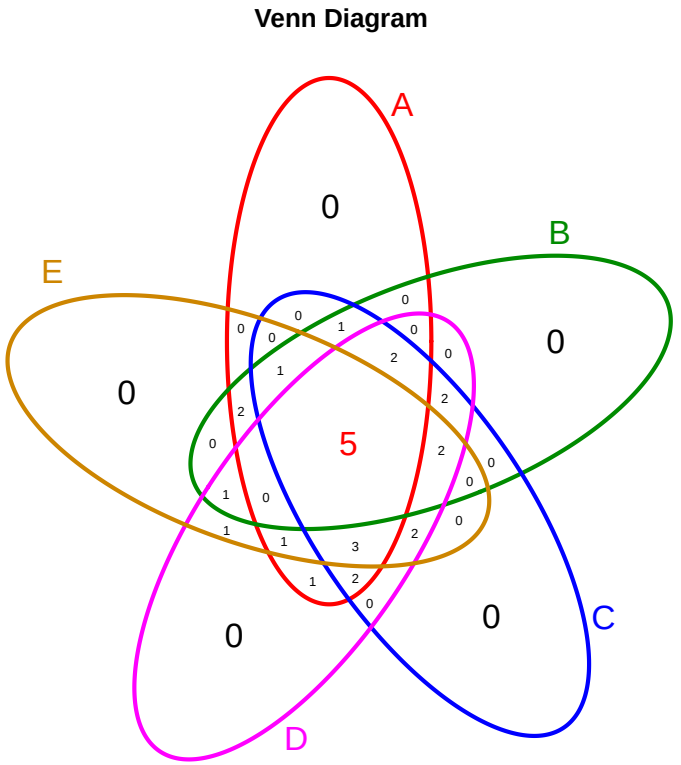
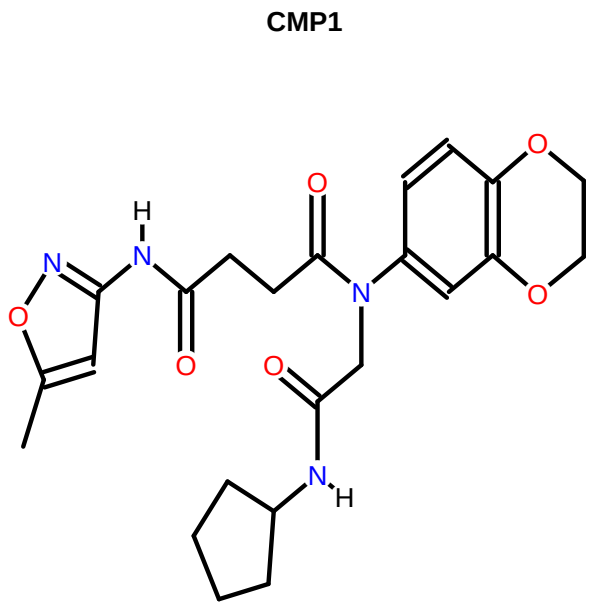


Figure : Venn Diagram

Compound Depictions with ChemmineR

```
> library(ChemmineR)
> data(sdfsample)
> plot(sdfsample[1], print=FALSE)
```



Outline

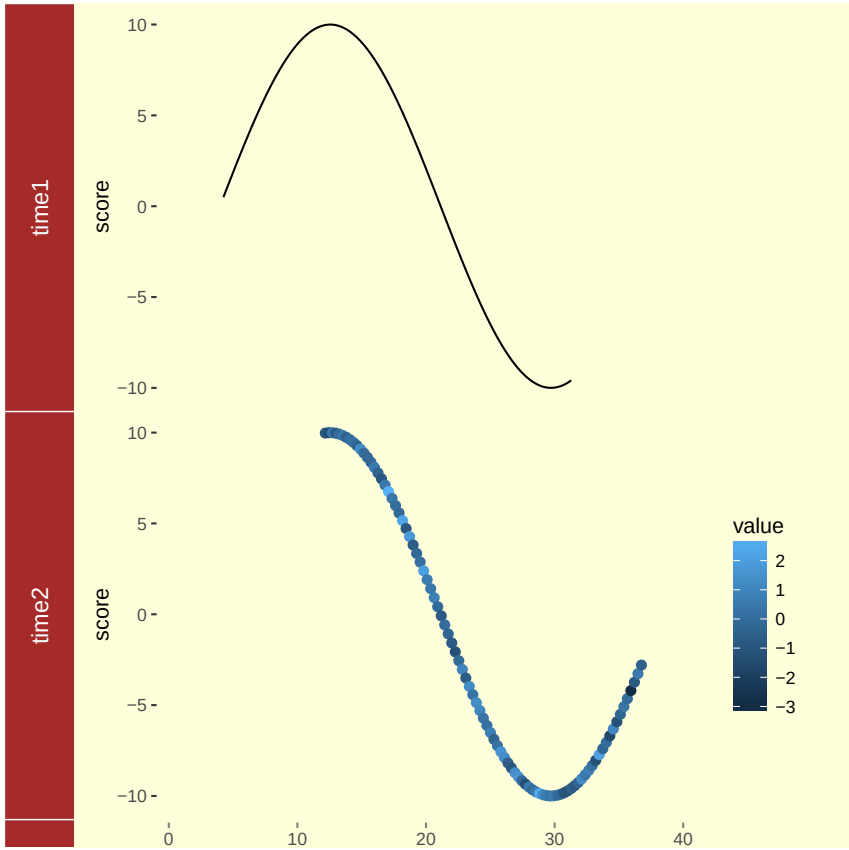
Outline

ggbio: A Programmable Genome Browser

- A genome browser is a visulalization tool for plotting different types of genomic data in separate tracks along chromosomes.
- The *ggbio* package (**?**) 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 Link.
- *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 serval new components useful for genomic data visualization. A detailed list is given in Table 1.2 of the vignette Link.
- Useful web sites:
  - *ggbio* manual Link
  - *ggbio* functions Link
  - `autoplot` demo Link

Tracks: Aligning Plots Along Chromosomes

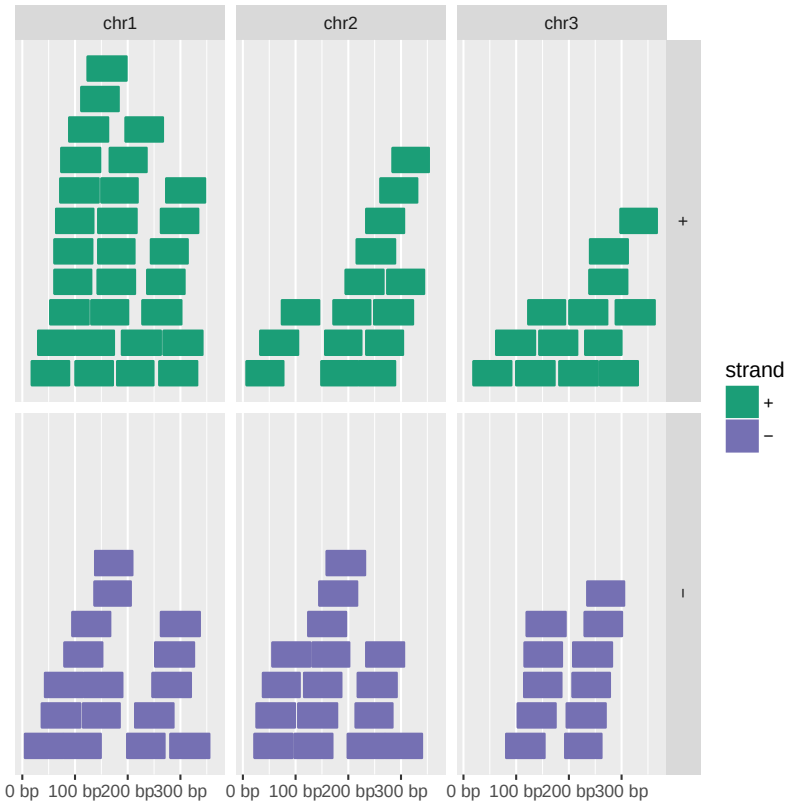
```
> library(ggbio)
> df1 <- data.frame(time = 1:100, score = sin((1:100)/20)*10)
> p1 <- qplot(data = df1, x = time, y = score, geom = "line")
> df2 <- data.frame(time = 30:120, score = sin((30:120)/20)*10, value = rnorm(120-30 +1))
> p2 <- ggplot(data = df2, aes(x = time, y = score)) + geom_line()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



Plotting Genomic Ranges

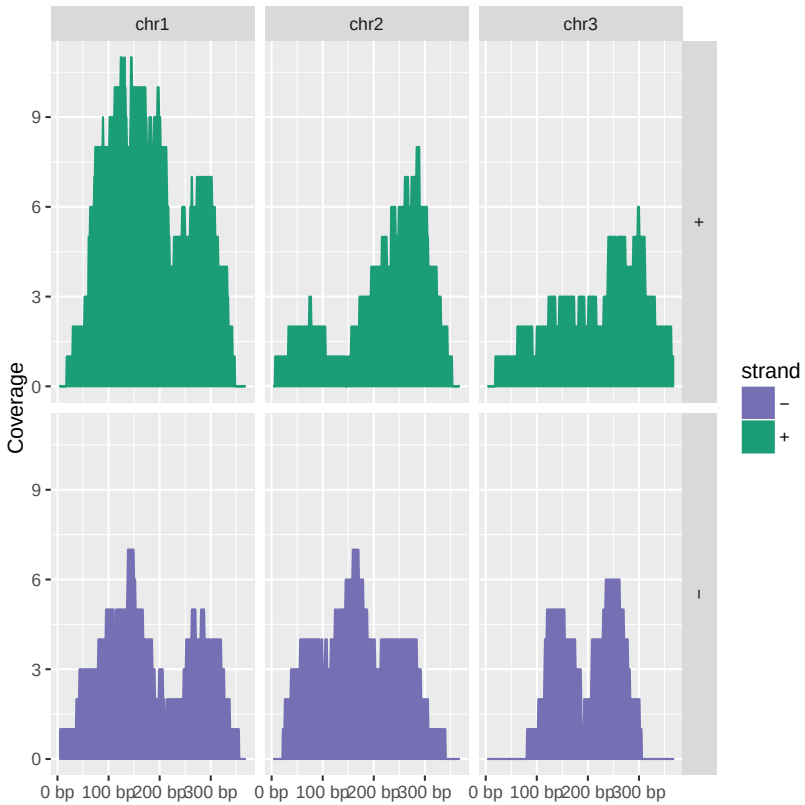
GRanges objects are essential for storing alignment or annotation ranges in R/Bioconductor. The following creates a sample GRanges object and plots its content.

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



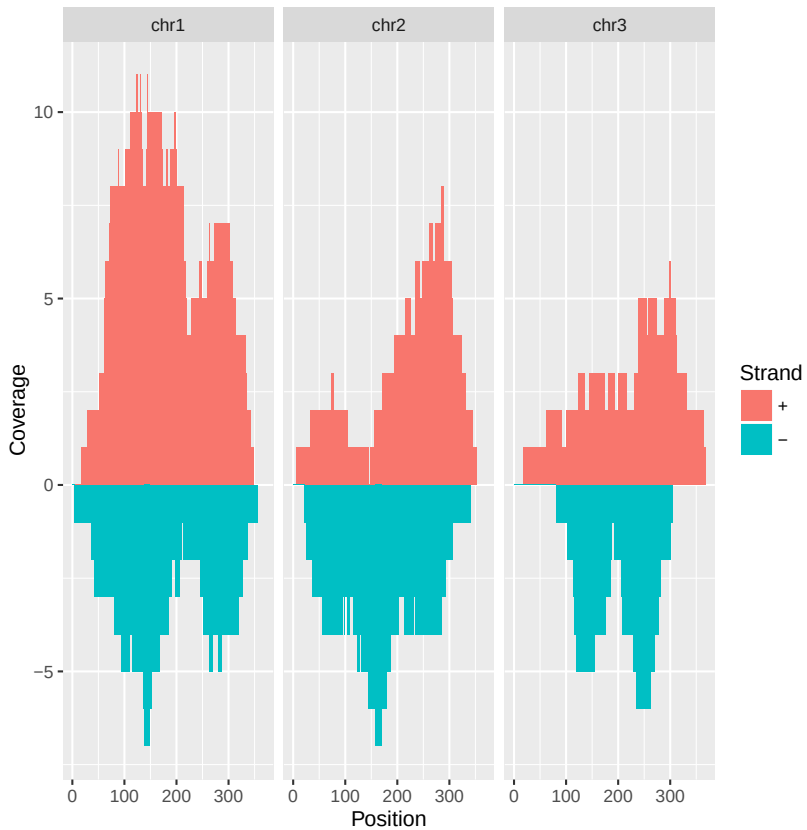
Plotting Coverage Instead of Ranges

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



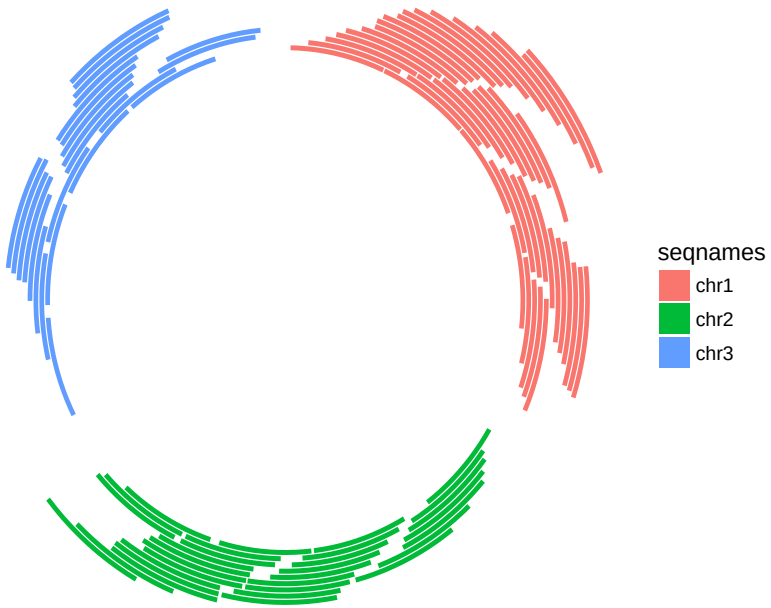
Mirrored Coverage Plot

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



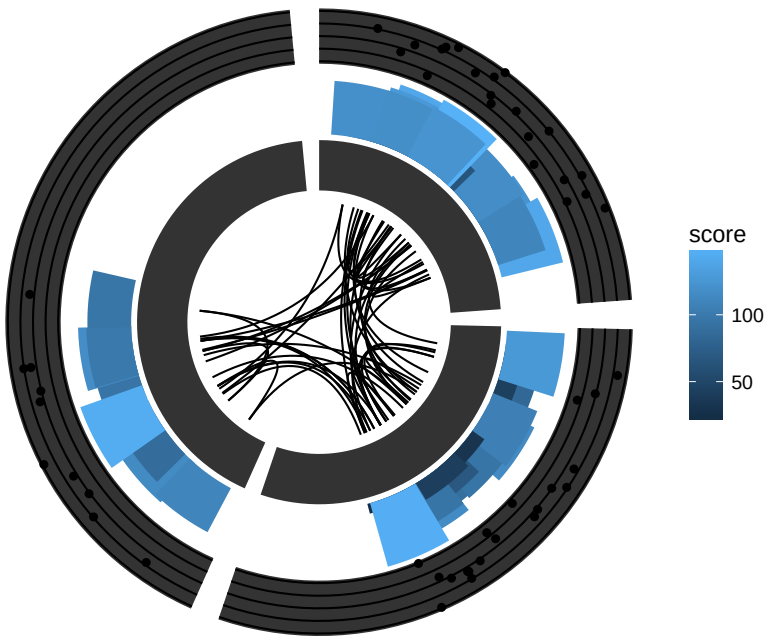
Circular Layout

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



More Complex Circular Example

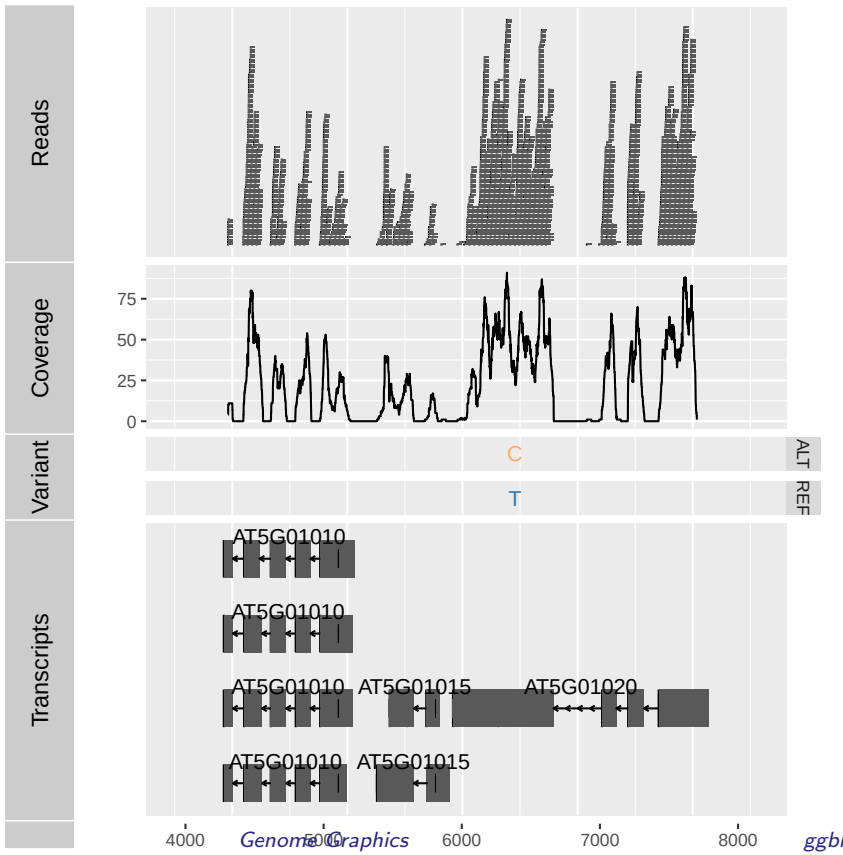
```
> seqlengths(gr) <- c(400, 500, 700)
> values(gr)$to.gr <- gr[sample(1:length(gr), size = length(gr))]
> idx <- sample(1:length(gr), size = 50)
> gr <- gr[idx]
> ggplot() + layout_circle(gr, geom = "ideo", fill = "gray70", radius = 7, trackWidth = 3) +
+   layout_circle(gr, geom = "bar", radius = 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)
```



Viewing Alignments and Variants

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

```
> library(rtracklayer); library(GenomicFeatures); library(Rsamtools); library(GenomicAlignments); library(V
> ga <- readGAlignments("./data/SRR064167.fastq.bam", use.names=TRUE, param=ScanBamParam(which=GRanges("Chr
> 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 = "
> 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 Sample Plots

- `autoplot` demo Link

Outline

Additional Packages for Visualizing Genome Data

- Gviz Link
- RCircos (**?**) Link
- Genome Graphs Link
- genoPlotR Link

Outline

Alignment Viewing in IGV

View results in IGV

- Download and open IGV Link
- 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/Rrnaseq/results/SRR064154.fast
http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rrnaseq/results/SRR064155.fast
http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rrnaseq/results/SRR064166.fast
http://faculty.ucr.edu/~tgirke/HTML_Presentations/Manuals/Workshop_Dec_6_10_2012/Rrnaseq/results/SRR064167.fast

- 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

- systemPipeR: utilities for building NGS analysis pipelines Link

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

Bibliography I