



The Elizabeth H.  
and James S. McDonnell III

**MCDONNELL  
GENOME INSTITUTE**

at Washington University

## GenViz Module 2: Using R for genomic data visualization and interpretation

Malachi Griffith, Obi Griffith, Zachary Skidmore  
Genomic Data Visualization and Interpretation  
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Berlin



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# Learning objectives of the course

- Module 1: Introduction to genomic data visualization and interpretation
- **Module 2: Using R for genomic data visualization and interpretation**
- Module 3: Introduction to GenVisR
- Module 4: Expression profiling, visualization, and interpretation
- Module 5: Variant annotation and interpretation
- Module 6: Q & A, discussion, integrated assignments, and working with your own data
- Tutorials
  - Provide working examples of data visualization and interpretation
  - Self contained, self explanatory, portable

# Learning objectives of module 2

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- Review basic R usage
- Learn to use R for basic data manipulation
- Learn to create publication quality graphs to display data
- Learn to create interactive graphics

# A brief history of R

- R is an implementation of the S programming language combined with lexical scoping semantics inspired by Scheme.
- S was created by John Chambers while at Bell Labs
- There are some important differences, but much of the code written for S runs unaltered.
- R was created by Ross Ihaka and Robert Gentleman at the University of Auckland, New Zealand
- Currently developed by the R Development Core Team, of which Chambers is a member.
- The R project was conceived in 1992, with an initial version released in 1995 and a stable beta version in 2000

# R is available via command-line or a number of integrated development environments (IDE)



R Project



Rstudio

```
Obis-MacBook-Air:~ ogriffit$ R
```

```
R version 3.4.1 (2017-06-30) -- "Single Candle"
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)
```

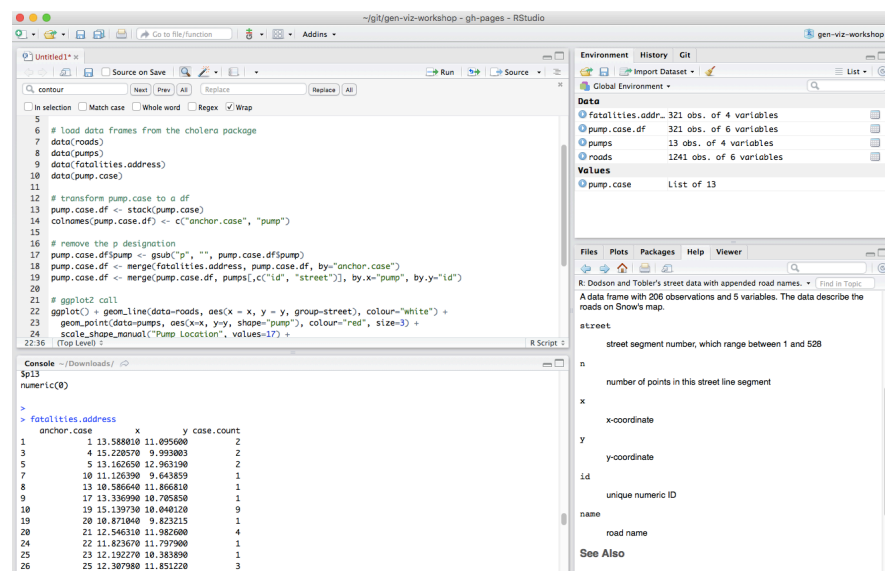
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.

```
> █
```



<https://cran.r-project.org/>

<https://www.rstudio.com/>

Open-source, non-profit

Open-source, free + commercial



# Installation and versions

- Rstudio installation is very simple
- R installation generally only a little more complicated
- Pre-compiled binaries exist for most operating systems
- Be aware of R versions
  - Occasionally some packages may be version dependent or interdependent
  - Less of an issue these days
  - Simplest to keep R, Rstudio and BioConductor updated to current/latest version
  - Rswitch - allows multiple versions of R/Rstudio to be maintained simultaneously

# CRAN and BioConductor

- 11,411 available packages
- All applications
  - ggplot2, cluster, dplyr, reshape2, randomForest, RColorBrewer
- <https://cran.r-project.org/>

```
install.packages()
```

- 1,381 available packages
- Genomic applications
  - AnnotationDBI, GenomicRanges, limma, biomaRt, affy, GEOquery
- <https://bioconductor.org/>

```
source("https://bioconductor.org/  
biocLite.R")  
biocLite()
```



# Getting help: ?, vignette(), and data()

- Type '?' before any function to get a manual style help page in R or Rstudio
- Similarly use vignette() together with a function/package name to get detailed usage vignettes
- Type data() to return a list of available demonstration datasets.

> ?apply



apply {base}

R Documentation

## Apply Functions Over Array Margins

### Description

Returns a vector or array or list of values obtained by applying a function to margins of an array or matrix.

### Usage

```
apply(X, MARGIN, FUN, ...)
```

### Arguments

- |               |   |
|---------------|---|
| <b>X</b>      | an array, including a matrix.   |
| <b>MARGIN</b> | a vector giving the subscripts which the function will be applied over. E.g., for a matrix 1 indicates rows, 2 indicates columns, c(1, 2) indicates rows and columns. Where X has named dimnames, it can be a character vector selecting dimension names. |
| <b>FUN</b>    | the function to be applied: see 'Details'. In the case of functions like +, %*%, etc., the function name must be backquoted or quoted.  |
| <b>...</b>    | optional arguments to FUN.  |

# Rseek.org to search CRAN, r-bloggers, support.rstudio.com, rpubs.com, etc



randomforest



All Packages Books Support Articles For Beginners

About 317,000 results (0.17 seconds)

Sort by: Relevance

powered by Google Custom Search

## [Package 'randomForest'](#)

<https://cran.r-project.org/web/packages/randomForest/randomForest.pdf>

File Format: PDF/Adobe Acrobat

Package 'randomForest'. October 7, 2015. Title Breiman and Cutler's Random Forests for Classification and Regression.

Version 4.6-12. Date 2015-10-06.

Labeled [Packages](#)

## [CRAN - Package randomForest](#)

<https://cran.r-project.org/package=randomForest>

Oct 7, 2015 ... **randomForest**: Breiman and Cutler's Random Forests for Classification and Regression. Classification and regression based on a forest of ...

## [randomForest citation info](#)

<https://cran.r-project.org/web/packages/randomForest/citation.html>

To cite **randomForest** in publications use: A. Liaw and M. Wiener (2002). Classification and Regression by **randomForest**. R News 2(3), 18--22. Corresponding ...

Labeled [Packages](#)

## [randomForest function | R Documentation](#)

<https://www.rdocumentation.org/packages/randomForest/versions/4.6-12/randomForest>

**randomForest** implements Breiman's **random forest** algorithm (based on Breiman and Cutler's original Fortran code) for classification and regression. It can also ...

Labeled [Packages](#) [Support](#)

## [Plotting trees from Random Forest models with ggraph | R-bloggers](#)

<https://www.r-bloggers.com/plotting-trees-from-random-forest-models-with-ggraph/>

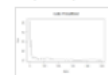


Mar 15, 2017 ... Today, I want to show how I use Thomas Lin Pederson's awesome ggraph package to plot decision trees from **Random Forest** models.

Labeled [Articles](#)

## [Rpubs - randomForest](#)

<https://rpubs.com/mbaumer/randomForest>



Dec 17, 2015 ... This example will utilize one of the most user-friendly approaches to predictive modeling: a **random forest**. A forest is a big group of trees, which ...

Labeled [Articles](#)

# Variables, Data Structure (Object) Types and Data types

- As with any programming language, you need to use variables to store information. When you create a variable you reserve some space in memory and keep a record of its location for later retrieval and use.
- The information you wish to store might be characters (e.g., text), integers, boolean (e.g., True/False) etc.
- In contrast to many other programming languages (e.g., C, java, etc), in R variables are not declared as a specific data type.
  - The variables are assigned with R-Objects and the data type of the R-object becomes the data type of the variable.
- The simplest R-object type is the atomic vector
  - There are six data types for atomic vectors, also termed as six classes of vectors: logical, numerical, integer, complex, character, and raw
- Lists are also vectors but are not atomic vectors, meaning that they can include multiple data types and can be recursive (contain lists of lists)
- The other R-Objects are built upon atomic vectors and include: factors, matrices, arrays, data frames,

# Understanding data and object types with class(), typeof() and is.\*()

x	class(x)	typeof(x)	is.*(x)
x <- 1.0	numeric	double	is.numeric(x)=TRUE is.double(x)=TRUE
x <- 1L	integer	integer	is.integer(x)=TRUE
x <- "a"	character	character	is.character(x)=TRUE
x <- TRUE	logical	logical	is.logical(x)=TRUE
x <- charToRaw("a")	raw	raw	is.raw(x)=TRUE
x <- 4 + 4i	complex	complex	is.complex(x)=TRUE
x <- matrix(1:4, nrow=2)	matrix	integer	is.matrix(x)=TRUE is.integer(x)=TRUE
x <- data.frame(x=1:2, y=c("a", "b"))	data.frame	list	is.data.frame(x)=TRUE is.list(x)=TRUE

# Vectors

- Typically defined with `c()` or extracted from other objects

```
> myVector <- c("foo", "bar", "baz")
```

```
> myVector2 <- c(2,3,5:10,15,20,25,30)
```

- Subsets of vectors can be extracted by index values

```
> myVector[3]  
[1] "baz"
```

- Conditional statements can be applied to vectors

```
myVector2 >= 5  
[1] FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
TRUE TRUE
```

# Dataframes

## Demo dataframe available in R: “mtcars”

```
> mtcars
```

	mpg	cyl	displacement	horsepower	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160.0	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160.0	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258.0	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360.0	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225.0	105	2.76	3.460	20.22	1	0	3	1
Duster 360	14.3	8	360.0	245	3.21	3.570	15.84	0	0	3	4
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Merc 280	19.2	6	167.6	123	3.92	3.440	18.30	1	0	4	4
Merc 280C	17.8	6	167.6	123	3.92	3.440	18.90	1	0	4	4
Merc 450SE	16.4	8	275.8	180	3.07	4.070	17.40	0	0	3	3
Merc 450SL	17.3	8	275.8	180	3.07	3.730	17.60	0	0	3	3
Merc 450SLC	15.2	8	275.8	180	3.07	3.780	18.00	0	0	3	3
Cadillac Fleetwood	10.4	8	472.0	205	2.93	5.250	17.98	0	0	3	4
Lincoln Continental	10.4	8	460.0	215	3.00	5.424	17.82	0	0	3	4
Chrysler Imperial	14.7	8	440.0	230	3.23	5.345	17.42	0	0	3	4
Fiat 128	32.4	4	78.7	66	4.08	2.200	19.47	1	1	4	1
Honda Civic	30.4	4	75.7	52	4.93	1.615	18.52	1	1	4	2
Toyota Corolla	33.9	4	71.1	65	4.22	1.835	19.90	1	1	4	1
Toyota Corona	21.5	4	120.1	97	3.70	2.465	20.01	1	0	3	1
Dodge Challenger	15.5	8	318.0	150	2.76	3.520	16.87	0	0	3	2
AMC Javelin	15.2	8	304.0	150	3.15	3.435	17.30	0	0	3	2
Camaro Z28	13.3	8	350.0	245	3.73	3.840	15.41	0	0	3	4
Pontiac Firebird	19.2	8	400.0	175	3.08	3.845	17.05	0	0	3	2
Fiat X1-9	27.3	4	79.0	66	4.08	1.935	18.90	1	1	4	1
Porsche 914-2	26.0	4	120.3	91	4.43	2.140	16.70	0	1	5	2
Lotus Europa	30.4	4	95.1	113	3.77	1.513	16.90	1	1	5	2
Ford Pantera L	15.8	8	351.0	264	4.22	3.170	14.50	0	1	5	4
Ferrari Dino	19.7	6	145.0	175	3.62	2.770	15.50	0	1	5	6
Maserati Bora	15.0	8	301.0	335	3.54	3.570	14.60	0	1	5	8
Volvo 142E	21.4	4	121.0	109	4.11	2.780	18.60	1	1	4	2

- Similar vectors, you can extract subsets of dataframes using [] but now with two dimensions: data[ROW,COL]
- You can also extract by row and column name:  
mtcars\$mpg

# Importing and Exporting Data

- R functions exist to import most common file formats
  - tsv, csv, excel, xml, json, etc
- `read.table()` is particularly useful for simple delimited data files

```
data <- read.table(file="my file or URL", header=TRUE, sep="\t",  
na.strings = c("NA","N/A","na"), as.is=c(1:27,29:30), row.names=1, ...)
```

- Read from file or web URL
- Tell R how you have encoded missing values
- Use `as.is` to prevent R from converting strings to factors

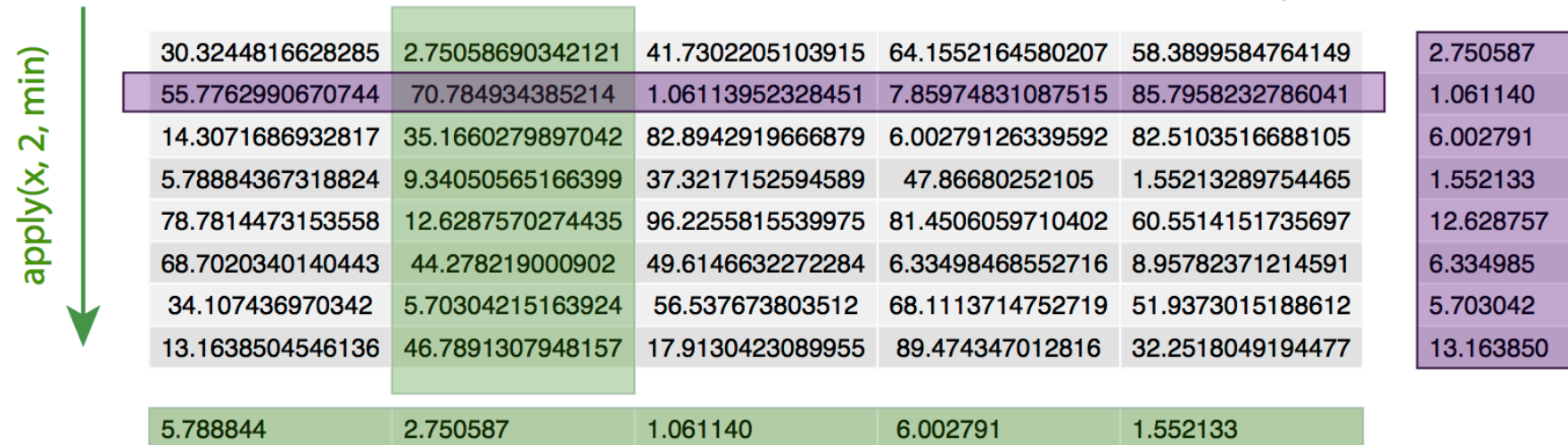
# Apply functions

```
# Create a matrix of 8 rows by 5 columns as above:  
x <- matrix(runif(n=40, min=1, max=100), ncol=5)
```

```
# Calculate min value for each row with a for loop  
for(i in 1:8){  
  print(min(x[i,]))  
}
```

```
# use apply function to do same thing  
apply(x, 1, min)
```

apply(x, 1, min)



30.3244816628285	2.75058690342121	41.7302205103915	64.1552164580207	58.3899584764149	2.750587
55.7762990670744	70.784934385214	1.06113952328451	7.85974831087515	85.7958232786041	1.061140
14.3071686932817	35.1660279897042	82.8942919666879	6.00279126339592	82.5103516688105	6.002791
5.78884367318824	9.34050565166399	37.3217152594589	47.86680252105	1.55213289754465	1.552133
78.7814473153558	12.6287570274435	96.2255815539975	81.4506059710402	60.5514151735697	12.628757
68.7020340140443	44.278219000902	49.6146632272284	6.33498468552716	8.95782371214591	6.334985
34.107436970342	5.70304215163924	56.537673803512	68.1113714752719	51.9373015188612	5.703042
13.1638504546136	46.7891307948157	17.9130423089955	89.474347012816	32.2518049194477	13.163850
5.788844	2.750587	1.061140	6.002791	1.552133	



# Custom functions

- Often necessary when an existing R function doesn't quite do what you need.
- Especially powerful in combination with `apply()` functions

- Basic structure:

```
myfun <- function(input){  
  output <- do_something(input)  
  return(output)  
}
```

```
apply(mydata, 1, myfun)
```

# Assignment - the age old “<-” vs “=” debate

- By convention in R, “<-” is used to assign a value to a variable and “=” is used for setting arguments in a function. For R purists, this is the preferred method.
- The “=” symbol will also generally work for assignment.
- Old keyboards had a “<-” key. Now its an extra key stroke.
- There is a difference in “scope”. Generally you may want values assigned within functions to stay inside the function.
- Let’s look at the simple ‘median’ function to illustrate
  - Usage: median(x, na.rm = FALSE, ...)

```
> data=c(1:10,NA,NA,3:5)
> median(x=data, na.rm=TRUE)
[1] 5
> x
Error: object 'x' not found

> median(x <- data, na.rm=TRUE)
[1] 5
> x
[1] 1 2 3 4 5 6 7 8 9 10 NA NA 3 4 5
```

# Assignment - the age old “<-” vs “=” debate

- With “<-” spacing matters. This drives some programmers crazy who think spacing should be a style matter and not change the way a program works

```
> x<-3
```

```
> x
```

```
[1] 3
```

```
> x <- 3
```

```
> x
```

```
[1] 3
```

```
> x < -3
```

```
> x
```

```
FALSE
```

# Assignment - the age old “<-” vs “=” debate

- More weirdness having to do with order of interpretation by R

```
x <- y <- 5 # x and y equal 5
```

```
x = y = 5 # x and y equal 5
```

```
x = y <- 5 # x and y equal 5
```

```
x <- y = 5 # errors!
```

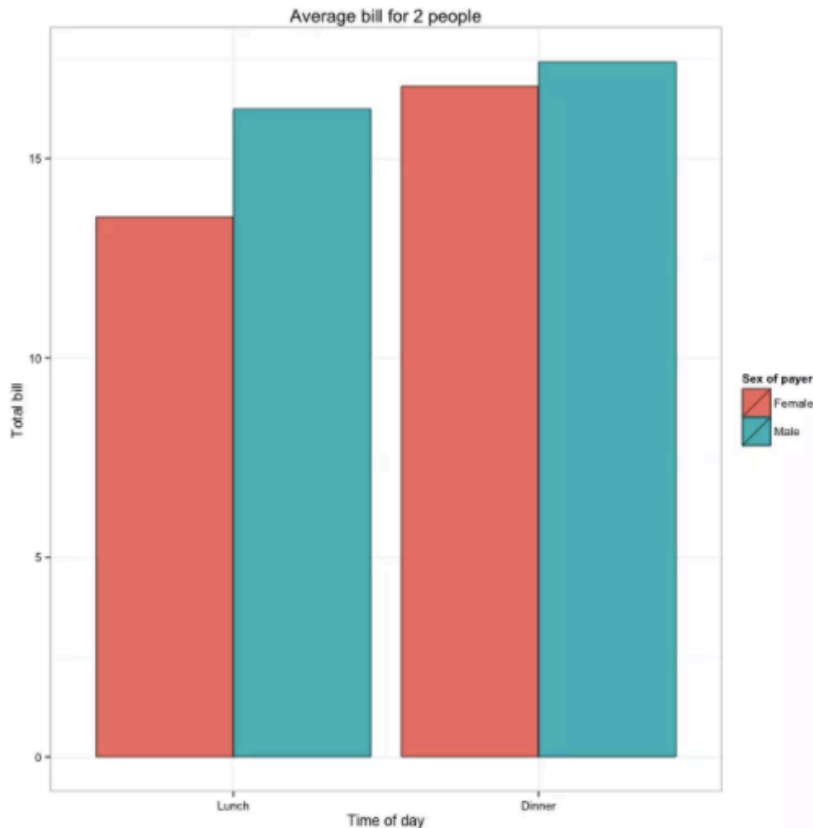
```
# Error in (x <- y) = 5 : could not find function "<-<-"
```

- We could keep going ...
- Use “<-” if you want to be a l33t R geek.
- I’ve been writing code for 15 years and use “=” for assignment. Never had a problem.
- formatR package (tidy\_\* functions) can be used to clean your code for publication

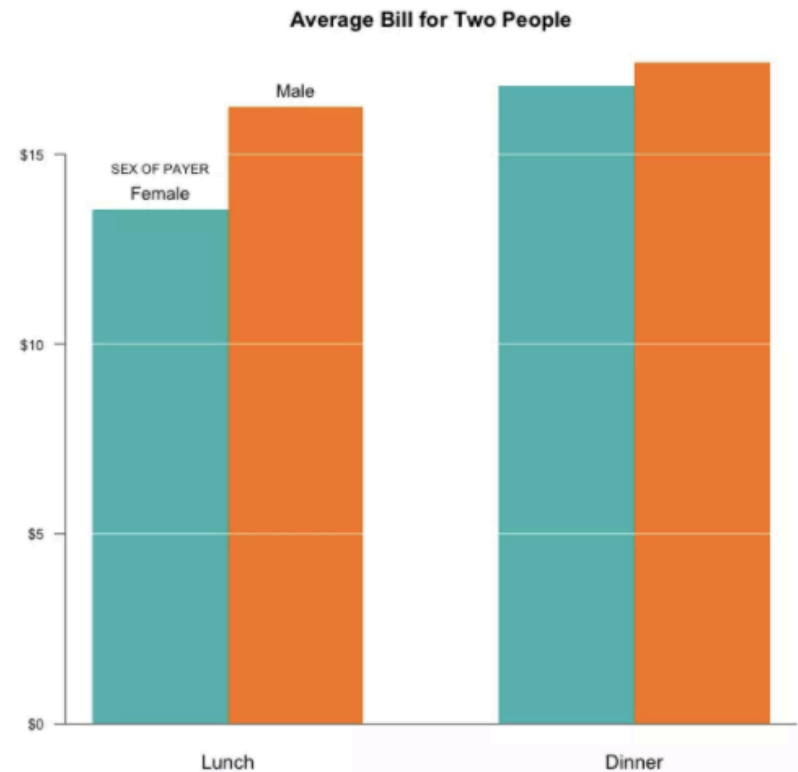
# Graphics options in R

- At least 3 primary graphics options in R
  - base R graphics
    - `plot()`, `par()`, etc
  - lattice
  - **ggplot2**
- ggplot2 consistently one of the top two most popular of all R packages

# Why use ggplot2? - “prettier” graphics in less lines of code



```
ggplot(data=dat1, aes(x=time, y=total_bill, fill=sex)) +  
  geom_bar(colour="black", stat="identity",  
           position=position_dodge(),  
           size=.3) +  
  scale_fill_hue(name="Sex of payer") +  
  xlab("Time of day") + ylab("Total bill") +  
  ggtitle("Average bill for 2 people") +  
  theme_bw()
```



```
par(cex=1.2, cex.axis=1.1)  
barplot(dat1mat, beside = TRUE, border=NA, col=mf_col,  
        main="Average Bill for Two People", yaxt="n")  
axis(2, at=axTicks(2), labels=sprintf("%$s", axTicks(2)),  
     las=1, cex.axis=0.8)  
grid(NA, NULL, lwd=1, lty=1, col="#ffffff")  
abline(0, 0)  
text(1.5, dat1mat["Female", "Lunch"], "Female", pos=3)  
text(2.5, dat1mat["Male", "Lunch"], "Male", pos=3)  
text(1.5, dat1mat["Female", "Lunch"]+0.7, "SEX OF PAYER",  
     pos=3, cex=0.75)
```

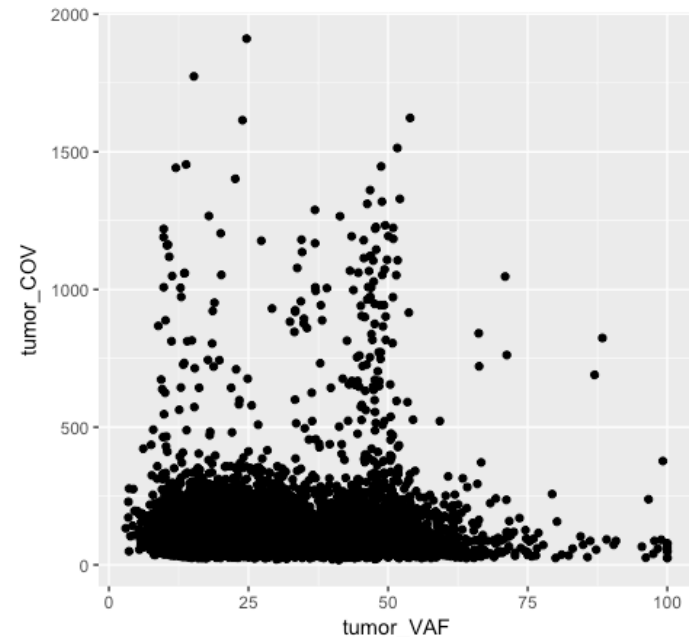
# ggplot2 syntax

```
ggplot(data=variantData, aes(x=tumor_VAF, y=tumor_COV)) + geom_point()
```

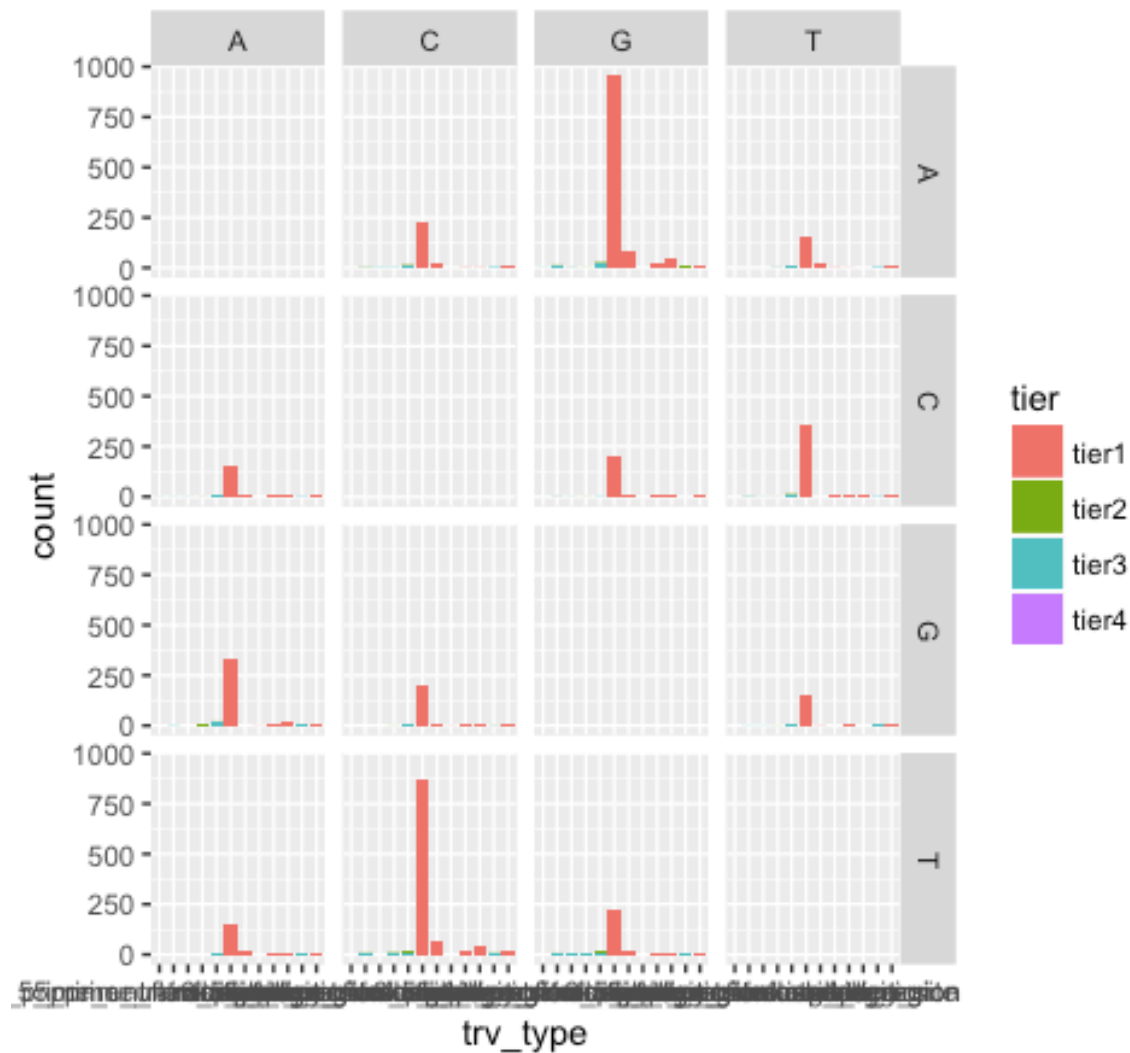
dataframe with  
data to be plotted

Aesthetic mappings describe how  
variables in the data are mapped to  
visual properties (aesthetics) of  
geometric objects (geoms)

geometric objects  
specify how data  
should be plotted

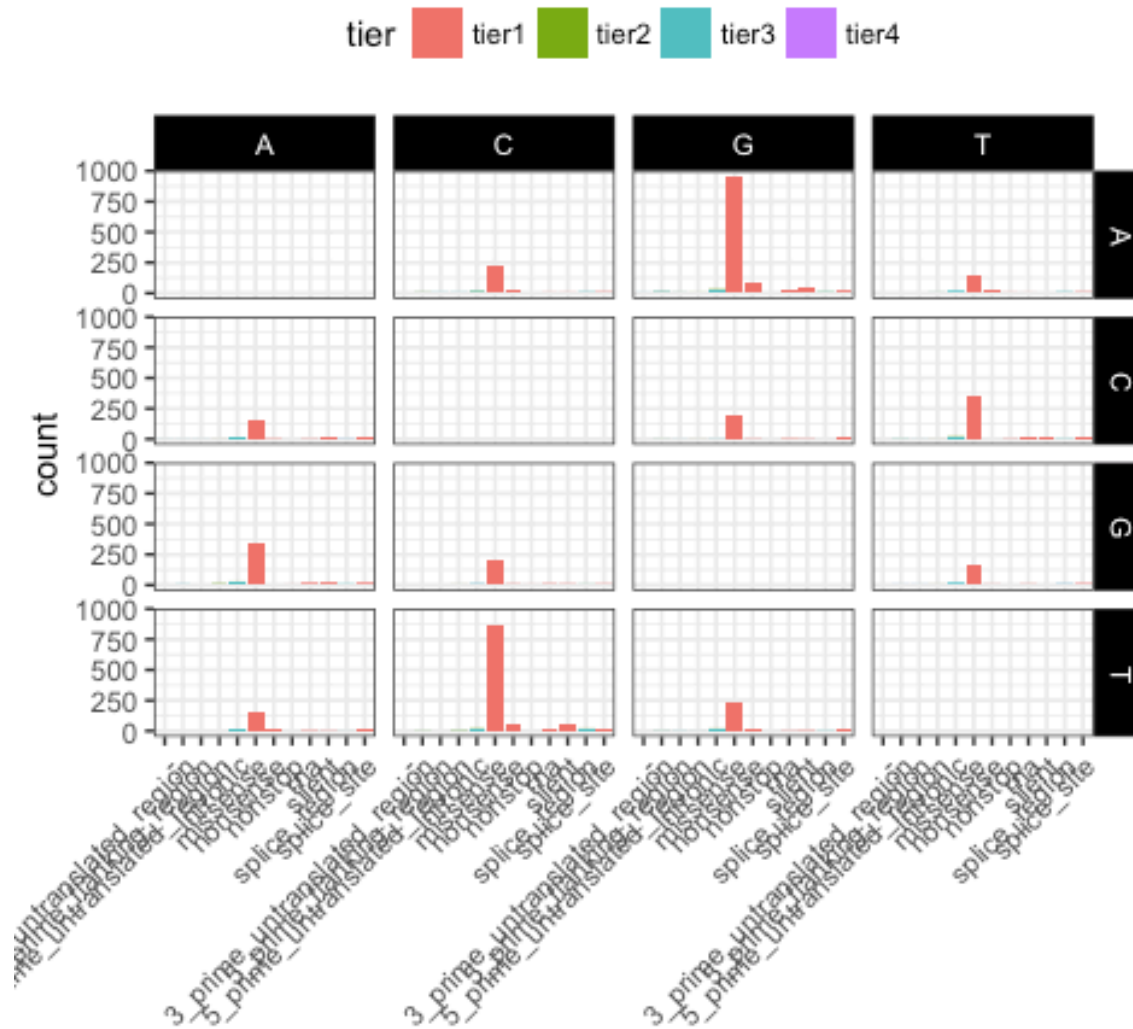


# Faceting allows multiple plots in a single page





# Themes allow stylistic improvements



# Wide vs long format

`melt(data=chrData, id.vars=c("region"))`



Long Format

region	variable	value
chr1	gc.content	0.43
chr4	gc.content	0.38
chr8	gc.content	40.00
chr1	mappability	63.00
chr4	mappability	47.00
chr8	mappability	40.00

Legend

- Value
- Variable Name
- ID Variable

Wide Format



`dcast(data=chrData, region ~ variable, value.var="value")`

region	gc.content	mappability
chr1	0.43	63
chr4	0.38	47
chr8	40.00	40

# Rmarkdown can be used to create publication ready documents presenting all code (analysis), comments, and results

myRprogram.Rmd  knitr  result.html

```
---  
title: "Introduction To Markdown"  
output: html_document  
---  
  
```\r setup, include=FALSE}  
knitr::opts_chunk$set(echo = TRUE)  
```\r
```

## ## Data description

The data used in this section is ...

```
```\r  
fl_data <- read.delim("~/Downloads/  
ggplot2ExampleData.tsv")  
```\r
```

## ## Data visualization

We will plot something...

```
```\r  
library(ggplot2)  
ggplot(fl_data, aes(x=tumor_VAF, fill=dataset)) +  
geom_density(alpha=.4)  
```\r
```

## Introduction To Markdown

### Data description

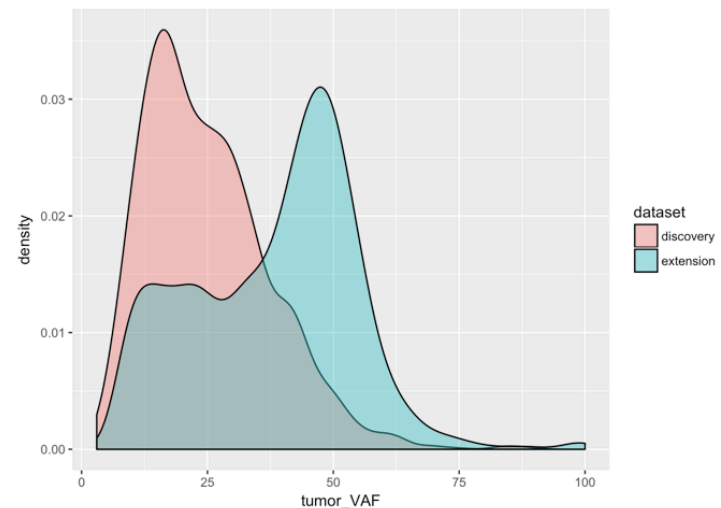
The data used in this section is ...

```
fl_data <- read.delim("~/Downloads/ggplot2ExampleData.tsv")
```

### Data visualization

We will plot something...

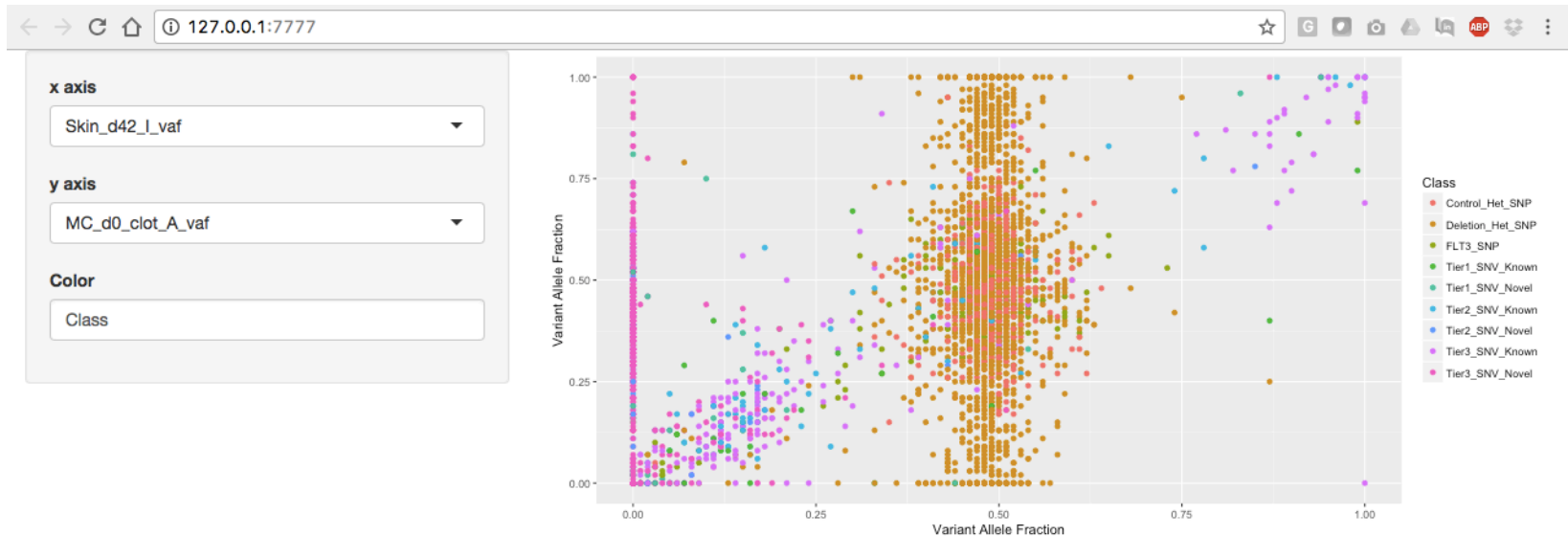
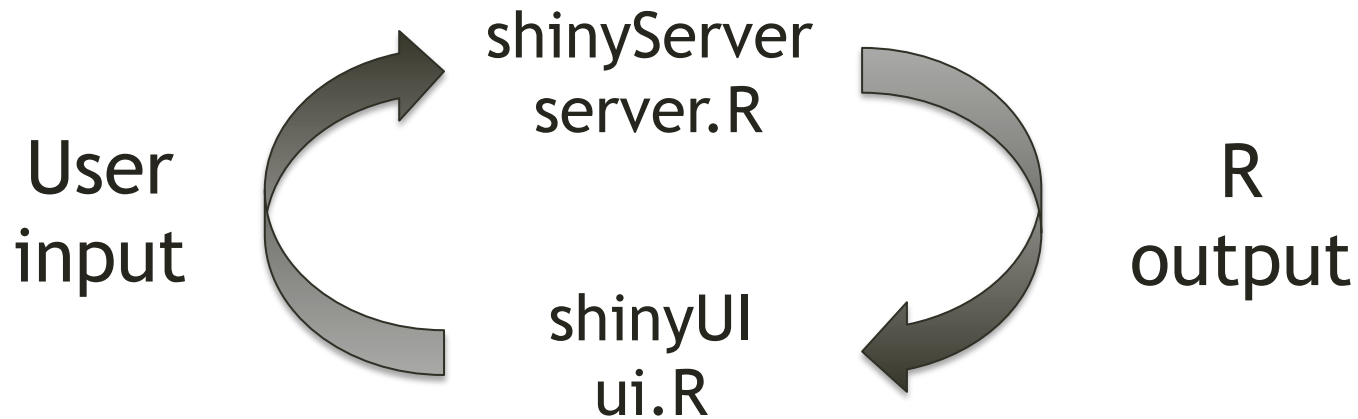
```
library(ggplot2)  
ggplot(fl_data, aes(x=tumor_VAF, fill=dataset)) + geom_density(alpha=.4)
```



# Interactive graphics with R shiny

- Optimizing a graphic often requires multiple iterative alterations
- Analysis and interpretation often benefits from active filtering, variable selection, and parameterization
- Interactive graphics allow end-users, especially non-experts, to more effectively explore data
- The R shiny package allows you to quickly and easily create sophisticated web-accessible interactive graphics

# Basic organization of a shiny application



Interactive User Interface (UI) = website

# Demo of shiny gallery genomics example

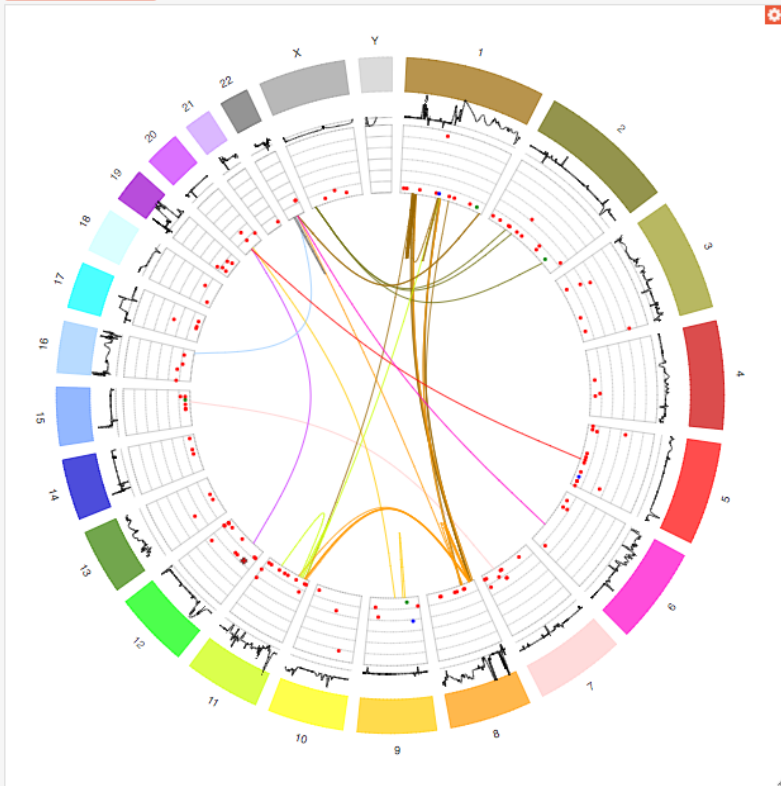
Shiny from RStudio

[Back to Gallery](#)



## ICGC PANCREATIC CANCER (DUCTAL ADENOCARCINOMA) - GENOME VIEWER

[More Information](#)



### Cohort Top ClinVar Gene Summary:

HGNC	Chr	Start	From	To	Consequence	Count
SMARCA4	19	11144847	C	T	missense_variant	18
TP53	17	7578437	G	A	stop_gained	18
KRAS	12	25398284	C	T	missense_variant	12
TP53	17	7578437	G	A	exon_variant	10
SMARCA4	19	11144847	C	T	exon_variant	8
TP53	17	7577121	G	A	downstream_gene_variant	6
TP53	17	7577121	G	A	missense_variant	6
KRAS	12	25398285	C	G	missense_variant	4
SMARCA4	19	11144847	C	T	downstream_gene_variant	4
TP53	17	7578437	G	A	downstream_gene_variant	4

Please select a donor ID:

DO49184

[SNP Consequences](#)

Resize Factor:



<https://shiny.rstudio.com/gallery/>

# Questions?