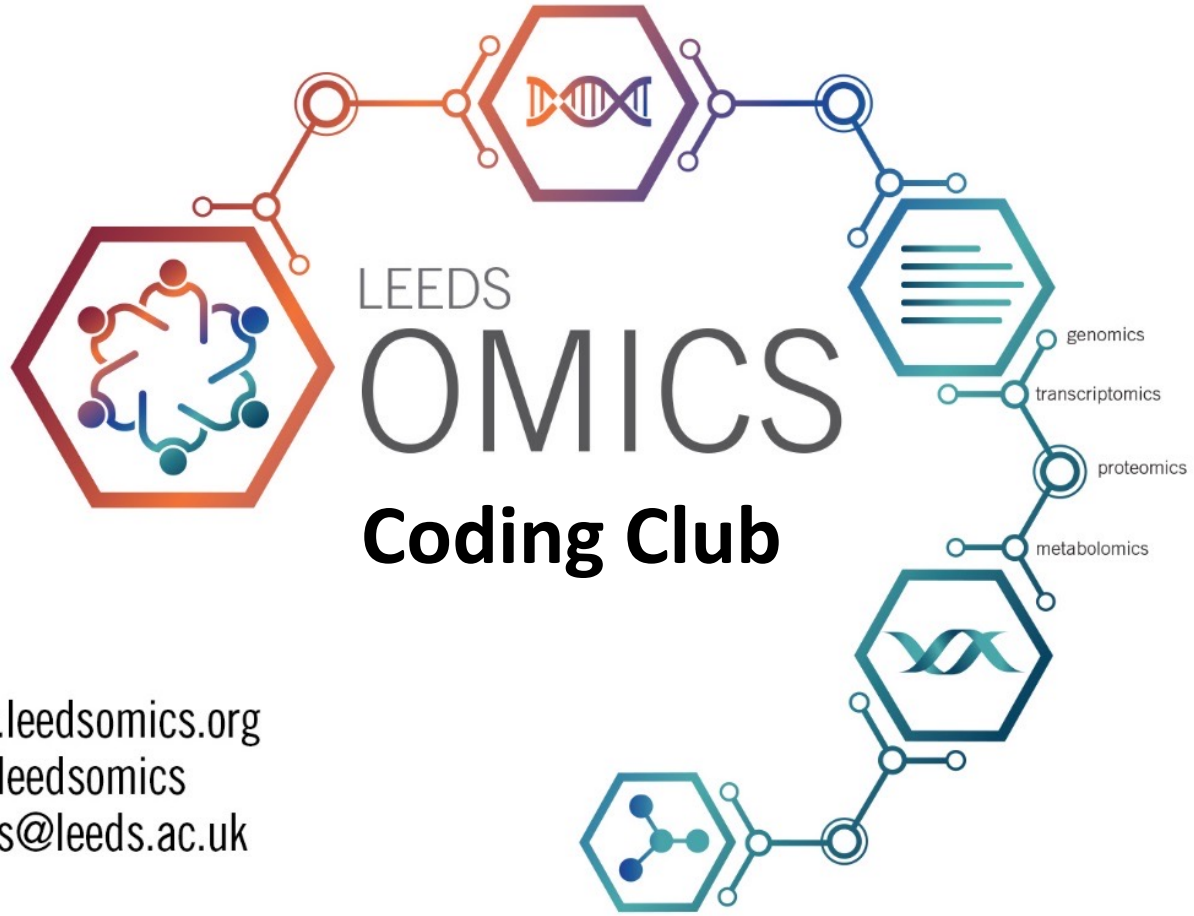

Coding Club

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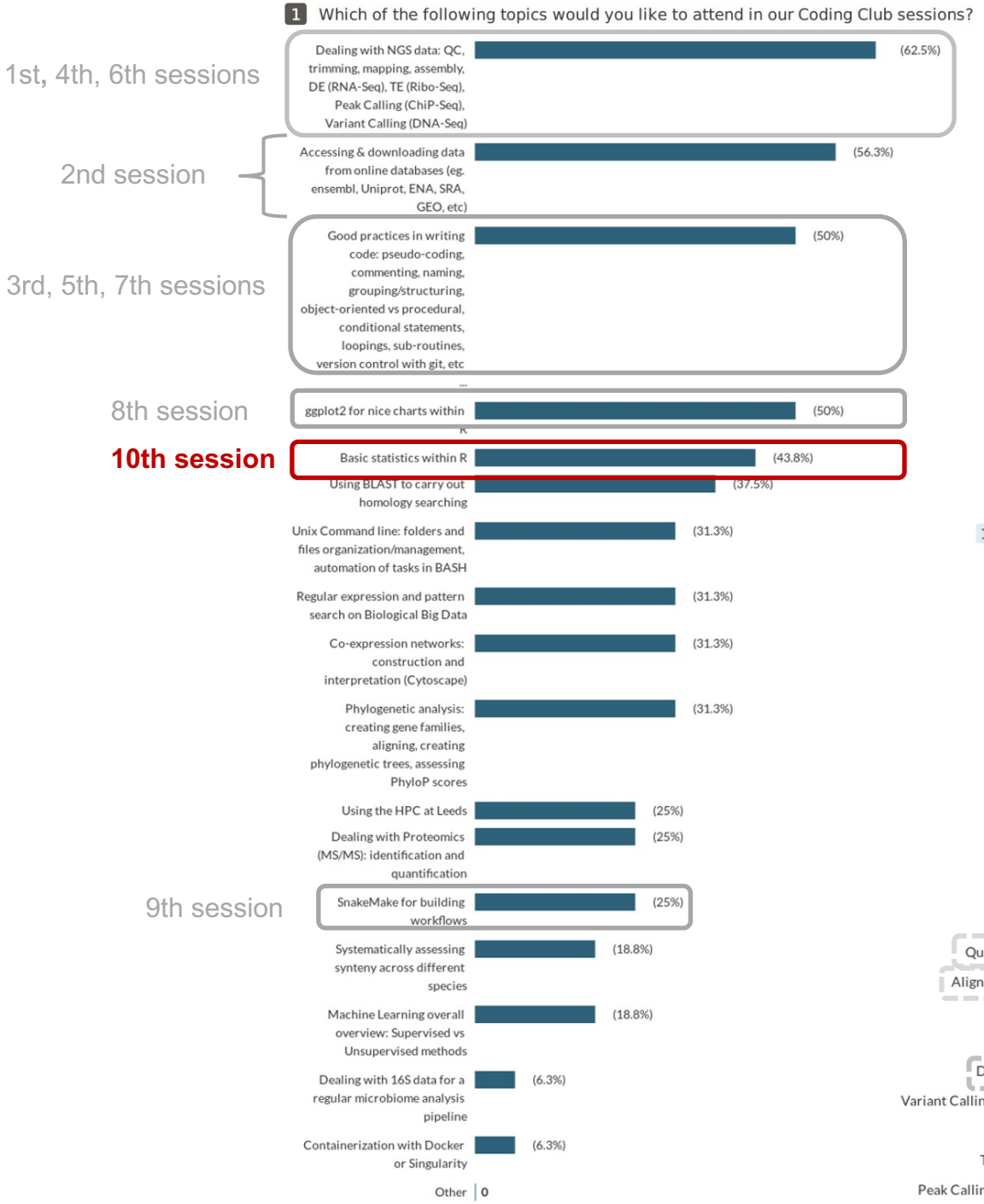
Basic Statistics within R

Club Moderators: Elton Vasconcelos and Euan McDonnell

Topics to be addressed on the **2020-21** season - **Survey Result**



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Survey Result (2020-2021)

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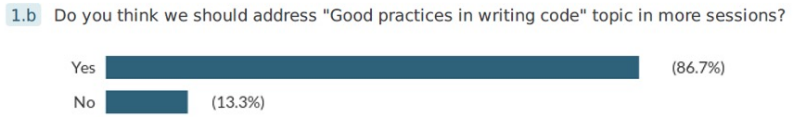
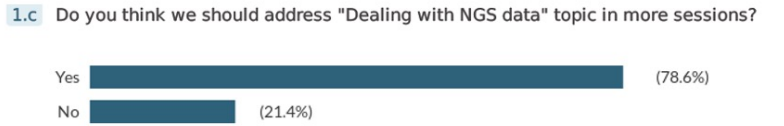
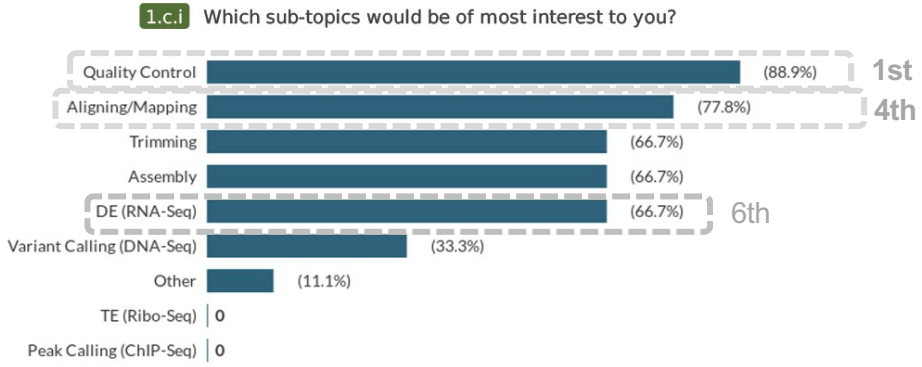






R has its own command line environment

Table of Useful R commands

https://cran.r-project.org/doc/contrib/Paradis-rdebuts_en.pdf

Command	Purpose
help()	Obtain documentation for a given R command
example()	View some examples on the use of a command
c(), scan()	Enter data manually to a vector in R
seq()	Make arithmetic progression vector
rep()	Make vector of repeated values
data()	Load (often into a data.frame) built-in dataset
View()	View dataset in a spreadsheet-type format
str()	Display internal structure of an R object
read.csv(), read.table()	Load into a data.frame an existing data file
library(), require()	Make available an R add-on package
dim()	See dimensions (# of rows/cols) of data.frame
length()	Give length of a vector
ls()	Lists memory contents
rm()	Removes an item from memory
names()	Lists names of variables in a data.frame
hist()	Command for producing a histogram
histogram()	Lattice command for producing a histogram
stem()	Make a stem plot
table()	List all values of a variable with frequencies
xtabs()	Cross-tabulation tables using formulas
mosaicplot()	Make a mosaic plot
cut()	Groups values of a variable into larger bins
mean(), median()	Identify "center" of distribution
by()	apply function to a column split by factors
summary()	Display 5-number summary and mean
var(), sd()	Find variance, sd of values in vector
sum()	Add up all values in a vector
quantile()	Find the position of a quantile in a dataset
barplot()	Produces a bar graph
barchart()	Lattice command for producing bar graphs
boxplot()	Produces a boxplot
bwplot()	Lattice command for producing boxplots

Command	Purpose
plot()	Produces a scatterplot
xyplot()	Lattice command for producing a scatterplot
lm()	Determine the least-squares regression line
anova()	Analysis of variance (can use on results of lm())
predict()	Obtain predicted values from linear model
nls()	estimate parameters of a nonlinear model
residuals()	gives (observed - predicted) for a model fit to data
sample()	take a sample from a vector of data
replicate()	repeat some process a set number of times
cumsum()	produce running total of values for input vector
ecdf()	builds empirical cumulative distribution function
dbinom(), etc.	tools for binomial distributions
dpois(), etc.	tools for Poisson distributions
pnorm(), etc.	tools for normal distributions
qt(), etc.	tools for student t distributions
pchisq(), etc.	tools for chi-square distributions
binom.test()	hypothesis test and confidence interval for 1 proportion
prop.test()	inference for 1 proportion using normal approx.
chisq.test()	carries out a chi-square test
fisher.test()	Fisher test for contingency table
t.test()	student t test for inference on population mean
qqnorm(), qqline()	tools for checking normality
addmargins()	adds marginal sums to an existing table
prop.table()	compute proportions from a contingency table
par()	query and edit graphical settings
power.t.test()	power calculations for 1- and 2-sample t
anova()	compute analysis of variance table for fitted model

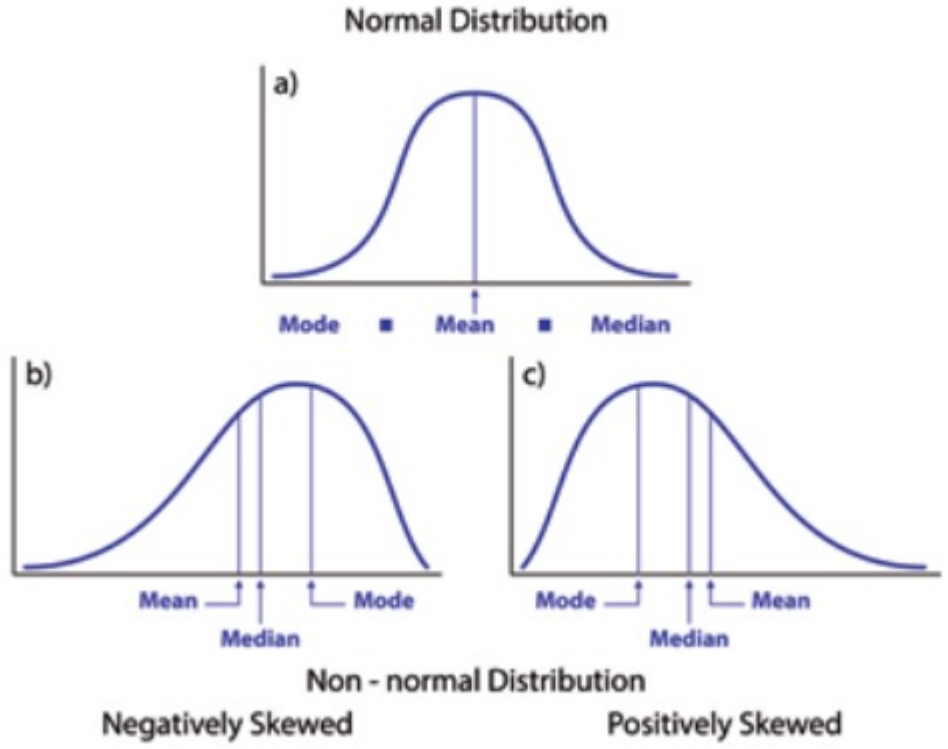
https://cran.r-project.org/doc/contrib/Paradis-rdebuts_en.pdf

http://www.math.umt.edu/olear/stat458/Rseminar_2.pdf

→ Other useful R material for beginners

Common practice prior running any statistics on your data

Check the distribution of whatever data values your samples have



https://heljves.com/gallery/vol_1_issue_1_2019_8.pdf (*Antonopoulos & Kakisis, 2019*)

Which test to use?

TYPE OF VARIABLE	Continuous									Categorical	
DISTRIBUTION	Normal distribution					Skewed distribution					
No of GROUPS	1 group	2 groups		>2 groups		1 group	2 groups		>2 groups		
Independence between GROUPS		Independent	Dependent	Independent	Dependent		Independent	Dependent	Independent	Dependent	Independent	Dependent
STATISTICAL TEST	1-sample t-test	Independent sample t-test	Paired sample t-test	ANOVA	Repeated-measures ANOVA	Sign test, Wilcoxon signed ranks test	Mann-Whitney U test	Sign test, Wilcoxon signed ranks test	Kruskal-Wallis H test	Friedman test	Chi-square test, Fischer exact test	McNemar's test
EXAMPLE	Mean age of all patients with AAA	Mean age of AAA patients treated with OSR vs. EVAR	Difference in aortic diameter in patients before vs. after EVAR	Mean age of AAA patients treated with OSR vs. EVAR vs. conservative treatment	Difference in aortic diameter in patients before vs. after 6 months vs. after 1 year of EVAR	Mean age of all patients with AAA	Mean age of AAA patients treated with OSR vs. EVAR	Difference in aortic diameter in patients before vs. after EVAR	Mean age of AAA patients treated with OSR vs. EVAR vs. conservative treatment	Difference in aortic diameter in patients before vs. after 6 months vs. after 1 year of EVAR	Difference in males/ females among patients treated with OSR vs. EVAR	Difference in number of patients with excluded/ non-excluded aneurysmal sac after 6 months vs. after 1 year of EVAR

Table 1. A statistical algorithm depicting which test to use, based on the type of variable, data distribution, number of groups and independence between groups

Abbreviations: AAA: Abdominal Aortic Aneurysm, ANOVA: Analysis of Variance, EVAR: Endovascular Aortic Repair, OSR: Open Surgical Repair

https://heljves.com/gallery/vol_1_issue_1_2019_8.pdf (*Antonopoulos & Kakisis, 2019*)

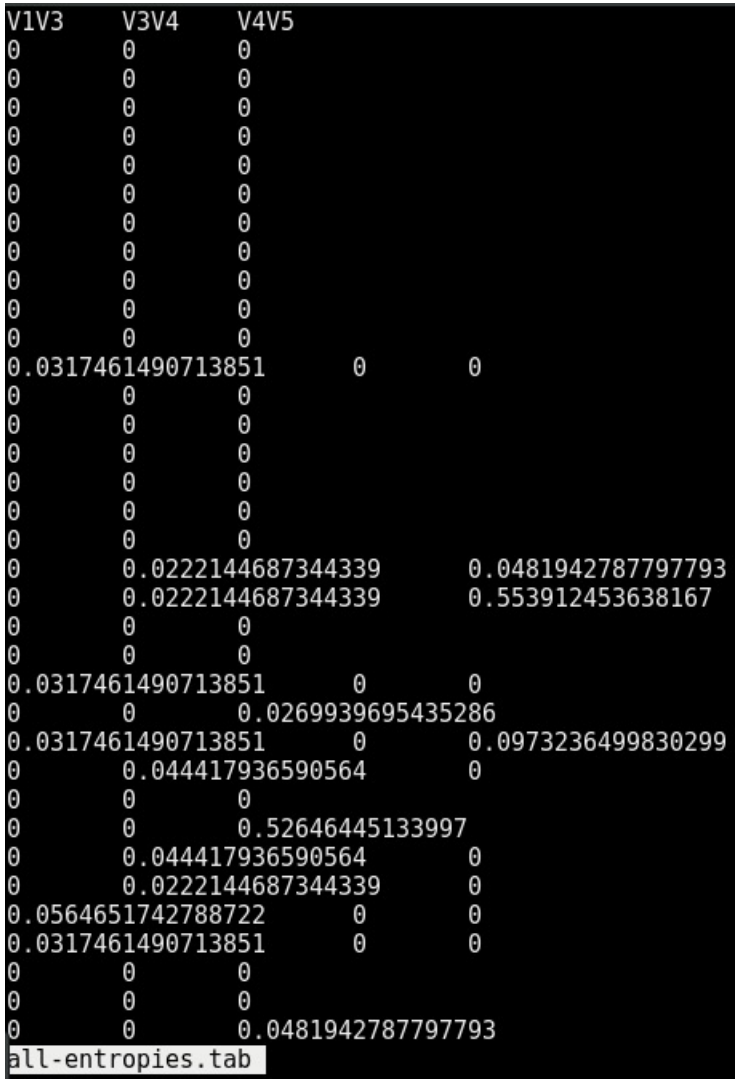
Summary of some basic statistical tests in R

R function	Test	Parametric (p) or Non-Parametric (np)	Purpose
t.test	T-test	p	pairwise
wilcox.test	Mann-Whitney-Wilcoxon	np	pairwise
aov	ANOVA	p	>2 groups
kruskal.test	Kruskal-Wallis	np	>2 groups
chisq.test	Chi-Square	np	Categorical: 2x2 contingency table
fisher.test	Fisher Exact Test	np	Categorical: 2x2 contingency table
binom.test	Binomial Test	np	#successes and failures on *n* trials
ks.test	Kolmogorov-Smirnov	np	Equality of cumulative distributions
cor.test(x, y, method = “pearson”)	Pearson Correlation (*r*)	p	Correlation coefficient from pairs of numerical vectors
cor.test(x, y, method = “spearman”)	Spearman Correlation (*rho*)	np	Correlation coefficient from pairs of numerical vectors

Type ? followed by the function name within R or visit https://www.statmethods.net/stats/index.html for more details

Practical example on an *Omics* context

→ Are there differences between variable regions from the 16S rRNA evolutionary marker gene regarding discriminatory power for taxonomic classification of vector-borne bacterial pathogens (VBPs)?



```
V1V3    V3V4    V4V5
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0.0317461490713851      0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0       0
0       0.0222144687344339      0.0481942787797793
0       0.0222144687344339      0.553912453638167
0       0       0
0       0       0
0.0317461490713851      0       0
0       0       0.0269939695435286
0.0317461490713851      0       0.0973236499830299
0       0.044417936590564       0
0       0       0
0       0       0.52646445133997
0       0.044417936590564       0
0       0.0222144687344339      0
0.0564651742788722      0       0
0.0317461490713851      0       0
0       0       0
0       0       0
0       0       0.0481942787797793
all-entropies.tab
```

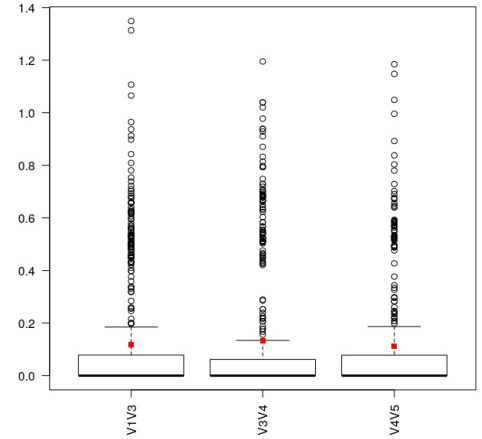
← **Input file**

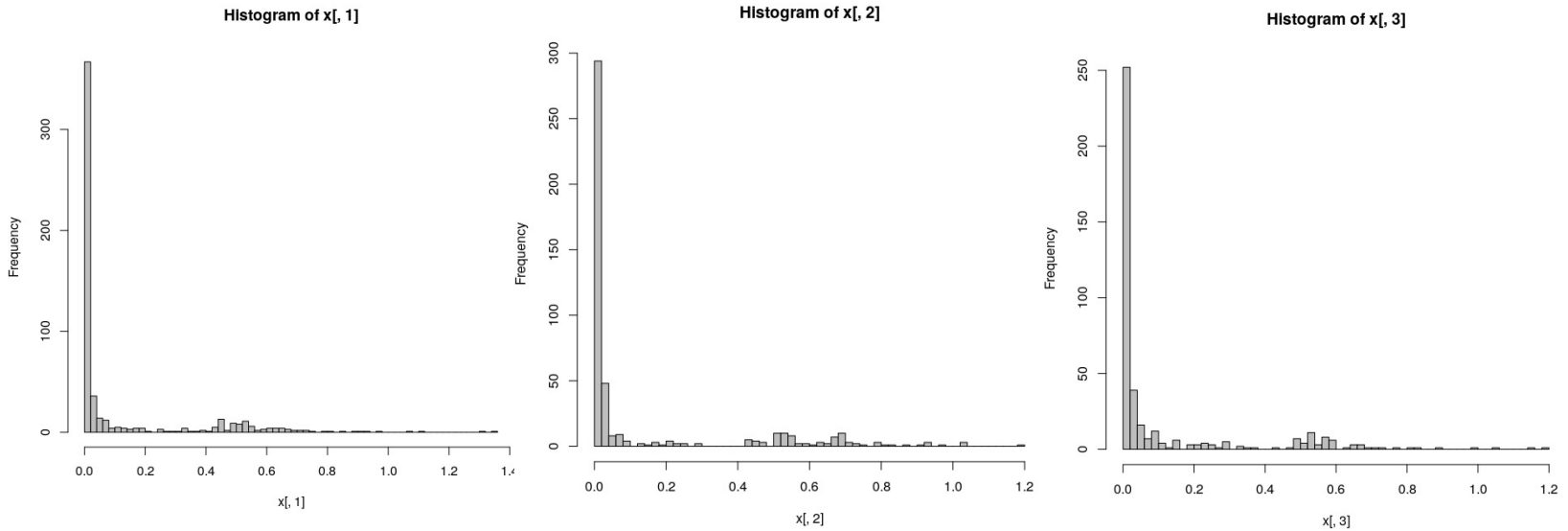
Shannon entropy values per individual position of a 320 VBPs-containing multiple sequence alignment (MSA) from three 16S variable regions

`diversity()` function from the ”vegan” R package

Checking entropy values' distribution with both boxplot and histograms

```
x = read.delim("all-entropies.tab")
dim(x)
head(x)
allVmeans = NULL
for(i in 1:3){ allVmeans = as.vector(c(allVmeans, mean(x[,i], na.rm = T))) }
boxplot(x, las=2)
points(allVmeans, pch = 15, col = "red")
hist(x[,1], col = "gray", breaks = 50)
hist(x[,2], col = "gray", breaks = 50)
hist(x[,3], col = "gray", breaks = 50)
```





Shapiro-Wilk Test of normality

`shapiro.test()`

p-value > 0.05 = normal distribution

p-value < 0.05 = non-normal distribution

Opting for non-parametric tests

```
> kruskal.test(x)

        Kruskal-Wallis rank sum test

data:  x
Kruskal-Wallis chi-squared = 1.2172, df = 2, p-value = 0.5441
```

```
> wilcox.test(x[,1], x[,2])$p.value
[1] 0.4414327
> wilcox.test(x[,1], x[,3])$p.value
[1] 0.3318844
> wilcox.test(x[,2], x[,3])$p.value
[1] 0.5765521
```

Answer:

No, the three assessed 16S variable regions have the same discriminatory power for the 320 VBP species/strains under study.

Bring your issues on!