ILS R Scripts

https://github.com/IntegrativeLifeScience

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r-crash-course

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half-day introduction to the R language

View the Project on GitHub

Description

This is intended to be a short introduction, or crash-course, to those wanting to learn the R language. It may be helpful to those with experience of other programming languages and familiar with general concepts of data analysis and programming. You might also use it as a refresher before more intermediate courses; such as our Data manipulation and Visualisation using R course

Materials

- Compiled
- Source (R markdown)

Further Reading and Viewing

https://bioinformatics-core-shared-training.github.io/r-crash-course/

- Has an intro into R and goes through basic aspects of R and programming
  - Variables
  - Functions
  - Vectors
  - Data frame
  - Subsetting data
  - Plotting
  - Statistical testing
  - Help

GPLv3 License

why?

- We are releasing scripts / code to anyone with an internet connection
- GPLv3 allows free use of the code but forbids people from modifying it and making the new, edited version, closed source – it must be freely published and remain under the GPLv3 license
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- A Quick Guide to GPLv3
- Why Upgrade to GPLv3
- Frequently Asked Questions about the GNU licenses
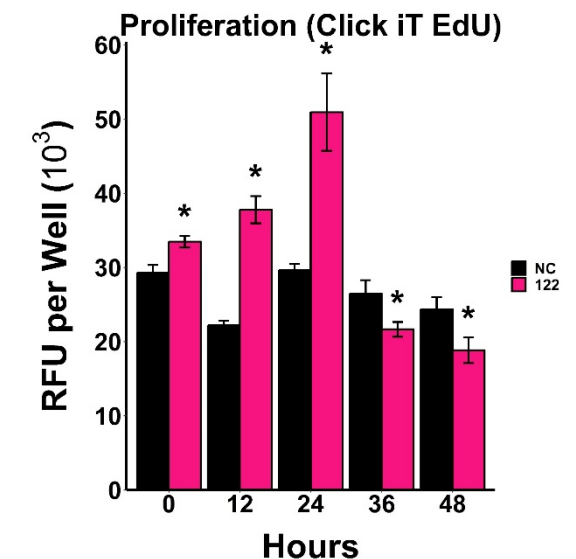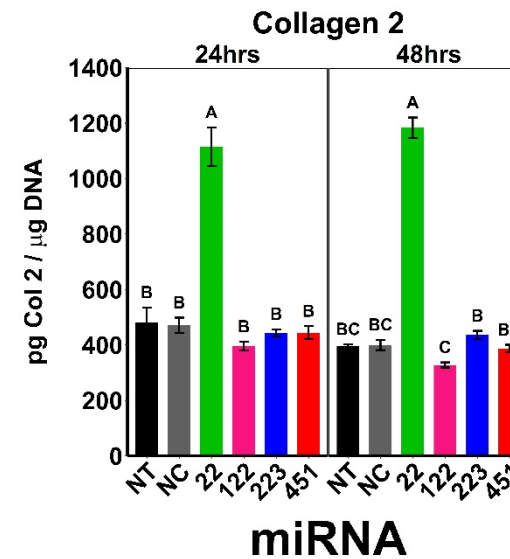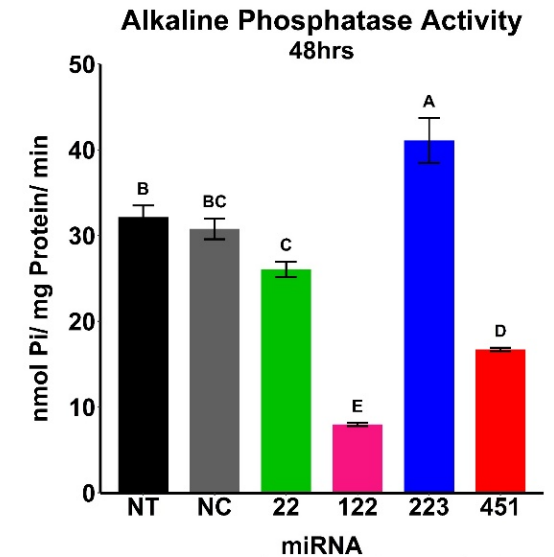- How to use GNU licenses for your own software

GPLV3
Free Software

histogram-anova-v3.3.R

https://github.com/IntegrativeLifeScience/Data-Visualization/tree/master/R-Scripts/histogram-anova

Functions

- Written for basic histograms
- Uses input file that specifies statistical tests & general appearance
- Statistical test:
  - 1 and 2 tailed outlier detection
  - ANOVA w/ Tukeys Post Hoc
  - Paired or Unpaired student t-test
- Can perform basic transformations
  - Dividing all values by X
  - Calculating treatment over control
  - Basic timecourse
- Setup batch creation & automatic save to file

Wales_StudentPres.R

https://github.com/IntegrativeLifeScience/Data-Visualization/tree/master/R-Scripts/wales-student-pres

- Available on ILS' github
- Walk through of many R functions
- Data file not on hand…
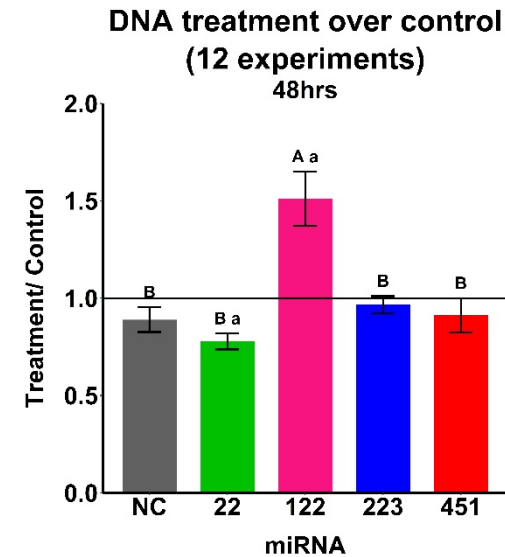
```
1  ##Editing and Making Publication Ready Plots
2  #Student Presentation: By Shea Wales
3
4  # ====================== Class outline ======================
5  #Today we are going to be discussing different ways to modify and customize your figures.
6
7  #(1) Let's talk: TYPES OF PLOTS
8  #We will briefly review some types of plots that you can make in r
9    ## Bar Plots / Histograms
10   ## Scatter Plots
11   ## Line Plots
12   ## Box Plots
13   ## Violin Plots
14
15 #(2) Let's talk: PRE-SETS
16 #I'll show you how to store/save a plot, and introduce you to some pre##set themes already available in ggplot2:
17   ## theme_gray
18   ## theme_bw
19   ## theme_linedraw
20   ## theme_light
21   ## theme_dark
22   ## theme_minimal
23   ## theme_classic
24   ## theme_void
25   ## theme_test
26
27 #(3) Let's talk: EDITING ANYTHING & EVERYTHING
28 #We will use histograms to demonstrate how you can alter almost anything within a ggplot to make it look the way you want it. We w
29   ## bin-width
30   ## plot title
31   ## axis and legend labels
32   ## How to add a theme to, and remove a theme from, a stored plot
33   ## How use color palettes, and make your own.
34   ## How to use alter default themes:
35      ## Text
36      ## Background color
37      ## Grid lines
38      ## Tick Marks
39      ## Legend location
40   ## Storing plots
41   ## Setting and defining themes for later use (AKA: Your personal publication style plots!)
42
43 # ====================== Class outline ====================== #
44
45 #### Setup: Load Libraries & Import Data ####
```

ENVrasters_test_for_correlation.R

https://github.com/IntegrativeLifeScience/Data-Analytics/tree/master/R-Scripts/ENV-rasters-correlation

```r
########### Working with rasters and performing environmental correlation test #############

install.packages(c("raster", "sp", "gdistance"), dependencies = TRUE)
install.packages("rgdal")
library(raster)
library(rgdal)
install.packages("dismo")
library(dismo)

install.packages("corrplot")
library(corrplot)

setwd("~/Desktop/modeling_materials_bio1-19_30s_bil")
```

- Available on ILS' github

	Longitude	Latitude	./alt23_pa	./bio1_pa	./bio10_p	./bio11_p	./bio12_p	./bio13_p	./bio14_p	./bio15_p	./bio16_p	./bio17_p	./bio18_p	./bio19_p	./bio2_pa	./bio3_pa	./bio4_pa	./bio5_pa	./bio6_pa	./bio7_pa	./bio8_pa	./bio9_pa
Longitude	1	-0.80543	-0.16233	0.168721	0.16966	0.161507	0.155068	-0.17658	0.532181	-0.6291	-0.25868	0.572274	0.611496	0.33477	-0.44521	0.595913	0.294702	-0.01685	0.265207	-0.73866	0.142447	0.12649
Latitude	-0.80543	1	-0.28554	0.255941	0.257043	0.259577	0.162887	0.205118	-0.04887	0.140719	0.263189	-0.07774	-0.31056	0.089062	-0.12725	-0.80807	0.151361	0.350737	0.208944	0.272709	0.288257	0.3242
./alt23_pa	-0.16233	-0.28554	1	-0.99544	-0.99529	-0.99427	-0.41018	-0.12754	-0.61702	0.547585	-0.05905	-0.62855	-0.44964	-0.63569	0.617065	0.554339	-0.86817	-0.9614	-0.98677	0.343884	-0.98916	-0.99476
./bio1_pa	0.168721	0.255941	-0.99544	1	0.999639	0.999636	0.398973	0.147034	0.592818	-0.50715	0.075501	0.604662	0.459077	0.622471	-0.58796	-0.54074	0.86192	0.971798	0.988125	-0.32305	0.990619	0.991399
./bio10_p	0.16966	0.257043	-0.99529	0.999639	1	0.999117	0.400391	0.14584	0.595633	-0.51035	0.074871	0.607539	0.46097	0.624727	-0.5889	-0.54324	0.871037	0.971773	0.987991	-0.32276	0.989438	0.991868
./bio11_p	0.161507	0.259577	-0.99427	0.999636	0.999117	1	0.406541	0.158986	0.592678	-0.50275	0.088368	0.603681	0.461702	0.625996	-0.58475	-0.54237	0.851816	0.97275	0.987538	-0.31927	0.99135	0.991396
./bio12_p	0.155068	0.162887	-0.41018	0.398973	0.400391	0.406541	1	0.79733	0.809548	-0.6415	0.78552	0.788826	0.801859	0.883629	-0.44404	-0.09125	0.262684	0.330567	0.451416	-0.41381	0.445749	0.438579
./bio13_p	-0.17658	0.205118	-0.12754	0.147034	0.14584	0.158986	0.79733	1	0.363145	-0.08603	0.9796	0.327918	0.552232	0.519365	0.060133	-0.07885	-0.07154	0.188462	0.139006	0.076063	0.184004	0.153172
./bio14_p	0.532181	-0.04887	-0.61702	0.592818	0.595633	0.592678	0.809548	0.363145	1	-0.91014	0.301773	0.993119	0.85941	0.908754	-0.76246	-0.00287	0.567313	0.439101	0.68085	-0.76378	0.619732	0.626991
./bio15_p	-0.6291	0.140719	0.547585	-0.50715	-0.51035	-0.50275	-0.6415	-0.08603	-0.91014	1	-0.0585	-0.93254	-0.70316	-0.80706	0.809322	-0.02643	-0.5607	-0.32918	-0.6043	0.82008	-0.52382	-0.54401
./bio16_p	-0.25868	0.263189	-0.05905	0.075501	0.074871	0.088368	0.78552	0.9796	0.301773	-0.0585	1	0.263821	0.47349	0.481164	0.098786	-0.10967	-0.13369	0.128351	0.064454	0.131451	0.118272	0.093124
./bio17_p	0.572274	-0.07774	-0.62855	0.604662	0.607539	0.603681	0.788826	0.327918	0.993119	-0.93254	0.263821	1	0.854005	0.910844	-0.79316	-0.00417	0.589787	0.443224	0.696042	-0.79414	0.623321	0.63201
./bio18_p	0.611496	-0.31056	-0.44964	0.459077	0.46097	0.461702	0.801859	0.552232	0.85941	-0.70316	0.47349	0.854005	1	0.804184	-0.47029	0.241473	0.415198	0.33896	0.529835	-0.60082	0.472237	0.451551
./bio19_p	0.33477	0.089062	-0.63569	0.622471	0.624727	0.625996	0.883629	0.519365	0.908754	-0.80706	0.481164	0.910844	0.804184	1	-0.65744	-0.13424	0.529317	0.514892	0.686773	-0.60144	0.646027	0.65945
./bio2_pa	-0.44521	-0.12725	0.617065	-0.58796	-0.5889	-0.58475	-0.44404	0.060133	-0.76246	0.809322	0.098786	-0.79316	-0.47029	-0.65744	1	0.237316	-0.59699	-0.40451	-0.69427	0.880361	-0.59793	-0.61587
./bio3_pa	0.595913	-0.80807	0.554339	-0.54074	-0.54324	-0.54237	-0.09125	-0.07885	-0.00287	-0.02643	-0.10967	-0.00417	0.241473	-0.13424	0.237316	1	-0.45649	-0.6377	-0.47363	-0.24873	-0.54005	-0.56514
./bio4_pa	0.294702	0.151361	-0.86817	0.86192	0.871037	0.851816	0.262684	-0.07154	0.567313	-0.5607	-0.13369	0.589787	0.415198	0.529317	-0.59699	-0.45649	1	0.81343	0.865584	-0.37186	0.834498	0.859315
./bio5_pa	-0.01685	0.350737	-0.9614	0.971798	0.971773	0.97275	0.330567	0.188462	0.439101	-0.32918	0.128351	0.443224	0.33896	0.514892	-0.40451	-0.6377	0.81343	1	0.92592	-0.09286	0.960544	0.960725
./bio6_pa	0.265207	0.208944	-0.98677	0.988125	0.987991	0.987538	0.451416	0.139006	0.68085	-0.6043	0.064454	0.696042	0.529835	0.686773	-0.69427	-0.47363	0.865584	0.92592	1	-0.46207	0.982104	0.983867
./bio7_pa	-0.73866	0.272709	0.343884	-0.32305	-0.32276	-0.31927	-0.41381	0.076063	-0.76378	0.82008	0.131451	-0.79414	-0.60082	-0.60144	0.880361	-0.24873	-0.37186	-0.09286	-0.46207	1	-0.3336	-0.33782
./bio8_pa	0.142447	0.288257	-0.98916	0.990619	0.989438	0.99135	0.445749	0.184004	0.619732	-0.52382	0.118272	0.623321	0.472237	0.646027	-0.59793	-0.54005	0.834498	0.960544	0.982104	-0.3336	1	0.990774
./bio9_pa	0.12649	0.3242	-0.99476	0.991399	0.991868	0.991396	0.438579	0.153172	0.626991	-0.54401	0.093124	0.63201	0.451551	0.65945	-0.61587	-0.56514	0.859315	0.960725	0.983867	-0.33782	0.990774	1

RNAseq analysis in R

https://bioinformatics-core-shared-training.github.io/RNAseq-R/

- Has R tutorials and presentations covering RNAseq in R

  - Alignment and counting
  - RNA-seq pre-processing
  - Differential expression

  - Annotation and visualization
  - Gene-set testing