

Useful R code

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Warning: package 'rmarkdown' was built under R version 3.5.2

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This document can be found at <https://github.com/darwinanddavis/UsefulCode>

Overview

This document outlines some useful R code for plotting, cool functions, and other random tidbits.

Install dependencies

Attributes

Access structural attributes of unique classes, such as raster and ggmap (bbox).

```
# Normal example
df <- data.frame("X"=c(1:5), "Y"=c(6:10))
str(df)
df$X

# `attr` method
require(ggmap)
map <- get_map("Atlanta", zoom=12, source="stamen", maptype="toner-lines")
str(map)
attr(map, "bb")$ll.lat
```

Classes

Convert character to factor to numeric without conversion error

```
read.table(f, header=T, sep=",", row.names=NULL, stringsAsFactors=FALSE, strip.white=TRUE)
f$V2<-as.numeric(f$V2)
```

See call options for class

```
methods(class="estUDm")
```

Set dynamic input for variable / assign variable to char vector

```
shadedens<-function(shadedens){ # set shade density to clumped (to match food) or sparse
  if (shadedens == "Random"){
    NLCommand("set Shade-density \"Random\" ")
  }else{
    NLCommand("set Shade-density \"Clumped\" ")
  }
}
shadedens("Clumped") # set clumped resources
```

D3 apps

Interactive network plots using d3

```
# Load package
install.packages("networkD3")
library(networkD3)

# Load energy projection data
URL <- "https://cdn.rawgit.com/christophergandrud/networkD3/master/JSONdata/energy.json"
Energy <- jsonlite::fromJSON(URL)
```

```

# Now we have 2 data frames: a 'links' data frame with 3 columns (from, to, value), and a 'nodes' data frame
head(Energy$links)
head(Energy$nodes)

# Thus we can plot it
sankeyNetwork(Links = Energy$links, Nodes = Energy$nodes, Source = "source",
              Target = "target", Value = "value", NodeID = "name",
              units = "TWh", fontSize = 12, nodeWidth = 30)

?sankeyNetwork

```

Dataframes

Optimal empty data frame

```

df <- data.frame(Date=as.Date(character()),
                 X=numeric(),
                 Y=integer(),
                 stringsAsFactors=FALSE)

```

Add df cols with mutate

```

require(dplyr)
df <- data.frame("a"=rnorm(10),"b"=(1:20))
df %>%
  mutate(
    "c"=rnorm(20),
    b = b *67
  )

```

Change df column names

```

colnames(data)[c(1,2,3)] <- c("TimeStamp","Lat","Long")

```

Remove multiple columns from df

```

### Remove multiple NA columns
rm_cols <- grep("NA", names(tt), ignore.case = F)
df[,colnames(df[,rm_cols])] <- list(NULL)

```

Check number of characters in each column

```

supply(meso1, function(x) sum(nchar(x)))

```

Generic functions

Generic useful functions that I can't place under any other headings here

```

# dput() for converting outputs such as copied text or data tables into vectors
xx <- "Some copied text or table from the internet"
dput(xx)

```

Round up integers to optimal rounded value

```

nn <- c(46,11,23)
round_any(nn,10)

```

```
round_any(nn,10,ceiling)
round_any(nn,10,floor)
```

Get summary stats for dataset (means)

```
means = aggregate(Cumulative_cerics ~ r*hb, data=df, FUN=mean)
```

ggplot functions

Remove annoying stock gridlines from plot window

```
plot + theme_bw() +
  theme(panel.border = element_blank(), panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
# alternative (after loading ggridges library)
theme_ridges(grid=F,center_axis_labels = T)
```

Setting global graphics theme for ggplot

```
plot_it_gg <- function(bg,family){ # bg = colour to plot bg, family = font family
  theme_tufte(base_family = family) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_rect(fill = bg,
                                         colour = bg),
        plot.background = element_rect(fill=bg))
  ) +
  theme(axis.line = element_line(color = "white")) +
  theme(axis.ticks = element_line(color = "white")) +
  theme(plot.title = element_text(colour = "white")) +
  theme(axis.title.x = element_text(colour = "white"),
        axis.title.y = element_text(colour = "white")) +
  theme(axis.text.x = element_text(color = "white"),
        axis.text.y = element_text(color = "white")) +
  theme(legend.key = element_rect(fill = bg)) + # fill bg of legend
  theme(legend.title = element_text(colour="white")) + # legend title
  theme(legend.text = element_text(colour="white")) # legend labels
}
```

Put plot in function to take dynamic data inputs

Ref: <http://jcborras.net/carpet/visualizing-political-divergences-2012-local-elections-in-helsinki.html>

```
hr.mass.plot <- function(d) {
  p <- ggplot(d, aes(HR, Mass, color = colfunc)) +
    geom_density_2d(data=d, aes(x = HR, y = Mass),
                   stat = "density2d",position="identity",
                   color=adjustcolor("orange",alpha=0.8), size=1.5, contour = T, lineend="square",line.lty=2)
  p <- p + geom_point(data=d, aes(x = HR, y = Mass),
                     color=colfunc,
                     fill=colfunc) +
    scale_color_manual(values = magma(8))
  p <- p + scale_y_continuous(limits=c(-200,200), name="Mass lost (g)")
  p <- p + scale_x_continuous(limits=c(0,0.35),name=expression("Home range area (km^2)"))
  p <- p + theme_classic()
```

```

    print(p)
  }
  hr.mass.plot(d)

```

Using ggplot when looping through for loop and saving to dir

```

pdf("mypdf.pdf", onefile = T)
for(i in 1:3){
  par(bty="n", las = 1)
  grid.arrange(
    ggplot(data, aes(x = X, y = Y, fill=..x..)) + # geom_density_ridges()
    # scale = overlap
    geom_density_ridges_gradient(scale = 5, size=0.2,color="black", rel_min_height = 0.01,panel_scaling=1) +
    geom_density_ridges(scale = 5, size=0.2,color="black", rel_min_height = 0.01,fill="white",alpha=0.2) +
    # geom_density_ridges(scale = 5, size=0.2,color="white", rel_min_height = 0.01,fill=col,alpha=0.5) +
    scale_fill_viridis(name = "Diameter", alpha=0.1, option = "magma",direction=-1) + # "magma", "inferno"
    xlim(c(0,25)) +
    labs(title = paste0("Title_",i)) +
    xlab("X") +
    ylab("Y") +
    # plot_it_gg("white")
  )
} # end loop
dev.off()

```

Converting lists and dataframes to usable format for ggplot (melt package)

```

# ----- plot individual outputs -----
mm_ = readRDS(paste0(model.path,fh,".R"))
cat("order = cerc, food, juv, adult, infected, infected shedding, host length, parasite mass")
# plot master
mm <- mm_[[2]]
y_m <- melt(mm);y_m
ggplot() +
  geom_point(data = y_m, aes(x = rep.int(1:n.ticks,max(L1)) , y = value, group = L1, colour=factor(L1)) +
  geom_line(data = y_m, aes(x = rep.int(1:n.ticks,max(L1)) , y = value, group = L1, colour=factor(L1)),
  #linetype=y_m$L1) +
  theme_tufte()
# + geom_text(x=,y=,label = max(value),check_overlap = TRUE)

```

Insert math expression in legend title

```

ggplot() +
  labs(title = bquote("Hello" ~ r[xy] ~ "and" ~ B^2))

```

Create double line break with expression in legend title (and labels)

```

ggplot() +
  scale_color_manual(
    expression(atop("text",
    atop(textstyle(epsilon))))
  )

```

Lists

Find maximum value in entire list

```
master <- list(1:10,100,rnorm(12))
do.call(max, master)
```

Plot all elements in a list

```
xx <- list(sample(5,1000,replace=T),rnorm(1000),sample(50,1000,replace=T))
plot(unlist(xx),type="l")
```

Loops

Save loop output in master list

```
pars <- seq(0,1,0.5)
master <- list()
t_list <- list()
for (p in 1:length(pars)){
  for(t in 5){
    tt <- rnorm(1000*t)
    t_list[t] <- tt
  }
  master[[length(master)+1]] <- t_list # store in master list
}
```

Messages

Display status message of progress

```
for(i in 1:10) {
  Sys.sleep(0.2)
  # Dirk says using cat() like this is naughty ;-)
  #cat(i, "\r")
  # So you can use message() like this, thanks to Sharpie's
  # comment to use appendLF=FALSE.
  message(i, "\r", appendLF=FALSE) # appendLF = new line
  flush.console()
}
```

Display popup progress bar

```
require(tcltk)
pb <- tkProgressBar("test progress bar", "Some information in %",
  0, 100, 50)
Sys.sleep(0.5)
u <- c(0, sort(runif(20, 0, 100)), 100)
for(i in u) {
  Sys.sleep(0.1)
  info <- sprintf("%d%% done", round(i))
  setTkProgressBar(pb, i, sprintf("test (%s)", info), info)
}
Sys.sleep(5)
close(pb)
```

NAs

Replace NAs with 0's

```
df[is.na(df)] <- 0
```

Replace X values less than given value (V) with 0

```
df$X[df$X<V] <- 0
```

Check for NAs

```
sapply(df, function(x) sum(is.na(x)))
```

Replace NaN and Inf values with NA

```
df$col1[which(!is.finite(df$col1))] <- NA
```

Fill in missing data values in sequence with NA

```
# /Users/malishev/Documents/Manuscripts/Chapter4/Sims/Chapter4_figs.R
library(zoo)
data <- data.frame(index = c(1:4, 6:10),
  data = c(1.5,4.3,5.6,6.7,7.1,12.5,14.5,16.8,3.4))
#you can create a series
z <- zoo(data$data, data$index)
#end extend it to the grid 1:10
z <- merge(zoo(,1:10), z)

#worked example
# fill in missing Tb values
minTb.d <- zoo(minTb$Tick,minTb$Days)
minTb.d <- merge(zoo(NULL,1:days), minTb.d) # make the minTb series match the temp series (117 days)
minTb.d <- as.numeric(minTb.d) # = time individuals reached VTMIN in ticks
minTb <- minTb.d - temp$Tick # get diff between starting time and time to reach VTMIN
minTb <- minTb/2 # convert ticks to minutes
minTb <- minTb/60 #convert to hours
minTb <- data.frame("Days"=1:days,"Time"=minTb)

# then fill in missing values
approx(minTb$Time,method = "linear")
```

Remove rows with NA

```
data <- data[!is.na(data$X),]
```

Turn NULLs in list into NAs to get numeric values (fix for 'cannot coerce double' error)

```
hl_list <- lapply(hl_list, function(x) ifelse(x == "NULL", NA, x))
```

Turn NaN or NAs in list into 0s

```
# NaN
global_output <- rapply(global_output, f=function(x) ifelse(is.nan(x),0,x), how="replace" )

# NA
global_output <- rapply(global_output, f=function(x) ifelse(is.na(x),0,x), how="replace" )
```

Packages

[rLandsat](#)

Sourcing, requesting, and downloading NASA Landsat 8 satellite data.

[Radix](#)

Improved RMarkdown output and interaction.

[rpanel](#)

[Reference guide](#)

Create interactive GUI control toggles from R. Like an early Shiny.

Plotting

Plot one plot window above and two below

```
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE))
```

Bookend axis ticks for plot E.g. at 0 and 100 when data is 1:99

```
axis(1,at=c(0,length(loco$X)),labels=c("", ""))# bookending axis tick marks
```

Optimal legend formatting for base

```
legend("right",legend=c("Small","Intermediate","Large"),col=c(colfunc[colvec[1:3]]),
      bty="n",pch=20,pt.cex=1.5,cex=0.7,y.intersp = 0.5, xjust = 0.5,
      title="Size class",title.adj = 0.3,text.font=2,
      trace=T,inset=0.1)
```

Plot inset plot in current plot (<https://stackoverflow.com/questions/17041246/how-to-add-an-inset-subplot-to-topright-of-an-r-plot>)

```
# calculate position of inset
plotdim <- par("plt")# get plot window dims as fraction of current plot dims
xleft    = plotdim[2] - (plotdim[2] - plotdim[1]) * 0.5
xright   = plotdim[2]  #
ybottom  = plotdim[4] - (plotdim[4] - plotdim[3]) * 0.5  #
ytop     = plotdim[4]  #

# set position for plot inset
par(fig = c(xleft, xright, ybottom, ytop),mar=c(0,0,0,0),new=TRUE)

boxplot(Eggs~Size,data=meso2,
        col=adjustcolor(colfunc[colvec[1:3]],alpha=0.5),
        notch = T,xlab="Week",ylab="Diameter (mm)",
        xaxs = "i", yaxs = "i"
        )
```

Interactive plots with rCharts (javascript and d3 viz)

<http://ramnathv.github.io/rCharts/>

```
require(devtools)
install_github('rCharts', 'ramnathv')
```

Cluster plot

<https://rpubs.com/dgrtwo/technology-clusters>


```

library(readr)
library(dplyr)
library(igraph)
library(ggraph)
library(ggforce)

# This shared file contains the number of question that have each pair of tags
# This counts only questions that are not deleted and have a positive score
tag_pair_data <- read_csv("http://varianceexplained.org/files/tag_pairs.csv.gz")

relationships <- tag_pair_data %>%
  mutate(Fraction = Cooccur / Tag1Total) %>%
  filter(Fraction >= .35) %>%
  distinct(Tag1)

v <- tag_pair_data %>%
  select(Tag1, Tag1Total) %>%
  distinct(Tag1) %>%
  filter(Tag1 %in% relationships$Tag1 |
         Tag1 %in% relationships$Tag2) %>%
  arrange(desc(Tag1Total))

a <- grid::arrow(length = grid::unit(.08, "inches"), ends = "first", type = "closed")

set.seed(2016)

relationships %>%
  graph_from_data_frame(vertices = v) %>%
  ggraph(layout = "fr") +
  geom_edge_link(aes(alpha = Fraction), arrow = a) +
  geom_node_point(aes(size = Tag1Total), color = "lightblue") +
  geom_node_text(aes(size = Tag1Total, label = name), check_overlap = TRUE) +
  scale_size_continuous(range = c(2, 9)) +
  ggforce::theme_no_axes() +
  theme(legend.position = "none")

```

Define global plotting graphics function.

The `plot_it.R` function is updated on the [plot_it Github page](#).

```

require(ggplot2)
require(ggthemes)
### set plotting params
plot_it <- function(manuscript,bg,cp1,cp2,alpha,family){ # plotting function (plot for MS or not, set b
  graphics.off()
  if(manuscript==0){
    if(bg=="black"){
      colvec <-- magma(200,1) # plot window bg # USES <-- OPERATOR
      par(bg = colvec[1],col.axis="white",col.lab="white",col.main="white",fg="white",bty="n",las=1,mar=
      border=adjustcolor("purple",alpha=0.5)
    }else{
      colvec <-- bpy.colors(200) # plot window bg # USES <-- OPERATOR
      par(bg = colvec[1],col.axis="white",col.lab="white",col.main="white",fg="white",bty="n",las=1,mar=
      border=adjustcolor("blue",alpha=0.5)
    }
  }
}

```

```

}else{
  # graphics.off()
  par(bty="n",las=1,family=family)
  colv<-"white"
}
# color palettes
# ifelse(manuscript==1,colvec<-adjustcolor(brewer.pal(9,cp1)[9], alpha = alpha),colvec <- adjustcolor
# colfunc <- colorRampPalette(brewer.pal(9,cp1),alpha=alpha)
cp1_info <- brewer.pal.info[cp1,]$maxcolors
cp2_info <- brewer.pal.info[cp2,]$maxcolors
colv <- brewer.pal(cp1_info,cp1) # USES <- OPERATOR
colv2 <- brewer.pal(cp2_info,cp2) # USES <- OPERATOR
}

# Setting ggplot theme graphics
plot_it_gg <- function(bg){ # bg = colour to plot bg, family = font family
  if(bg=="white"){
    bg <- "white"
    fg <- "black"
    theme_tufte(base_family = "HersheySans") +
      theme(panel.border = element_blank(),panel.grid.major = element_blank(),panel.grid.minor = element_blank(),
            theme(axis.line = element_line(color = fg)) +theme(axis.ticks = element_line(color = fg)) + theme
  }
}# end gg

### Set plotting function

require("RCurl")
script <- getURL("https://raw.githubusercontent.com/darwinanddavis/plot_it/master/plot_it.R", ssl.verif
eval(parse(text = script))

cat("plot_it( \n0 for presentation, 1 for manuscript, \nset colour for background, \nset colour palette
plot_it(0,"blue","Spectral","Greens",1,"mono") # set col function params
plot_it_gg("white") # same as above

```

Make plot cycle on one page

```
plot(m_abundance$gam,pages=1)
```

Get plot summaries and values from plot

```

plot.gam(m_abundance$gam,shade=T,pages=1,seWithMean = T)[1] # everything
plot.gam(m_abundance$gam,shade=T,pages=1,seWithMean = T)[1][[1]]$x #subset x
plot.gam(m_abundance$gam,shade=T,pages=1,seWithMean = T)[1][[1]]$fit #get values to produce fit curve

```

Package for stock world maps

```

#worldmap
library(choroplethrMaps)

```

Circle packing, tree, dendrogram, network plots

```

# dendrogram tree nested bubble circle packing network
# https://www.r-graph-gallery.com/313-basic-circle-packing-with-several-levels/

# circle packing plot
# Libraries

```

```

p <- c("ggraph", "igraph", "tidyverse", "DeducerSpatial", "Rcpp", "car")
install.packages(p, dependencies = T)
lapply(p, library, character.only=T)

# We need a data frame giving a hierarchical structure. Let's consider the flare dataset:
edges=flare$edges
# edges cols = character

# Usually we associate another dataset that give information about each node of the dataset:
vertices = flare$vertices
# vertices cols = character, numeric, character

# Create a subset of the dataset (I remove 1 level)
edges = flare$edges %>% filter(to %in% from) %>% droplevels()
vertices = flare$vertices %>% filter(name %in% c(edges$from, edges$to)) %>% droplevels()
vertices$size=runif(nrow(vertices))

# Then we have to make a 'graph' object using the igraph library:
mygraph <- graph_from_data_frame( edges, vertices=vertices )

# circle packing
ggraph(mygraph, layout = 'circlepack', weight="size", sort.by=NULL, direction="out") +
  geom_node_circle(aes(fill=depth)) +
  geom_node_text(aes(label=shortName, filter=leaf, fill=depth, size=size)) + # add text
  # geom_node_label(aes(label=shortName, filter=leaf, size=size)) + # add text boxes
  theme_void() +
  # theme(legend.position="F") + #show legend
  scale_fill_viridis(alpha=0.5, direction=-1, option="magma") +
  # scale_fill_distiller(palette = "Blues")

#circular dendro
str(mygraph)
ggraph(mygraph, layout='dendrogram', circular=T) +
  geom_edge_diagonal(flipped=F,
                    label_colour = "black",
                    label_alpha = 1,
                    angle_calc = "rot",
                    force_flip = TRUE, label_dodge = NULL, label_push = NULL,
                    show.legend = NA) +
  theme_void() +
  # theme(legend.position="none") +
  scale_fill_distiller(palette = "Blues")

# tree map
ggraph(mygraph, 'treemap', weight = 'size') +
  geom_node_tile(aes(fill = depth), size = 0.25) +
  theme_void() +
  theme(legend.position="none")

# circular partition
ggraph(mygraph, 'partition', circular = TRUE) +
  geom_node_arc_bar(aes(fill = depth), size = 0.25) +
  theme_void() +

```

```

theme(legend.position="none")

# node
ggraph(mygraph) +
  geom_edge_link() +
  geom_node_point() +
  theme_void() +
  theme(legend.position="none")

```

Insert an animal silhouette into a plot

```

#1. Get image from http://www.phylopic.org
library(png)
ima <- readPNG("thething.png")
plot(1:3,1:3)
rasterImage(image=ima, xleft=2,ybottom=1.8,
             xright=2.7,ytop=2.7)

```

Create an empty plot window

```

# 1
plot(0,type='n',axes=FALSE,ann=FALSE)
# 2
plot(1, type="n", xlab="", ylab="", xlim=c(0, 10), ylim=c(0, 10))
# 3
plot.new()

```

Set color gradient, palette for smoothing data points

```

require(RColorBrewer)

alpha <- 0.8 # transparency (0 to 1 value)
set.seed(5000)
rr <- rnorm(5000)

# user defined gradient
col<-colorRampPalette(c("steelblue","lightblue","orange","red")) # set your own col gradient with as many colors as you want
colfunc <- col(length(rr))[as.numeric(cut(rr,breaks = length(rr)))] # define breaks in col gradient
plot(rr,col=colfunc,pch=20)

# gradient from palette
display.brewer.all()
col <- "Greens"
col<-colorRampPalette(brewer.pal(brewer.pal.info[col,]$maxcolors,col)) # col gradient
colfunc <- col(length(rr))[as.numeric(cut(rr,breaks = length(rr)))] # define breaks in col gradient
plot(rr,col=colfunc,pch=20)

```

Add plot point every nth element

```

n <- 3
plot(runif(10, 0, 1), type = "o", pch = c(20, rep(NA, n)))

```

Create function to make line as default type in plot

```

lplot <- function(...) plot(..., type="l")
lplot(runif(200))

```

Stack dataframe columns automatically in plot

```
head(outplot)
# time      N      P      S      I
# 1 0.00 200.000000 200.0000 20.00000 2.000000
# 2 0.01  78.245140 177.1952 20.58217 2.067159
# 3 0.02  34.785145 168.9650 21.12174 2.136073
dats <- zoo(outplot)
plot(dats)
```

Make 3D scatterplot

```
require(scatterplot3d)
xx <- rnorm(1000)
yy <- runif(1000)
dens <- c(rep(0.0001,500),rep(1,500))
controls <- runif(3)
add.control <- 1
dens_val <- 1*10^-10 # 0 or 1*10^-10. value to knock out blanket of colour on plot surface
#linear model of r/ship between coords
dens_lm <- lm(dens ~ xx + yy)

xlim <- c(min(xx),max(xx)); ylim <- c(min(yy),max(yy)); zlim=c(min(dens),max(dens)) # set lims
colv <- "Blues"
colvv<-colorRampPalette(brewer.pal(brewer.pal.info[colv,]$maxcolors,colv)) # col gradient
colvv<-colorRampPalette(c("steelblue","lightblue","orange","red")) # set your own col gradient with as many colours as you want
# colvv<-colorRampPalette(magma(length(dens))) # set your own col gradient with as many colours as you want

# set col palette
colfunc <- colvv(length(dens))[as.numeric(cut(dens,breaks = length(dens)))] # define breaks in col gradient
bg <- bpy.colors(1)
alpha <- 0.8

# pdf(paste0(plot.dir,strat,"_",density,"_",stage,"_kudspdf.pdf"),width=8.27,height=11.69,paper="a4r")
scatterplot3d(x=xx,y=yy,z=dens,
              # color=ifelse(col_heat==1, adjustcolor(colfunc, alpha=1),adjustcolor("lightgreen",alpha=1),
              color=ifelse(dens<=dens_val,adjustcolor(ifelse(bg==bpy.colors(1),bpy.colors(1),"white"),alpha=1),
              # col.axis="light green",
              las=1,
              pch=15,
              type="p",
              lty.hplot = 1,
              xlim=xlim,
              ylim=ylim,
              zlim=zlim,
              xlab="X",
              ylab="Y",
              zlab="Density",
              main="Main",
              box=F,
              lty.axis=par(1),
              grid=F,
              col.grid = adjustcolor("gray",1),
              lty.grid=par(3),
              #cex.symbols=dens*3,
```

```

      #cex.symbols = ifelse(z<=0,0,0.5),
      # highlight.3d=T, # ignores color arg if T
      # angle=70,
      axis=T
      # add below part to end of scatterplot3d plot
    )#$plane3d(dens_lm, # add 3d linear model plane. # ??plane3d(Intercept, x.coef = NULL, y.coef = NULL, l
#      lty="dashed",
#      lty.box = NULL,
#      draw_lines = F, draw_polygon = T,
#      polygon_args = list(border = NA, col = adjustcolor("light green",alpha=0.4)))
# add control dates
if(add.control==1){par(new=T); scatterplot3d(x=rep(0,length(controls)),y=controls,z=rep(max(dens),length(controls)),lty="dashed",lty.box=NULL,draw_lines=F,draw_polygon=T,polygon_args=list(border=NA,col=adjustcolor("light green",alpha=0.4)))}

```

Adding title from separate list to plot in loop (ggplot)

```

# plot all sim results in one window
gspl <- list()
ttl_list <- c("cerc","food", "juv", "adult", "infec", "infec (shed)", "host L", "parasite mass")

# choose sim to plot
global_sim_plot <- global_detritus

for(g in 1:10){
  gspl[[g]] <- ggplot() +
    geom_line(data = y_m, aes(x = rep.int(1:n.ticks,max(L1)) , y = value, group = L1, colour=factor(L1)),
      # scale_color_manual(values = viridis(length(mm))) +
      #linetype=y_m$L1) +
    theme_tufte() +
    labs(title=ttl_list[g],x="",y="") +
    if(g==length(global_sim_plot)){
      theme(legend.title=element_text(size=0.2),
        legend.text=element_text(size=0.2)) +
      theme(legend.position = "top")
      labs(x="Time")
    }else{
      theme(legend.position="none")
    }
  }
# + geom_text(x=,y=,label = max(value),check_overlap = TUE)
do.call(grid.arrange,gspl) # plot in one window

```

Using math expressions in plot labels

```

plot(rnorm(1000),
  xlab=expression(paste("X values"~^2)),
  ylab=expression(paste("Y values"~^3,hat(beta)))
)

```

Adding faint gridlines to plot

```

# add gridlines
grid(nx=NA,ny=NULL)

```

Storing current par variables for plotting

```
og_pars <- par(no.readonly = T) # store current par values
```

Reading in files/data

Read in file manually

```
get.file.vol <- read.table(file.choose())#read file manually  
v.file <- get.file.vol[1:100,1]#get the volume
```

Loop through files from dir and append to list

```
# option 1  
# reading in spdf (hrpath) files from drive  
setwd("/Users/camel/Desktop/Matt2016/Manuscripts/MalishevBullKearney/Resubmission/2016/barcoo sims/barcoo")  
file.list<-list.files()  
hrs75<-as.list(rep(1,100)) # empty list  
for (f in 1:100){  
  load(file.list[f])  
  hrs75[f]<-hrpath  
}  
  
# working version  
#converting spdf into mcp(spdf,100,unout="m2")  
ghr<-list()  
for (i in hrs75[1:10]) {  
  m<-mcp(i,100,unout='m2')  
  ghr<-c(ghr,m)  
};ghr  
  
# option 2  
wd <- getwd()  
me_list <- list() # create list  
for(me_day in c("A","B","C")){  
  for(me_im in 1:5){  
    mes <- readRDS(paste0(wd,resource_type,"_meday_",me_day,"_meim",me_im,".R")) # read .R files from d  
    cat("\n",paste0(wd,resource_type,"_meday_",me_day,"_meim",me_im,".R"))  
    names(mes) <- c("cerc", "food", "juv", "adult", "infected", "infected shedding", "mean host length"  
    mes <- mes$"cerc" # get cercs (as list) use mes$"cerc"[[1]] for numeric  
    names(mes) <- paste0(me_day,"_",me_im) # name list elements according to loop iterations  
    me_list <- c(me_list,mes) # bind to master list  
  }  
}
```

Read in PDF files from online source in R and save to drive.

```
# from https://github.com/ropensci/pdftools  
  
require(pdftools)  
url <- "https://raw.githubusercontent.com/darwinanddavis/499R/master/exp_pop_growth.pdf"  
dir <- "FOLDER ON YOUR COMPUTER WHERE YOU WANT THE FILE SAVED"  
f <- "NAME OF THE FILE"  
f <- paste0(f,".pdf")  
  
# run all this  
download.file(url, paste0(dir,"/",f), mode = "wb")
```

```

txt <- pdf_text(paste0(dir,"/",f))

# first page text
page <- 1 # enter the page number
cat(txt[page])

toc <- pdf_toc(paste0(dir,"/",f))

require(jsonlite)
# Show as JSON
jsonlite::toJSON(toc, auto_unbox = TRUE, pretty = TRUE)

# show author, version, etc
info <- pdf_info(f)

# renders pdf to bitmap array
bitmap <- pdf_render_page(f, page = 1)

# save bitmap image
png::writePNG(bitmap, "page.png")
jpeg::writeJPEG(bitmap, "page.jpeg")
webp::write_webp(bitmap, "page.webp")

```

Read .txt files

```
readLines("search_terms.txt") # must have a blank line at end of file to avoid line read error
```

Load in data to avoid 'magic number error'

```

# avoid load()
readRDS("path to file .R") # can use .R and .Rdata
source("path to file .R")

```

Regular expressions (regex)

Get just numbers or characters

```

vec <- "16-Feb-2018 20:08:04 PM"
vecN <- gsub("[^[:digit:]]", "", vec); vec; print(paste0("Just numbers: ",vecN))
vecC <- gsub("[[:digit:]]", "", vec); vec; print(paste0("Just characters: ", vecC))

# with tidyr. requires data frame
require(tidyr)
df <- data.frame(N1=c("APPLE348744", "BANANA77845", "OATS2647892", "EGG98586456"))
print("tidyr doesn't work with strings separated by spaces")
df %>%
  separate(N1, into = c("text", "num"), sep = "(?<=[A-Za-z])(?=[0-9])")

```

Insert or replace a character in a string at a specific location

```

require(stringi)
vec <- "ABCEF"
stri_sub(vec, 4, 2) <- "d"
print(paste0("Original: ABCEF")); print(paste0("New: ",vec))

```


Testing regex expressions and their output

```
# Testing regex expressions and their output  
  
# https://regex101.com/r/ksY7HU/2
```

Removing multiple cols from df using grep

```
packages <- c("dplyr", "purrr")  
  
fh <- "LEC100testrecords.txt"  
tt <- read.delim(paste0(wd, "/", fh), header=T, sep="\t")  
  
# Enter data column you want to search  
col2search <- "Title"  
keyterms <- c("evidence", "human", "africa")  
  
# 1. find key terms  
final <- tt[grep(keyterms, tt[,col2search], ignore.case = T),] #  
length(final[,col2search]) # get number of results  
tt[final[,col2search],col2search] # show raw outputs
```

R Markdown

Hide unwanted code output, such as inherent examples for functions

```
# ``{r, cache = TRUE, tidy = TRUE, lazy = TRUE, results='markup'}
```

Math notation in R Markdown

```
x=y $x = y$  
x<y $x < y$  
x>y $x > y$  
x y $x \le y$  
x y $x \ge y$  
xn $x^{n}$  
xn $x_{n}$  
x $\overline{x}$  
x̂ $\hat{x}$  
x̃ $\tilde{x}$  
ab $\frac{a}{b}$  
f x $\frac{a}{b}$  
f x $\displaystyle \frac{a}{b}$  
(nk) $\binom{n}{k}$  
x1+x2+...+xn $x_{1} + x_{2} + \cdots + x_{n}$  
x1,x2,...,xn $x_{1}, x_{2}, \dots, x_{n}$  
x=x1,x2,...,xn $\mathbf{x} = \langle x_{1}, x_{2}, \dots, x_{n} \rangle$  
x A $x \in A$  
|A| $|A|$  
x A $x \in A$  
A B $A \subset B$  
A B $A \subseteq B$  
A B $A \cup B$  
A B $A \cap B$  
X (n, ) $X \sim \text{\sf Binom}(n, \pi)$
```

```

P(X x)= (x,n, )  $\mathrm{P}(X \leq x) = \texttt{pbinom}(x, n, \pi)$ 
P(A B)  $\mathbb{P}(A \mid B)$ 
P(A B)  $\mathrm{P}(A \mid B)$ 
{1,2,3}  $\{1, 2, 3\}$ 
sin(x)  $\sin(x)$ 
log(x)  $\log(x)$ 
ba  $\int_a^b$ 
( baf(x)dx)  $\left( \int_a^b f(x) \, dx \right)$ 
[  $\int_a^b f(x) \, dx$  ]  $\left[ \int_{-\infty}^{\infty} f(x) \, dx \right]$ 
F(x) | ba  $\left. F(x) \right|_a^b$ 
bx=af(x)  $\sum_{x=a}^b f(x)$ 
bx=af(x)  $\prod_{x=a}^b f(x)$ 
limx→af(x)  $\lim_{x \rightarrow a} f(x)$ 
limx→af(x)  $\displaystyle \lim_{x \rightarrow a} f(x)$ 

```

Greek Letters

```

A  $\alpha$  A
N  $\nu$  N
B  $\beta$  B
Ξ  $\xi$  Xi
Γ  $\gamma$  Gamma
oO  $\omicron$  (omicron)
Δ  $\delta$  Delta
Π  $\pi$  Pi
E  $\epsilon$  epsilon
P  $\rho$  rho
Z  $\zeta$  Zeta
Σ  $\sigma$  Sigma
H  $\eta$  H
T  $\tau$  T
Θ  $\theta$  Theta
Υ  $\upsilon$  Upsilon
I  $\iota$  I
Φ  $\phi$  Phi
K  $\kappa$  K
X  $\chi$  X
Λ  $\lambda$  Lambda
Ψ  $\psi$  Psi
M  $\mu$  M
Ω  $\omega$  Omega

```

Subsetting

Select specific rows E.g. select rows of speed_move not in foodh

```

library(sqldf)
a1NotIna2_h <- sqldf('SELECT * FROM speed_move EXCEPT SELECT * FROM foodh')
a1NotIna2_l <- sqldf('SELECT * FROM speed_move EXCEPT SELECT * FROM foodl')
# select rows from speed_move that also appear in foodh
a1Ina2_h <- sqldf('SELECT * FROM speed_move INTERSECT SELECT * FROM foodh')
a1Ina2_l <- sqldf('SELECT * FROM speed_move INTERSECT SELECT * FROM foodl')

```

Count occurrences of values in data frame

```
table(unlist(df$X))
```

Remove a specific column from a data frame

```
within(df, rm("Col1"))
```

Web scraping

Scraping web tables

http://web.mit.edu/~r/current/arch/i386_linux26/lib/R/library/XML/html/readHTMLTable.html%5Bhttp://web.mit.edu/~r/current/arch/i386_linux26/lib/R/library/XML/html/readHTMLTable.html%5D

```
library(XML)
readHTMLTable()
```

Scraping Twitter timelines

See complete example at <http://varianceexplained.org/r/trump-tweets/>

```
# https://cran.r-project.org/web/packages/twitterR/
library(dplyr)
library(purrr)
library(twitterR)
```