

# Basic statistical computing in R

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# Outline

- ▶ Reshaping data
  - ▶ Manipulating datasets with tidyr
  - ▶ Applying functions over datasets (for loops, apply and plyr)
- ▶ Data visualization
  - ▶ Base graphics and ggplot2
- ▶ Presenting data
  - ▶ Reproducible reports and presentations in Rmarkdown

# Reshaping data

- ▶ We often want to go between 'long' and 'wide' formats

- ▶ Long:

```
##      Line Rep Location      Value
## 1 Line1    1      Home 46.57751
## 2 Line1    2      Home 71.13049
## 3 Line1    3      Home 41.15104
## 4 Line1    1     Away 113.06042
## 5 Line1    2     Away 104.80377
## 6 Line1    3     Away 110.50241
```

- ▶ Wide:

```
##      Line Rep      Away      Home
## 1 Line1    1 113.06042 46.57751
## 2 Line1    2 104.80377 71.13049
## 3 Line1    3 110.50241 41.15104
## 4 Line2    1  94.91813 45.99226
## 5 Line2    2  88.39580 46.69039
## 6 Line2    3 106.61620 53.15883
```

# Reshaping data: 'spread' and 'gather'

- ▶ Rice data set (Zhao et al 2011): 34 traits for 413 rice accessions (not all have phenotypes)
  - ▶ 'Wide' format: traits listed as different columns
  - ▶ We'll use flowering time at three locations as an example

```
Rice <- read.table(url("http://ricediversity.org/data/sets/44kgwas/RiceDiversity_44K_Phenotypes_34traits_F  
                    sep = "\t", header = T)[1:5]  
dim(Rice)
```

```
## [1] 413 5
```

# Reshaping data: 'spread' and 'gather' functions

- ▶ Convert it to long format using the gather function
  - ▶ gather(data, name for combined column, name for value column, names of columns to be combined)

```
Rice_long <- gather(Rice, Location, Value,  
                    Flowering.time.at.Arkansas:Flowering.time.at.Aberdeen,  
                    factor_key = T)  
dim(Rice_long)
```

```
## [1] 1239    4  
dim(Rice)
```

```
## [1] 413    5  
#Give the locations a shorter name  
Rice_long$Location <- sub("Flowering.time.at.", "", Rice_long$Location)
```

# Reshaping data: 'spread' and 'gather' functions

- ▶ Convert long to wide format using the spread function
  - ▶ spread(data, name of the column to be expanded, name for value column)

```
Rice_wide <- spread(data = Rice_long, key = Location, value = Value)  
dim(Rice_wide)
```

```
## [1] 413 5  
dim(Rice)
```

```
## [1] 413 5
```

# Applying functions over data

- ▶ In the simplest case we want to get a summary for each trait (flowering time at each location) or for each line
  - ▶ If the data is in wide format just take the column means
- ▶ Mean flowering time at each location:

```
#Mean of each trait  
#colMeans  
colMeans(Rice_wide[3:5], na.rm = T)
```

```
##  Aberdeen  Arkansas  Faridpur  
## 107.05014  87.94439  71.77049  
#Alternatively use apply and apply the function  
#over columns (indicated by 2)  
apply(Rice_wide[3:5], 2, mean, na.rm = T)
```

```
##  Aberdeen  Arkansas  Faridpur  
## 107.05014  87.94439  71.77049
```

# Applying functions over data

## ► Mean flowering time for each line:

```
#Mean for each line
```

```
head(rowMeans(Rice_wide[3:5], na.rm = T))
```

```
## [1] 101.13889 90.72222 89.12500 89.91667 72.50000 92.08333
```

```
#Alternatively use apply and apply the function
```

```
#over rows (indicated by 1)
```

```
head(apply(Rice_wide[3:5], 1, mean, na.rm = T))
```

```
## [1] 101.13889 90.72222 89.12500 89.91667 72.50000 92.08333
```



# Applying functions over data

- Suppose we measure a trait at multiple time points and the day of measurement is stored in one column. What can we do if we want to take the mean at each time point for each line?

```
Longit <- read.csv("PSA.cleaned.csv", header = T)
head(Longit)
```

```
##   NSFTV.ID Exp Rep DayOfImaging   PSA
## 1  NSFTV_1  E1  1             1 18780
## 2  NSFTV_1  E1  1             2 25434
## 3  NSFTV_1  E1  1             3 29431
## 4  NSFTV_1  E1  1             4 35704
## 5  NSFTV_1  E1  1             5 50058
## 6  NSFTV_1  E1  1             6 59267
```

```
Longit$DayOfImaging <- as.factor(Longit$DayOfImaging)
```

# Applying functions over data: for loops

- For each day, subset the data frame, transform it to the wide format and take the mean

```
ResList <- list()
for (i in 1:length(unique(Longit$DayOfImaging))){
  #subset
  tmpdata <- Longit[Longit$DayOfImaging
                    %in% unique(Longit$DayOfImaging)[i] ,]
  tmpdata <- spread(tmpdata, key = NSFTV.ID, value = PSA)
  ResList[[i]] <- colMeans(tmpdata[4:length(tmpdata)], na.rm = T)
}
head(ResList[[20]])
```

```
##   NSFTV_1  NSFTV_10 NSFTV_101 NSFTV_102 NSFTV_103 NSFTV_104
## 318417.3 260199.0 295836.8 390416.0 229428.0 376634.7
```

# Applying functions over data: plyr

- ▶ Sometimes for loops are necessary, but try to use an alternative if it exists
- ▶ `ddply`: apply some function to subsets of dataframe and combine the results into a nice dataframe

```
#. (NSFTV.ID, DayOfImaging) these are the columns that we will subset on  
Longit_means <- ddply(Longit, .(NSFTV.ID, DayOfImaging), summarise, MeanPSA = mean(PSA, na.rm = T))  
  
head(Longit_means)
```

```
##   NSFTV.ID DayOfImaging  MeanPSA  
## 1  NSFTV_1           1 16164.00  
## 2  NSFTV_1           2 20688.67  
## 3  NSFTV_1           3 23542.33  
## 4  NSFTV_1           4 29838.00  
## 5  NSFTV_1           5 39872.67  
## 6  NSFTV_1           6 46087.33
```

- ▶ Also check out other plyr functions: `dlply`, `ldply`, etc.

# Plotting with the R base graphics

```
pdf("Base_plot.pdf", h=3, w=6, useDingbats = F,
    pointsize = 10)
par(mar=c(3,4,2,0.5), mgp=c(1.8,0.5,0),
    mfrow=c(1,2), cex.lab = 0.75, cex.axis = 0.75)
#Formula, data, color, etc
boxplot(MeanPSA ~ DayOfImaging, data = Longit_means,
        col = colors()[1:20], ylab = "PSA",
        xlab = "Days of Imaging", cex = 0.3)

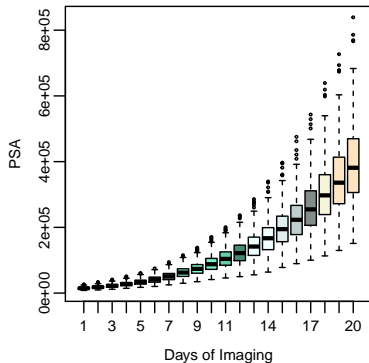
mtext("A", line = 1, side = 3, adj = -0.25)

tmp.df <- spread(Longit_means[Longit_means$DayOfImaging %in% c(19,20) ],
                 DayOfImaging, MeanPSA)

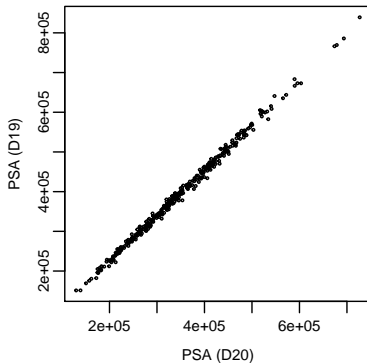
plot(tmp.df$`19`, tmp.df$`20`, pch = 21, cex = 0.3,
     ylab = "PSA (D19)", xlab = "PSA (D20)")
mtext("B", line = 1, side = 3, adj = -0.25)
dev.off()
```

# Plotting with the R base graphics

A



B



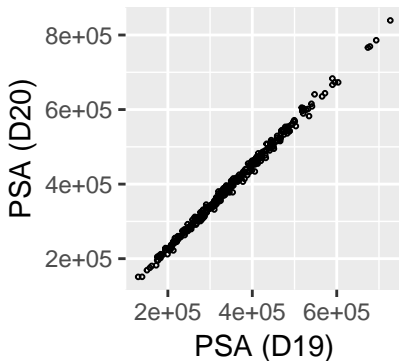
# Plotting with ggplot

- ▶ Aesthetics: specify the variables in data sets
  - ▶ Position, color, shape of points; height of a bar
- ▶ Geoms: Specify the type of graph
  - ▶ Scatter plot (`geom_point`), bar (`geom_bar`), line (`geom_line`), heatmap (`geom_tile`)
- ▶ Others: statistics, themes, legend, labels, etc.

# Plotting with ggplot

```
tmp.df <- spread(Longit_means[Longit_means$DayOfImaging %in%  
                    c(19,20) ],,  
                  DayOfImaging, MeanPSA)  
  
NicePlot <- ggplot(tmp.df) +  
  geom_point(aes(x=`19`, y=`20`), pch = 21, size = 0.5) +  
  ylab("PSA (D20)") +  
  xlab("PSA (D19)")
```

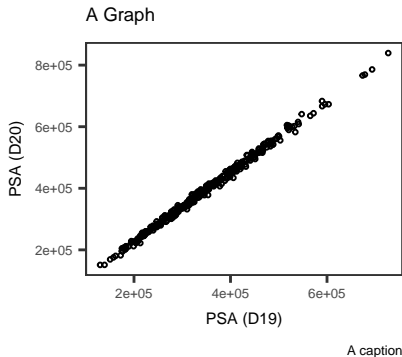
NicePlot



# Plotting with ggplot

```
NicePlot <- NicePlot + theme_bw() +  
  theme(panel.grid.major = element_blank(),  
        panel.grid.minor = element_blank(),  
        text = element_text(size = 6)) +  
  labs(title = "A Graph",  
        caption = "A caption")
```

NicePlot





# Generating reproducible reports with R markdown

- ▶ Markdown: Markdown is a language (?) for creating HTML, PDF, and MS Word
- ▶ Using the Knitr package reports can be made within R studio
- ▶ 'rmdformats' package has several pre-made templates
  - ▶ Picture of 'rmdformats'

# Generating reproducible reports with R markdown

- From Rstudio: File -> New File -> Rmarkdown...

The screenshot shows the RStudio interface with a new R Markdown file being created. The 'New R Markdown' dialog box is open, showing the 'Document' template selected. The 'Title' field is 'Untitled', and the 'Author' field is 'Malachy Campbell'. The 'Default Output Format' is set to 'HTML'. Below the dialog, the R Markdown source file is visible, showing a plot of 'PSA (D19)' vs 'PSA (D20)' using ggplot2. The plot is a scatter plot with a linear trend line. The 'Plots' pane on the right shows the preview of the plot, titled 'A Graph', with the x-axis labeled 'PSA (D19)' and the y-axis labeled 'PSA (D20)'. The plot shows a positive correlation between the two variables.

```
# Plotting with ggplot
\footnotesize
NicePlot <- NicePlot + theme_bw() +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank()) +
  labs(title = "A Graph",
        caption = "A caption")
NicePlot
```

Generating reproducible reports with R markdown

Markdown: Markdown is a language (?) for creating HTML documents.

Using the Knitr package reports can be made within R.

'rmdformats' package has several pre-made templates

Picture of 'rmdformats'

Generating reproducible reports with R markdown

From Rstudio: File -> New File -> Rmarkdown...

Generating reproducible reports with R markdown

Console Terminal R Markdown

```
~/Documents/Dropbox/Work/Presentations/Japan/IntroToR/
+ labs(title = "A Graph",
+       caption = "A caption")
+ NicePlot
+
+ 
```

Environment History Connections

```
plot(trp.dfs$19 ~ trp.dfs$20, pch = 21, cex = 0.3,
      ylab = "PSA (D19)", xlab = "PSA (D20)")
NicePlot <- ggplot(tmp.df) +
  geom_point(aes(x=19, y=20), pch = 21, size = 0.5) +
  ylab("PSA (D20)") +
  xlab("PSA (D19)")
lot <- NicePlot + theme_bw() +
  (panel.grid.major = element_blank(),
   .grid.minor = element_blank()) +
  title = "A Graph",
  an = "A caption")
lot
```

Plots Packages Help Viewer

A Graph

2e+05 4e+05 6e+05

PSA (D19)

A caption

# Generating reproducible reports with R markdown

- ▶ Demo

# Presentations with R markdown

- From Rstudio: File -> New File -> Rmarkdown...

The screenshot shows the RStudio interface with the 'New R Markdown' dialog box open. The dialog box has four tabs: Document, Presentation, Shiny, and From Template. The 'Presentation' tab is selected. The 'Title' field is 'Untitled' and the 'Author' field is 'Malachy Campbell'. The 'Default Output Format' section has three options: HTML (ioslides) (selected), HTML (Sliidy), and PDF (Beamer). The HTML (ioslides) option is selected, and its description is: 'HTML presentation viewable with any browser (you can also print ioslides to PDF with Chrome)'. The HTML (Sliidy) option is described as 'HTML presentation viewable with any browser (you can also print Sliidy to PDF with Chrome)'. The PDF (Beamer) option is described as 'PDF output requires TeX (MiKTeX on Windows, MacTeX 2013+ on OS X, TeX Live 2013+ on Linux)'. The 'OK' button is highlighted.

The background shows the R Markdown editor with the following content:

```
## Generating reproducible reports with R markdown
- From Rstudio: File -> New File -> Rmarkdown...
\begin{center}
\includegraphics[height=255px]{Rmd.open}
\end{center}
## Generating reproducible reports with R markdown
- Demo
## Presentations with R markdown
- From Rstudio: File -> New File -> Rmarkdown...
```

The console shows the output of the R Markdown presentation:

```
Output created: IntroToR3.html
Warning message:
MathJax doesn't work with self_contained when not using the rmarkdown "default" template.
```

The rendered presentation is visible in the bottom right pane, showing a histogram of `rnorm(100, 10, 2)` with the title 'ogram of rnorm(100, 1'.