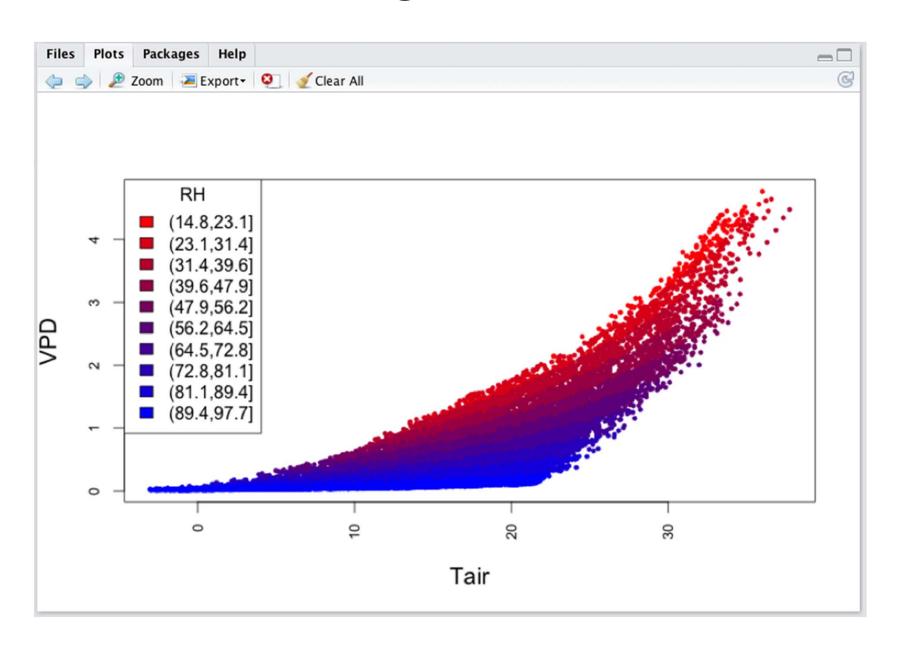
## Introduction to R – Tuesday PM

### Visualising data

- Plotting in RStudio
- Plot types
- Formatting plots
  - Getting to know 'par'
  - Setting up a plotting device
- Exporting plots
- Examples and exercises

## Plotting in RStudio

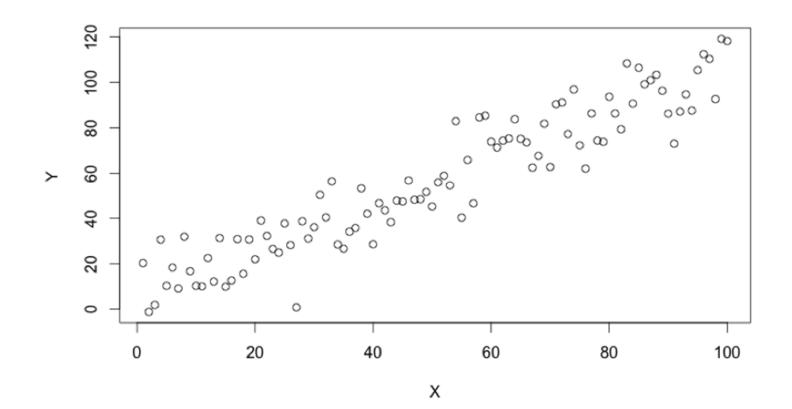


# Plot types

Function	Graph type
plot	Scatter plots and line plots
barplot	Bar plot, with a dizzying number of options
hist	Histograms and (relative) frequency diagrams
curve	Plots curves given some mathematical expression
pie	Pie charts (for less scientific uses)
boxplot	Box-and-whisker plots
symbols	As scatter plot, but symbols sized by another variable

### Basic plotting (e.g., scatter plot)

```
# Option 1:
with(dfr, plot(X, Y))
# Option 2:
plot(Y ~ X, data = dfr)
```



## 'par' options

Graphical parameter	Description		
pch	Sets the types of symbols that are used in the plot; see points() for a		
	list of options.		
type	Decides whether to plot points, lines, both, or other (see ?plot)		
col	Sets the colour of the plotting symbols and the lines.		
lty	Sets the line type (1=solid, 2=dashed, etc.)		
lwd	Sets the line width		
cex	Controls the size of text and points in the plot area. Short for 'character		
	expansion', it acts as a multiplier of the default value.		
cex.axis, cex.lab	Character expansion of axes and the labels.		
cex.main	Character expansion of the title of the plot.		
family Sets the font for labels and titles. Varies by system, but 'se			
	and 'mono' should always work.		
bty	Sets the type of box, if any, to be drawn around the plot.		
las	Sets the orientation of the text labels relative to the axis		
mar	Sets the number of lines in each margin, in the order bottom, left, top,		
	right.		
xaxs, yaxs	Preset functions for calculating axis intervals.		
xaxp, yaxp	Sets the coordinates for tick marks on each axis.		
xaxt, yaxt	Sets axis type, but can also suppress plotting axes by specifying 'n'.		

type 'par()' or, e.g., par('pch') at the command line to get current settings

### 'par' options

Change options within current plot:

```
plot(1:10, 1:10, cex.lab = 1.2)
```

Change options globally (for all subsequent plots):

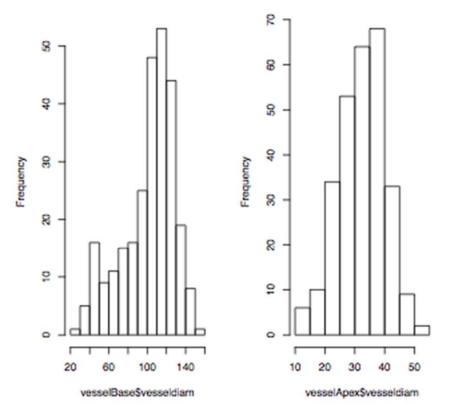
```
par(cex.lab = 2)
plot(1:10, 1:10)
```

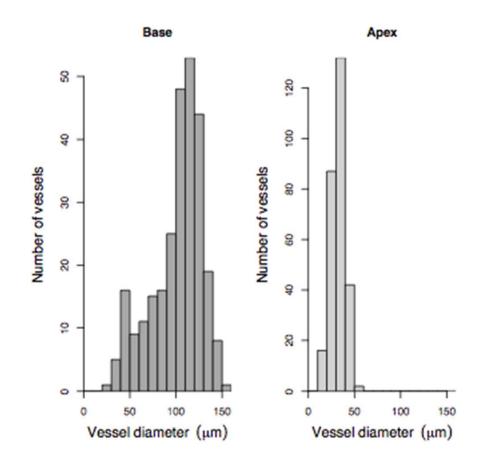
type 'par()' or, e.g., par('cex.lab') at the command line to get current settings

```
# Read vessel data, and make two datasets (one for 'base' data, one for
# 'apex' data).
vessel <- read.csv("vessel.csv")</pre>
vesselBase <- subset(vessel, position == "base")</pre>
vesselApex <- subset(vessel, position == "apex")</pre>
# Set up two figures next to each other:
par(mfrow = c(1, 2))
# Simple histograms, default setting.s
hist(vesselBase$vesseldiam)
```

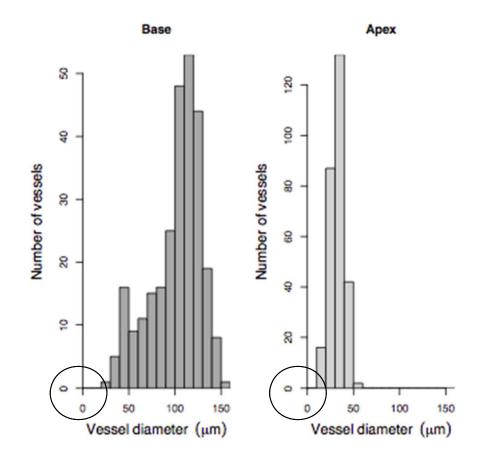
hist(vesselApex\$vesseldiam)



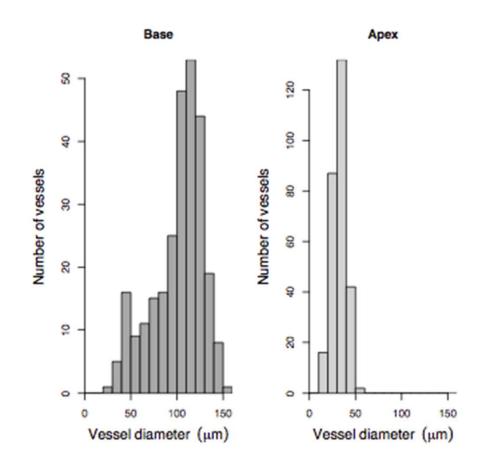




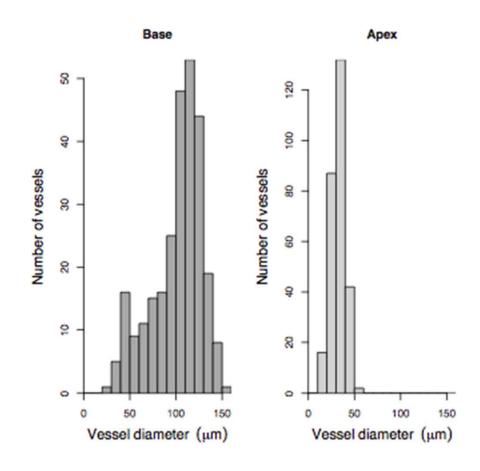
Intercept type



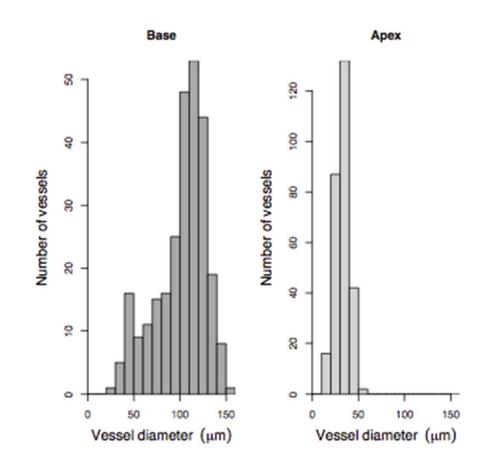
- Intercept type
- Axis range



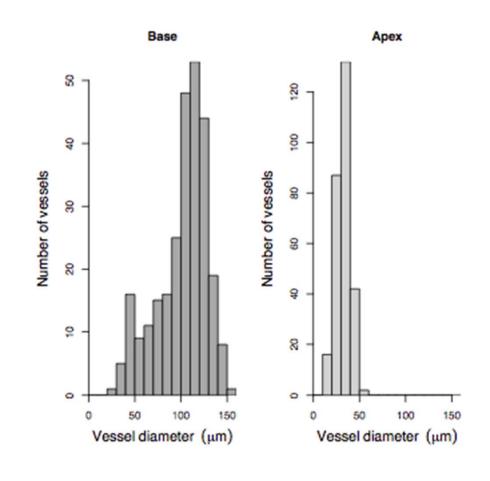
- Intercept type
- Axis range
- Breaks



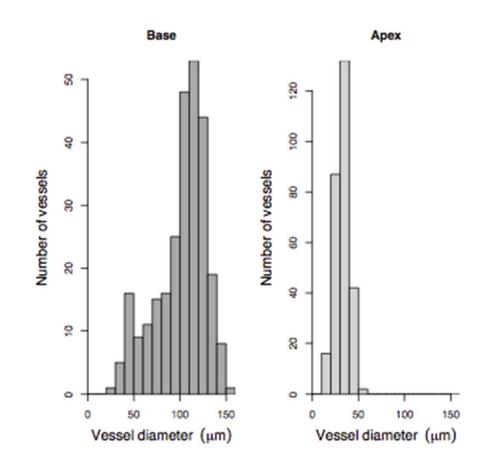
- Intercept type
- Axis range
- Breaks
- Colours



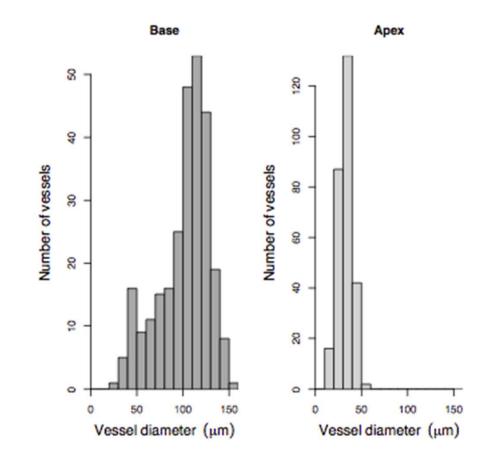
- Intercept type
- Axis range
- Breaks
- Colours
- Main title



- Intercept type
- Axis range
- Breaks
- Colours
- Main title
- Axis labels



- Intercept type
- Axis range
- Breaks
- Colours
- Main title
- Axis labels
- Margins, text size

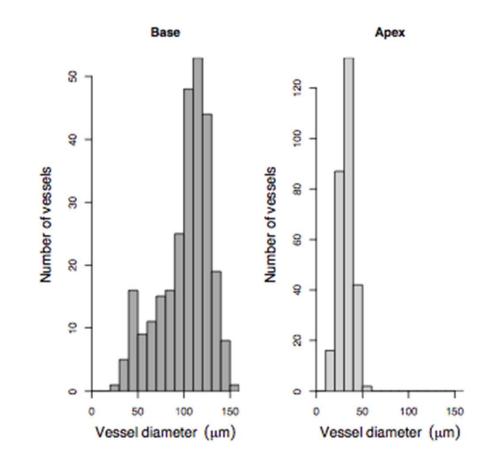


#### On Mac OS X:

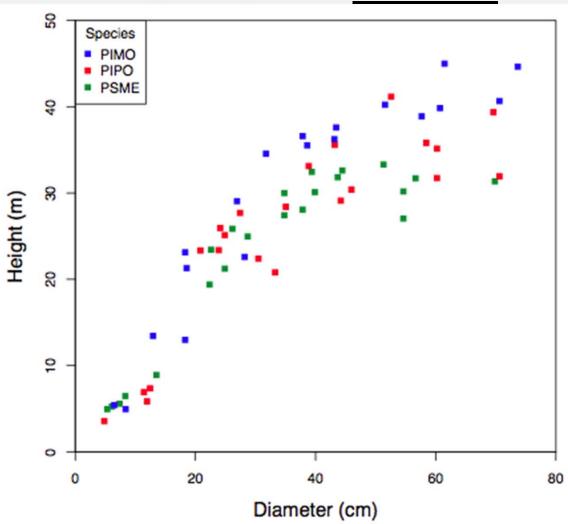
- quartz()
- X11()

On Linux

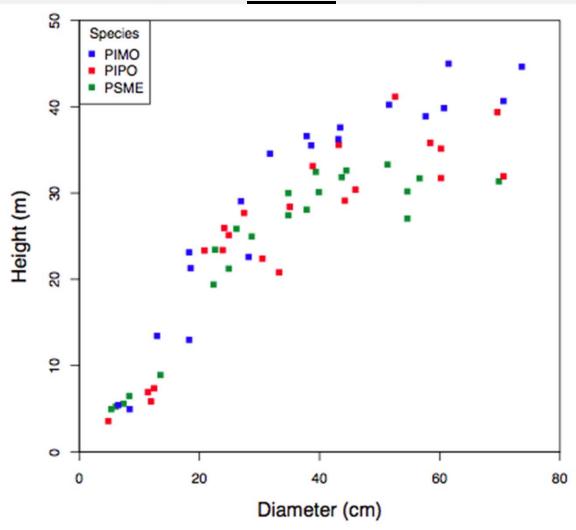
• X11()



```
par(xaxs = "i", yaxs = "i", cex.lab = 1.4)
palette(c("blue", "red", "forestgreen"))
plot(height ~ diameter, col = species, data = allom, pch = 15, xlim = c(0, 80),
    ylim = c(0, 50), xlab = "Diameter (cm)", ylab = "Height (m)")
# Add a legend
legend("topleft", levels(allom$species), pch = 15, col = palette(), title = "Species")
```



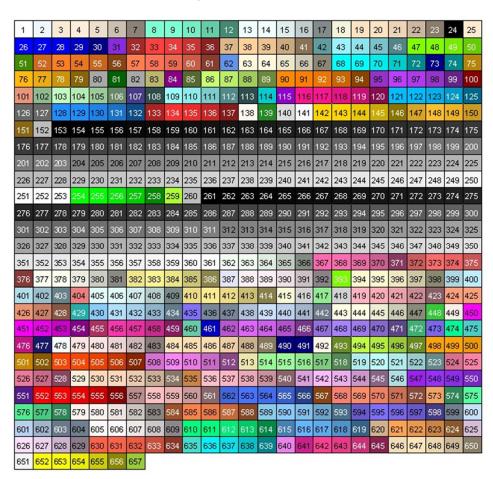
```
par(xaxs = "i", yaxs = "i", cex.lab = 1.4)
palette(c("blue", "red", "forestgreen"))
plot(height ~ diameter, col = species, data = allom, pch = 15, xlim = c(0, 80),
    ylim = c(0, 50), xlab = "Diameter (cm)", ylab = "Height (m)")
# Add a legend
legend("topleft", levels(allom$species), pch = 15, col = palette(), title = "Species")
```



### par('pch')

0: 🔲	10: 🕀	20: •	A: <b>A</b>
1: 🔾	11:🂢	21: 🛑	a: <b>a</b>
2: 🛆	12: ⊞	22: 📕	B: <b>B</b>
3: +	13: 💢	23: 🔷	b: <b>b</b>
4: ×	14: 🔽	24: 📥	S: <b>S</b>
5: 🔷	15: 🔼	25: 🔻	`: `
6: 🗸	16: 🛑	@:@	.: •
7: 🖂	17: 📥	+: +	,: <b>,</b>
8: *	18: 🔷	%: <mark>%</mark>	?: <mark>?</mark>
9: 🕁	19: 🔵	#: #	*; *

### par('col')



http://research.stowers-institute.org/efg/R/Color/Chart/

#### Indexing par('col') using a factor:

9

0

```
> palette()
                        "forestgreen"
[1] "blue"
             "red"
> levels(allom$species)
[1] "PIMO" "PIPO" "PSME"
> str(allom$species)
Factor w/ 3 levels "PIMO", "PIPO", ...: 3 3 3 3 3 3 3 3 3 ...
> as.numeric(allom$species)
[51] 1 1 1 1 1 1 1 1 1 1 1 1 1 1
> .
                        Species
                        PIMO
                        PIPO
                        PSME
                  Height (m)
```

40

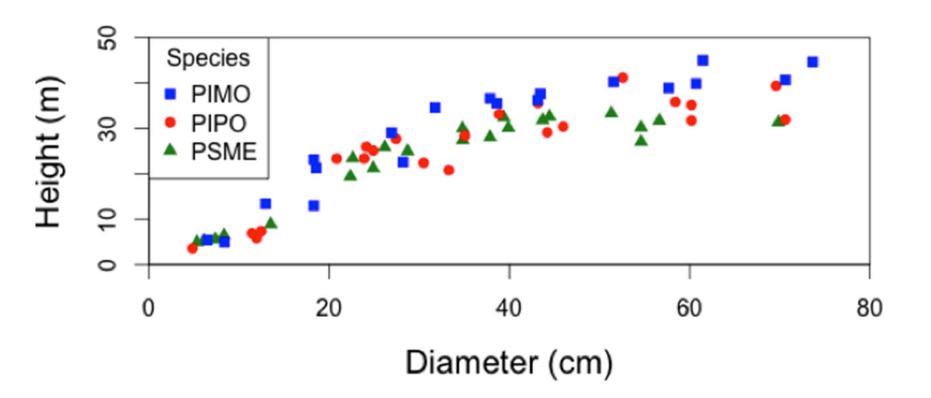
Diameter (cm)

20

60

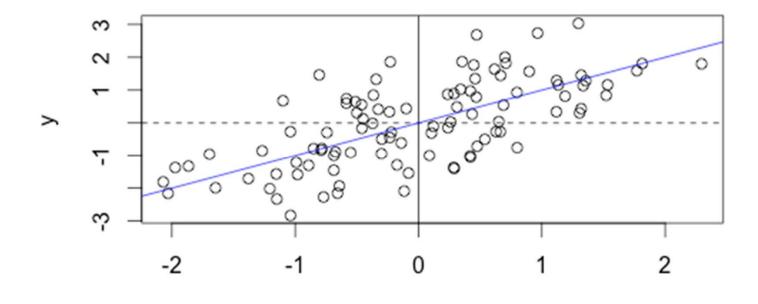
80

#### Indexing par('pch') using a factor:



### Adding to plots

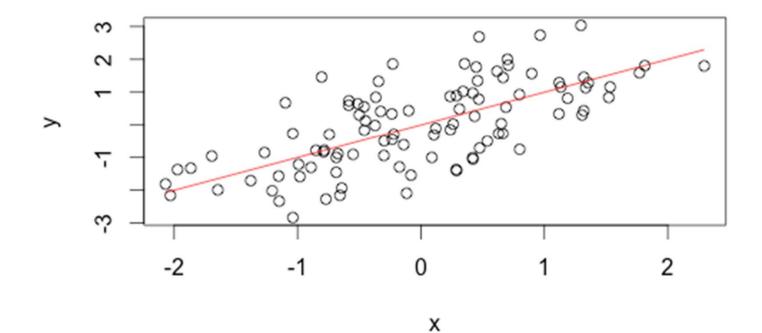
```
> x <- rnorm(100)
> y <- x + rnorm(100)
> plot(y ~ x)
>
> abline(v=0)
> abline(h=0, lty='dashed')
> abline(0, 1, col='blue')
```



Х

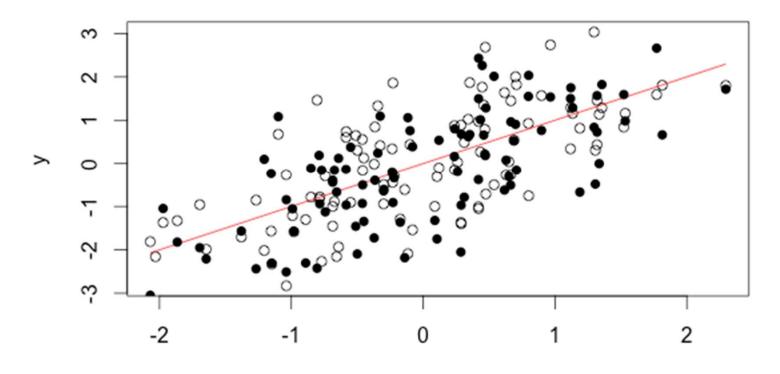
### Adding to plots

```
> plot(y ~ x)
> library(plotrix)
> ablineclip(0, 1, x1=min(x), x2=max(x), col='red')
```

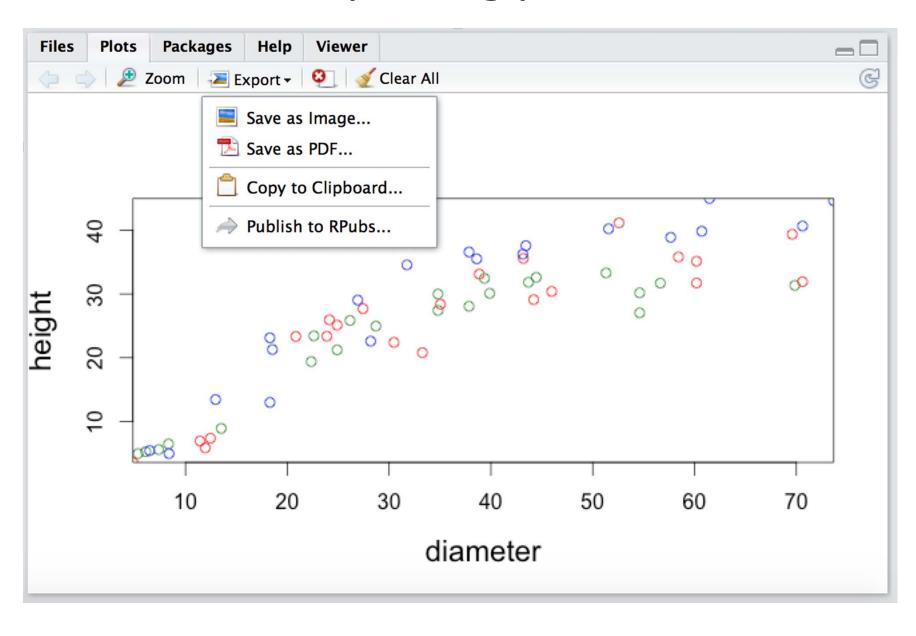


### Adding to plots

```
> plot(y ~ x)
> ablineclip(0, 1, x1=min(x), x2=max(x), col='red')
> 
> z <- x - rnorm(100)
> points(z ~ x, pch=16)
```



### **Exporting plots**



### Exporting plots from command line

Save plot as pdf/eps file (best quality):

```
windows(4,4)
par(mar=c(5,5,2,2))
plot(x,y)
dev.copy2pdf(file="Figure1.pdf")
dev.copy2eps(file="Figure1.eps")
```

Save plot at tiff/jpeg/png file (smaller file size):

```
# First make a plot..
plot(1)

# Example from ?dev.print

# Make a large PNG file of the current plot.
dev.print(png, file = "myplot.png", width = 1024, height = 768)
```

Or just use software to grab image from screen and save as tiff/jpeg/png to ensure plot is saved as displayed on screen.

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