

# ggplot2: visualizing our data and IO

Peter D Smits

Committee on Evolutionary Biology  
University of Chicago

January 25, 2013

# Introduction

Last time, we covered the basics of ggplot2 and how we modify plots.

Today's talk will be in two parts.

1. introduction to maps and ggplot
2. Sample workflow from IO through summarising to visualizing.

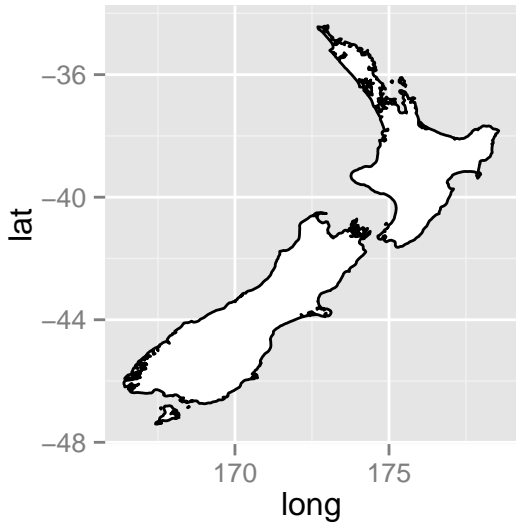
# Maps

```
library(ggplot2)
library(maps)
nz <- map_data('nz')
```

	long	lat	group	order	region	subregion
1	172.74	-34.44	1.00	1	North.Island	
2	172.80	-34.46	1.00	2	North.Island	
3	172.85	-34.45	1.00	3	North.Island	
4	172.90	-34.42	1.00	4	North.Island	
5	172.96	-34.43	1.00	5	North.Island	
6	173.02	-34.40	1.00	6	North.Island	

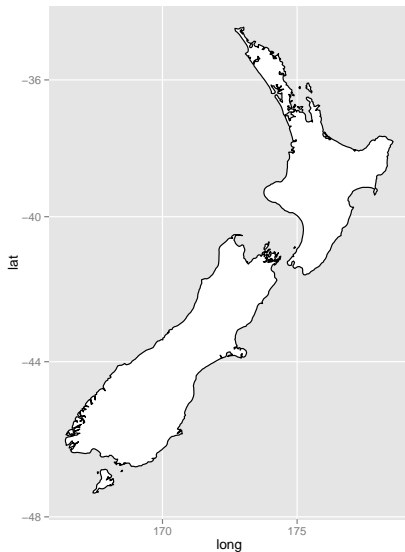
# Looking at NZ: Cartesian coordinates

```
nzmap <- ggplot(nz, aes(x = long, y = lat, group = group))  
nzmap <- nzmap + geom_polygon(fill = 'white', colour = 'black')  
nzmap
```



# Looking at NZ: Mercator projection

```
library(mapproj)  
nzmap + coord_map()
```



# Looking NZ: Other projections

```
nzmap + coord_map('cylindrical')

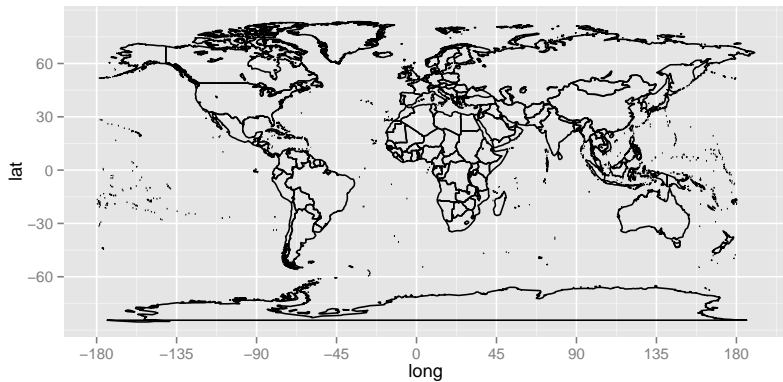
nzmap + coord_map('azequalarea',
                  orientation = c(-36.92, 174.6, 0))

## ?mapproject for coordinate systems and their parameters
## there are a lot of them
```

# World map!

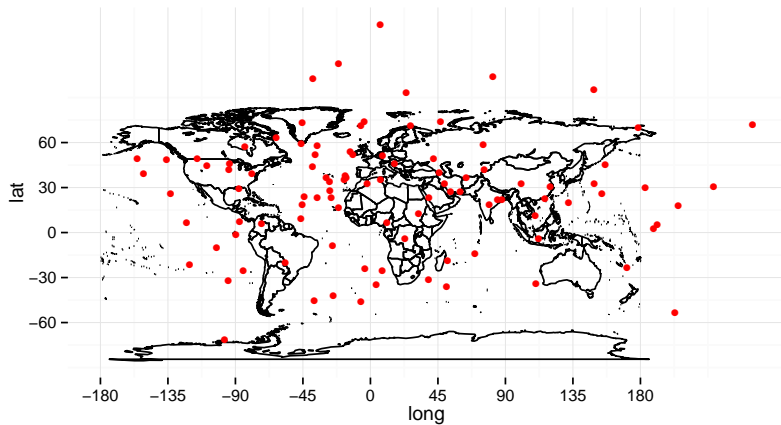
```
world <- map_data('world')
worldmap <- ggplot(world, aes(x = long, y = lat, group = group))
worldmap <- worldmap + geom_path()
worldmap <- worldmap + scale_y_continuous(breaks = (-2:2) * 30) +
  scale_x_continuous(breaks = (-4:4) * 45)
worldmap <- worldmap + coord_equal()
```





## Lets add random dots to it!

```
x.long <- rnorm(100, mean = mean(world$long), sd = sd(world$long))
y.lat <- rnorm(100, mean = mean(world$lat), sd = sd(world$lat))
rpoints <- data.frame(x.long, y.lat)
## there are prettier ways to do this, but they are more complicated
worldmap <- worldmap + geom_point(data = rpoints,
                                mapping = aes(x = x.long,
                                                y = y.lat,
                                                group = NULL),
                                colour = 'red')
worldmap <- worldmap + theme_minimal()
```



## More on maps

Try a lot of projections to get the one that distorts your reality the least.

You can cut down the amount of the map displayed. You can look that up on your own.

Shape files can be read into R and used as maps. (maptools)

There are packages to use google maps. (RGoogleMaps, ggmap)

Input/Output: the act of getting things in and out of your program/script/what have you.

```
read.table()
read.csv()
read.tree()
read.nexus()
dget()
## etc.

write.table()
write.csv()
write.tree()
write.nexus()
dput()
save()
save.image()
ggsave() # save ggplot object
## etc.
```

# Anatomy of read.table()

```
args(read.table)

## function (file, header = FALSE, sep = "", quote = "\"'", dec = ".",
##      row.names, col.names, as.is = !stringsAsFactors, na.strings = "NA",
##      colClasses = NA, nrows = -1, skip = 0, check.names = TRUE,
##      fill = !blank.lines.skip, strip.white = FALSE, blank.lines.skip = TRUE,
##      comment.char = "#", allowEscapes = FALSE, flush = FALSE,
##      stringsAsFactors = default.stringsAsFactors(), fileEncoding = "",
##      encoding = "unknown", text)
## NULL
```

returns an object of class “data.frame”

## (Review of) reading in a file

```
pantheria <- read.table(file = 'pantheria_mung.csv',  
                        sep = ',', header = T, row.names = 1)
```

# Very rough summary

summary(pantheria)

```
##          order          family          genus
## Rodentia      :2277 Muridae      : 730 Crocidura   : 172
## Chiroptera    :1116 Cricetidae   : 681 Myotis      : 103
## Soricomorpha  : 428 Vespertilionidae: 407 Rhinolophus : 77
## Primates      : 376 Soricidae    : 376 Sorex       : 77
## Carnivora     : 286 Sciuridae    : 278 Hipposideros: 67
## Artiodactyla  : 240 Pteropodidae : 186 Rattus      : 66
## (Other)       : 693 (Other)      :2758 (Other)     :4854
##          species      adultbodymass adultforearmrlen adultheadbodylen
## australis: 15 Min.      : 0.7 Min.      :3 Min.      : 3
## thomasi   : 15 1st Qu.: 3.2 1st Qu.:4 1st Qu.: 5
## macrotis  : 14 Median   : 4.6 Median   :4 Median   : 5
## major     : 14 Mean     : 5.5 Mean     :4 Mean     : 6
## grandis   : 11 3rd Qu.: 7.2 3rd Qu.:4 3rd Qu.: 6
## minor     : 11 Max.     :18.9 Max.     :6 Max.     :10
## (Other)   :5336 NA's    :1874 NA's    :4513 NA's    :3475
## basalmtrate basalmtratemass dietbreadth homerange
## Min.      : 2 Min.      : 1 Min.      :1 Min.      : 0
## 1st Qu.: 4 1st Qu.: 3 1st Qu.:1 1st Qu.: 0
## Median   : 5 Median   : 5 Median   :2 Median   : 0
## Mean     : 5 Mean     : 5 Mean     :3 Mean     : 234
## 3rd Qu.: 6 3rd Qu.: 7 3rd Qu.:4 3rd Qu.: 1
## Max.     :12 Max.     :13 Max.     :8 Max.     :79245
## NA's     :4843 NA's     :4843 NA's     :3255 NA's     :4709
## terrestriality weaningage
```



# Summarizing

Hadley coined term “split-apply-combine” in his J. Stat. Soft. paper on “plyr”.

This is essentially using higher-order functions to ease aspects of data munging.

EXTREME munging will not be covered here (plug for other course) because it requires a lot of knowledge of the R language as an actual language. Here, we do a quick usage of the function `ddply()`

# Summarize by order

```
library(plyr)
order.summary <- ddply(pantheria, .(order), summarise,
  mean.mass = mean(adultbodymass, na.rm = TRUE),
  mass.count = length(na.omit(adultbodymass)),
  mean.body = mean(adultheadbodylen, na.rm = TRUE),
  body.count = length(na.omit(adultheadbodylen)),
  mean.metrage = mean(basalmetrage, na.rm = TRUE),
  metrage.count = length(na.omit(basalmetrage)))
```

## Summarize by order

	order	mean.mass	mass.count	mean.body	body.count	mean.metrate	metrate.count
1	Afrosoricida	3.58	39	4.76	32	4.04	13
2	Artiodactyla	10.87	210	7.16	146	9.25	12
3	Carnivora	8.66	250	6.49	241	7.99	62
4	Cetacea	13.44	76	8.48	45		0
5	Chiroptera	2.95	695	4.58	158	3.48	80
6	Cingulata	7.65	20	5.88	10	6.52	9
7	Dasyuromorphia	4.00	61	5.10	29	4.16	20
8	Dermoptera	7.07	2	5.94	2		0
9	Didelphimorphia	4.31	64	4.89	66	5.25	11
10	Diprotodontia	7.58	121	5.96	55	6.21	25
11	Erinaceomorpha	5.69	12	5.27	20	5.39	5
12	Hyracoidea	7.96	4	6.17	3	6.60	3
13	Lagomorpha	7.03	60	5.80	69	6.72	6
14	Macroscelidea	4.46	14	5.01	9	4.16	7
15	Microbiotheria	3.22	1	4.66	1		0

# Reshaping

Wide versus long format. ggplot likes long, we think in wide.

```
library(reshape2)
```

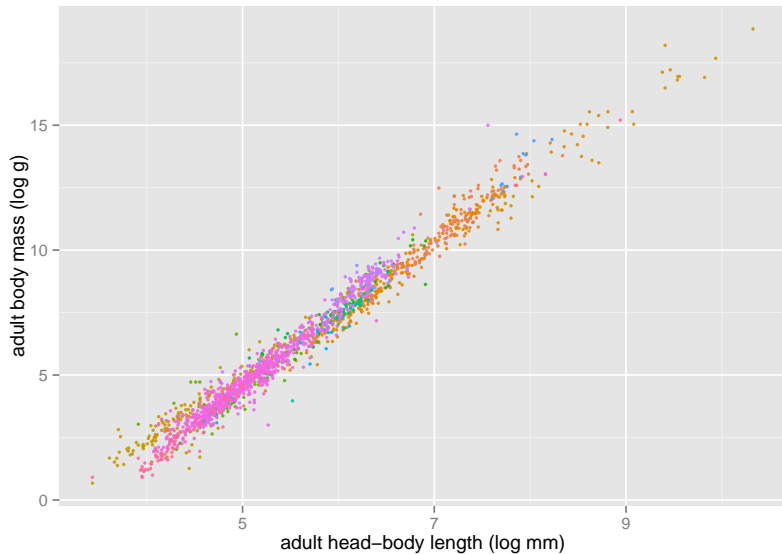
I won't be covering this as a part of this lecture.

Stay tuned for a proper munging lecture.

# Visualizing

```
gpan <- ggplot(pantheria, aes(x = adultheadbodylen,  
                             y = adultbodymass,  
                             colour = order))  
gpan <- gpan + geom_point(alpha = 0.9, size = 1, na.rm = TRUE)  
gpan <- gpan + theme(legend.position = 'none')  
gpan <- gpan + labs(x = 'adult head-body length (log mm)',  
                   y = 'adult body mass (log g)')
```

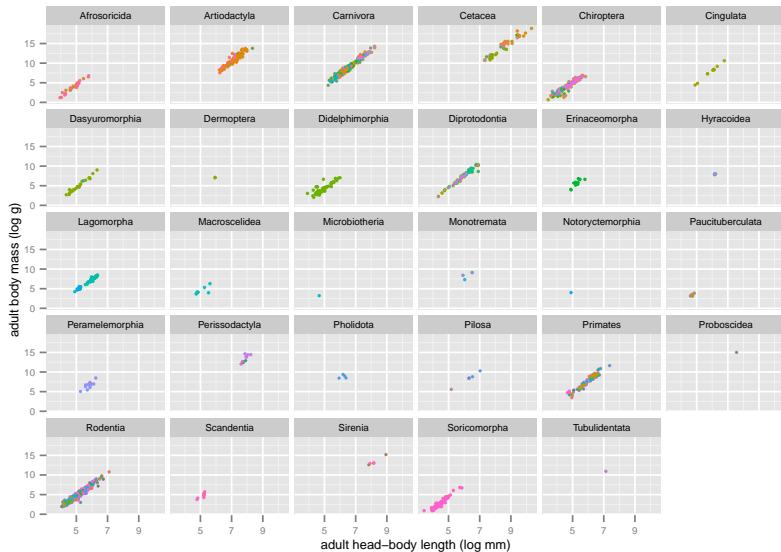
# Visualizing



# Visualizing

```
gpan <- gpan + geom_point(alpha = 0.9, size = 0.7,  
                           mapping = aes(colour = family))  
gpan <- gpan + theme(axis.text = element_text(size = 6),  
                     axis.title = element_text(size = 8),  
                     strip.text = element_text(size = 6))  
gpan <- gpan + facet_wrap(~ order)
```

# Visualizing

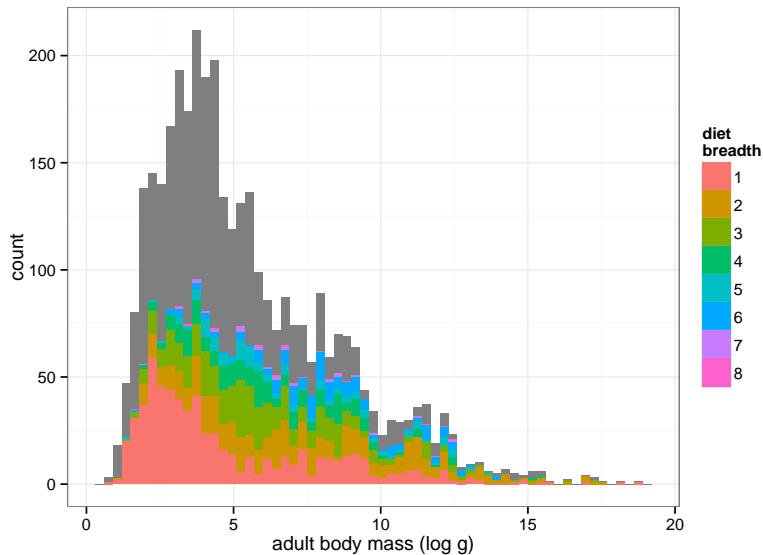




# Visualizing

```
gdiet <- ggplot(pantheria, aes(x = adultbodymass,  
                              fill = factor(dietbreadth)))  
gdiet <- gdiet + geom_histogram(binwidth = 0.3)  
gdiet <- gdiet + theme_bw()  
gdiet <- gdiet + scale_fill_discrete(name = 'diet\nbreadth')  
gdiet <- gdiet + labs(x = 'adult body mass (log g)')
```

# Visualizing



# Save our plot

If you aren't using knitr/Sweave (you should!), you can save your ggplot for use later.

```
ggsave(filename = 'pantheria_facet.png',  
        plot = gpan)
```