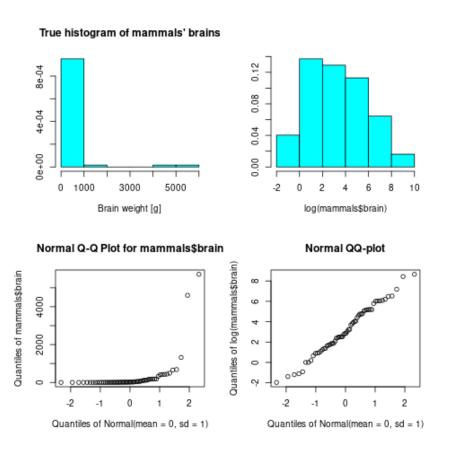
In the last lecture, you saw some plots from the mammals data frame of the MASS package, giving body weights and brain weights for 62 animals.



The Animals2 data frame from the robustbase package gives the same characterizations for a different set of animals.

In both cases, the row names for these data frames identify these animals, and the objective of this exercise is to examine the differences between the animals characterized in these data frames:

1. Make the required packages available.

Tip: packages need to be installed (once) and loaded (per session).

Use this code block to start a session and run the necessary commands:

. . .

Remember when asked to start the session in the same directory where your practice file resides.

— SOLUTION —

- Install MASS and robustbase install using install.packages. You have to do this only once (unless you upgrade or change your version of R).
- Load the packages.

```
library(MASS)
library(robustbase)
```

2. The rownames function returns a vector or row names for a data frame, and the intersect function computes the intersection of two sets, returning a vector of their common elements.

Using these functions, construct and display the vector commonAnimals of animal names common to both data frames.

How many animals are included in this set? Tip: you can check the length of a vector with the function length.

— SOLUTION —

• Check both data frames with str.

```
str(Animals2)
str(mammals)
```

```
'data.frame': 65 obs. of 2 variables:
$ body : num   1.35 465 36.33 27.66 1.04 ...
$ brain: num   8.1 423 119.5 115 5.5 ...
'data.frame': 62 obs. of 2 variables:
$ body : num   3.38 0.48 1.35 465 36.33 ...
$ brain: num   44.5 15.5 8.1 423 119.5 ...
```

• Look at row names with rownames.

```
rownames(Animals2)
rownames(mammals)
```

- Check the use of intersect with help(intersect).
- Store the intersection using intersect in commonAnimals.

commonAnimals <- intersect(rownames(Animals2), rownames(mammals))</pre> commonAnimals • Check the length of commonAnimals with length or str. length(commonAnimals) str(commonAnimals) [1] 58 chr [1:58] "Mountain beaver" "Cow" "Grey wolf" "Goat" "Guinea pig" "Asian ele 3. The setdiff function returns a vector of elements contained in one set but not in the other: setdiff(A,B)~ returns a vector of elements in set A that are not in set B. Use setdiff to display the animals present in mammals that are not present in Animals2. — SOLUTION setdiff(rownames(mammals), rownames(Animals2)) "Arctic ground squirrel" "Patas monkey" [1] "Arctic fox" [4] "Mole rat" 4. Use setdiff to display the animals present in Animals2 that are not present in mammals. — SOLUTION setdiff(rownames(Animals2), rownames(mammals)) [1] "Dipliodocus" "Potar monkey" "Triceratops" [4] "Brachiosaurus" "Mole" "Artic fox" [7] "Artic ground squirrel"

5. Can you give a simple (qualitative) characterization of these differences between the two sets of animals?

Tip: you have to look at the output of the last two tasks to identify these differences.

— SOLUTION —

- (a) The Animals2 data frame contains three dinosaurs ("Triceratops", "Dipliodocus", and "Brachiosaurus")
- (b) The word "Arctic" is misspelled in Animals2 "Arctic fox" and "Arctic ground squirrel" are actually in both data frames.
- (c) mammals lists "Mole rat" while Animals2 lists "Mole" but body and brain weights are the same:

```
mammals["Mole rat",]
Animals2["Mole",]
```

body brain
Mole rat 0.122 3

body brain
Mole 0.122 3

More detailed using which for indices and rownames with ==:

```
mammals[which(rownames(mammals) == "Mole rat"),]
Animals2[which(rownames(Animals2) == "Mole"),]
```

body brain
Mole rat 0.122 3
body brain

(d) mammals lists "Patas monkey" while Animals2 lists "Potar monkey" but body and brain weights are the same:

```
mammals["Patas monkey",]
Animals2["Potar monkey",]
```

body brain

3

Patas monkey 10 115

body brain

Mole 0.122

Potar monkey 10 115

6. Make some meaningful plots! (Next week.)