

# Exercise 1

*Your Name*

*11 Dec 2015*

```
genome.size <- c(3102, 2731, 169, 100, 12)
coding.genes <- c(20774, 23139, 13937, 20532, 6692)
species.name <- c("H. sapiens", "M. musculus",
                  "D. melanogaster", "C. elegans",
                  "S. cerevisiae")
names(genome.size) <- species.name
names(coding.genes) <- species.name
```

```
coding.bases <- coding.genes*0.0015
coding.bases
```

```
##      H. sapiens      M. musculus D. melanogaster      C. elegans
##      31.1610         34.7085         20.9055         30.7980
##      S. cerevisiae
##      10.0380
```

```
coding.pc <- coding.bases/genome.size*100
coding.pc
```

```
##      H. sapiens      M. musculus D. melanogaster      C. elegans
##      1.004545         1.270908         12.370118         30.798000
##      S. cerevisiae
##      83.650000
```

```
coding.bases[1]/coding.bases[5]
```

```
## H. sapiens
##  3.104304
```

```
genome.size[1]/genome.size[5]
```

```
## H. sapiens
##  258.5
```