Introduction to randomisation, bootstrap, and Monte Carlo methods in R

https://stirlingcodingclub.github.io/randomisation/randomisation_notes.html

Brad Duthie

6 Februrary 2019

Randomisation in R for statistical analyses

Being able to generate random numbers or sample random subsets of a list is very useful for all types of modelling

Randomisation in R for statistical analyses

Being able to generate random numbers or sample random subsets of a list is very useful for all types of modelling

1. The R programming languages includes many base functions for random number and list sampling
    - `rnorm`, `runif`, `rbinom`, `rpois`
    - `sample`

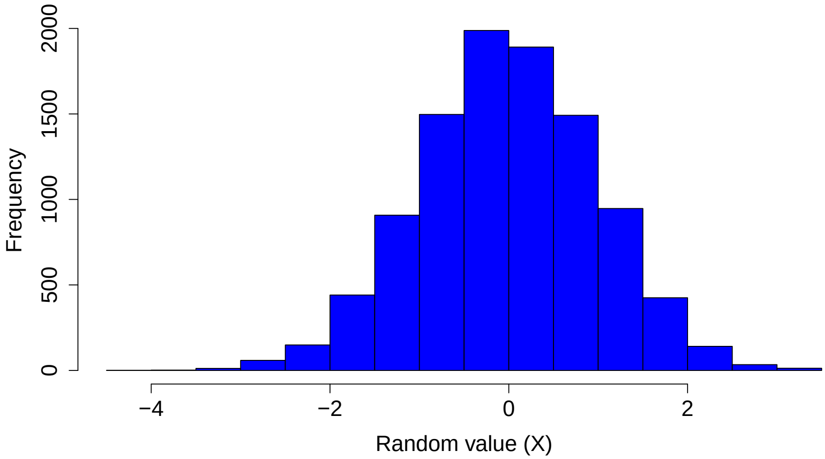
Randomisation in R for statistical analyses

Being able to generate random numbers or sample random subsets of a list is very useful for all types of modelling

1. The R programming languages includes many base functions for random number and list sampling
   - `rnorm`, `runif`, `rbinom`, `rpois`
   - `sample`
2. Look at each of these functions briefly, then show how they can be used in frequentist statistics
   - Hypothesis testing (i.e., getting p-values)
   - Confidence intervals

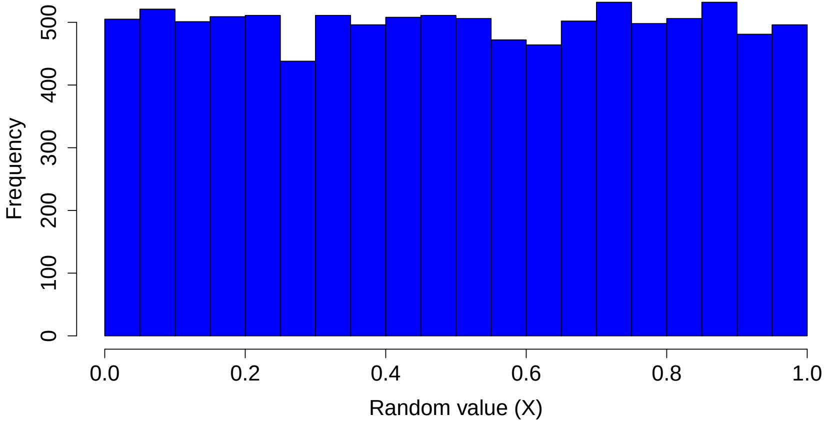
Random sampling using base functions in R: `rnorm`

```
random_norms <- rnorm(n = 10000, mean = 0, sd = 1);
```



Random sampling using base functions in R: `runif`

```r
rand_unifs <- runif(n = 10000, min = 0, max = 1);
```



Random sampling using base functions in R: `rbinom`

The `rbinom` function is a bit more tricky.

- `n`: Number of observations
- `size`: Number of independent trials *within an observation*
- `prob`: Probability that a trial is successful

If we want to flip one fair coin 1000 times:

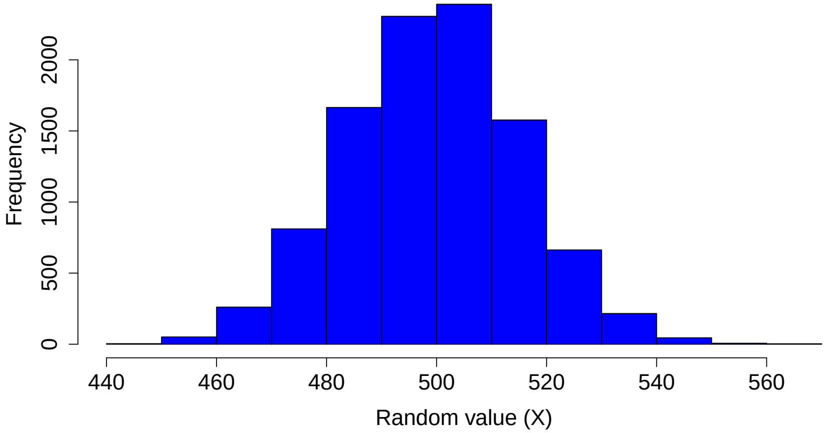
```
rand_binoms <- rbinom(n = 1, size = 1000, prob = 0.5);
```

If we want to flip 10 fair coins 1000 times:

```
rand_binoms <- rbinom(n = 10, size = 1000, prob = 0.5);
```

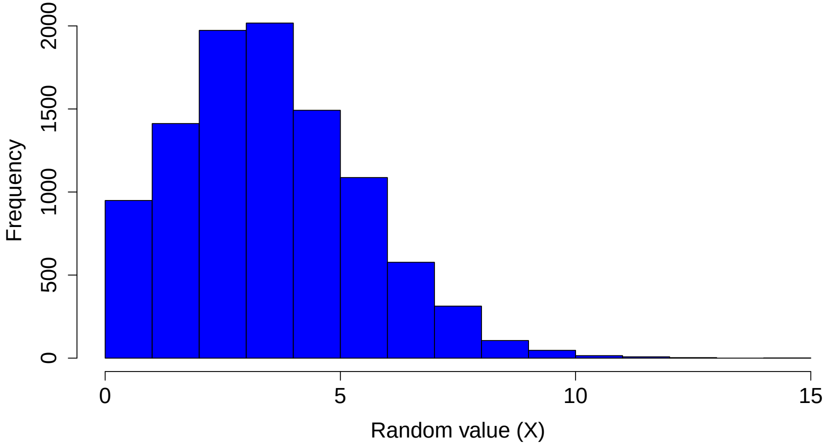
Random sampling using base functions in R: rbinom

```r
rand_binoms <- rbinom(n = 10000, size = 1000, prob = 0.5);
```



Random sampling using base functions in R: `rpois`

```r
rand_poissons <- rpois(n = 10000, lambda = 4);
```



The availability of randomisation for statistical models

Computational speed greatly increased in the late 20^{th} century

- New methods for approaching statistics became possible
- Programming tools makes custom analyses easier

The availability of randomisation for statistical models

Computational speed greatly increased in the late 20^{th} century

- New methods for approaching statistics became possible
- Programming tools makes custom analyses easier

Coding in R with randomisation & resampling very useful

- Custom analyses for non-standard statistical questions
- Modelling biological systems accessible (e.g., IBMS)

The availability of randomisation for statistical models

Computational speed greatly increased in the late 20^{th} century

- New methods for approaching statistics became possible
- Programming tools makes custom analyses easier

Coding in R with randomisation & resampling very useful

- Custom analyses for non-standard statistical questions
- Modelling biological systems accessible (e.g., IBMS)

The logic of randomisation for frequentist statistics

Logic of frequentist statistics becomes more intuitive when using randomisation and resampling methods

- **P-value**: For a particular statistical model, given that the null hypothesis is true, what is the probability of getting a statistic as or more extreme than the one observed?

The logic of randomisation for frequentist statistics

Logic of frequentist statistics becomes more intuitive when using randomisation and resampling methods

- **P-value**: For a particular statistical model, given that the null hypothesis is true, what is the probability of getting a statistic as or more extreme than the one observed?
- **Confidence interval**: An interval within which the parameter mean would be expected to be contained with some confidence (e.g., 95%) if the population were repeatedly resampled

The logic of randomisation for frequentist statistics

Logic of frequentist statistics becomes more intuitive when using randomisation and resampling methods

- **P-value**: For a particular statistical model, given that the null hypothesis is true, what is the probability of getting a statistic as or more extreme than the one observed?
- **Confidence interval**: An interval within which the parameter mean would be expected to be contained with some confidence (e.g., 95%) if the population were repeatedly resampled

By using randomisation and re-sampling, we can do statistical tests using a process that better reflects the logic underlying the frequentist approach.

The basic idea: a t-test

```r
data(iris); # Remove one of the three species below
dat <- iris[iris[,5] != "setosa",];
dat <- dat[,c(1, 5)]; # Remove unneeded columns
```

	Sepal.Length	Species
51	7.0	versicolor
52	6.4	versicolor
53	6.9	versicolor
54	5.5	versicolor
55	6.5	versicolor

- Two species include versicolor and virginica
- Want to know difference between sepal lengths is significant

The basic idea: a t-test

```r
t.test(dat[,1] ~ dat[,2], alternative = "two.sided");
```

```
##
##  Welch Two Sample t-test
##
## data:  dat[, 1] by dat[, 2]
## t = -5.6292, df = 94.025, p-value = 1.866e-07
## alternative hypothesis: true difference in means is not
## 95 percent confidence interval:
##  -0.8819731 -0.4220269
## sample estimates:
## mean in group versicolor  mean in group virginica
##                    5.936                    6.588
```

The basic idea: a t-test

A different way to state the null hypothesis: *Species identity does not have any effect on the mean difference between sepal lengths*

1. If we randomly assign species to sepal lengths, then calculate the difference between species means, the size of this difference is due to chance
2. If we repeat step 1 many times, we can generate a null distribution of differences between species means (i.e., what magnitudes of differences between sepal lengths are expected by chance)
3. We can compare the *actual observed* difference between species mean sepal lengths to the null distribution generated in step 2.

Proportion of differences that are as extreme or more extreme than the *actual observed* difference in the null distribution **is a p-value**.

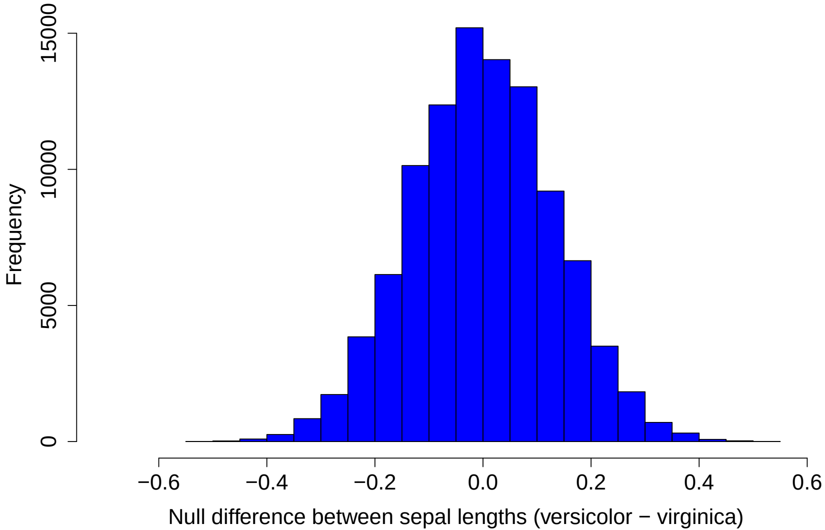
Randomisation to test for a difference between means

We can code the algorithm 1-3 below

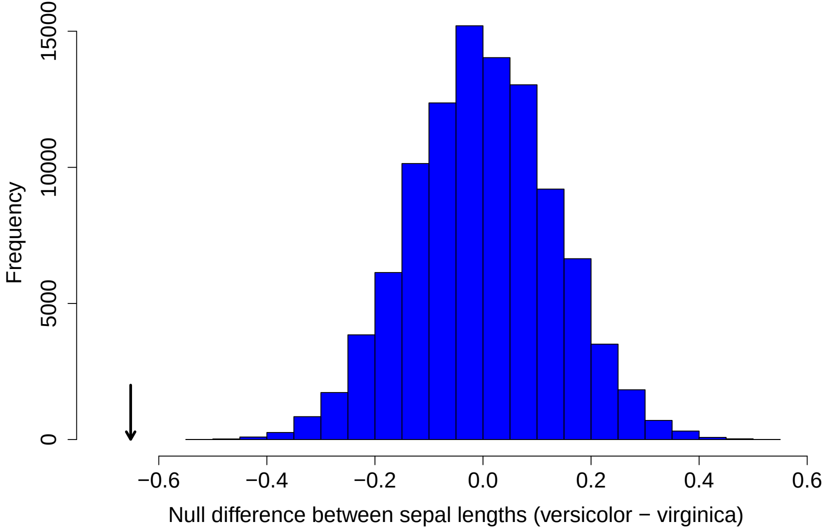
```r
iter <- 99999;           # Total iterations
diff <- NULL;
N    <- dim(dat)[1];   # Total number of sepals
for(i in 1:iter){
    sepal_smp   <- sample(x = dat[,2], size = N);
    versicolor  <- which(sepal_smp == "versicolor");
    virginica   <- which(sepal_smp == "virginica");
    mn_samp_ve  <- mean(dat[versicolor, 1]);
    mn_samp_vi  <- mean(dat[virginica, 1]);
    diff[i]     <- mn_samp_ve - mn_samp_vi;
}
```

We now have a null distribution of mean differences between sepal lengths (`diff`)

Randomisation to test for a difference between means



Randomisation to test for a difference between means



Randomisation to test for a difference between means

The actual difference between versicolor and virginica group means is -0.652.

```r
more_extreme <- sum(abs(diff) >= abs(obs_diff));
```

There were 0 values as or more extreme in the null distribution generated with 99999 values

$$P < \frac{0+1}{99999+1} = 0.00001.$$

This is consistent with the value from `t.test`

Practice problems

1. Using the base R data set `mtcars`, use a randomisation test to see if there is a significant correlation between car miles per gallon (`mpg`) and car weight (`wt`)

2. Using your own data, generate a 95% confidence interval around some mean value.

`https://stirlingcodingclub.github.io/randomisation/randomisation_notes.html`