Simulating data in R

stirlingcodingclub.github.io/simulating_data

Stirling Coding Club

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Why simulate data?

Simulating data uses generating random data sets with known properties using code (or some other method). This can be useful in a lot of contexts.

- Better understand statistical methods
- Plan ahead for actual data collection
- Visualise data sets and distributions
- Run some statistical analyses (randomisation)

How can data be simulated in R?

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- ‘rnorm‘ generates random values from a normal distribution.
- ‘rpois‘ generates random values from a poisson distribution.
- ‘rbinom‘ generates random values from a binomial distribution.
- ‘sample‘ samples values from any given vector with or without replacement.

Other R packages, such as the MASS library, can simulate full data sets with pre-defined correlation stuctures.

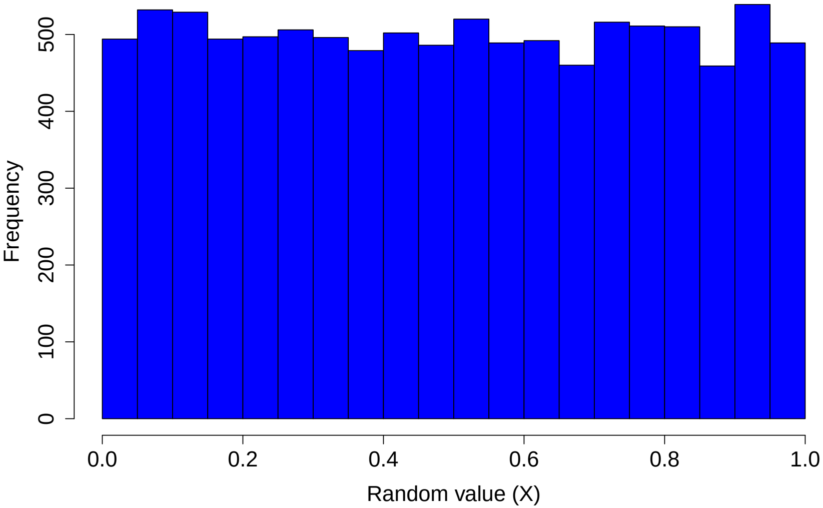
The runif function in R

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

```
##  [1] 0.71739297 0.75035000 0.56013160 0.24498652 0.68830
##  [7] 0.67665735 0.20360831 0.52135276 0.48068556 0.55222
## [13] 0.66911110 0.85938387 0.58939530 0.73200866 0.72432
## [19] 0.12922075 0.57770871 0.98332661 0.28403160 0.72911
## [25] 0.96192536 0.13342066 0.90172250 0.54101509 0.49679
## [31] 0.85583746 0.15100820 0.07010486 0.83421067 0.94163
## [37] 0.94881335 0.89494764 0.85449798 0.32408480
```

The `runif` function in R

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



The runif function in R

```
int verify_seed(int x){
  x=abs(x) % 30000;
  return(++x);
 } /* Easy way of getting seeds */

double as183(int seeds[]){
  double unidev; /* Code below verifies the 3 seeds */
  seeds[0] = verify_seed(seeds[0]);
  seeds[1] = verify_seed(seeds[1]);
  seeds[2] = verify_seed(seeds[2]);
  /* Code below gets a decimal to be added to unidev */
  seeds[0] = (171 * seeds[0]) % 30269;
  seeds[1] = (172 * seeds[1]) % 30307;
  seeds[2] = (170 * seeds[2]) % 30323;
  /* unidev gets a random uniform number between zero and one */
  unidev = seeds[0]/30269.0 + seeds[1]/30307.0 + seeds[2]/30323.
  /* Return just the decimal, subtract integer of unidev */
  return(unidev - (int)unidev);
} /* We now have one random uniform number */
```

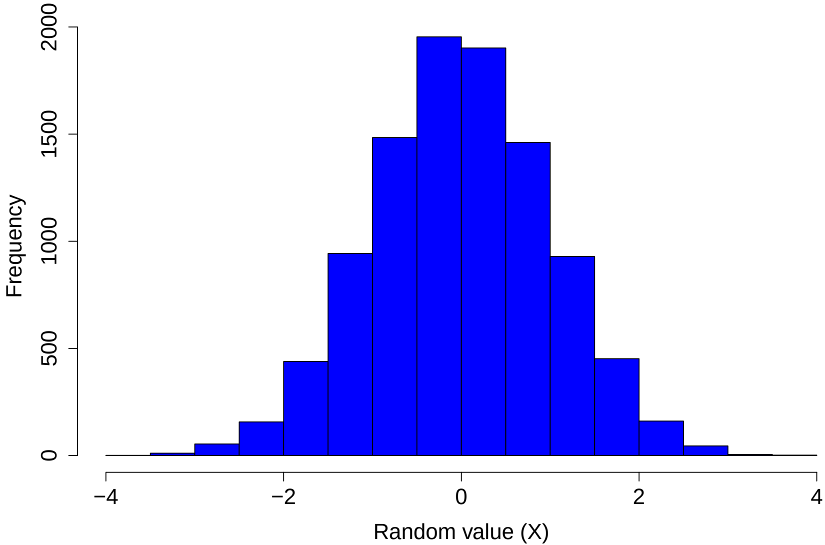
The rnorm function in R

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

```
##  [1]  0.94726152  0.68356269  0.49704858  0.44813645  0.
##  [7]  0.24372762  1.53200867  0.51274151  0.59188341  1.
## [13]  0.98859434 -1.32302537  0.12578028  0.78844279  0.
## [19] -0.60932700 -0.38531844 -1.07812230  0.44641907  0.
## [25] -1.60425962  0.98398122  2.03062832 -1.55893601 -1.
## [31]  0.10309797  0.62000705  0.41811461  1.26991674 -0.
## [37] -0.83093977 -0.31985344  0.93327407  0.19218058
```

The rnorm function in R

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



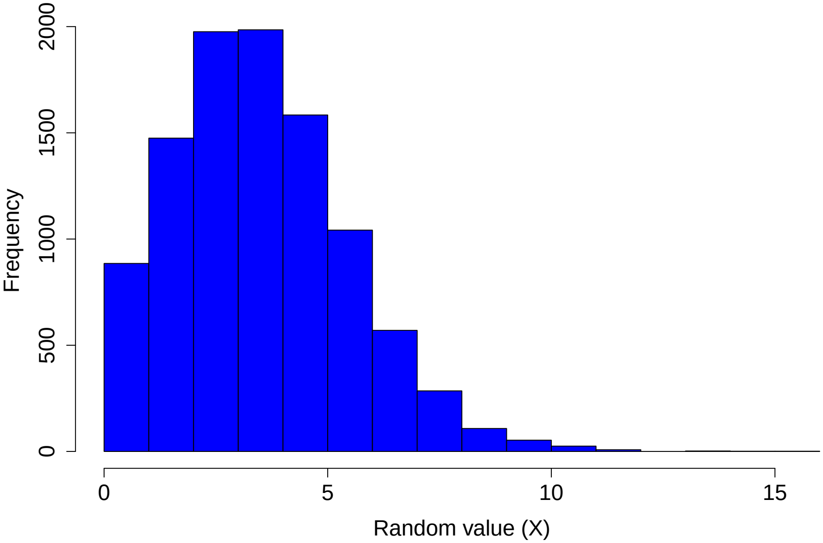
The rpois function in R

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

```
##  [1]  0  7  3  3  4  5  5  2  4  6  6  0  6  5  7  7  6
## [26]  3  5  7  3  3  3  3  3  7  3  4  5  3  9  4
```

The rpois function in R

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



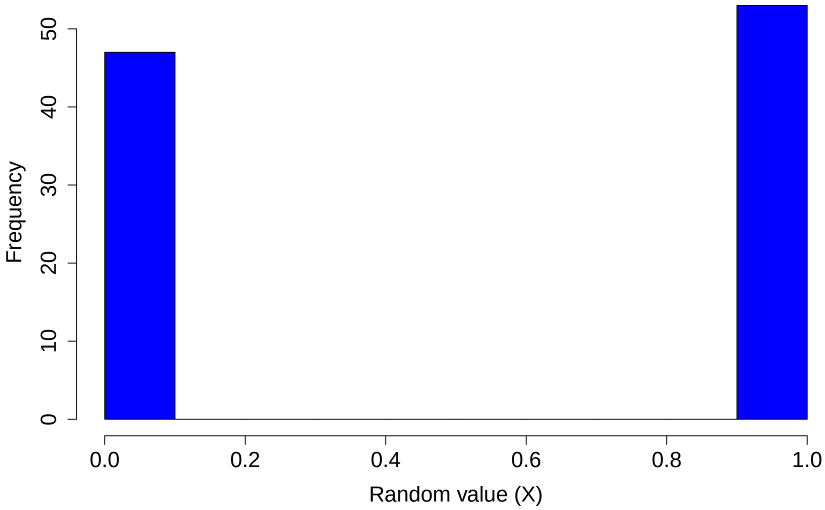
The rbinom function in R

```r
rand_rbinom <- rbinom(n = 100, size = 1, prob = 0.5);
```

```
##  [1] 0 0 1 0 1 1 1 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 1 0
## [39] 1 1
```

The rpois function in R

```r
rand_rbinom <- rbinom(n = 100, size = 1, prob = 0.5);
```



Using sample in R

Create a vector of numbers from which to sample.

```
my_sample_vec <- 1:10;
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

Using `sample` in R

Create a vector of numbers from which to sample.

```
my_sample_vec <- 1:10;
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

Use `sample` to randomly sample numbers from `my_sample_vec`

```
my_sample <- sample(x = my_sample_vec, size = 4);
```

```
## [1] 7 6 5 8
```

Using sample in R

Can sample with or without replacement.

```
sample_no_replace <- sample(x = my_sample_vec,
                            size = 10, replace = FALSE);
```

```
##  [1]  9  2  8  1 10  3  5  7  4  6
```

Using sample in R

Can sample with or without replacement.

```r
sample_no_replace <- sample(x = my_sample_vec,
                            size = 10, replace = FALSE);
```

```
##  [1]  9  2  8  1 10  3  5  7  4  6
```

```r
sample_replace <- sample(x = my_sample_vec,
                         size = 10, replace = TRUE);
```

```
##  [1]  6 10  6  9  6 10  5  5  5  8
```

Using sample in R

Can also change the probabilities of being sampled

```r
# Vector values must sum to 1
pr_vector  <- c(0, 0, 0, 0, 0,
                0.2, 0.2, 0.2,
                0.2, 0.2);
new_sample <- sample(x = 1:10, size = 10,
                     replace = TRUE,
                     prob = pr_vector);
```

```
##  [1] 10  8  6  7 10  8  9 10  6  7
```

Using sample in R

Can also sample strings instead of numbers

```r
species   <- c("species_A", "species_B", "species_C");
sp_sample <- sample(x = species, size = 12,
                    replace = TRUE,
                    prob = c(0.5, 0.25, 0.25)
                    );
```

```
##  [1] "species_B" "species_A" "species_C" "species_A" "sp
##  [7] "species_B" "species_A" "species_A" "species_B" "sp
```

Building a simple simulated dataset

```
N          <- 12;
species    <- c("species_A", "species_B");
sp_sample  <- sample(x = species,
                    size = N, replace = TRUE);
sp_mass    <- rnorm(n = N, mean = 100, sd = 4);
for(i in 1:N){
  if(sp_sample[i] == "species_A"){
    sp_mass[i] <- sp_mass[i] + rnorm(n = 1,
                                     mean = 4, sd = 1);
  }
}
sim_data  <- data.frame(sp_sample, sp_mass);
```

Building a simple simulated dataset

sp_sample	sp_mass
species_B	97.58065
species_B	96.96083
species_B	104.09267
species_A	105.05708
species_A	102.81067
species_A	106.13235
species_A	104.61697
species_A	107.89034
species_B	101.01198
species_B	96.17857
species_B	100.64885
species_B	103.06411

Building a simple simulated dataset

```r
t.test(sp_mass ~ sp_sample, data = sim_data);
```

```
##
##  Welch Two Sample t-test
##
## data:  sp_mass by sp_sample
## t = 3.7314, df = 9.8585, p-value = 0.003999
## alternative hypothesis: true difference in means betwee
## 95 percent confidence interval:
##  2.156122 8.578935
## sample estimates:
## mean in group species_A mean in group species_B
##               105.30148                99.93395
```

Building a simple simulated dataset

```r
N         <- 120;
species   <- c("species_A", "species_B");
sp_sample <- sample(x = species, size = N,
                    replace = TRUE);
sp_mass   <- rnorm(n = N, mean = 100, sd = 4);
for(i in 1:N){
  if(sp_sample[i] == "species_A"){
    sp_mass[i] <- sp_mass[i] + rnorm(n = 1,
                                     mean = 4, sd = 1);
  }
}
sim_data  <- data.frame(sp_sample, sp_mass);
```

Building a simple simulated dataset

```r
t.test(sp_mass ~ sp_sample, data = sim_data);
```

```
##
##  Welch Two Sample t-test
##
## data:  sp_mass by sp_sample
## t = 4.7219, df = 92.007, p-value = 8.341e-06
## alternative hypothesis: true difference in means betwee
## 95 percent confidence interval:
##  2.087618 5.118701
## sample estimates:
## mean in group species_A mean in group species_B
##                104.0913                100.4882
```

Setting a seed gives the same numbers

Try it once

```r
set.seed(10);
rnorm(n = 10);
```

```
##  [1]  0.01874617 -0.18425254 -1.37133055 -0.59916772  0.
##  [7] -1.20807618 -0.36367602 -1.62667268 -0.25647839
```

Try it again

```r
set.seed(10);
rnorm(n = 10);
```

```
##  [1]  0.01874617 -0.18425254 -1.37133055 -0.59916772  0.
##  [7] -1.20807618 -0.36367602 -1.62667268 -0.25647839
```