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?

Random data with different properties can be generated in R using several base R functions.

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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.

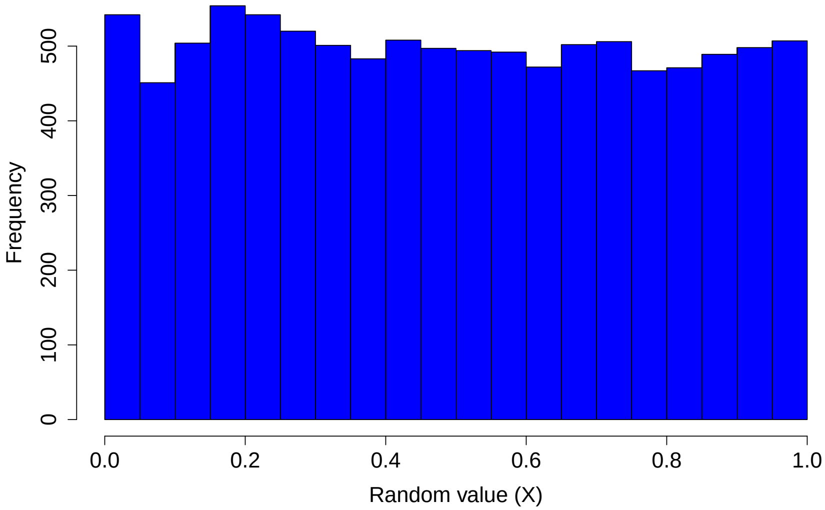
The runif function in R

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

```
##  [1] 0.8670857768 0.5615415513 0.6288375359 0.7923040655
##  [6] 0.1095961148 0.2355039727 0.8978011261 0.6879017937
## [11] 0.5624286113 0.9375209641 0.3825901572 0.5472148873
## [16] 0.7698536073 0.4487606222 0.8535867573 0.7288415928
## [21] 0.0934886276 0.0524177891 0.6597115695 0.1274242669
## [26] 0.7071376585 0.7218166539 0.9343405771 0.0041327698
## [31] 0.8715531109 0.1296939508 0.3870098493 0.0009932041
## [36] 0.6261875923 0.5429373912 0.1288557602 0.7124097436
```

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 */
```

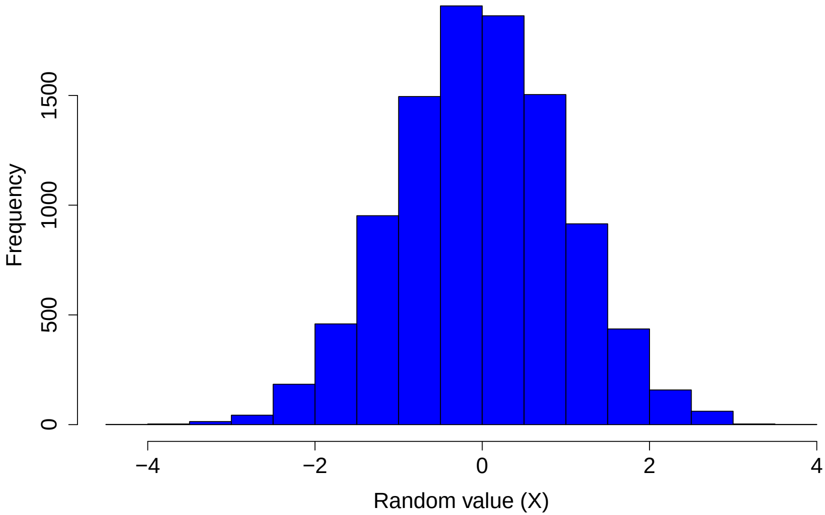
The rnorm function in R

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

```
##  [1] -0.238818449 -0.410411347  0.277909056  0.305590858
##  [6] -0.492572290 -0.397795630  0.135767266  0.312741598
## [11]  0.247555343 -0.565200403  0.486173016  0.835464508
## [16] -0.282386781 -0.490972178 -0.415299952  0.303614862
## [21]  0.533060260 -0.866063628  0.153560803 -0.122009959
## [26] -0.024995795  1.538472460  0.909788815 -2.154001653
## [31] -0.441665950 -0.681505811  0.746111719  1.192287230
## [36]  0.286682273  0.518682453  0.871770365  0.961401125
```

The rnorm function in R

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



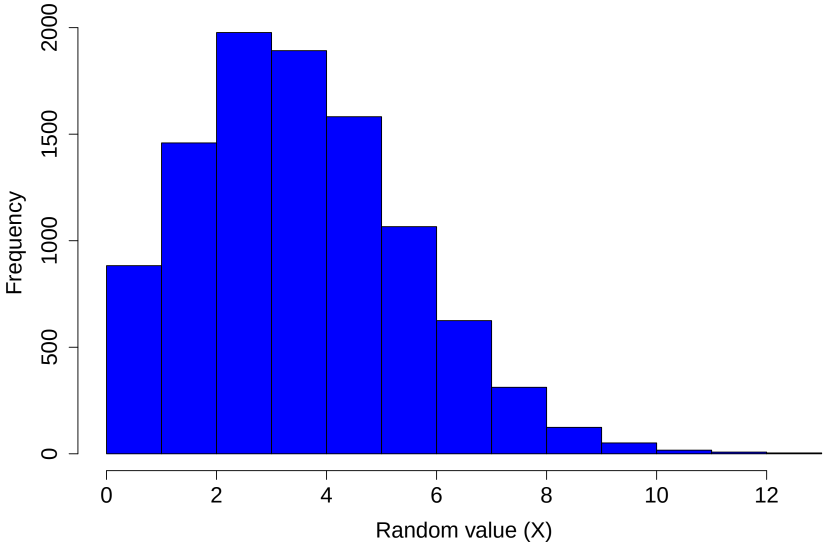
The rpois function in R

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

```
##  [1]  3  6  3 10  5  4  3  3  5  7  4  4  3  7  4  3  5
## [26]  7  1  4  4  4  7  3  2  3  1  4  3  5  2  1
```

The rpois function in R

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



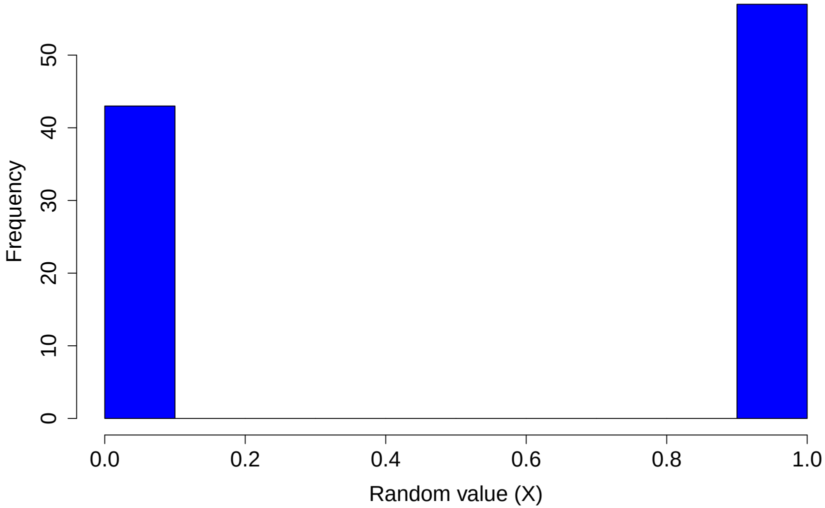
The rbinom function in R

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

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

The rpois function in R

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



Using sample in R

Create a vector of numbers from which to sample.

```r
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.

```r
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`

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

```
## [1]  7 10  4  2
```

Using `sample` in R

Can sample with or without replacement.

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

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

Using sample in R

Can sample with or without replacement.

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

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

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

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

Using `sample` in R

Can also change the probabilities of being sampled

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

Using `sample` in R

Can also sample strings instead of numbers

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

Building a simple simulated dataset

```r
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 = 2, sd = 1);
  }
}
sim_data  <- data.frame(sp_sample, sp_mass);
```

Building a simple simulated dataset

sp_sample	sp_mass
species_B	102.12150
species_B	103.63621
species_B	100.80428
species_A	97.01569
species_A	104.27227
species_A	104.20936
species_A	96.13937
species_A	99.41683
species_B	106.52525
species_A	103.54237
species_A	99.59500
species_B	105.38609

Building a simple simulated dataset

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

```
##
##  Welch Two Sample t-test
##
## data:  sp_mass by sp_sample
## t = -1.8637, df = 9.9981, p-value = 0.09197
## alternative hypothesis: true difference in means between
## 95 percent confidence interval:
##  -6.7975205  0.6055819
## sample estimates:
## mean in group species_A mean in group species_B
##                100.5987                103.6947
```

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 = 2, 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 = 3.5696, df = 117.23, p-value = 0.0005193
## alternative hypothesis: true difference in means between
## 95 percent confidence interval:
##  1.09329 3.81812
## sample estimates:
## mean in group species_A mean in group species_B
##                102.25269                99.79699
```

Setting a seed gives the same numbers

Try it once

```
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

```
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
```