Exercice n°1

Variance calculation

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I Variance calculation

The aim of this first exercice is to approache the difficulties of computer simulation and to get used to R and R Markdown. In order to illustrate these problems we will use the variance calculation through 4 different algorithms and the "var" function provided by R.

As starting point, we will use theese lines to include libraries and create our datasets

```
library(microbenchmark)#Allows the use of the microbenchmark library

set.seed(11220221)#Create random data
x1 <- rnorm(100)
x2 <- rnorm(100, mean=1000000)
x3 <- rnorm(100, mean=0.0000001)
```

I.1 Algorithme n°1: (two-pass algorithme)

The first algorithm follows the traditional variance formula: $s_n^2 = \frac{1}{(n-1)} \sum_{i=1}^{n} (x_i - x_n)^2$. It needs to read all the data twice, once to calculate the mean and once to calculate the variance.

```
precise <- function(x) {
  sum <- 0
  n <- length(x)

  #First pass: mean calculation
  for (i in x) {
    sum <- sum + i
  }
  mean <- sum/n

  variance <- 0
  #Second pass: variance calculation
  for(i in x) {
    variance <- variance + (i - mean)^2
  }
  variance <- variance/(n-1)
  return(variance)
}
```

I.2 Algorithme n°2: (one-pass algorithme)

The second algorithm use the Variance Decomposition princips : $s_n^2 = \frac{1}{(n-1)}(\sum_{i=1}^{n} x_i^2 - \frac{1}{n}(\sum_{i=1}^{n} x_i)^2)$. This allows the algorithm to read the data only once.

```
excel <- function(x) {
  P1 <- 0
  P2 <- 0
  n <- length(x)
  variance <- 0

  for (i in x) {
    P1 <- P1 + i^2
    P2 <- P2 + i
  }
  P2 <- (P2^2)/n
  variance <- (P1-P2)/(n-1)
  return(variance)
}
```

I.3 Algorithme n°3: (shifted one-pass algorithme)

The third algorithm works with the Scale Invariance property : $s_x^2 = s_{x-c}^2$ with c a constant. That gives us the following formula :

$s_n^2 = \frac{1}{(n-1)}(\sum_{i=1}^{n} (x_i - c)^2 - (\frac{1}{n}\sum_{i=1}^{n}(x_i - c))^2)$

The default c-value is the first value in the dataset

```
shifted <- function(x, c=x[1]) {
  P1 <- 0
  P2 <- 0
  n <- length(x)
  variance <- 0

  for (i in x) {
    P1 <- P1 + (i-c)^2
    P2 <- P2 + i-c
  }
  P2 <- (P2^2)/n
  variance <- (P1-P2)/(n-1)
  return(variance)
}
```

Consider what would be a good value for c ?

Considering the compututation pinciples of a computer, it would be interesting to work with small number (i.e: approaching 0) so giving c the mean value should be interessting.

I.4 Algorithme n°4: (online algorithme)

The last algorithm is based on the online calculation of the variance :

$$\bar{x}_n = \bar{x}_{n-1} + \frac{x_n - \bar{x}_{n-1}}{n}, \quad n > 1$$

$$S_n^2 = \frac{n-2}{n-1} S_{n-1}^2 + \frac{(x_n - \bar{x}_{n-1})^2}{n}, \quad n > 1$$

```
online <- function(x) {
  #initalisation
  n <- 2
  mean <- (x[1]+x[2])/2
  variance <- (x[1]-mean)^2 + (x[2]-mean)^2

  #Mean and variance are computed after each element in x
  for (i in 3:length(x)) {
    n <- n+1
    variance <- ((n-2)/(n-1)) * variance + ((x[i]-mean)^2/n)
    mean <- mean + (x[i]-mean)/n
  }
  return(variance)
}
```

II Comparison

To facilitate the comparison between the different algorithms we will use a wrapper function that call every algorithm

```
variances <- function(x){
  return(c(precise(x), excel(x), shifted(x), online(x),var(x)))
}
```

First we will examine the result obtained by each algorithm on the same two datasets we have set up earlier.

Table 1: Variance calulation

	precise	excel	shifted	online	var
x1	1.1244184	1.1244184	1.1244184	1.1244184	1.1244184
x2	0.9419366	0.9416035	0.9419366	0.9419366	0.9419366

It appears that the excel algorithm isn't robust. For samples with big means it doesn't return a precise value for the variance and differs from the others.

II.1 Computation time

Let's focus on the computation time, we will run each algoritm 100 times thank to the microbenchmark function using the x1 dataset.

```
microx1 <- microbenchmark(precise(x1), excel(x1), shifted(x1), online(x1),var(x1),  times=100)
knitr::kable(summary(microx1), caption ="x1 computation times")
```

Table 2: x1 computation times

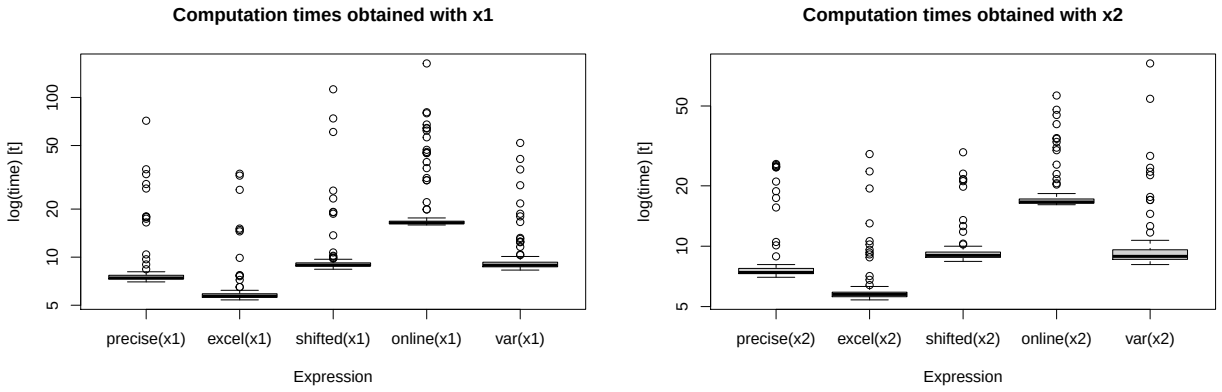
expr	min	lq	mean	median	uq	max	neval	cld
precise(x1)	7.0	7.3	9.588	7.4	7.7	71.5	100	ab
excel(x1)	5.4	5.6	6.832	5.7	5.9	33.3	100	a
shifted(x1)	8.4	8.8	11.858	8.9	9.2	112.5	100	b
online(x1)	15.9	16.2	23.580	16.4	16.8	163.3	100	c
var(x1)	8.3	8.7	10.771	8.9	9.3	51.9	100	ab

```
microx2 <- microbenchmark(precise(x2), excel(x2), shifted(x2), online(x2),var(x2),  times=100)
knitr::kable(summary(microx2), caption ="x2 computation times")
```

Table 3: x2 computation times

expr	min	lq	mean	median	uq	max	neval	cld
precise(x2)	7.0	7.3	9.008	7.40	7.75	25.7	100	b
excel(x2)	5.4	5.6	6.617	5.75	5.90	28.8	100	a
shifted(x2)	8.4	8.8	9.972	9.00	9.35	29.4	100	b
online(x2)	16.1	16.4	18.986	16.60	17.20	56.4	100	c
var(x2)	8.1	8.6	11.135	8.90	9.60	81.5	100	b

```
boxplot(microx1, main="Computation times obtained with x1")
boxplot(microx2, main="Computation times obtained with x2")
```



Thank to the boxplot it clearly appears that the excel algorithm is the speediest one and the online one is the worth. By the way, switching x1 dataset to x2 dataset doesn't impact the computational time so much and doesn't change the ranking either.

Would you know another way in R to compare computing times?

Recording computing time in R can also be done with the system time :

```
start_time <- Sys.time()
invisible(excel(x1))
end_time <- Sys.time()
```

```
computation_time = end_time-start_time
print(computation_time)
```

```
## Time difference of 0.002043009 secs
```

II.2 Scale invariance property

Thanks to the scale invariance property, we can assume that $s_x^2 = s_{x+c}^2$ with c a constant. We can investigate this property with the shifted algorithm by changing the c-value. Therefor we will use the *condition number*: $S = \sum_{i=1}^{n}(x_i - x_n)^2 = (n-1) * s_n^2$. It gives a idea of how a small change in the inputs will causes a change in the output. The closet is k to 1 the best it is because it would mean our variance remain trustful with some noise errors in the input.
Influence of the c-value on the condition number

```
condition_number <- function(mean, n , S){
  return(sqrt(1+(mean^2*n)/S))
}
```

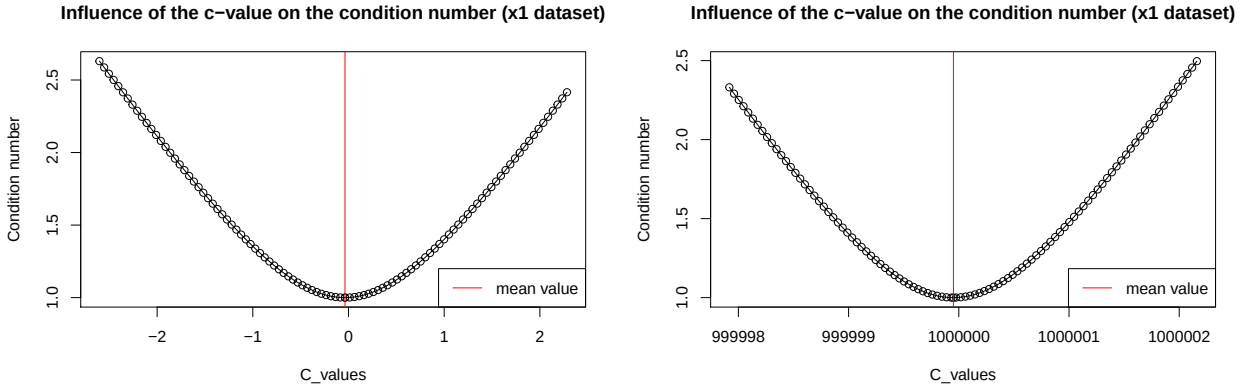
To observe the c_value influence, we will compute the condition number with 10 c-values tooked between the min and the max of the data set and we will also compute the condition number with the mean as c-value.

```
c_val_influence <- function(x){
  minimum <- min(x)
  maximum <- max(x)
  c_list <- seq(from=minimum, to=maximum, length.out=100)
  c_list <- sort(append(c_list, mean(x)))
  condition_numb <- matrix(nrow = 2, ncol = 101)
  for(i in 0:length(c_list)){
    mean <- mean(x) - c_list[i]
    n <- 100
    S <- shifted(x,c_list[i])*(n-1)
    condition_numb[1,i] <- c_list[i]
    condition_numb[2,i] <- condition_number(mean, n ,S)
  }
  return(condition_numb)
}

cond_numb_x1 <- c_val_influence(x1)
cond_numb_x2 <- c_val_influence(x2)

plot(cond_numb_x1[2,], x=cond_numb_x1[1,], main="Influence of the c-value on the condition number (x1 da
abline(v=mean(x1), col='red')
legend("bottomright", "mean value", col="red", lty=1)

plot(cond_numb_x2[2,], x=cond_numb_x2[1,], main="Influence of the c-value on the condition number (x1 da
abline(v=mean(x2), col='red')
legend("bottomright", "mean value", col="red", lty=1)
```



As expected, the best condition number is obtained for the mean as c-value.

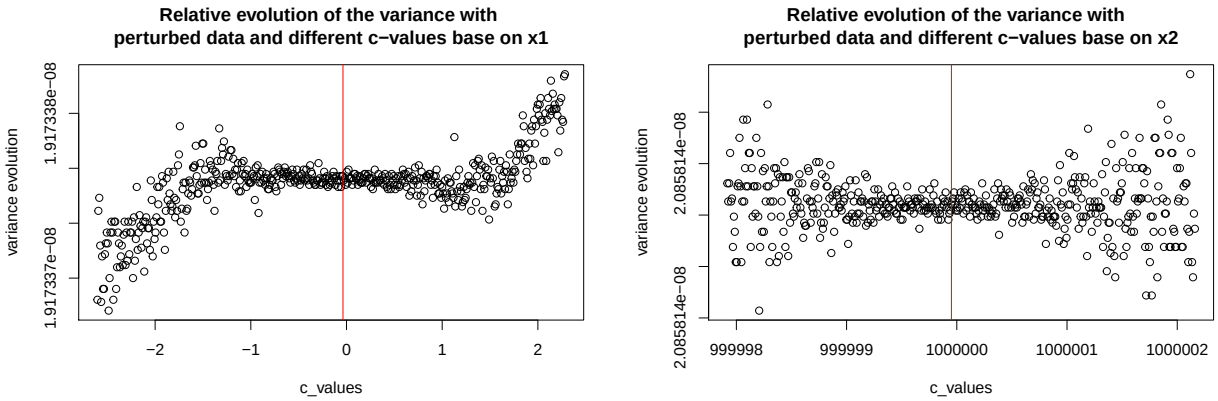
Influence of input changement on the variance with different c-value

On the previous point, we shows that the c-value of the shifted variance algorithm influence the condition number. Since the condition number defines how a small change in the input impact the output, we can investigate the impact of this input changement on the variance value for different c-values.

```
var_evolution <-function(x){
  minimum <- min(x)
  maximum <- max(x)
  c_list <- seq(from=minimum, to=maximum, length.out=500)
  pertubated_sample = x + rnorm(100,0)*0.0000001
  variance <- c()
  perturbed_variance <- c()
  evolution<- c()
  for( i in 0:length(c_list)){
    variance <- append(variance, shifted(x,c_list[i]))
    perturbed_variance <- append(perturbed_variance, shifted(pertubated_sample,c_list[i]))
    evolution<- append(evolution, abs(perturbed_variance[i]-variance[i])/variance[i])
  }
  result <- data.frame(variance,perturbed_variance,evolution,c_list)
  return(result)
}

data <- var_evolution(x1)
plot(data$c_list,data$evolution, xlab = "c_values", ylab = "variance evolution", main = "Relative evolu
abline(v = mean(x1), col="red")

data <- var_evolution(x2)
plot(data$c_list,data$evolution, xlab = "c_values", ylab = "variance evolution", main = "Relative evolu
abline(v = mean(x2), col="red")
```



This plot confirms the plot previous graph. It shows that with a c-value close to the dataset mean the relative evolution of the shifted algorithm output is less important with small pertutbations in the input. The importance of the perturbation (1e-8 here) will impact all points in the same way.

3 Condition number

We will focus on the importance of the dataset's mean for the condition number

```
res <- c()
res <- append(res,condition_number(mean(x1), 100,var(x1)*(100-1)))
res <- append(res,condition_number(mean(x2), 100,var(x2)*(100-1)))
res <- append(res,condition_number(mean(x3), 100,var(x3)*(100-1)))
res <- as.data.frame(res, row.names=c('x1 mean=0','x2 mean=1 000 000','x3 mean=0.000 000 1'))
knitr::kable(res , col.names="k", caption="Condition numbers for different dataset mean")
```

Table 4: Condition numbers for different dataset mean

	k
x1 mean=0	1.000609e+00
x2 mean=1 000 000	1.035551e+06
x3 mean=0.000 000 1	1.013128e+00

We can assume that the condition number is pretty sensitive. Between the condition number of x1 (mean(x1)=0) and x3 (mean(x3)=0.000 000 1) we have a difference of 1e-2.