Non-life — Assignment NL1

Niels Keizer* and Robert Jan Sopers†

September 18, 2016

Generating multinormal and multi-student r.v.'s

Q1

First we run the following script:

```
> set.seed(1)
> sum(duplicated(runif(1e6))) ## = 120
[1] 120
> sum(duplicated(rnorm(1e8))) ## = 0
[1] 0
```

The function `duplicated` returns a logical array where unique numbers are marked with 0 and duplicates are marked with 1 (the first occurence of the number is marked with a 0). Summming this array thus gives the total number of duplicates. The uniform distribution gives 120 duplicates in a much smaller sample size than the normal distribution, which gives 0 duplicates.

In the assignment, the expected number of different numbers is derived to be

$$\mathbb{E}[N_n] = \frac{1 - f^n}{1 - f} \tag{1}$$

The number of duplicates is then given by $n - \mathbb{E}[N_n]$ We run the following script:

```
> m <- 2^32;n <- 1e6
> f <- 1 - 1/m
> num_dup_unif <- n - (1-f^n)/(1-f)
> num_dup_unif
[1] 116.3988
```

The expected result of 116.4 is quite close to the generated result. The outcome of 120 is therefore consistent with the assumption that `runif` produces different values uniformly.

*Student number: 10910492
†Student number: 99999999

The resolution of `rnorm` is somewhere in the 2^{50}'s. Directly calculating $1 - f^n$ will give 1, because f is so close to 1. First, we use to approximation given in the assignment.

$$f^n = \left(1 - \frac{1}{m}\right)^n \approx 1 - \frac{n}{m} + \frac{n^2}{2m^2} \tag{2}$$

Inserting this into our equation for the number of different numbers gives

$$\frac{1 - f^n}{1 - f} \approx \frac{1 - 1 + \frac{n}{m} - \frac{n^2}{2m^2}}{1 - \left(1 - \frac{1}{m}\right)} = \frac{\frac{n}{m} - \frac{n^2}{2m^2}}{\frac{1}{m}} = n - \frac{n^2}{2m} \tag{3}$$

This results in the following equation for the expected number of duplicates.

$$n - \left(n - \frac{n^2}{2m}\right) = \frac{n^2}{2m} \tag{4}$$

Next we check in `R` if the number of duplicates is consistent with values for m of 10^{15}, 10^{16}, 10^{17} or 10^{18}, when n is 10^8

```
> n_norm <- 1e8
> m_norm <- c(1e15,1e16,1e17,1e18)
> num_dup_norm <- n_norm^2/(2*m_norm)
> num_dup_norm
[1] 5.000 0.500 0.050 0.005
```

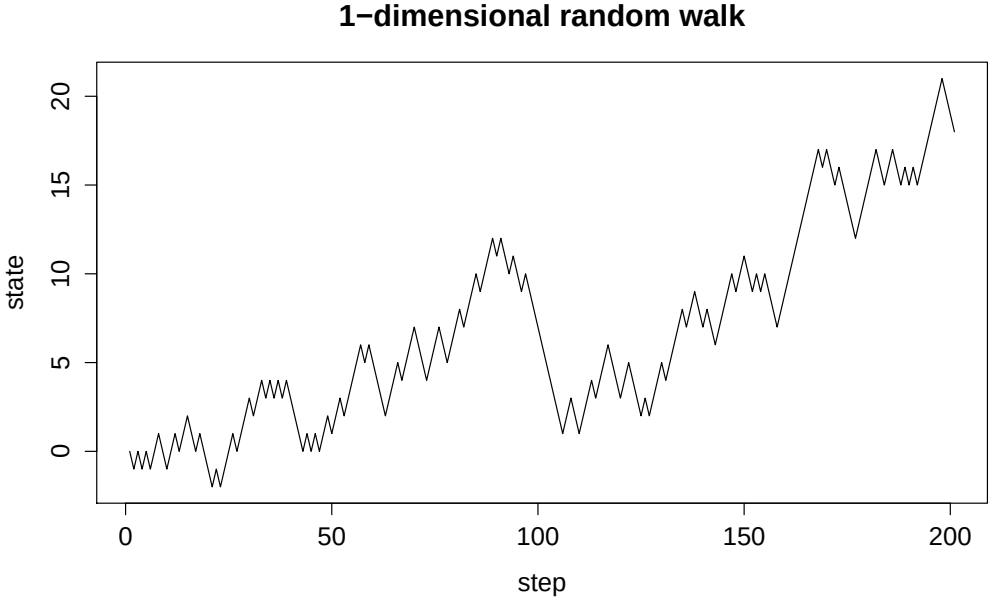
The obtained result seems to be consistent with a resolution of 10^{16} or higher.

Q2

The following code is executed in `R`.

```
> n <- 200; p <- 0.52
> x <- c(0,cumsum(2*rbinom(n,1,p)-1))
> plot(x, type="l", lwd=1, ylab="state", xlab="step", main="1-dimensional random walk")
```

This gives the following biased random walk:



Q3

Given that X, $Y \sim N(0,1)$, we want to transform (X,Y) into (X,Y^*), with $Y^* = aX + bY$, with a, b chosen in such a way that $\text{Var}[Y^*] = 1$ and $r(X,Y^*) = 0.8$.

$$r(X,Y^*) = \frac{\mathbb{E}[XY^*] - \mathbb{E}[X]\,\mathbb{E}[Y*]}{\sqrt{\text{Var}[X]\,\text{Var}[Y^*]}} = \frac{\mathbb{E}[aX^2 + bXY] - 0 \cdot \mathbb{E}[Y^*]}{\sqrt{1 * 1}} \tag{5}$$

$$= a * \mathbb{E}[X^2] + b * \mathbb{E}[XY] = a(\text{Var}[X] - \mathbb{E}[X]^2) = a \tag{6}$$

Here we use that $\mathbb{E}[X] = 0$, $\text{Var}[X] = \text{Var}[Y] = \text{Var}[Y^*] = 1$. Also $\mathbb{E}[XY] = \mathbb{E}[X]\,\mathbb{E}[]Y] = 0$, because X and Y are independent. Next we use the condition that the variance of Y^* must also be 1.

$$\text{Var}[Y^*] = \text{Var}[aX + bY] = a^2\,\text{Var}[X] + b^2\,\text{Var}[Y] + 2ab\,\text{Cov}[X,Y] = a^2 + b^2 = 1 \tag{7}$$

We can conclude from this that $a = 0.8$ and $b = \sqrt{1 - a^2} = 0.6$.

In `R` code:

```
set.seed(2004); options(digits=2)
X <- rnorm(1000); Y <- rnorm(1000)
a <- .8; b <- sqrt(1 - a^2); Y <- a*X + b*Y
```

Q4

The variance-covariance matrix Σ of the random vector (X,Y^*) is equal to the correlation matrix because $\text{Var}[X] = \text{Var}[Y^*] = 1$. It is given by the following expression.

$$\Sigma = \begin{pmatrix} \text{Cov}[X,X] & \text{Cov}[X,Y^*] \\ \text{Cov}[Y^*,X] & \text{Cov}[Y^*,Y^*] \end{pmatrix} = \begin{pmatrix} \text{Var}[X] & r(X,Y^*) \\ r(X,Y^*) & \text{Var}[Y^*] \end{pmatrix} = \begin{pmatrix} 1 & 0.8 \\ 0.8 & 1 \end{pmatrix} \tag{8}$$

Q5

If A is to be the Cholesky decomposition of Σ, it should be a lower triangular matrix with real and positive entries and $AA^* = \Sigma$, where A^* is the conjugate transpose of A. Checking this gives

$$\begin{pmatrix} 1 & 0 \\ a & b \end{pmatrix} \begin{pmatrix} 1 & a \\ 0 & b \end{pmatrix} = \begin{pmatrix} 1 & a \\ a & a^2 + b^2 \end{pmatrix} = \begin{pmatrix} 1 & a \\ a & 1 \end{pmatrix} = \begin{pmatrix} 1 & 0.8 \\ 0.8 & 1 \end{pmatrix} = \Sigma \tag{9}$$

Q6

We execute the following `R` code.

```
> c(mean(X), var(X), mean(Y), var(Y), cor(X,Y))
[1] 0.051 0.983 0.070 0.994 0.796
```

The means of X and Y^* are close to 0. The variances close to 1 and the correlation is close to 0.8. This resembles the theoretical values quite close.

Q7

Let (X, Y) be bivariate Normal with $\mathbb{E}[X] = \mathbb{E}[Y] = 0$, $\mathrm{Var}[X] = \mathrm{Var}[Y] = 1$ and $r(X, Y) = r$. W is independent of (X, Y). Then

$$r(XW, YW) = \frac{\mathbb{E}[XWYW] - \mathbb{E}[XW]\,\mathbb{E}[YW]}{\sqrt{\mathrm{Var}[XW]\,\mathrm{Var}[YW]}} \tag{10}$$

$$= \frac{\mathbb{E}[W^2]\,\mathbb{E}[XY] - \mathbb{E}[W]^2\,\mathbb{E}[X]\,\mathbb{E}[Y]}{\sqrt{\left(\mathbb{E}[W^2]\,\mathbb{E}[X^2] - \mathbb{E}[W]^2\,\mathbb{E}[X]^2\right)\left(\mathbb{E}[W^2]\,\mathbb{E}[Y^2] - \mathbb{E}[W]^2\,\mathbb{E}[Y]^2\right)}} \tag{11}$$

$$= \frac{\mathbb{E}[W]^2\,\mathbb{E}[XY] - 0}{\sqrt{\left(\mathbb{E}[W^2]\,\mathbb{E}[X^2] - 0\right)\left(\mathbb{E}[W^2]\,\mathbb{E}[Y^2] - 0\right)}} \tag{12}$$

$$= \frac{\mathbb{E}[W^2]}{\sqrt{\mathbb{E}[W^2]^2}} \frac{\mathbb{E}[XY]}{\mathrm{Var}[X]\,\mathrm{Var}[Y]} = r \cdot \frac{\mathbb{E}[W^2]}{\sqrt{\mathbb{E}[W^2]^2}} = r \tag{13}$$

When $\mathbb{E}[W^2]$ is finite, the final step in the derivation is allowed. This is equivalent with demanding $\mathrm{Var}[W]$ to be finite.

Q8

We take X and Y^* as defined earlier. $V \sim \chi^2_k$ and $W = \sqrt{k/V}$ with $k = 5$. The population mean of XW is 0 because $\mathbb{E}[XW] = \mathbb{E}[X]\,\mathbb{E}[W] = 0$. The same holds for Y^*W. $r(XW, Y^*W) = 0.8$ has been proven in question 7. Next we determine the variance of XW.

$$\mathrm{Var}[XW] = \mathbb{E}[X]^2\,\mathrm{Var}[W] + \mathrm{Var}[X]\,\mathbb{E}[W]^2 + \mathrm{Var}[X]\,\mathrm{Var}[W] \tag{14}$$

$$= 0 + \mathrm{Var}[X](\mathbb{E}[W]^2 + \mathrm{Var}[W]) = \mathrm{Var}[X]\,\mathbb{E}[W^2] \tag{15}$$

$$= 1 \cdot \mathbb{E}[k/V] = k\,\mathbb{E}[1/V] = \frac{k}{k-2} \tag{16}$$

Here we use that $\mathbb{E}[1/V] = 1/(k-2)$, which we will derive below. We use that $f_{\chi^2}(x; k)$ is the probability density function of the chi-squared distribution with k degrees of freedom.

$$\mathbb{E}[1/V] = \int_0^\infty \frac{1}{x} f_{\chi^2}(x; k)dx = \int_0^\infty \frac{1}{x} \frac{x^{(k/2-1)} e^{-x/2}}{2^{k/2}\Gamma(k/2)} dx = \int_0^\infty \frac{x^{(k/2-2)} e^{-x/2}}{2^{k/2}\Gamma(k/2)} dx \tag{17}$$

$$= \int_0^\infty \frac{x^{((k-2)/2-1)} e^{-x/2}}{2^{k/2}\Gamma(k/2)} dx = \int_0^\infty \frac{x^{((k-2)/2-1)} e^{-x/2}}{2 \cdot 2^{(k-2)/2} \frac{k-2}{2} \Gamma(\frac{k-2}{2})} dx \tag{18}$$

$$= \frac{1}{k-2} \int_0^\infty f_{\chi^2}(x; k-2)dx = \frac{1}{k-2} \tag{19}$$

In the derivation, we use $\Gamma(k/2) = \Gamma(\frac{k-2}{2} + 1) = \frac{k-2}{2}\Gamma(\frac{k-2}{2})$.

Now we execute the following `R` code.

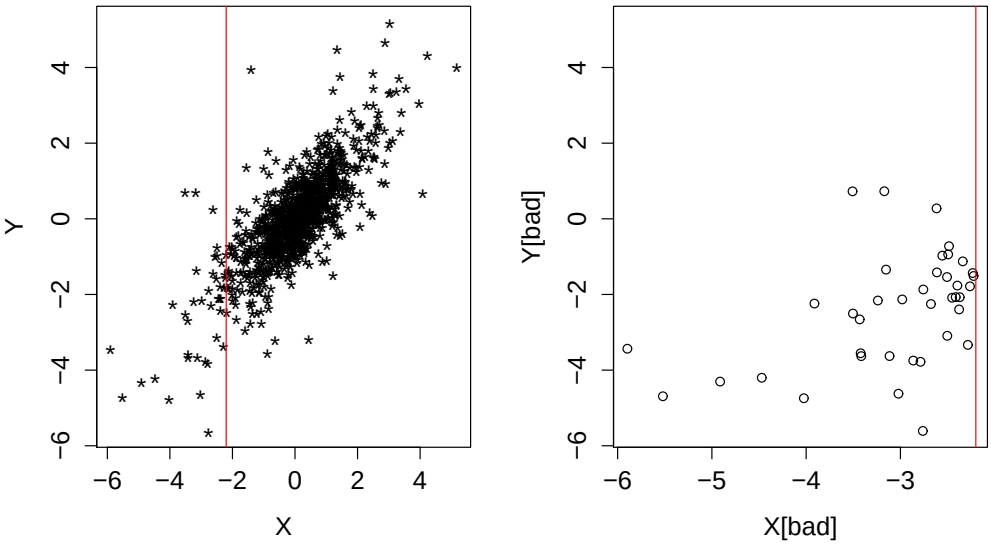
```
> chi5 <- sqrt(rchisq(1000, df=5)/5)
> X <- X/chi5; Y <- Y/chi5
> c(mean(X), var(X), mean(Y), var(Y), cor(X,Y))
[1] 0.038 1.525 0.068 1.528 0.786
```

We see that the means are close to 0, as expected, the variances differ by about 0.1 and the correlation is quite close to 0.8.

Q9

As instructed in an earlier example, we execute the following R code to obtain side by side scatterplots.

```
> par(mfrow=c(1,2))
> plot(X,Y, pch="*")
> d <- -2.2
> abline(v=d, col="red")
>
> bad <- (X < d)
> plot(X[bad], Y[bad], ylim=range(Y))
> abline(v=d, col="red")
> cor(X[bad],Y[bad])
[1] 0.44
```



We can see a tail dependence for the multiStudent distribution in the plot on the right hand side. The tail correlation of 0.44 is lower than 0.8, but is is a lot larger than 0. This means that there is a tail dependence.

Q10

Let $\vec{Z}$ be a correlated multinormal random vector with mean $\vec{\mu}$ and covariance matrix Σ. We denote ρ as the correlation matrix and we use shorthand notation $\rho(Z_i, Z_j) = \rho_{i,j}$ and $\text{Cov}(Z_i, Z_j) = \Sigma_{i,j}$.

By definition, $\rho(Z_i, Z_j) = \frac{\text{Cov}(Z_i, Z_j)}{\sqrt{\text{Var}[Z_i]\,\text{Var}[Z_j]}}$. Using the shorthand, we derive Σ to be.

$$\Sigma_{i,j} = \rho_{i,j}\sqrt{\mathrm{Var}[\vec{Z}_i]\,\mathrm{Var}[\vec{Z}]_j} \tag{20}$$

$$= \rho_{i,j}\sqrt{(\mathrm{Var}[\vec{Z}]\,\mathrm{Var}[\vec{Z}]^T)_{i,j}} \tag{21}$$

$$\Sigma = \rho\sqrt{\mathrm{Var}[\vec{Z}]\,\mathrm{Var}[\vec{Z}]^T} \tag{22}$$

$$= \rho\sqrt{\mathrm{Var}[\vec{Z}] \otimes \mathrm{Var}[\vec{Z}]} \tag{23}$$

In the first step, we rewrite from index notation to vector notation as can be seen on the wikipedia page of the outer product. We then drop the indexes and use that the outer product can be written as a matrix multiplication of a vector and its own transpose.

We execute the following code:

```
> library(MASS)
> mu <- c(1,3,5); sig2 <- c(1,2,5)
> Corrmat <- rbind(c(1., .3, .3),
+                  c(.3, 1., .4),
+                  c(.3, .4, 1.))
> Varmat <- Corrmat * sqrt(sig2 %*% t(sig2))
> Z <- mvrnorm(100, mu, Varmat)
> options(digits=7)
> colMeans(Z); diag(cov(Z)); cor(Z)
[1] 0.9497085 2.8927698 4.7217666
[1] 0.9276677 2.1010010 5.4895002
[,1]      [,2]      [,3]
[1,] 1.0000000 0.1696436 0.1025938
[2,] 0.1696436 1.0000000 0.4265725
[3,] 0.1025938 0.4265725 1.0000000
```

`colMeans(Z)` estimates the mean of each column. Therefore `colMeans` should be close to the mean vector $\vec{\mu}$. `diag(cov(Z))` gives the diagonal elements of the covariance matrix. The diagonal elements of the covariance matrix contains the estimated variance of each element of Z. This should be close to to $\mathrm{Var}[\vec{Z}]$ (or `sig2`). `cor(Z)` contains the estimated correlation between the three elements of Z.

Q11

We execute the following code in `R`:

```
> no_sims = 1e6
> VaR <- rep(0,10)
> for (i in (1:10)){
+   Z <- mvrnorm(no_sims, mu, Varmat)
+   VaR[i] <- quantile(rowSums(Z),0.9999)
+ }
> VaR
[1] 22.34890 22.27627 22.24395 22.40076 22.29522 22.23880 22.33798 22.17733 22.32926 22.31303
> c(mean(VaR),sd(VaR))
[1] 22.29615014  0.06445194
```

We are asked to determine the $F_Z^{-1}(0.9999)$, where $Z = Z_1 + Z_2 + Z_3$, with Z_i as defined in question 10. Because Z_i are random normally distributed, so is the sum Z. The mean of Z is given by the following equation.

$$\mathbb{E}[Z] = \mathbb{E}[Z_1] + \mathbb{E}[Z_2] + \mathbb{E}[Z_3] = 1 + 3 + 5 = 9 \tag{24}$$

The variance is given by the following formula:

$$\text{Var}[Z] = \text{Var}[Z_1] + \text{Var}[Z_2] + \text{Var}[Z_2] + 2(\text{Cov}(Z_1, Z_2) + \text{Cov}(Z_1, Z_3) + \text{Cov}(Z_2, Z_3)) \tag{25}$$

The right hand side of this equation is equal to the sum of the elements of covariance matrix from the previous question. The theoretical value is then computed by executing the following code in R.

```
> Var_t <- qnorm(0.9999, sum(mu), sqrt(sum(Varmat)))
> Var_t
[1] 22.26391
```

The estimated value of 22.296 is close to the theoretical value of 22.264.

Q12

We generate 10^6 independent drawings from a trinormal random vector $(X, Y, Z) \sim N(\vec{\mu} = \vec{0}; \Sigma)$, with the covariance matrix Σ having ones on the diagonal and $\rho = 1/6$ outside the diagonal. Translated to `R` this gives.

```
> n <- 1e6
> mu <- c(0,0,0)
> sigma <- rbind(c(1,1/6,1/6),
+                c(1/6,1,1/6),
+                c(1/6,1/6,1))
> Z <- mvrnorm(n, mu,sigma)
```

Q13

We construct $V_i = X_i + Y_i + Z_i$ by executing the following code in `R`.

```
> V <- rowSums(Z)
```

Q14

We use the `quantile` function to estimate the 97.5% quantile $d = F_V^{-1}(0.975)$ by executing the following code in `R`.

```
> d <- quantile(V,0.975)
> d
97.5%
3.918903
```

The estimate for the $97,5\%$ quantile of `V` is 3.92.

Q15

We execute the following code in `R`, where we use the definition of the stoploss premium to estimate it for V at level 97.5%.

```
> stoploss_premium <- mean(pmax(V-d,0))
> stoploss_premium
[1] 0.01884366
```

The estimated stoploss premium is 0.0188.

Q16

By definition, the random variables X_i, Y_i and Z_i are normally distributed. The sum of normally distributed variables is also normally ditributed, therefore V_i is also normally distributed. The mean and variance of V_i can be obtained in the same manner as in question 11.

We run the following code in `R` to obtain the mean and standard devation of V_i.

```
> mean <- sum(mu); sd <- sqrt(sum(sigma))
> c(mean, sd)
[1] 0 2
```

Q17

First, we calculate the theoretical value of d, after which we use formula (3.104) from MART.

```
> d_new <- qnorm(0.975, mean, sd)
> stoploss_premium_mart <- sd * dnorm((d_new - mean)/sd) - (d_new - mean)*(1 - pnorm((d_new - 
> stoploss_premium_mart
[1] 0.01889194
```

The theoretical stoploss premium of 0.01889 is really close to its estimated value of 0.01884.

Q18

We use a sample size of 10^6 toestimate the ES of V', where V' is a sum of multi-student t random variables. The multi-normal random variables used to generate the student t variables have equal $\vec{\mu}$ and Σ as in question 12. The χ^2_k distribution used to transform the sum of normal variables into a student t variable has 5 degrees of freedom. We then repeat the methods from questions 12 to 15.

```
> n <- 1e6
> k <- 5
> mu <- c(0,0,0)
```

```
> sigma <- rbind(c(1,1/6,1/6),
+                c(1/6,1,1/6),
+                c(1/6,1/6,1))
> Z <- mvrnorm(n, mu,sigma)
> chi5 <- sqrt(rchisq(n, df=5)/5)
> Z_prime <- Z/chi5
> V_prime <- rowSums(Z_prime)
> d <- quantile(V_prime,0.975)
> d
97.5%
5.137715
> stoploss_premium <- mean(pmax(V_prime-d,0))
> stoploss_premium
[1] 0.04811667
```

We estimate the expected shortfall $ES = 0.0481$.

Q19

A univariate Student(k) distribution is found by dividing $T \sim N(0,1)$ by a r.v. $\sqrt{U/k}$, with $U \sim \chi^2_k$, independent of T. We define $V = X + Y + Z$. V is standard normally distributed with mean $\mu = 0$ and standard deviation $\sigma = 2$. The transform to a student distribution requires $\sigma = 1$, so we need to scale V by sigma. We can then conclude that $V/(\sigma\sqrt{(U/k)})$ has a student t distribution with k degrees of freedom. We define $V' = V/\sqrt{(U/k)}$, with cumulative distribution function $F_{V'}(x)$. It then follows that

$$F_{V'}(x) = \Pr[V' \leq x] = \Pr[V/\sqrt{(U/k)} \leq x] = \Pr[V/(\sigma\sqrt{(U/k)}) \leq x/\sigma] = F_{st}(x/\sigma; k) \tag{26}$$

, where $F_{st}(x/\sigma; k)$ is the cumulative distribution function of the student distribution. We can now calculate the 97.5% quantile d by the following derivation.

$$F_{st}(d/\sigma; k) = 0.975 \implies d = \sigma F^{-1}_{st}(0.975; k) \tag{27}$$

Using formula (1.33) from MART, we can then determine the equation for the expected shortfall ES.

$$ES = \int_d^\infty [1 - F_{st}(x/\sigma; k)]dx \tag{28}$$

We use the following functions in the next bit of `R` code. `qt()` gives the quantiles of the student t distribution, `pt` is the distribution function of the student t distribution.

```
> sd <- sqrt(sum(sigma))
> d_new <- sd * qt(0.975,5)
> f <- function(x) {1 - pt(x/sd,5)}
> ES <- integrate(f, d_new, Inf)
> ES$value
[1] 0.04754977
```

The theoretical value of 0.0475 is very close to the estimated value of 0.0481.

Makeham and Gompertz survival distributions

Q1

Let $Y = \log(1 + \frac{V\log(c)}{b})/\log(c) = \log_c(1 + \frac{V\log(c)}{b})$ and $V \sim$ exponential(1). Then a straightforward calculation gives the result:

$$c^Y - 1 = c^{\log_c(1+\frac{V\log(c)}{b})} - 1 = 1 + \frac{V\log(c)}{b} - 1 = \frac{V\log(c)}{b} \tag{29}$$

and because $V \sim$ exponential(1) we have that

$$P[c^Y - 1 \leq x] = P[V\frac{\log(c)}{b} \leq x] = P[V \leq x\frac{b}{\log c}] \tag{30}$$

so that $c^Y - 1 \sim$ exponential($\frac{b}{\log(c)}$). Then using the explicit form of the CDF of the exponential distribution we find using $Z = c^Y - 1$

$$\begin{aligned} P[Y > x] &= P[c^Y - 1 > c^x - 1] \\ &= P[Z > c^x - 1] = 1 - P[Z \leq c^x - 1] \\ &= 1 - F_Z(c^x - 1) = 1 - (1 - \exp(-\frac{b}{\log c}(c^x - 1))) \\ &= \exp(-\frac{b}{\log c}(c^x - 1)) \end{aligned} \tag{31}$$

which is equal to equation (2) from the exercises with $a = 0$ so $Y \sim$ Gompertz(b, c).

Q2

If the following code is entered into Rstudio

```
gen.Sample <- function(n, a, b, c)
{if (any(a<0,b<0,c<1)) stop("Invalid parameters")
  lifetimes <- log(1+rexp(n)*log(c)/b)/log(c)
  if (a>0) lifetimes <- pmin(lifetimes, rexp(n)/a)
  return(lifetimes)}
set.seed(2525); G <- gen.Sample(2000, 0, 8e-5, 1.08)
set.seed(2525); M <- gen.Sample(2000, 5e-4, 8e-5, 1.08)
all(G>=M)
mean(M==G)
rbind(Gompertz=summary(G), Makeham=summary(M))
```

we obtain the output:

```
> all(G>=M)
[1] TRUE
> mean(M==G)
[1] 0.959
> rbind(Gompertz=summary(G), Makeham=summary(M))
           Min. 1st Qu. Median  Mean 3rd Qu.  Max.
Gompertz 4.9450   73.72  85.12 81.98   93.73 116.6
Makeham  0.2809   71.85  84.15 80.08   93.35 116.6
```

Since the Makeham distribution is defined as $X = min(Y, Z)$ with $Y \sim$ Gompertz(b, c) and $Z \sim$ exponential(a) the results of the Makeham distribution are always smaller or equal to the Gompertz results. This is verified by the result `all(G>M)` is TRUE.
The result of `mean(M==G)` is 0.959 which implies that in 95,9% of the cases the cause of death is equal to the Gompertz results. The probability of dying of old ages with these parameters is therefore 0.959.

Q3

We run the following code to assess the effect of changes on the parameters on the mean life-time.

```
S <- function(x, a, b, c) exp(-a*x - b/log(c)*(c^x-1))
a <- 5e-4; b <- 8e-5; c <- 1.09
mean.age <- integrate(S, 0, Inf, a, b, c)$value
mean(gen.Sample(1e6, a, b, c))
integrate(S, 0, Inf, 1.02*a, b, c)$value / mean.age
integrate(S, 0, Inf, a, 1.02*b, c)$value / mean.age
integrate(S, 0, Inf, a, b, 1.02*(c-1)+1)$value / mean.age
```

and obtain the following results

```
> integrate(S, 0, Inf, 1.02*a, b, c)$value / mean.age
[1] 0.9996164
> integrate(S, 0, Inf, a, 1.02*b, c)$value / mean.age
[1] 0.9969848
> integrate(S, 0, Inf, a, b, 1.02*(c-1)+1)$value / mean.age
[1] 0.9844023
```

The results imply that a 2% increase in the parameter a leads to a very small percentage decline of the mean life-time of approximately 0.04%. The impact of a 2% increase in the b parameter leads to a slightly larger decrease on the mean life-time of approximately 0.3%. The impact of the scaling of the c parameter leads to approximately a 1.6% decrease of the mean life-time. Increasing the paramters therefore leads to an increase in mortality.

Q4

By using the logarithm of the likelihood function we evade the problem of limited machine precision. If we let R calculate the following lines

```
exp(-8300)
exp(-10000)
exp(-5000)
exp(-100)
exp(-10)
```

we obtain the answers

```
> exp(-8300)
```

```
[1] 0
> exp(-10000)
[1] 0
> exp(-5000)
[1] 0
> exp(-100)
[1] 3.720076e-44
> exp(-10)
[1] 4.539993e-05
```

which implies that R does not have the capacity to differentiate between the numbers $\exp(-10000)$, $\exp(-8300)$ and $\exp(-5000)$ for example. Only if the exponent is sufficiently small R will have the ability to differentiate between the numbers and find an optimum. By passing to the logarithm of the likelihood function we circumvent this problem.

Q5

To obtain ML-estimates for the M sample the code given in the exercise is the following:

```
log.Lik <- function(p) {- sum(log.fx(M, p[1], p[2], p[3]))} ## Makeham on Makeham
a <- 5e-4; b <- 8e-5; c <- 1.08
oMM <- optim(c(a,b,c), log.Lik)
oMM$value ## 8428.489
oMM$par ## a=7.3e-04 b=6.0e-05 c=1.083

log.Lik <- function(p) {-sum(log.fx(M, 0, p[1], p[2]))} ## Gompertz on Makeham
a <- 0; b <- 8e-5; c <- 1.08
oGM <- optim(c(b,c), log.Lik) ## 13x NaN
oGM$value ## 8456.258
oGM$par ## a=0 b=1.3e-4 c=1.074
```

with the following output

```
> log.Lik <- function(p) {- sum(log.fx(M, p[1], p[2], p[3]))} ## Makeham on Makeham
> a <- 5e-4; b <- 8e-5; c <- 1.08
> oMM <- optim(c(a,b,c), log.Lik)
There were 26 warnings (use warnings() to see them)
> oMM$value ## 8428.489
[1] 8428.489
> oMM$par ## a=7.3e-04 b=6.0e-05 c=1.083
[1] 7.338301e-04 5.993626e-05 1.083515e+00
>
> log.Lik <- function(p) {-sum(log.fx(M, 0, p[1], p[2]))} ## Gompertz on Makeham
> a <- 0; b <- 8e-5; c <- 1.08
> oGM <- optim(c(b,c), log.Lik) ## 13x NaN
There were 13 warnings (use warnings() to see them)
> oGM$value ## 8456.258
```

```
[1] 8456.258
> oGM$par ## a=0 b=1.3e-4 c=1.074
[1] 0.0001292634 1.0741178742
>
```

To find the ML-estimates for the G sample we use the following code

```
log.Lik <- function(p) {-sum(log.fx(G, p[1], p[2], p[3]))} ## Makeham on Gompertz
a <- 5e-4; b <- 8e-5; c <- 1.08
oMG <- optim(c(a,b,c), log.Lik) ## 13x NaN
oMG$value
oMG$par

log.Lik <- function(p) {-sum(log.fx(G,0, p[1], p[2]))} ## Gompertz on Gompertz
a <- 0; b <- 8e-5; c <- 1.08
oGG <- optim(c(b,c), log.Lik) ## 13x NaN
oGG$value
oGG$par
```

With results

```
> log.Lik <- function(p) {-sum(log.fx(G, p[1], p[2], p[3]))} ## Makeham on Gompertz
> a <- 5e-4; b <- 8e-5; c <- 1.08
> oMG <- optim(c(a,b,c), log.Lik) ## 13x NaN
There were 33 warnings (use warnings() to see them)
> oMG$value
[1] 8245.877
> oMG$par
[1] 1.585592e-04 5.928508e-05 1.083783e+00
>
> log.Lik <- function(p) {-sum(log.fx(G,0, p[1], p[2]))} ## Gompertz on Gompertz
> a <- 0; b <- 8e-5; c <- 1.08
> oGG <- optim(c(b,c), log.Lik) ## 13x NaN
There were 13 warnings (use warnings() to see them)
> oGG$value
[1] 8248.117
> oGG$par
[1] 7.088547e-05 1.081598e+00
```

Summarizing the output we have the following results

	a	b	c	ML
Makeham on Makeham sample	7.338301e-04	5.993626e-05	1.083515e+00	8428.489
Gompertz on Makeham sample	0	0.0001292634	1.0741178742	8456.258
Makeham on Gompertz sample	1.585592e-04	5.928508e-05	1.083783e+00	8245.877
Gompertz on Gompertz sample	0	7.088547e-05	1.081598e+00	8248.117

Q6

We have the following formulas for the AIC

$$AIC = -2\log L + 2k \tag{32}$$

and for the BIC criteria

$$BIC = -2\log L + k\log n \approx -2\log L + 7.6k \tag{33}$$

where the approximation is for the current situation. For the Makeham model there are 3 paramters ($k = 3$) and for the Gompertz model there are 2 parameters ($k = 2$).

Via R we compute the values for the AIC and BIC criteria in the optima for the different situations and test if the Makeham model has a smaller AIC or BIC

```
AIC.MM <- 2*oMM$value + 2 * 3;
AIC.GM <- 2*oGM$value + 2 * 2;
AIC.MG <- 2*oMG$value + 2 * 3;
AIC.GG <- 2*oGG$value + 2 * 2;

BIC.MM <- 2*oMM$value + 7.6 * 3;
BIC.GM <- 2*oGM$value + 7.6 * 2;
BIC.MG <- 2*oMG$value + 7.6 * 3;
BIC.GG <- 2*oGG$value + 7.6 * 2;

(AIC.MM<AIC.GM)
(AIC.MG<AIC.GG)
(BIC.MM<BIC.GM)
(BIC.MG<BIC.GG)
```

which gives the following output

```
> (AIC.MM<AIC.GM)
[1] TRUE
> (AIC.MG<AIC.GG)
[1] TRUE
> (BIC.MM<BIC.GM)
[1] TRUE
> (BIC.MG<BIC.GG)
[1] FALSE
```

As regards to AIC the Makeham model is better on both samples. As regards to the BIC the Makeham model is better on the Makeham sample but the Gompertz model is better on the Gompertz sample.

Q7

If the following code is submitted in R

```
S <- function(x, a, b, c) exp(-a*x - b/log(c)*(c^x-1))
x <- 0:110
```

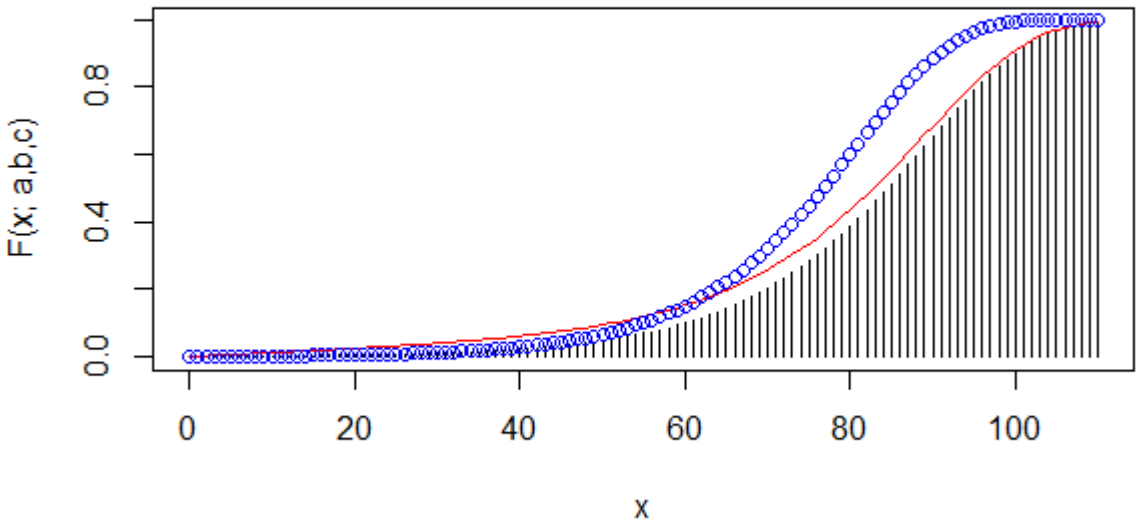


Figure 1: The bar chart describes a Gompertz distribution with b = 8e-5 and c=1.08. The red line is a Makeham distribution with a=1e-3 and b,c equal to the Gompertz distribution. The blue dots represent the Gompertz distribution with the parameter c = 1.09.

```
plot(x, 1-S(x, 0, 8e-5, 1.08), type="h", ylab="F(x; a,b,c)")
lines(x, 1-S(x, 1e-3, 8e-5, 1.08), col="red")
points(x, 1-S(x, 0, 8e-5, 1.09), col="blue")
```

R generates the plot as seen in Figure 1.

The difference between the Gompertz (bars in Figure) and Makeham distribution (red line) can clearly be seen in the figure. Since Makeham also has a 'accident' part in the model the cdf shows higher probabilities at low ages. For old ages the two distribution converge and are appoximately equal. The blue dots represent a Gompertz distribution with a higher parameter c. The effect of increasing the c paramter leads to an increase in the cdf especially for older ages.

Q8

If the following code is submitted in R

```
mu <- function(x, a, b, c) (a + b*c^x)
x <- 0:110
plot(x, mu(x, 0, 8e-5, 1.08), type="h", ylab="F(x; a,b,c)")
lines(x, mu(x, 1e-3, 8e-5, 1.08), col="red")
points(x, mu(x, 0, 8e-5, 1.09), col="blue")
```

the output from R is given in figure 2.

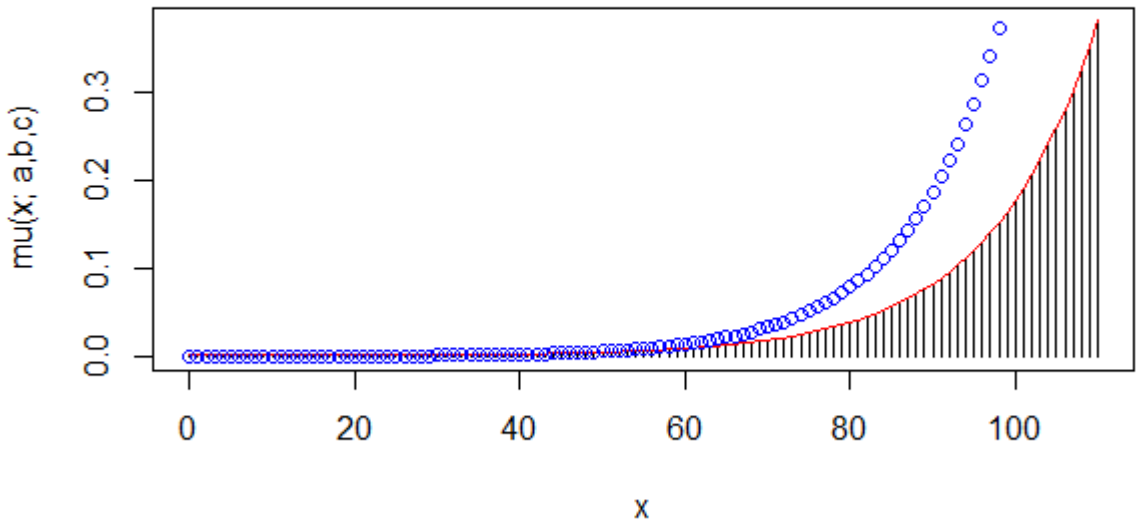


Figure 2: The bar chart describes the mortality rate for Gompertz' law with b = 8e-5 and c=1.08. The red line is the Makeham extension with a=1e-3 and b,c equal to the Gompertz case. The blue dots represent the Gompertz case with the parameter c = 1.09.

The Makeham mortality rate with $a = 1e-3$ is almost indistiguishable from the Gompertz mortality rate. Changing the paramter c to 1.09 has a large impact on the mortality rate. At ages higher than 70 years old the mortality rate increases dramatically.

Q9

Since $q_x = \frac{S(x-1)-S(x)}{S(x-1)}$ we can fill the dots in the code in the following way using the `diff(c)` and `head()` functions and optimize

```
S <- function(x, a, b, c) exp(-a*x - b/log(c)*(c^x-1))
agerange <- 1:nages ## denotes the range of ages accounted for when finding ML
LogLik <- function(p)
{ ddfs <- S(0:nages, p[1], p[2], p[3])
q.x <- -diff(ddfs)/head(ddfs,nages)
-sum(dbinom(D.x[agerange], e.x[agerange], q.x[agerange], log=TRUE))}
a <- 1e-4; b <- 8e-5; c <- 1.08
o <- optim(c(a,b,c), LogLik)
o$value
o$par
```

which gives the following results

```
There were 22 warnings (use warnings() to see them)
```

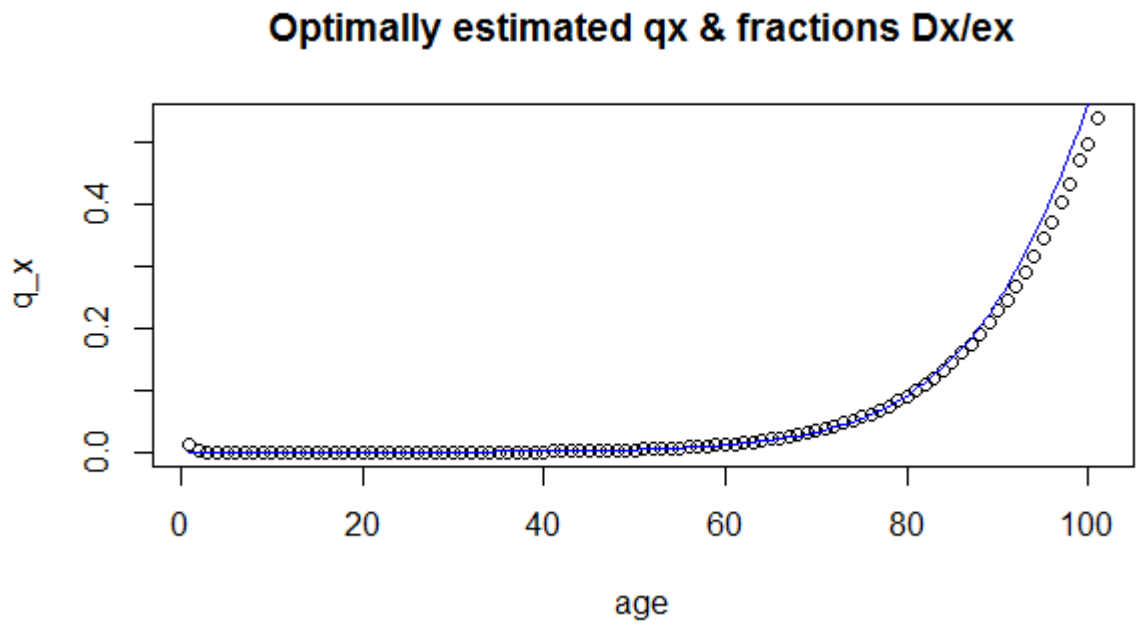


Figure 3: Plot of the ML estimate and the fractions D_x/e_x

```
> o$value
[1] 172666.1
> o$par
[1] 1.076124e-03 1.433849e-06 1.166235e+00
```

so the ML-estimates for a,b and c are $a = 1.077e-3, b = 1,433e-6$ and $c = 1.166$.
Submitting the code

```
ddfs <- S(0:nages, o$par[1], o$par[2], o$par[3])
q.x <- -diff(ddfs)/head(ddfs,nages)

plot(1:nages,D.x[1:nages]/e.x[1:nages],type="p",
     main="Optimally estimated qx & fractions Dx/ex",xlab="age",ylab="q_x")
lines(1:nages, q.x[1:nages], col="blue")
```

gives the plot in figure 3.

The Makeham fit is not valid for ages in $(0, 1]$ and the expectation is that the estimation is better when $x = 1$ is left out. If we run the following code in R we obtain the result without $x = 1$.

```
S <- function(x, a, b, c) exp(-a*x - b/log(c)*(c^x-1))
agerange <- 2:nages ## denotes the range of ages accounted for when finding ML
LogLik <- function(p)
{ ddfs <- S(0:nages, p[1], p[2], p[3])
q.x <- -diff(ddfs)/head(ddfs,nages)
```

```
-sum(dbinom(D.x[agerange], e.x[agerange], q.x[agerange], log=TRUE))}
a <- 1e-4; b <- 8e-5; c <- 1.08
o2 <- optim(c(a,b,c), LogLik)
o2$value
o2$par

ddfs <- S(0:nages, o2$par[1], o2$par[2], o2$par[3])
q2.x <- -diff(ddfs)/head(ddfs,nages)

plot(1:nages,D.x[1:nages]/e.x[1:nages],type="p",
     main="Optimally estimated qx & fractions Dx/ex",xlab="age",ylab="q_x")
lines(1:nages, q.x[1:nages], col="blue")
lines(1:nages, q2.x[1:nages], col="red")
```

with the following output

```
> o2$value
[1] 15217.31
> o2$par
[1] 0.0004726379 0.0000246149 1.1095517146
```