Computer Practical 1 Outline Solutions
Simulation Basics

1. *Transformation Methods*

   Recall the Box-Muller method which transforms pairs of uniformly-distributed random variables to obtain a pair of independent standard normal random variates. If

   $$U_1, U_2 \overset{\text{iid}}{\sim} \mathsf{U}[0,1]$$

   and

   $$\begin{aligned} X_1 &= \sqrt{-2\log(U_1)} \cdot \cos(2\pi U_2) \\ X_2 &= \sqrt{-2\log(U_1)} \cdot \sin(2\pi U_2) \end{aligned}$$

   then $X_1, X_2 \overset{\text{iid}}{\sim} \mathsf{N}(0,1)$.

   (a) Write a function which takes as arguments two vectors $(\mathbf{U}_1, \mathbf{U}_2)$ and returns the two vectors $(\mathbf{X}_1, \mathbf{X}_2)$ obtained by applying the Box-Muller transform elementwise.

   ```
   box.muller <- function(U1,U2) {
       X1 <- sqrt(-2*log(U1)) * cos(2*pi*U2)
       X2 <- sqrt(-2*log(U1)) * sin(2*pi*U2)
       rbind(X1,X2)
   }
   ```

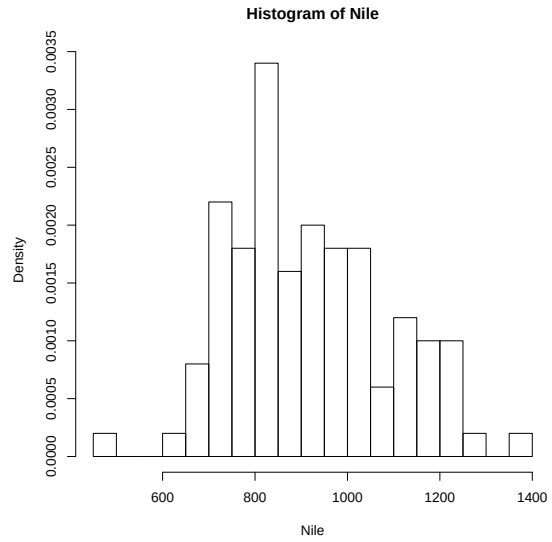
   (b) The R function `runif` provides access to a PRNG. The type of PRNG can be identified using the `rngkind` command; by default it will be a Mersenne-Twister (`http://en.wikipedia.org/wiki/Mersenne_twister`). Generate 10,000 $\mathsf{U}[0,1]$ random variables using this function, convert this to two vectors of 5,000 elements in the same way as you did with the RANDU values.

   ```
   unif.mt <-runif(10000)
   unif.mt.odd <-unif.mt[seq(1,10000,2)]
   unif.mt.even <-unif.mt[seq(2,10000,2)]
   ```

2. *The Bootstrap:* This question can be answered in two ways. The more direct (and perhaps more informative, if you have the time to do so and the inclination to implement a bootstrap algorithm from scratch) is to use the `sample` function to obtain bootstrap replicates and to compute the required confidence intervals by direct means. More pragmatically, the `boot` library provides a function `boot` to obtain bootstrap samples and another, `boot.ci` which will provide various bootstrap confidence intervals.

   (a) The `Nile` dataset shows the rivers. Use a histogram or other visualisation to briefly explore this data.

```
hist(Nile,n=20,prob=T)
```



There's apparently some *skewness* in the data. We'll consider it as a time series later...

(b) What's the mean and median length of a river in this category?

```
mean(Nile)
```
919.35
```
median(Nile)
```
893.5
Further evidence of positive skewness.

(c) Treating the data as a simple random sample, appeal to asymptotic normality to construct a confidence interval for the mean annual flow of the Nile.

The lazy solution:

```
sigma.hat <-sqrt(var(Nile)/length(Nile))
```
Estimate variance.

```
c(qnorm(0.025),qnorm(0.975))*sigma.hat + mean(Nile)
```
Compute interval.

Leading to: [886.182, 952.518]

(d) Using the `boot::boot` function to obtain the sample and `boot::boot.ci` to obtain confidence intervals from that sample, or otherwise, obtain a *bootstrap percentile interval* for both the mean and median of the Nile's annual flow. For the median you may also wish to obtain the interval obtained by an optimistic appeal to asymptotic normality combined with a bootstrap estimate of the variance (`boot::boot.ci` will provide this).

Note the following: `boot::boot` does the actual bootstrap resampling; it needs a function which takes two arguments to compute the statistic for each bootstrap sample, the first contains the *original* data and the second the index of the values included in a particular bootstrap resampling.

Load the relevant library:

```
library(boot)
```
Construct an appropriate evaluation function:

```
f.mean <- function (x,i) { mean(x[i]) }
```
Obtain the bootstrap resamples:

```
boot.mean <-boot::boot(Nile,f.mean,9999,stype='i')
```
Obtain the bootstrap percentile confidence intervals:

```
boot::boot.ci(boot.mean,type='perc')
```
On this occasion leading to: (886.7, 952.7)

Moving on to the median, we repeat the same strategy:

```
f.median <- function (x,i) {median(x[i])}
boot.median <-boot::boot(Nile,f.median,9999,stype='i')
boot::boot.ci(boot.median,type='perc')
```

On this occasion leading to: (845, 940)

```
boot::boot.ci(boot.median,type='norm')
```

While the normal approximation leads to: (846.2, 947.9)

(e) Are there any interesting qualitative differences between the various confidence intervals? How does this relate to the data?

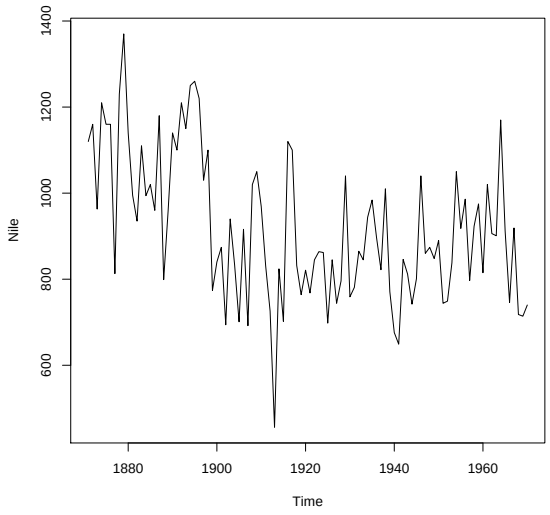
Interesting is a relative term and you might identify other things, but something which I find interesting is that the BPIs are not symmetric around the mean or median and this reflects the fact that even the mean of a small sample of non-normal random variables is not normally distributed.

(f) Are your findings stable? If you repeat the bootstrap sampling do you recover similar behaviour?

This depends on the sample size you use, there is a reasonable degree of stability with the sample size used here. This is a convenient point to emphasize that one should *always* attempt to assess the sensitivity of computational procedures to their design parameters and other factors which may influence their performance before depending upon their output.

(g) Are there any reasons to doubt the accuracy of these confidence intervals?

Absolutely. The computational method is irrelevant, the data is a time series and plotting it shows a clear departure from independence so any method predicated on it is untrustworthy, `ts.plot(Nile)`:



3. *Convergence of Sample Approximations*

(a) The `stats::ecdf` and `stats::plot.ecdf` functions compute and plot empirical distribution functions from a provided sample.

i. Show plots of the empirical distribution function of samples of a variety of sizes ranging from 10 to 10,000 from a $\mathsf{U}[0,1]$ distribution. Add to your plots the distribution function of the $\mathsf{U}[0,1]$ distribution.

The following code produces the type of plots required, which illustrate the Glivenko-Cantelli Theorem.

```
ru  <- runif(10000)
F10  <- ecdf(ru[1:10])
F50  <- ecdf(ru[1:50])
F500 <- ecdf(ru[1:500])
```

```
F3000 <- ecdf(ru[1:3000])
F10000 <- ecdf(ru)

seq <- seq(0,1,1/1000)
plot.ecdf(F10,main='Sample␣Size␣n=10')
lines(seq,punif(seq),col='red')

plot.ecdf(F50,main='Sample␣Size␣n=50')
lines(seq,punif(seq),col='red')

plot.ecdf(F500,main='Sample␣Size␣n=500')
lines(seq,punif(seq),col='red')

plot.ecdf(F3000,main='Sample␣Size␣n=3␣000')
lines(seq,punif(seq),col='red')

plot.ecdf(F10000,main='Sample␣Size␣n=10␣000')
lines(seq,punif(seq),col='red')
```

ii. Repeat part *i.* with a standard normal distribution.

Slight modifications of the above code suffice...

iii. Repeat part *i.* with a Cauchy distribution.

Slight modifications of the above code suffice...

(b) For each of the three distributions considered in the previous part, determine $\sup_x |\hat{F}_n(x) - F(x)|$ for each n considered (consider only the sup over the sampled values of x) and plot these quantities against n. Do you notice anything interesting?

Having implemented the 3 slight variants of the code for part *(a) i.* this is reasonably straightforward:

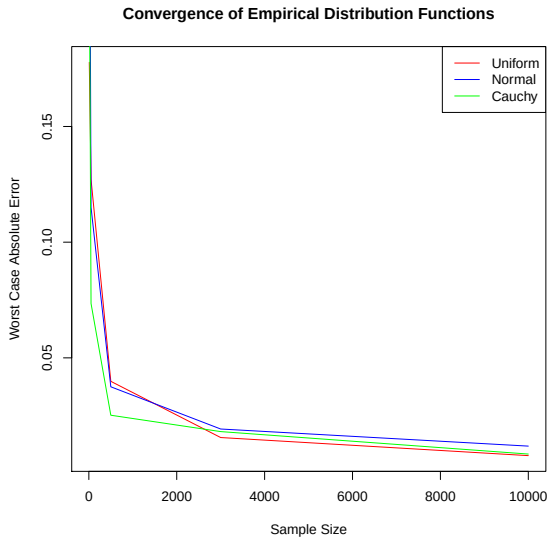
```
eu <- c(10, max(abs(F10(ru[1:10]) - punif(ru[1:10]))))
eu <- rbind(eu, c(50, max(abs(F50(ru[1:50]) - punif(ru[1:50])))))
eu <- rbind(eu, c(500, max(abs(F500(ru[1:500]) - punif(ru[1:500])))))
eu <- rbind(eu, c(3000, max(abs(F3000(ru[1:3000]) - punif(ru[1:3000])))))
eu <- rbind(eu, c(10000, max(abs(F10000(ru[1:10000]) - punif(ru[1:10000])))))

en <- c(10, max(abs(Fn10(rn[1:10]) - pnorm(rn[1:10]))))
en <- rbind(en, c(50, max(abs(Fn50(rn[1:50]) - pnorm(rn[1:50])))))
en <- rbind(en, c(500, max(abs(Fn500(rn[1:500]) - pnorm(rn[1:500])))))
en <- rbind(en, c(3000, max(abs(Fn3000(rn[1:3000]) - pnorm(rn[1:3000])))))
en <- rbind(en, c(10000, max(abs(Fn10000(rn[1:10000]) - pnorm(rn[1:10000])))))

ec <- c(10, max(abs(Fc10(rc[1:10]) - pcauchy(rc[1:10]))))
ec <- rbind(ec, c(50, max(abs(Fc50(rc[1:50]) - pcauchy(rc[1:50])))))
ec <- rbind(ec, c(500, max(abs(Fc500(rc[1:500]) - pcauchy(rc[1:500])))))
ec <- rbind(ec, c(3000, max(abs(Fc3000(rc[1:3000]) - pcauchy(rc[1:3000])))))
ec <- rbind(ec, c(10000, max(abs(Fc10000(rc[1:10000]) - pcauchy(rc[1:10000])))))

plot(eu,type='l',col='red',main='Convergence␣of␣Empirical␣Distribution␣Functions'
    ,xlab='Sample␣Size', ylab='Worst␣Case␣Absolute␣Error')
lines(en,col='blue')
lines(ec,col='green')
legend('topright',c('Uniform','Normal','Cauchy'), lty=1, col=c('red','blue','
    green'))
```

And leads to the following graph:



The striking feature of which is that performance is just as good for the Cauchy distribution as for the uniform or the normal; indeed, as the distribution function maps all of these things onto $[0, 1]$ this is well behaved even for distributions which often misbehave. Whether the resulting distributional approximation is good enough for particular tasks, of course, depends on what those tasks are.

⋆ Indicates questions which can easily be done later if you're short of time.