1 Survival time

As a small example, the survival times of 9 rats were 10, 27, 30, 40, 46, 51, 52, 104, and 146 days. Because of the skewness in the data, consider estimating the population median survival time θ through the sample median.

```
CODE FILENAME: ../R/01_01_load_data.R*****

  survival_times <- c(10, 27, 30, 40, 46, 51, 52, 104, 146)
  sample_median <- median(survival_times)
  sample_mean <- mean(survival_times)
  seed <- 7
  B1 <- 1000; B2 <- 50
  n <- 9

  bootstrap_fn <- function(estimate = "median", meth = "percentile") {
    # taking 1st level boot
    survival_boot <- sample(survival_times, n, replace = TRUE)

    if (estimate == "median") {
      est_boot <- median(survival_boot)
      if (meth == "percentile") {
        return(est_boot)
      } else if (meth == "bootstrap_t") {
        sample_est <- median(survival_times)
        # taking 2nd level boot
        est_boot2 <- replicate(B2, {
          survival_boot2 <- sample(survival_boot, n, replace = TRUE)
          median(survival_boot2)
        })
      }
    } else if (estimate == "mean") {
      est_boot <- mean(survival_boot)
      if (meth == "percentile") {
        return(est_boot)
      } else if (meth == "bootstrap_t") {
        sample_est <- mean(survival_times)
        #taking 2nd level boot
        est_boot2 <- replicate(B2, {
          survival_boot2 <- sample(survival_boot, n, replace = TRUE)
          mean(survival_boot2)
        })
      }
    }

    se_boot <- sd(est_boot2)
    t_boot <- (est_boot - sample_est) / se_boot
    result_list <- list(r = est_boot, t = t_boot)
    return(result_list)
  }
end------------------------------------------------------------------------
```

1.1 Bootstrap-t method: median

Compute a 95% CI for θ using the bootstrap-t method. Use $B_1 = 1000$ first-level bootstrap samples and $B_2 = 50$ second level bootstrap samples (to estimate the standard error).

We are 95% confident that the true value of the median is between 20.46346 and 78.24754.

```
CODE FILENAME: ../R/01_02_bst_median.R*****

  set.seed(seed)
  res = sapply(1:B1, function(.){bootstrap_fn(estimate = "median",
                                               meth = "bootstrap_t")})
  ses <- unlist(res[1,])
  tbs <- unlist(res[2,])

  se_median <- sd(ses) #bootstrap estimate of the SE
  lower <- sample_median - quantile(tbs,.975)*se_median
  upper <- sample_median - quantile(tbs,.025)*se_median
  #c(lower,upper)

end-----------------------------------------------------------------------
```

1.2 Bootstrap percentile CI: median

Compute a 95% CI for θ using the bootstrap percentile CI with B = 1000 bootstrap samples.

We are 95% confident that the true value of the median is between 27 and 53.3.

```
CODE FILENAME: ../R/01_03_percentile_median.R*****

  set.seed(seed)
  res_median = sapply(1:B1, function(.){bootstrap_fn(estimate = "median",
                                                      meth = "percentile")})
  #c(quantile(res_median,.025), quantile(res_median,.975))

end-----------------------------------------------------------------------
```

1.3 Reverse bootstrap percentile CI (basic bootstrap): mean

Compute a 95% confidence interval for the mean time between failures θ using the basic bootstrap method with B = 1000 bootstrap samples.

We are 95% confident that the true value of the mean is between 29.21667 and 78.66944.

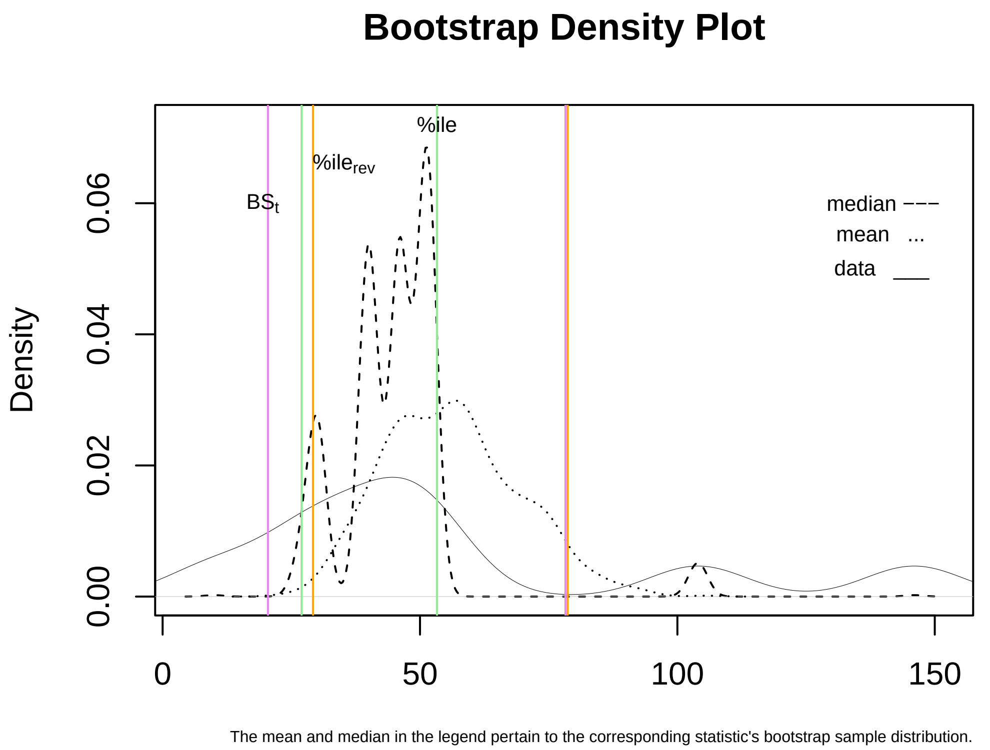
```
CODE FILENAME: ../R/01_04_reversepercentile_mean.R*****

  set.seed(seed)
  res_mean = sapply(1:B1, function(.){bootstrap_fn(estimate = "mean",
                                                    meth = "percentile")})
  #c(2*sample_mean - quantile(res_mean,.975),
  #  2*sample_mean - quantile(res_mean,.025))



end-----------------------------------------------------------------------
```

1.4 Density estimate

Plot a density estimate of the data. In R, you can do this through the density function. Compare the results in parts 1.1, 1.2, and 1.3.

For the selected seed, the percentile CI captures the bulk of the median values from the bootstrap samples. The bootstrap-t (median) CI appears to cover areas of large concentration from both the percentile (median) and reverse percentile CI (mean).

I also tried a number of seeds and noticed across all cases that: 1) The lower CI endpoint of the basic and the percentile intervals are close to each other. 2) The upper CI endpoint of basic and bootstrap-t intervals are close to each other but the lower CI endpoint of the latter is always less than that of the former. 3) Bootstrap-t captures the bulk of the statistics (mean and median). 4) The upper limit of the percentile interval could be erratic due to the presence of outliers.




```
CODE FILENAME: ../R/01_05_density_plot.R*****

    plot(density(res_median),
         ylim = range(density(res_median)$y, density(ses)$y),
         lty = 'dashed', main = "Bootstrap Density Plot", xlab = '')
    lines(density(res_mean), lty = 'dotted')
    lines(density(survival_times), lwd = 0.25)

    abline(v=2*sample_mean - quantile(res_mean,.975),col="orange")
    abline(v=2*sample_mean - quantile(res_mean,.025),col="orange")
    text(2*sample_mean - quantile(res_mean,.975)+6, 0.066,
         expression(paste("%il", e[rev])), cex=0.7)

    abline(v=quantile(res_median,.025),col="lightgreen")
```

```
abline(v=quantile(res_median,.975),col="lightgreen")
text(quantile(res_median,.975), 0.072,
     expression(paste("%", ile)), cex=0.7)

abline(v=quantile(lower,.025),col="violet")
abline(v=quantile(upper,.975),col="violet")
text(quantile(lower,.025)-1, 0.06, expression(BS[t]), cex=0.7)

text(140, 0.06, "median ---", cex=0.7)
text(139.5, 0.055, "mean   ...", cex=0.7)
text(139.7, 0.05, "data   ___", cex=0.7)
title(
  sub=paste("The mean and median in the legend pertain to the",
            "corresponding statistic's bootstrap sample distribution."),
  adj=1, line=2.5, cex.sub = 0.5)
```

end--

2 Spatial test

Consider the spatial test data from Table 14.1 of Efron and Tibshirani (1993) shown below. From the table's description, it is clear that the measurements A and B are paired. Suppose the data consist of a random sample from an unknown joint distribution of A and B. Whenever ratios are scientifically or statistically preferred to differences, we gain stability by considering the logarithm of the ratios. Let $\theta_1 = \log E\left(\frac{A_i}{B_i}\right)$, $\theta_2 = E\left(\log \frac{A_i}{B_i}\right)$ for all i. Exclude observation #14 because the logarithm of its ratio is undefined. Use 2000 bootstrap samples.

2.1 Bootstrap percentile CI for θ_1

Compute a bootstrap percentile confidence interval for θ_1.

We are 95% confident that the true value of θ_1 is between -0.06867 and 0.16487.

CODE FILENAME: ../R/02_02_percentile_logmean.R*****

```
B <- 2000

plug_in_estimator <- function(A,B, est = "theta_1"){
  if (est == "theta_1") {
    return(log(mean(A/B)))
  } else if (est == "theta_2") {
    return(mean(log(A/B)))
  }
}

theta_1_hat_star <- c()
theta_2_hat_star <- c()
set.seed(7)
for (b in 1:B) {
  bs_sample <- spatial_test_data[sample(spatial_test_data[,1],
                                        n1,
                                        replace = TRUE),]
```

```
    theta_1_hat_star[b] <- plug_in_estimator(bs_sample$A,
                                             bs_sample$B,
                                             est = "theta_1")
    theta_2_hat_star[b] <- plug_in_estimator(bs_sample$A,
                                             bs_sample$B,
                                             est = "theta_2")
  }

  theta_1_pci <- c(quantile(theta_1_hat_star,.025),
                   quantile(theta_1_hat_star,.975))
  theta_1_pci
```

```
end-------------------------------------------------------------------------
```

2.2 BC_a CI for θ_1

Compute a BC_a confidence interval for θ_1. Interpret the CI.

We are 95% confident that the true value of θ_1 is between -0.05756 and 0.17511.

```
CODE FILENAME: ../R/02_03_bca_logmean.R*****
```

```
  # helper functions=========================================================

  bias_correction <- function(bootstrap_estimates,
                              plug_in_estimate,
                              B){
    return(qnorm(sum(bootstrap_estimates < plug_in_estimate)/B))
  }

  acceleration_parameter <- function(data = spatial_test_data,
                                     est = "theta_1"){

    th.jack <- sapply(1:n1, function(x){plug_in_estimator(data$A[-x],
                                                          data$B[-x],
                                                          est = est)})

    L <- mean(th.jack) - th.jack

    return( sum(L^3)/(6 * sum(L^2)^1.5) )
    }

  alpha <- function(confid = .975,
                    est = "theta_1",
                    bootstrap_estimates = theta_1_hat_star,
                    plug_in_estimate = plug_in_estimate_theta_1){

    bc <- bias_correction(bootstrap_estimates = bootstrap_estimates,
                          plug_in_estimate = plug_in_estimate,
                          B = B)

    ap <- acceleration_parameter(data = spatial_test_data,
```

```
                              est = est)

    return(pnorm(bc + (bc + qnorm(confid))/(1-(ap*(bc + qnorm(confid))))))
  }

  BC_a <- function(confid = .975,
                   est = "theta_1",
                   bootstrap_estimates = theta_1_hat_star,
                   plug_in_estimate = plug_in_estimate_theta_1
  ){
    return(c(quantile(bootstrap_estimates,
                      alpha(1-confid, est = est,
                            bootstrap_estimates = bootstrap_estimates,
                            plug_in_estimate = plug_in_estimate)),
             quantile(bootstrap_estimates,
                      alpha(confid, est = est,
                            bootstrap_estimates = bootstrap_estimates,
                            plug_in_estimate = plug_in_estimate))))
  }

  # BCa for logmean computation ============================================

  plug_in_estimate_theta_1 <- plug_in_estimator(spatial_test_data$A,
                                                spatial_test_data$B,
                                                est = "theta_1")

  theta_1_BCa <- BC_a(confid = .975,
                      est = "theta_1",
                      bootstrap_estimates = theta_1_hat_star,
                      plug_in_estimate = plug_in_estimate_theta_1)

  theta_1_BCa
  #if bc & ap are 0: (-0.06867057, 0.16486927)

end---------------------------------------------------------------------------
```

2.3 BC_a CI for θ_2

Compute a BC_a confidence interval for θ_2.

We are 95% confident that the true value of θ_2 is between -0.15372 and 0.11496.

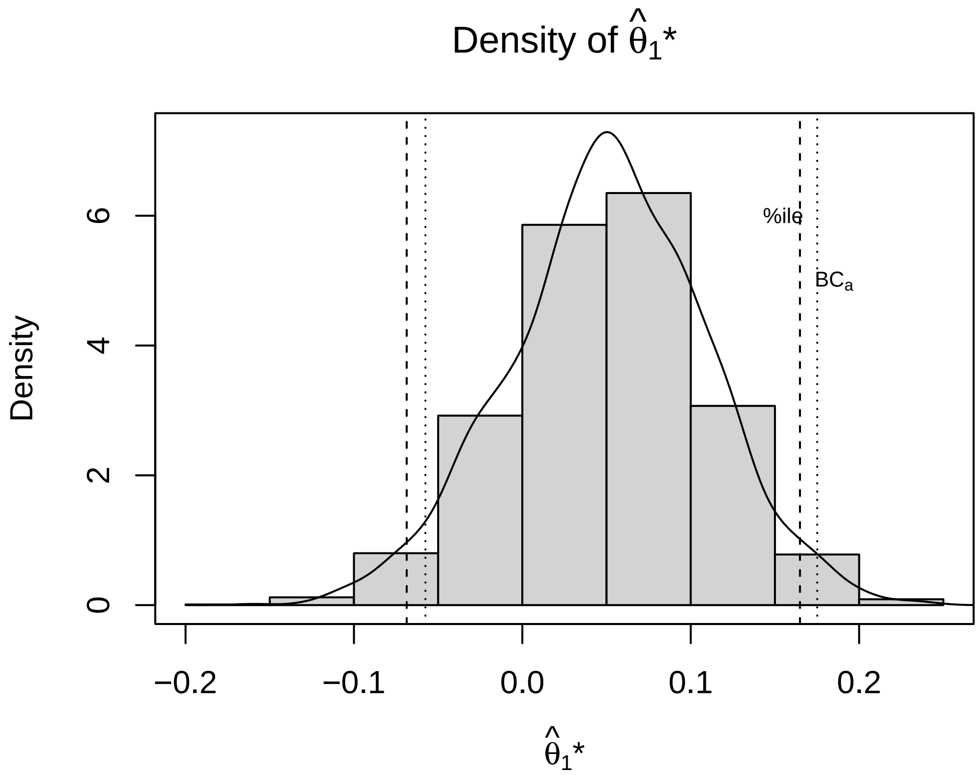
```
CODE FILENAME: ../R/02_05_bca_meanlog.R*****

  plug_in_estimate_theta_2 <- plug_in_estimator(spatial_test_data$A,
                                                spatial_test_data$B,
                                                est = "theta_2")

  theta_2_BCa <- BC_a(confid = .975,
                      est = "theta_2",
                      bootstrap_estimates = theta_2_hat_star,
```

```
                        plug_in_estimate = plug_in_estimate_theta_2)

    #theta_2_BCa

  end------------------------------------------------------------------------
```

2.4 Bootstrap percentile vs BC_a CI for θ_1

Compare your CIs in 2.1 and 2.2. How different are the two CIs?

The endpoints of the BC_a CI are found to the right of the bootstrap percentile CI but they are not hugely different. It is possible that the plug-in estimator is a little biased, resulting to that characteristic. Percentile CI works best if $\hat{\theta}_1$ is an unbiased estimator of θ_1. In our case, we only have bootstrap resamples that are centered around the mean, 0.05077 which is also a little different from the original sample's plug-in estimate 0.05458. BC_a corrects for the bias.




```
  CODE FILENAME: ../R/02_06_compare_ci.R*****

    hist(theta_1_hat_star,
         prob = TRUE,
         main = expression(paste("Density of ", hat(theta)[1], "*")),
         xlab = expression(paste(hat(theta)[1], "*")),
         ylim = range(density(theta_1_hat_star)$y, density(theta_1_hat_star)$y))

    lines(density(theta_1_hat_star))

    box(col = "black")

    abline(v=theta_1_pci[1],lty="dashed")
```

```
abline(v=theta_1_pci[2],lty="dashed")
text(theta_1_pci[2]-0.01, 6, expression(paste("%", ile)), cex=0.7)

abline(v=theta_1_BCa[1],lty="dotted")
abline(v=theta_1_BCa[2],lty="dotted")

#abline(v=mean(theta_1_hat_star))
#abline(v=plug_in_estimate_theta_1)
text(theta_1_BCa[2]+0.01, 5, expression(BC[a]), cex=0.7)
```

end---

3 References

Efron, B., & Tibshirani, R. (1993). *An introduction to the bootstrap.* Chapman & Hall/CRC.

4 Appendix

4.1 Code to read data for item 2

CODE FILENAME: ../R/02_01_load_data.R

```
data <- "../../../problems/ps_02/datasets/spatial_test_data.RData"

if (file.exists(data)) {
  print(paste(c("The file exists; loading", data), collapse = ' '))
  load(data)
} else {
  paste(c("The file does not exist; creating, loading and saving", data),
        collapse = ' ')
  spatial_test_data <- data.frame(
    'i' = 1:25,
    'A' = c(48, 36, 20, 29, 42, 42, 20, 42, 22, 41, 45, 14, 6,
            33, 28, 34, 4, 32, 24, 47, 41, 24, 26, 30, 41),
    'B' = c(42, 33, 16, 39, 38, 36, 15, 33, 20, 43, 34, 22, 7,
            34, 29, 41, 13, 38, 25, 27, 41, 28, 14, 28, 40)
  )
  n1 <- dim(spatial_test_data)[1]
  seed <- 7

  save(spatial_test_data, seed, n1, file=data)
}

rm(data)
```