

Question 2 a)

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```
data <- read.csv("Infectious.csv")
```

```
# From Tutorial 7 but modified for with replacement
createInclusionProbFn <- function(N, sampSize) {
  n <- sampSize
  f <- function(u) rep( 1 - (1 - 1/N)^n, length(u))
  return(f)
}

createJointInclusionProbFn <- function(N, sampSize) {
  n <- sampSize
  f <- function(u, v) ifelse(u == v, 1 - (1 - 1/N)^n, 1 - 2 * (( (N-1) / N )^n) + ( (N - 2)/N)^n)
  return(f)
}

createHTestimator <- function(pi_u_fn) {
  f <- function(sample_idx, variateFn)
    sum(sapply(sample_idx, function(u) variateFn(u)/ pi_u_fn(u)))
  return(f)
}

createHTVarianceEstimator <- function(pi_u_fn, pi_uv_fn) {
  f = function(sample_idx, variateFn) {
    sum(outer(sample_idx, sample_idx, FUN = function(u, v) {
      pi_u <- pi_u_fn(u)
      pi_v <- pi_u_fn(v)
      y_u <- variateFn(u)
      y_v <- variateFn(v)
      pi_uv <- pi_uv_fn(u, v)
      Delta_uv <- pi_uv - pi_u * pi_v
      return((Delta_uv * y_u * y_v) / (pi_uv * pi_u * pi_v))
    })))
  }
  return(f)
}

createGenericVariateFn <- function(popData, expression, ...) {
  # Save extra arguments to extra_args
  extra_args <- list(...)
  # A formality; instead of evaluating, return the unevaluated expression.
  evalable <- substitute(expression)
```

```

# Evaluate expression in the context of popData, restricted to indices u, and any extra_args.
f <- function(u) with(extra_args, eval(evalable, popData[u,]))
return(f)
}

```

Provide an estimate of the total number of individuals who died in country A because of the infectious disease

```

n = 100 # samples
N = 486 # population

inclusionProb      <- createInclusionProbFn(N, sampSize = n)
inclusionJointProb <- createJointInclusionProbFn(N, sampSize = n)

deceasedHTEstimator <- createHTEstimator(inclusionProb)
HTVarianceEstimator <- createHTVarianceEstimator(pi_u_fn = inclusionProb,
                                                  pi_uv_fn = inclusionJointProb)

deceased.infected <- createGenericVariateFn(data, Deceased.Prop * Infected * 12.5)

estimated.deceased.infected <- deceasedHTEstimator(seq(100), deceased.infected)
cat('Estimate of total number of individuals who died in country A because
    of the infectious disease: ', estimated.deceased.infected)

```

```

## Estimate of total number of individuals who died in country A because
##   of the infectious disease: 134137.6

```

Provide the standard error of your estimate as well as a 95% confidence interval for the number of individuals who died of the infectious

```

standard.error <- sqrt(HTVarianceEstimator(seq(100), deceased.infected))
cat('Standard Error of Estimate: ', standard.error)

```

```

## Standard Error of Estimate: 8304.263

```

```

confidence.interval <- estimated.deceased.infected + 2*standard.error*c(-1,1)
cat('95% Confidence Interval: ', confidence.interval)

```

```

## 95% Confidence Interval: 117529.1 150746.1

```