

1D Monte Carlo simulation of microbial exposure

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This document offers a 1D Monte Carlo probabilistic solution in R for the daily microbial exposure from drinking water consumption, swimming in surface water and shellfish consumption for [Example 6.18](#) from pages 215-216 of:

[Quantitative Microbial Risk Assessment, 2nd Edition](#) by Charles N. Haas, Joan B. Rose, and Charles P. Gerba. (Wiley, 2014).

```
# A 1D Monte Carlo simulation for the daily microbial exposure from drinking
# water consumption, swimming in surface water, and shellfish consumption for
# Example 6.18 from Quantitative Microbial Risk Assessment, 2nd Edition by
# Charles N. Haas, Joan B. Rose, and Charles P. Gerba. (Wiley, 2014).

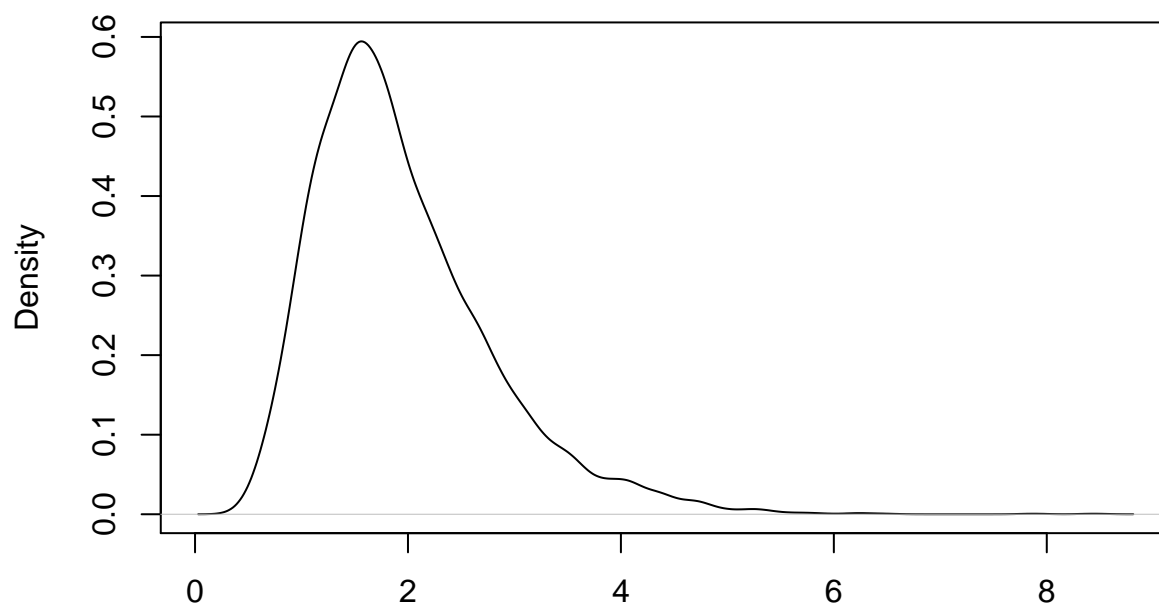
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# Define additional variables provided in the example for three exposure types.
#
# Shellfish consumption
shell.viral.load <- 1
shell.cons <- 9e-4 * 150 # 9e-4 Person-Days per year * 150 g per occurrence
# Drinking water consumption
dw.viral.load <- 0.001
# Surface water consumption while swimming
sw.viral.load <- 0.01
sw.daily.IR <- 50 # Ingestion rate in mL of surface water
sw.frequency <- 7 # Exposure frequency of 7 swims per year

# Generate 5000 random values from a log-normal distribution to estimate
# exposure from consumption of drinking water (mL/day). Divide by 1000 mL/L
# to get consumption in liters/day. Values for meanlog and sdlog are from the
# QMRA textbook (Haas, 2014), page 216, Table 6.30.
set.seed(1)
water.cons.L <- rlnorm(5000, meanlog = 7.49, sdlog = 0.407) / 1000

# Plot the kernel density curve of the generated values just as a check.
plot(density(water.cons.L))
```

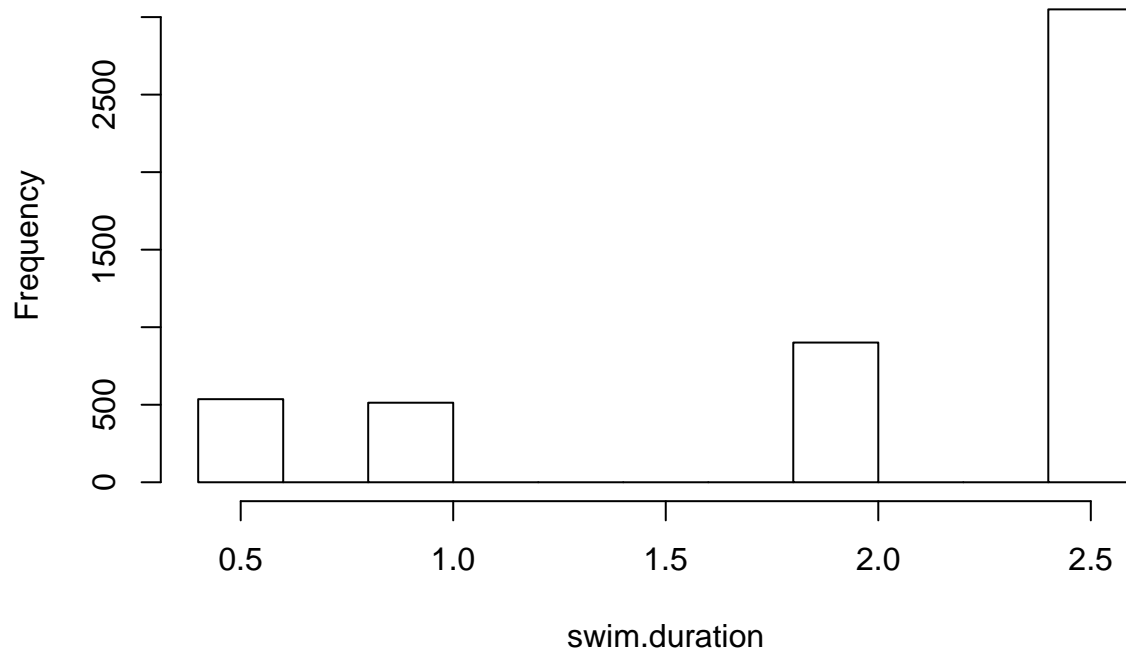
density.default(x = water.cons.L)



N = 5000 Bandwidth = 0.1241

```
# Sample 5000 times from a discrete distribution of swim duration with  
# assigned probabilities of each outcome. These values are hypothetical and  
# are not found in the text, but are defined here to provide an example of  
# sampling from a discrete distribution.  
set.seed(1)  
swim.duration <- sample(x = c(0.5, 1, 2, 2.6), 5000, replace = TRUE,  
                        prob = c(0.1, 0.1, 0.2, 0.6))  
  
# Create a simple histogram of our distribution as a check.  
hist(swim.duration)
```

Histogram of swim.duration

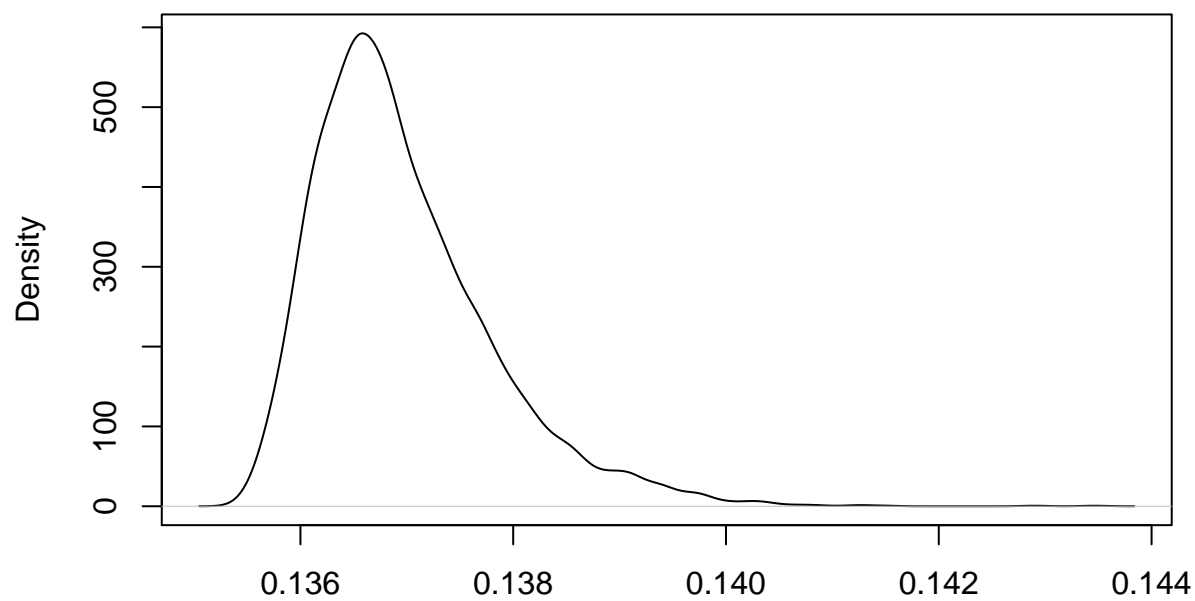


```
# Define a function to calculate microbial exposure risk.
Risk.fcn <- function(shell.vl, shell.cons, water.cons.L, dw.vl, sw.vl,
                     sw.daily.IR, sw.duration, sw.frequency) {
  ((shell.vl * shell.cons) + (water.cons.L * dw.vl) +
   ((sw.vl * (sw.daily.IR * sw.duration * sw.frequency)) / 365 / 1000))
}

# Run the simulation 5000 times.
daily.dose <- sapply(1:5000,
                    function(j) Risk.fcn(water.cons.L = water.cons.L[j],
                                           sw.duration = swim.duration[j],
                                           shell.vl = shell.viral.load,
                                           dw.vl = dw.viral.load,
                                           shell.cons = shell.cons,
                                           sw.vl = sw.viral.load,
                                           sw.daily.IR = sw.daily.IR,
                                           sw.frequency = sw.frequency))

# Plot the results of the simulation.
plot(density(daily.dose))
```

density.default(x = daily.dose)



N = 5000 Bandwidth = 0.0001241