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Simulations of the effect of sample size on the maximum observed age in a fish population

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This technical report provides the R computer code for performing the Monte Carlo simulations described in the publication:

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# simulating the maximum age in samples of size n drawn from
# a population in equilibrium with constant recruitment and
# constant mortality rate with respect to age and time

# This simulation is in support of the article by John Hoenig
# which examines several expressions in the literature for the
# expected value of the maximum age in a sample drawn at one
# point in time. These expressions were derived by Sarhan (1954),

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# generate growth of a population from time 0 to 200 assuming
# constant recruitment and mortality starting at time 0. (For
# Z = .2, the population approaches steady state after about 60
# years. Hence, we can sample the population at time 200, say,
# and have approximately equilibrium conditions (although,
# strictly speaking, the oldest age can't be more than 200))

# note: I reset the random number seed several times to
# prevent recycling of the number stream

# Generate 40 million times of birth distributed uniformly in
# the interval (0,200)
set.seed(45)
birth.times <- runif(20000000, 0, 200)
set.seed(23)
birth.times <- c(birth.times, runif(20000000, 0, 200))

# generate a corresponding duration of life for each birth
# from an exponential distribution with mortality rate Z
set.seed(14)
Z = .2 # instantaneous mortality rate (hazard function), i.e., 1/mean
life.dur <- rexp(20000000, Z)
set.seed(17)
life.dur <- c(life.dur, rexp(20000000, Z))
max(life.dur)  # longest life among the 40 million lives generated: [1] 98.91561

# quality control checks
1/mean(life.dur) # Check mean is consistent with Z, i.e., close to 1/Z: [1] 0.2000247

# check on distribution of life durations
opar <- par(mfrow=c(2,2))
out <- hist(life.dur, main="life durations", xlab="duration of life")
plot(out$breaks[1:(length(out$breaks)-1)], log(out$counts), ylab="log(Frequency)",
     xlab="duration of life")
out2 <- hist(life.dur[life.dur>70], main="life durations > 70", xlab="duration of life")
plot(out2$breaks[1:(length(out2$breaks)-1)], log(out2$counts), ylab="log(Frequency)",
     xlab="duration of life")
pars(opar)

# slight departure from linearity on the log scale at the extreme right
# is due to fact that one can't observe any animal abundances between
# 0 and 1, hence the linear regression can't extend below the x-axis
# which begins at y = log(1 animal) = 0

annual.recruit <- 40000000/200 ; annual.recruit # 200,000

# compute time of death for each fish as birth time + length of life
deadtimes <- birth.times + life.dur

# look at the population that is alive at time 200
time <- 200
# find all animals alive at time=time
alive.t <- birth.times[birth.times<time & time < death.times]
length(alive.t) # size of the population # [1] 999470
quality control checks

look at the population that is alive as a function of time to

see the evolution of the population ### THIS RUNS VERY SLOWLY

```r
pop <- rep(NA, 200)
for (time in 1:200){
# find all animals alive at time=time
  alive.t <- birth.times[birth.times<time & time < death.times]
  pop[time] <- length(alive.t)  # size of the population
}
plot(1:200, pop, typ="l", xlab="time", ylab="population size")
plot(50:200, pop[50:200], typ="l", xlab="time", ylab="population size")
# population grows steadily towards an equilibrium value and has largely
# reached the equilibrium after 50 years. There is not much variability
# in abundance after 50 years.
```

```
# make histogram of the times of birth for those animals alive
# at time=200 ###### THIS CREATES FIGURE 1 for the paper ######
opar <- par(las=1, cex.axis=1.2)
out <- hist(alive.t, axes=F, main="", col=1,
  xlab=list("Birth time", cex=1.5), ylab = list("Frequency (thousands)",cex=1.5))
axis(2, at= seq(0, 600000, 100000), labels = seq(0, 600, 100), las=1)
axis(1, at = out$breaks, labels = out$breaks)
box()
```

```r
ages <- time - alive.t
max(ages)  # find the oldest animal alive at time=time: [1] 62.97065
```
hist(ages, las=0)
box()
par(opar)

#########
# Now let's look at how maximum age varies with changes in sample size.
# We will draw samples of size n (= 100, 500 and 1000) 100,000 times
### NOTE: THIS IS VERY SLOW ###
obs.max.age <- matrix(NA, nrow=100000, ncol = 3) # hold the 300,000 maximum ages

### THIS WILL BE SLOW ###
n <- c(100, 500, 1000)
for (i in 1:3) {
  for (j in 1:100000){
    samp <- sample(ages, n[i])       # draw a sample
    obs.max.age[j, i] <- max(samp)   # note the maximum age in sample
  }
}

mean.obs.max <- apply(obs.max.age, 2, mean) # [1] 25.87964 34.01604 37.62368
# NOTE: the use of the nested loops above is obviously inefficient but
# I perform the computations this way to make them as easy for the reader
# to follow as possible

# now compute the expected values for each sample size using the equations
# given by Johnson and Kotz (called expec), Hoenig (called Hoe), Holt (called Holt)
# and Kenchington (called Ken). Also compute the variance by the formula of
# Johnson and Kotz (called varexpec)
expec <- rep(NA, 3)
Hoe <- rep(NA, 3)
Holt <- rep(NA, 3)
Ken <- rep(NA, 3)
varexpec <- rep(NA, 3)

for (i in 1:3) {
  ind <- 1:n[i]
  expec[i] <- 1/(Z) * sum(1/ind)
  Hoe[i] <- log(2 * n[i] + 1)/Z
  Holt[i] <- (.577 + log(n[i]))/Z
  Ken[i] <- log(2 * n[i] * Z + 1)/Z
  varexpec[i] <- (1/Z) * sum(1/ind^2)
}

sqrt(varexpec)

answer = cbind(n, round(mean.obs.max, 2), round(expec, 2), round(Ken, 2), round(Holt, 2), round(Hoe, 2))
colnames(answer) <- c("n", "obs", "expect", "Kench", "Holt", "Hoe appr")
answer

#     n   obs  expect Kench  Holt Hoe appr
# [1,] 100 25.90  25.94 18.57 25.91    26.52
# [2,] 500 34.05  33.96 26.52 33.96    34.54
# [3,] 1000 37.59  37.43 29.97 37.42    38.01

##### THIS CREATES FIGURE 2 ######

opar = par(las=1, cex.axis=1.2)

plot(n, mean.obs.max, typ="l", ylim=c(17, 38), xlab=list("Sample size", cex=1.5),
ylab=list("Mean oldest age", cex=1.5, lty=3, lwd=2)
points(n, expec, typ="l", lty=1, lwd=2)
points(n, Ken, typ="l", lty=4, lwd=2)
# points(n, Holt, typ="l", lty=5, pch=5, lwd=2)
points(n, Hoe, typ="l", lty=2, lwd=2)

leg <- c("Hoenig approx.", "observed", "Sarhan", "Kenchighton")
text(800, 23.5, "top to bottom")
legend("bottomright", legend=leg, lty=c(2,3,1,4), bty="n")
#title("maximum age when M = 0.2")

par(opar)

####################################

# Now compare Kenchington's formula (called ken) to the one in
# Johnson and Kotz (called true) for values of mortality rate
# varying from 0.05 to 1.5, for 3 sample sizes

##### THIS CREATES FIGURE 3 ######
Zvec <- seq(.05, 1.5, .1); Zvec
n <- c(100, 500, 1000)

compare <- function(Z, n) { # compute E(Tmax) from Sarhan &
    # Kenchington formulae
    true <- sum(1/1:n)/Z
    ken <- log(2 * n * Z + 1)/Z
    return(c(true, ken))
}

results100 <- t(sapply(Zvec, compare, 100))
results500  <- t(sapply(Zvec, compare, 500))
results1000 <- t(sapply(Zvec, compare, 1000))

# first do n = 1000
wid <- 2
opar = par(las=1, cex.axis=1.2, fig=c(0,1,0,1), bty="o")
plot(Zvec, results1000[,1], typ="l", lty=1, lwd=wid, xlab=list("Mortality rate", cex=1.5),
     ylab=list("Maximum age", cex=1.5))
points(Zvec, results1000[,2], typ="l", lty=2, lwd=wid)

leg <- c("correct, n=1000","Kenchington, n=1000")
legend("topright", leg, lty=c(1,2), bty="n")

par(new=T, fig=c(x1=.271, x2=.991, y1=.25, y2=.85), bty="l")
plot(Zvec[6:15], results1000[6:15,1], typ="l", lty=1, lwd=wid, xlab="",
     ylab="", ylim=c(4,14), yaxt="n")
points(Zvec[6:15], results1000[6:15,2], typ="l", lty=2, lwd=wid)
axis(2, at = seq(4, 14, 2), labels = c("4","", "8","", "12",""))

par(opar)

# now do n= 100
wid <- 2
opar = par(las=1, cex.axis=1.2, fig=c(0,1,0,1))
plot(Zvec, results100[,1], typ="l", lty=1, lwd=wid, xlab=list("Mortality rate", cex=1.5),
     ylab=list("Maximum age", cex=1.5), bty="o")
points(Zvec, results100[,2], typ="l", lty=2, lwd=wid)
leg <- c("correct, n=100", "Kenchington, n=100")
legend("topright", leg, lty=c(1,2,3,4), bty="n")
par(new=T, fig=c(x1=.271, x2=.991, y1=.25, y2=.85), bty="l")
plot(Zvec[6:15], results100[6:15,1], typ="l", lty=1, lwd=wid, xlab="", ylab="", ylim=c(4,14), yaxt="n")
points(Zvec[6:15], results100[6:15,2], typ="l", lty=2, lwd=wid)
axis(2, at = seq(4, 14, 2), labels = c("4","", "8","", "12",""))
par(opar)

# Annual (not continuous) reproduction case

set.seed(45)
Z = .2

# We generate birth times up to time 201 so that when we truncate the
# birth time to an integer we will have some animals born at time 200,
# in other words, the age composition at time = 200 will include animals
# of age 0
birth.times <- floor(runif(20000000, 0, 201))
set.seed(23)
birth.times <- c(birth.times, floor(runif(20000000, 0, 201)))
range(birth.times)  # this gives births ranging from time 0 to 200
hist(birth.times)

# the first bar of the histogram is higher than the others because
# it represents the animals born from year 0 to year 10 (11 years)
# while all the other bars represent 10 years of births (11 to 20,
# 21 to 30, 31 to 40, etc.)

set.seed(14)
life.dur <- rexp(20000000, Z)
set.seed(17)
life.dur <- c(life.dur, rexp(20000000, Z))
max(life.dur)

1/mean(life.dur)  # Check that mean is consistent with a Z of 0.5
deadth.times <- birth.times + life.dur

# Look at the population at time 200
time <- 200
alive.t <- birth.times[birth.times<=time & time < death.times]

length(alive.t)  # size of the population
hist(alive.t, main="birth times for fish alive at time=200",
     xlab=list("Birth time", cex=1.5), ylab = list("Frequency",cex=1.5))

ages <- time - alive.t
max(ages)  # [1] 63

# Now let's look at how maximum age varies with changes in sample size

#### THIS RUNS SLOWLY

obs.max.age <- matrix(NA, nrow=100000, ncol = 3)

n <- c(100, 500, 1000)

for (i in 1:3) {
    for (j in 1:100000) {
        samp <- sample(ages, n[i])
    }
}
obs.max.age[j, i] <- max(samp)
}
}

mean.obs.max <- apply(obs.max.age, 2, mean)

expec <- rep(NA, 3)
Hoe <- rep(NA, 3)
Ken <- rep(NA, 3)
Holt <- rep(NA, 3)
for (i in 1:3) {
  ind <- 1:n[i]
  expec[i] <- 1/(Z) * sum(1/ind)
  Hoe[i] <- log(2 * n[i] + 1)/Z
  Ken[i] <- log(2 * n[i] * (1 - exp(-Z)) + 1)/Z
  Holt[i] <- (0.577 + log(n[i]))/Z
}

answer = cbind(n, round(mean.obs.max, 2), round(expec, 2), round(Ken, 2), round(Hoe, 2),
                round(Holt,2))
colnames(answer) <- c("n", "obs", "expect", "Kench", "Hoe appr", "Holt") ; answer

##### THIS CREATES FIGURE 4 ######
par(las=1, cex.axis=1.2, bty="o")
plot(n, Hoe, typ="l", ylim=c(18, 40), xlab=list("Sample size", cex=1.5),
     ylab=list("Mean oldest age", cex=1.5), lty=2, lwd=2)
points(n, expec, typ="l", lty=1, lwd=2)
points(n, mean.obs.max, typ="l", lty=3, lwd=2)
points(n, Ken, typ="l", lty=4, lwd=2)
# points(n, Holt, typ="b", lty=5, pch=5, lwd=2, col=2) # Holt is on top of expec
leg <- c("Hoenig approx.", "expected (expon)", "observed", "Kenchington")
legend("bottomright", legend=leg, lty = c(2, 1, 3, 4), bty="n")
text(790, 24.7, "top to bottom")
par(opar)