BIOl 410 Tutorial 3

Population growth

Cohort life table analysis

Exponential population growth

$$N_t = N_0 e^{rt}$$

- The doubling time of an exponentially growing population is given by

$$t_{double} = \frac{\ln(2)}{r}$$

Exponential population growth

- The human population is expected to double in approximately 50 years.
- Assuming exponential population growth calculate r for the human population.
- If the current population size is 7.3 billion (2015), calculate the projected population size in 2030.

```
# Exponential population general framework
years <- c(2015:2020)
t <- c(1:length(years))
N0 <- 12    # initial population size
r <- 0.6    # instantaneous rate of population increase

N <- N0*exp(r*t)
plot(years, N,col="blue", type ="l")
```

Exponential growth

- Estimating r from data
- Plot the logarithm of population size vs time
- The slope of a best fit line approximates r under exponential growth

Exponential growth

- For five consecutive days the population of a flatworm is recorded as 100, 158, 315, 398, 794.
- Using this data, and assuming exponential growth, estimate r, and plot the projected population growth from an initial population size of 100.

```
worms <- c(100,158,315,398,794)
days <- c(1:5)
plot(days,worms)
```

Exponential growth

```
worms <- c(100,158,315,398,794)
days <- c(1:5)
plot(days,worms)

plot(days,log(worms))

r <- (log(794)-log(100))/(5-1)
N0 <- 100
day <- seq(1,4,0.01)

N <- N0*exp(r*day)

plot(days,worms)
points(c(1,day+1),c(N0,N),type="l“,col=“red”)
```

Logistic population growth

$$N_t = \frac{K}{1 + [(K - N_0)/N_0]e^{-rt}}$$

```
# Model 5: Logistic population growth
years <- c(2015:2030)
t <- seq(1,length(years),0.01)
N0 <- 1     # initial population size
b <- 0.8    # instantaneous birth rate
d <- 0.2    # instantaneous death rate
r <- b - d  # instantaneous rate of population increase
K <- 60

N <- K/(1+((K-N0)/N0)*exp(-r*t))
plot(t, N, type ="l")
```

Logistic population growth

- A population of butterflies is growing according to the logistic equation. Assuming a carrying capacity of 500, and a intrinsic rate of increase (r) of 0.1, what is the maximum rate of growth of the population?

Logistic population growth

```
# Butterflies
t <- c(1:120)
N0 <- 1     # initial population size
r <- 0.1    # instantaneous rate of population increase
K <- 500

N <- K/(1+((K-N0)/N0)*exp(-r*t))
plot(t, N, type ="l")

dndt <- r*(1-(1/K)*N)*N
par(mfrow=c(2,1))
plot(t, N, type ="l")
plot(N, dndt,ylab="dN/dt")

jpeg("butterfly_max_growth.jpg")
  par(mfrow=c(2,1))
  plot(t, N, type ="l")
  plot(N, dndt,ylab="dN/dt")
dev.off()
```

Cohort life table analysis

```
# Cohort life table analysis
# Song sparrow example
years <- c(2009:2015)
age <- c(0:6)
S <- c(115,25,19,12,2,1,0)
b <- c(0,0,1,2,3,1,1)

lt <- data.frame(years,age,S,b)
lt

plot(lt$years,lt$S,xlab="Years",yl
ab="Number in cohort")
```

Survival schedule

Survivorship schedule $$l(x) = \frac{S(x)}{S(0)}$$

Survival probability $$g(x) = \frac{l(x+1)}{l(x)}$$

```
S0    <- lt$S[1]  # Cohort size at start of age
lt$l  <- lt$S/S0  # Survivorship Schedule
g     <- lt$l[2:length(S)]/lt$l[1:length(S)-1] # Survival probability
lt$g  <- c(g,0) # Survival probability added to life table

lt
```

Net reproductive rate R_0

$$R_0 = \sum_{x=0}^{k} l(x) b(x)$$

```
lt$lb <- lt$l*lt$b  # Births * survivorship
R0    <- sum(lt$l*lt$b)  # Net Reproductive Rate
R0
```

Generation Time (G)

$$G = \frac{\sum_{x=0}^{k} l(x)\, b(x)\, x}{\sum_{x=0}^{k} l(x)\, b(x)}$$

```
lt$lbS <- lt$l*lt$b*lt$age # Births * survivorship weighted by age
G      <- sum(lt$l*lt$b*lt$age)/sum(lt$l*lt$b) # Generation time
```

Estimating r

$$r \approx \frac{ln(R_0)}{G}$$

```
aprox.r <- log(R0)/G        # Estimation of r
aprox.r
```

Euler's Equation

```
lt$euler.part <- exp(-aprox.r*lt$age)*lt$l*lt$b  # Euler partial calculation
euler <- sum(exp(-aprox.r*lt$age)*lt$l*lt$b)     # Euler equation
Lt

lt[,5:9] <- round(lt[,5:9],2)

euler
```

Does euler == 1?

Calculation of r using Euler's equation

```
rtests <- seq(aprox.r-aprox.r/2,aprox.r+aprox.r/2,0.001) # vector of possible r values
euler_1 <- rep(NA,1,length(rtests))  # Storage vector for associated Euler values

for(i in 1:length(rtests)){          # loop through potential values and calculate Euler
   euler_1[i] <- sum(exp(-rtests[i]*lt$age)*lt$l*lt$b)
}

plot(rtests,euler_1)   # Plot Euler as a function of r

r.location <- match(1,round(euler_1,2))    # Find the location of the lowest suitable r
value
r.fit <- rtests[match(1,round(euler_1,2))] # Find the lowest suitable r value
```