BIOL 410

Tutorial 4
Life table analysis
Leslie matrix population model
Lefkovitch matrix population model

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
```

Leslie population matrix

```
# Leslie matrix population model
# one time step
A <- matrix(c(0,1.4,1.6,0.2,0.8,0,0,0,0,0.5,0,0,0,0,0.25,0),
nrow=4, byrow=TRUE)
N0 <- matrix(c(200,0,0,0),ncol=1)
A
N0

N1 <- A %*% N0
N1
```

- What is the transition probability from age class 2 to 3
- What is the average fecundity of age class 2
- Does the age class distribution of N1 make sense

Leslie matrix population model

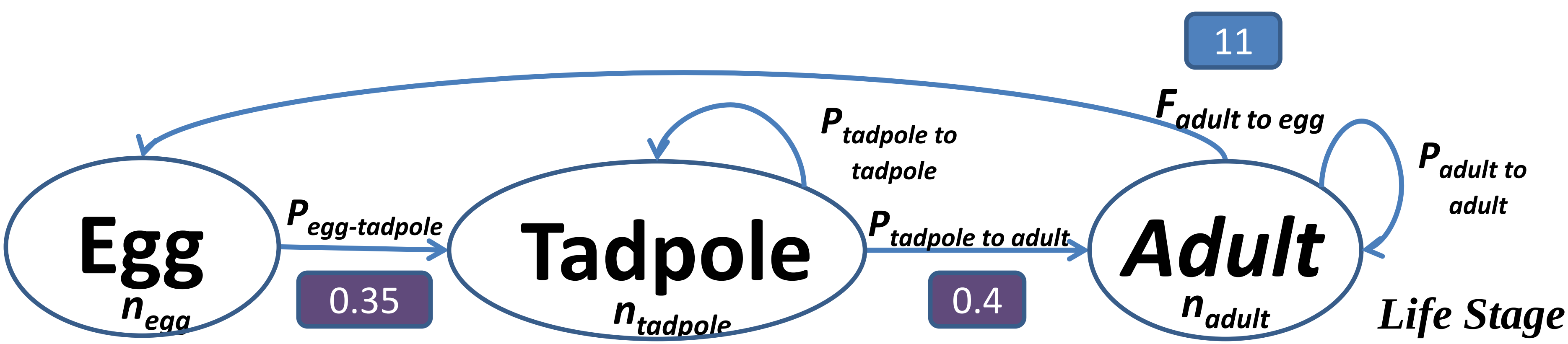
```
# Leslie matrix population model
A <- matrix(c(0,1.4,1.6,0.2,0.8,0,0,0,0,0.5,0,0,0,0,0.25,0), nrow=4,
byrow=TRUE)
N0 <- matrix(c(6,10,15,4),ncol=1)

years <- 6
N.projections <- matrix(0,nrow=nrow(A),ncol = years +1)
N.projections[,1]<- N0

for(year in 1:years){
    N.projections[,year+1]<- A %*% N.projections[,year]
}

N.projections
```

- Has the population reached a stable age distribution by year 7? What happens by year 12?

```
par(ylog = TRUE, cex = 1.2, cex.axis=1.2, cex.lab=1.2)
matplot(1:(years+1), t(N.projections),log="y",type = "l", lty = 1:nrow(A), col =
rainbow(nrow(A)),lwd=2, ylab = "Abundance by age class", xlab = "Year")
```

Leslie matrix population model

- Construct a Leslie matrix population model from this diagrammatic life table
- Initialize the population with 34,12,5 (e,t,a) individuals and project forward for 8 generations



Lefkovitch stage structured models

- Create the following stage structured model and project population forward for 10 time units.
- Initialize the population with 34,12,5 (e,t,a)