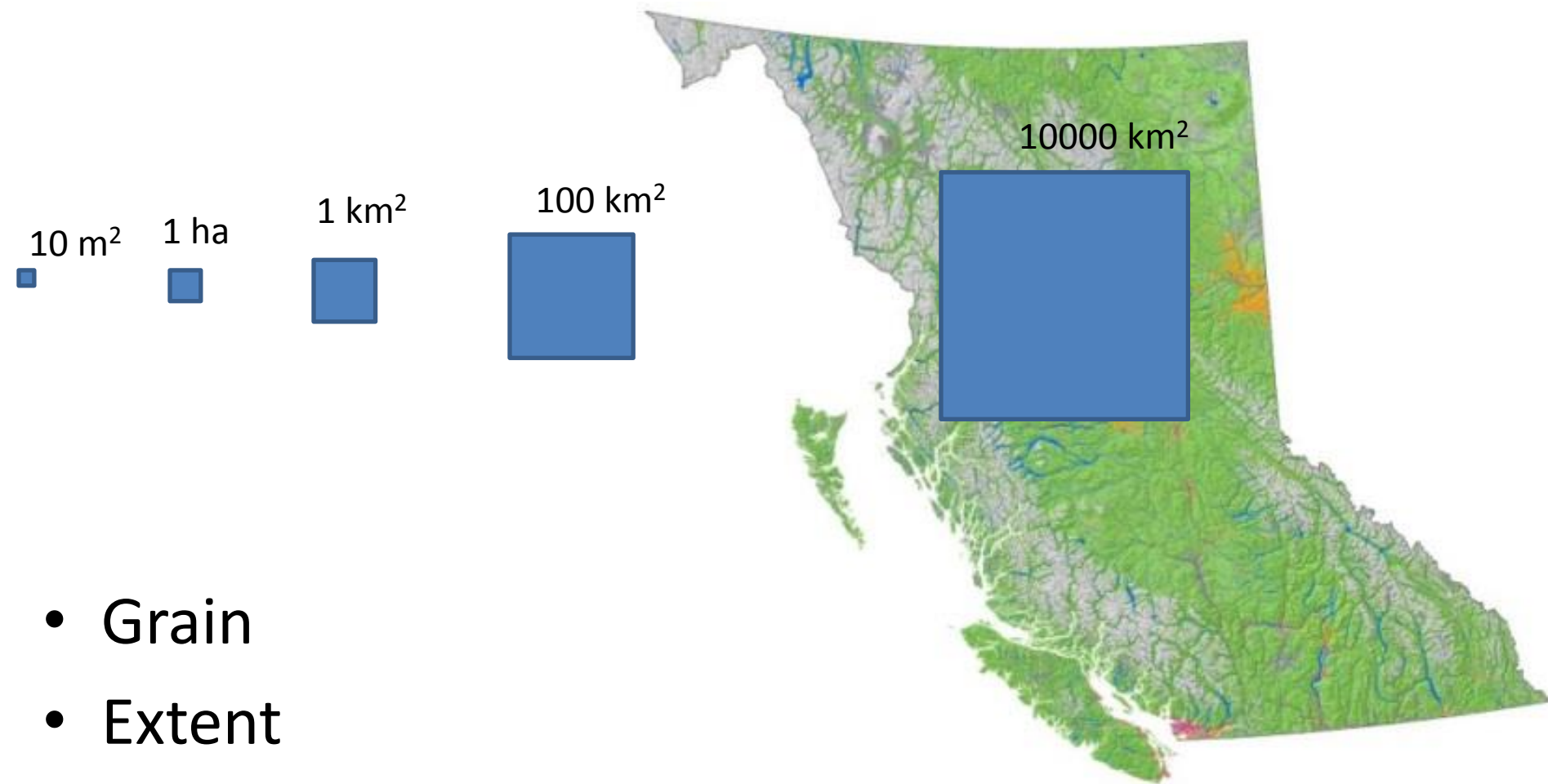


# BIOL 410 Population and Community Ecology

Density-independent growth

# Spatial scales



- Grain
- Extent
- Relevant ecological unit
- Relevant ecological processes

# What is scale in a population ecology context?

- Ecological scale
  - Related to:
    - The structures and processes that define the phenomenon under study
    - The sampling method
    - The statistical analysis
  - Grain and extent need to be defined for all studies

# Importance of scale

- What scale should a population be assessed at?
- At what scale do the processes that influence the population operate on?
- As the scale changes, the controls on pattern and process change
  - E.g. relationship between climate and vegetation
- As the scale changes, the system may switch between closed and open.

What factors will influence the extent and grain of the population model?

# Scale of spatial heterogeneity



Homogeneous?

## Grain size

- Small enough to be homogeneous within cell
- Large enough to minimize # of cells.



Heterogeneous?

## Abiotic

- Elevation
- Aspect
- Slope
- Soil depth

## Biotic

- Organism
- Scale of interactions

# Spatial scale

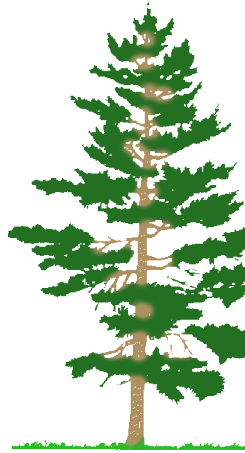
Relevant ecological unit?



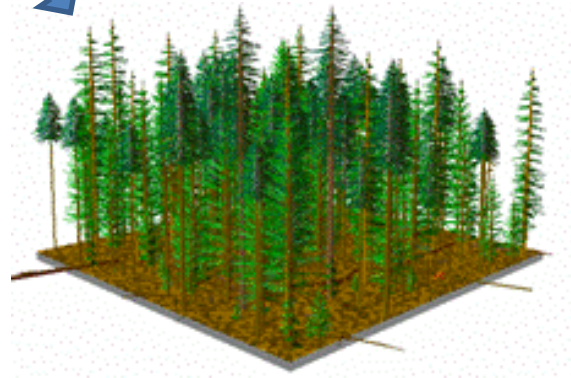
Cell



Branch  
(organism component)



Tree



Stand  
(population / community)



Region



# Spatial scale

- Relevant processes?
  - Competition?
  - Predation?
  - Dispersal?



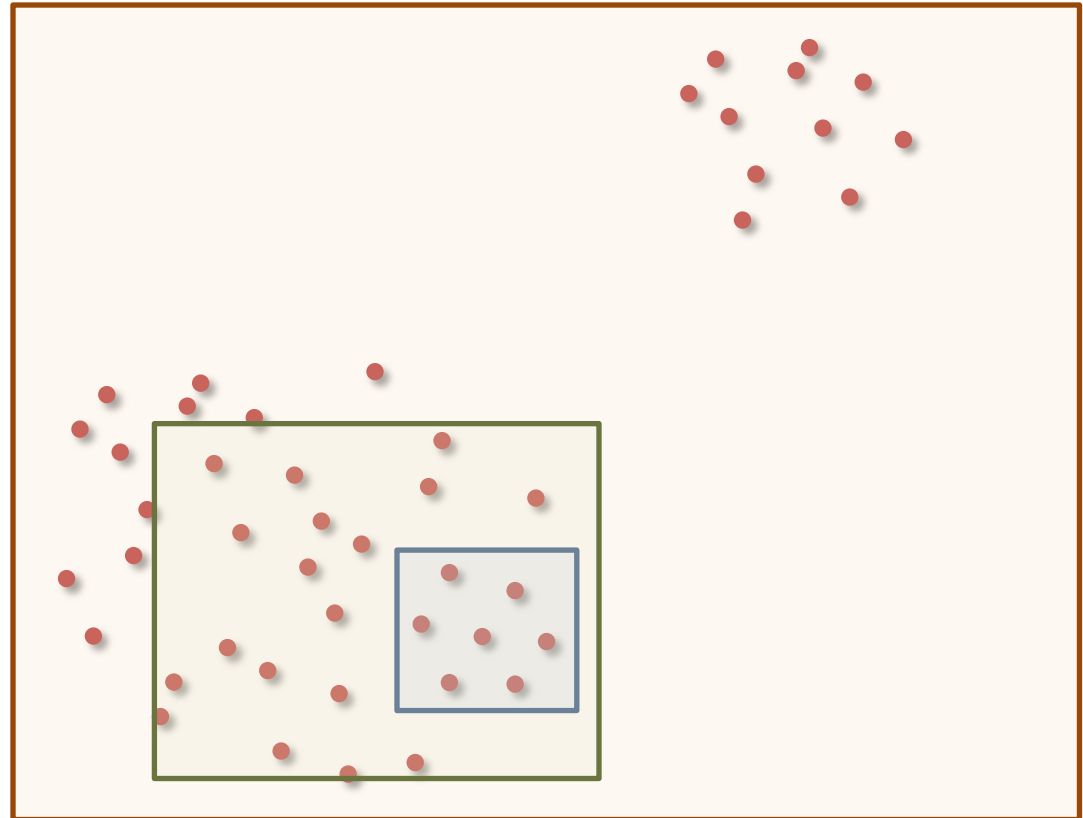
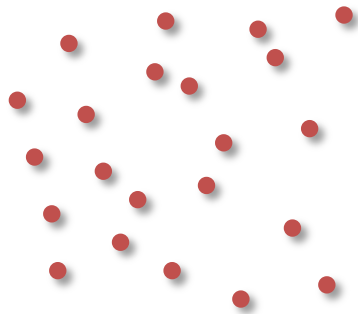


# Scale and ecology

- Key points when considering scaling issues:
  1. Description of phenomenon can be conditional on the scale of observation and resulting analysis
  2. Relating patterns to processes is dependent on the appropriate choice of scale
  3. Scale might be a continuous process without discrete borders or breaks
  4. Identifying variability between units or process can be used to identify appropriate scales
    - Domain: sharp transition from dominance of one set of factors to dominance by other sets

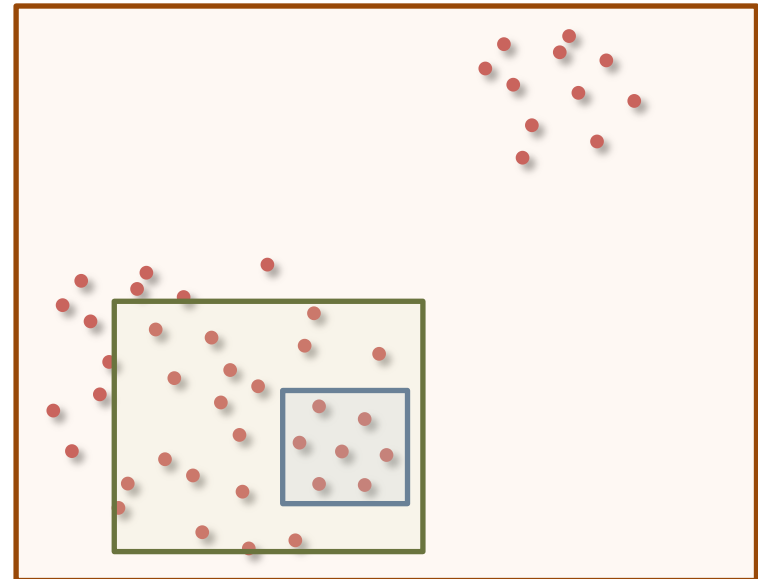
# Scale of observation can influence your ecological conclusions

- Pattern
- Process



# Scale of observation can influence your ecological conclusions

- Estimation of population mean
- Estimation of population variance
- Characterization of spatial or temporal autocorrelation
- Process rate
- Gradients, functional forms



# Scale of study in population and community ecology

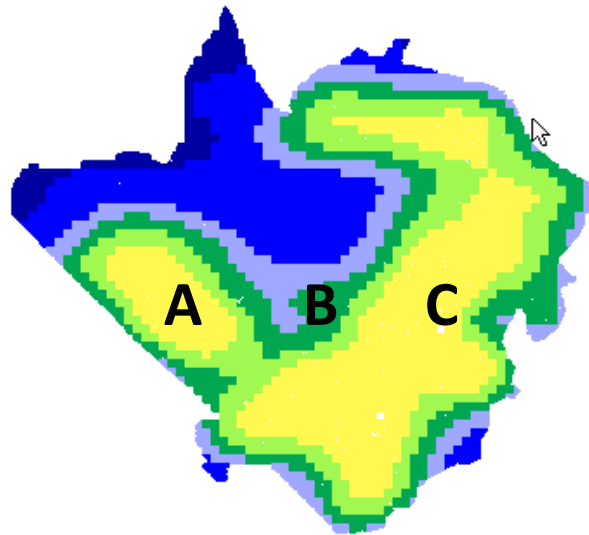
- Individual?
- Population?
- Geographic range?
- Species range?



Question, objective dependent

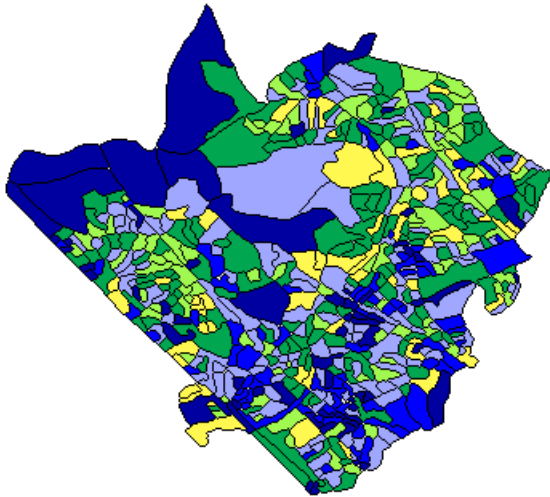
# Quantitative methods for identifying scale

- Are spatially close points more similar?
- Variance plotted against distance classes
- Autocorrelation value plotted against distance classes



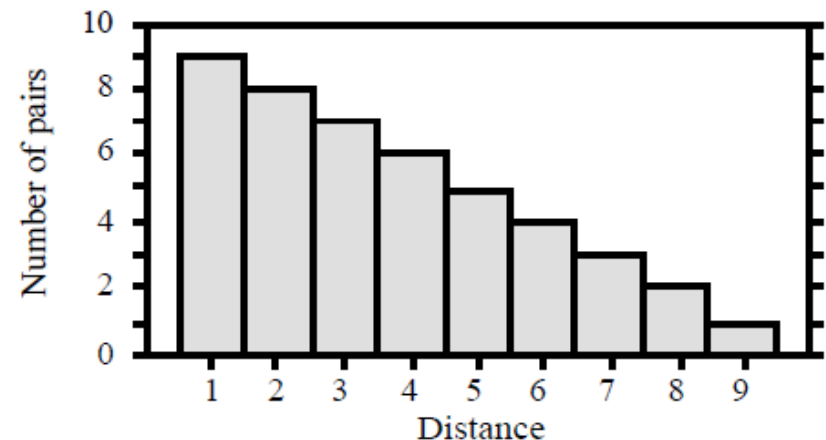
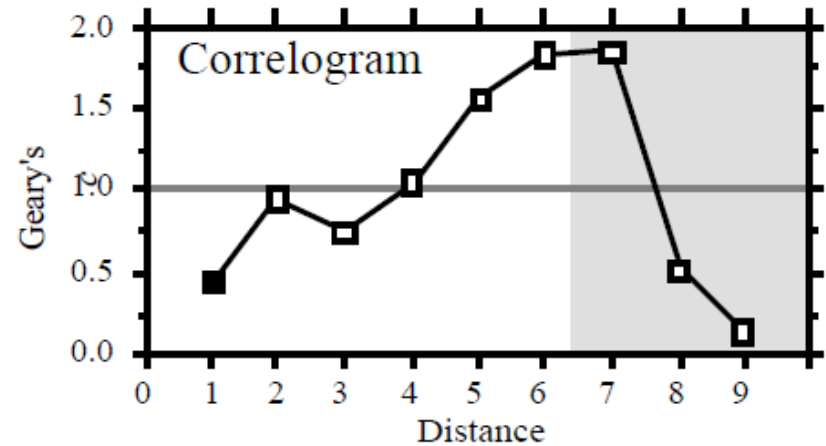
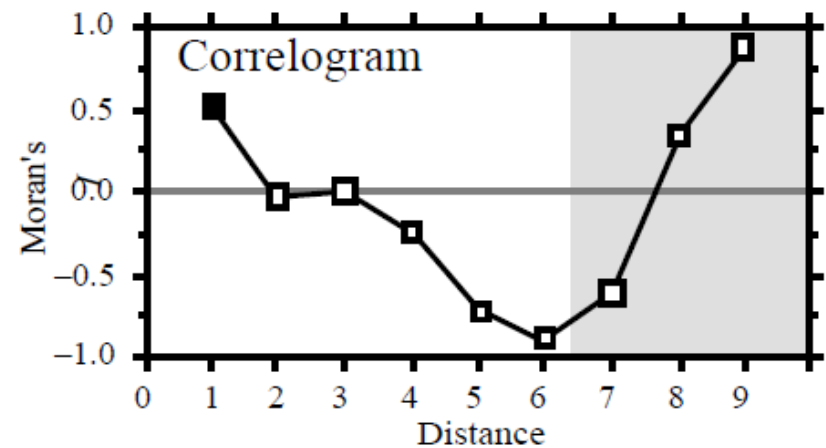
# Correlogram

> 0 positive



< 1 positive

- Distance at which correlogram lines cross the neutral value indicates “patch size” or “spatial range of the pattern”





Population growth  
density independent

# Key concepts

- Density independence
- Birth and death rates
- Population growth rate
- Exponential population growth
- Closed vs. Open populations
- Discrete vs. overlapping generations
- Discrete vs. continuous growth
- Deterministic vs. stochastic model

# Most basic population

$$N_{t+1} = N_t + B - D$$

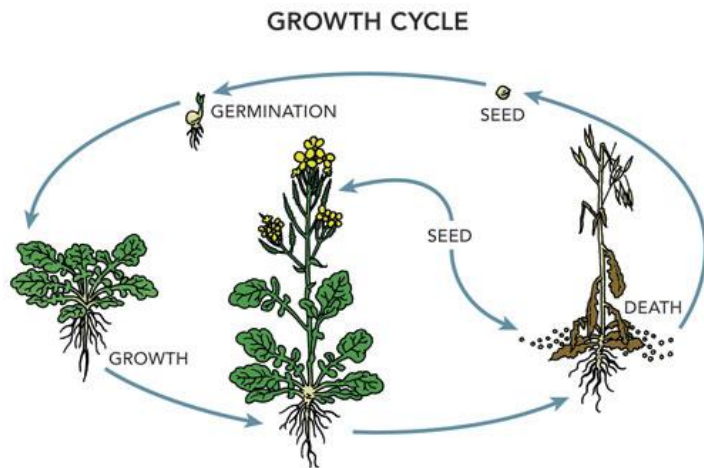
N: number of individuals in population

t: time (discrete unit)

B: number of births time interval

D: number of deaths per time interval

# Non-overlapping generations



Caterpillars Emerging from Egg Masses



Larva



Life Cycle of the Gypsy Moth



Female Moth

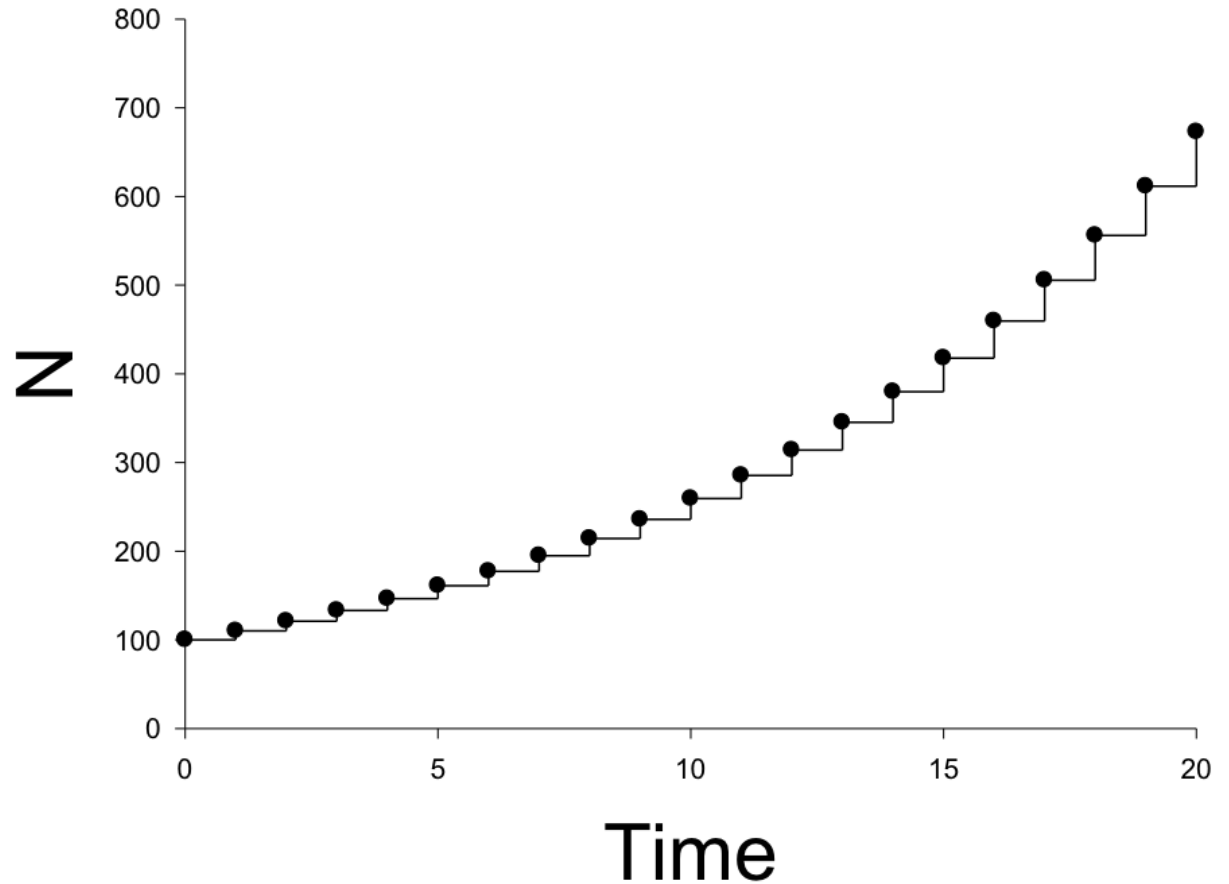


Male Moth



Pupae

# Discrete population growth



# Most basic population

$$N_{t+1} = N_t + B - D$$

- Discrete time steps
- Closed population
- No spatial structure
- No demographic structure

How will the population density change?

- $N_t = 12$ ,  $B = 5$ ,  $D = 3$

```
# State variables (abiotic)
years <- 2011:2015
Nt <- rep(NA,length(years))

# State variables (biological)
N <- c(1,3,8,27,81)
B <- 5 # births per year
D <- 3 # deaths per year

# Model 1
N <- 12
for(year in years) {
  t <- match(year,years)
  Nt[t] <- N + B - D
  N <- Nt[t]
}
plot(years,Nt)
```



$$N_{t+1} = N_t + b \cdot N_t - m \cdot N_t$$

b: birth **rate** (births **per individual** per time step)

m: mortality rate (death rate per individual per time step)

**Rate coefficient**, not fixed parameter



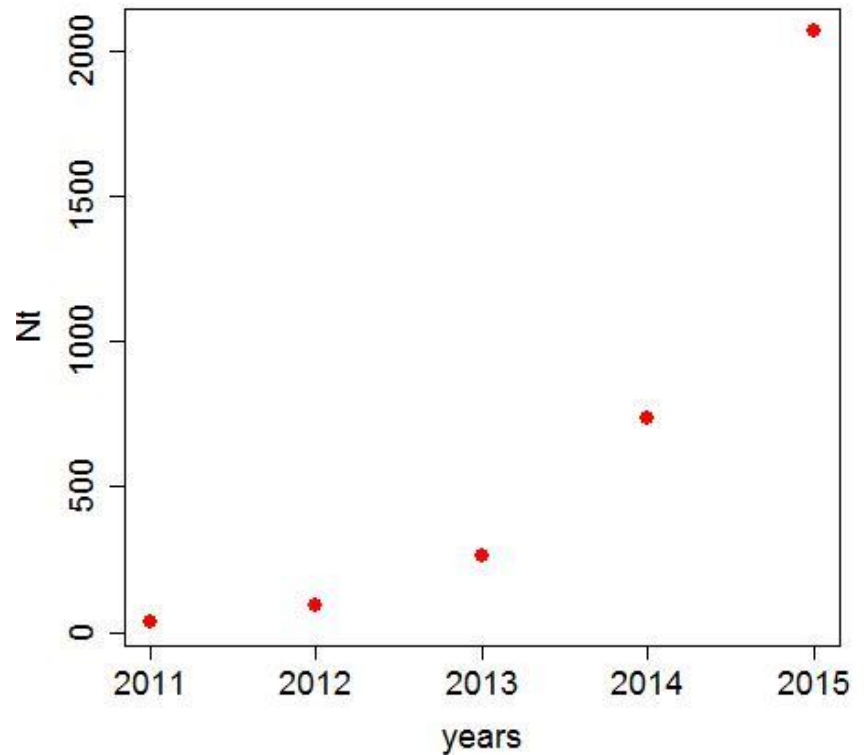
```
# Model 2
N <- 12
# Rate coefficient (parameter)
b <- 2 # birth rate per individual
m <- 0.2 # death rate per individual

for(year in years){
  t <- match(year, years)
  Nt[t] <- N + N*b - N*m
  N <- Nt[t]
}
plot(years, Nt)
```

$$N_{t+1} = N_t + b \cdot N_t - m \cdot N_t$$

```
# Model 2
N <- 12
# Rate coefficient (parameter)
b <- 2 # birth rate per individual
m <- 0.2 # death rate per individual

for(year in years){
  t <- match(year,years)
  Nt[t] <- N + N*b - N*m
  N <- Nt[t]
}
plot(years,Nt)
```



## Geometric population growth

$$N_{t+1} = N_t + b \cdot N_t - m \cdot N_t$$

$$N_{t+1} = N_t + N_t \cdot (b - m)$$

$$rd = b - m$$

$$N_{t+1} = N_t + N_t \cdot rd$$

rd: discrete population  
growth factor



```
# Model 3
# Rate coefficient (parameter)
b <- 2 # birth rate per individual
m <- 0.2 # death rate per individual
rd <- b - m # discrete population growth factor
N <- 12
for(year in years){
  t <- match(year, years)
  Nt[t] <- N + N*rd
  N <- Nt[t]
}
```

$$N_{t+1} = N_t + N_t \cdot rd$$

What happens when  $rd$  is:

$> 0$

$= 0$

$< 0$

$$N_{t+1} = N_t + N_t \cdot rd$$

$$N_{t+1} = N_t \cdot (1 + rd)$$

$$\lambda = (1 + rd)$$

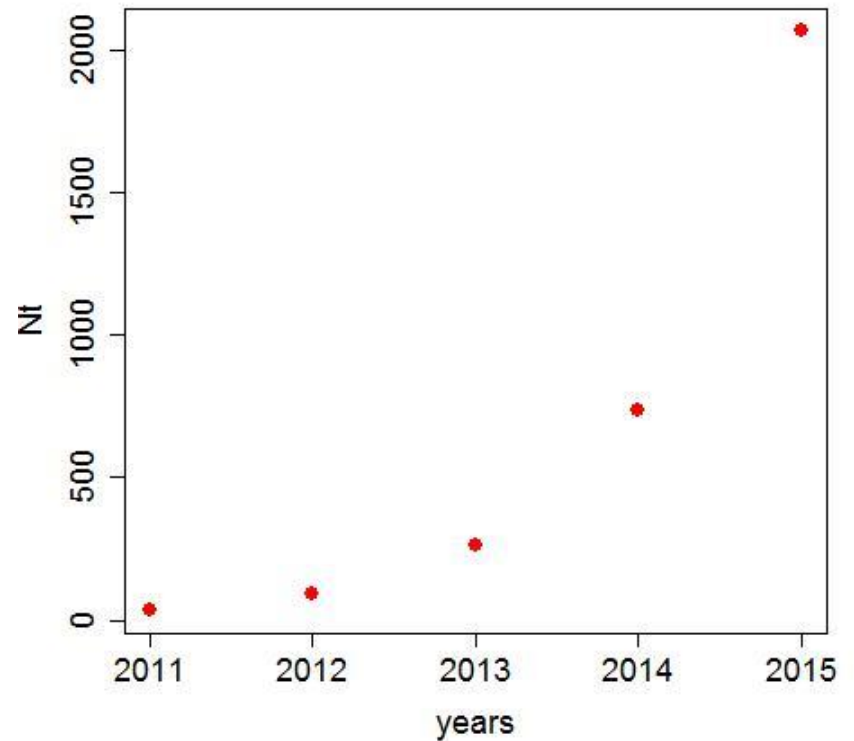
$$N_{t+1} = N_t \cdot \lambda$$

$\lambda$  : the finite  
rate of increase

```
# Model 4
# Finite rate of increase
b <- 2# birth rate per individual
m <- 0.2# death rate per individual
rd <- b - m# per individual population growth rate
lambda <- 1 + rd# Finite rate of per individual
population increase
N <- 12
for(year in years){
  t <- match(year,years)
  Nt[t] <- lambda*N
  N <- Nt[t]
}
```

$$N_{t+1} = N_t \cdot \lambda$$

```
# Model 4
# Finite rate of increase
b <- 2# birth rate per individual
m <- 0.2# death rate per individual
rd <- b - m# per individual population growth rate
lambda <- 1 + rd# Finite rate of per individual
population increase
N <- 12
for(year in years){
  t <- match(year,years)
  Nt[t] <- lambda*N
  N <- Nt[t]
}
```





# Discrete population growth

## Geometric population growth

$$N_{t+1} = N_t \cdot \lambda$$

$\lambda$

- Always a positive number
- Represents the proportional change in a population from one time unit to the next
- As a ratio it is a dimensionless number

# Projected population size at any time

$$N_{t+1} = N_t \cdot \lambda$$

$$N_{t+2} = N_t \cdot \lambda \cdot \lambda$$

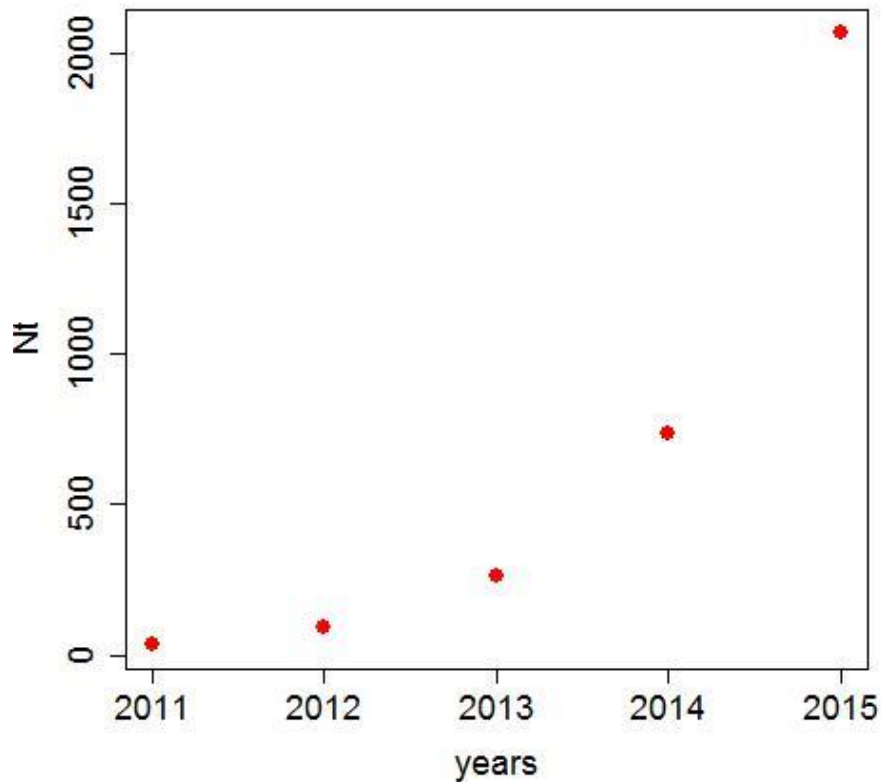
$$N_{t+2} = N_t \cdot \lambda^2$$

Recursion equation

$$N_t = N_0 \cdot \lambda^t$$

# Discrete population growth

$$N_t = N_0 \cdot \lambda^t$$



```
# Model 5
# Finite rate of increase
b <- 2 # birth rate per individual
d <- 0.2 # death rate per individual
R <- b - d # per individual population growth rate
lambda <- 1 + R # Finite rate of increase
N0 <- 12
t <- c(1:5)
Nt[t] <- (lambda^t)*N0
```

# Discrete population growth

$$N_t = N_0 \cdot \lambda^t$$

## Assumptions

- Population is closed (No I or E)
- No genetic structure
- No age or size structure
- Constant b and d ( $\lambda$  constant)
  - Unlimited space, food, resources
  - b and m resource independent
  - b and m density independent

$$N_t = N_0 \cdot \lambda^t$$

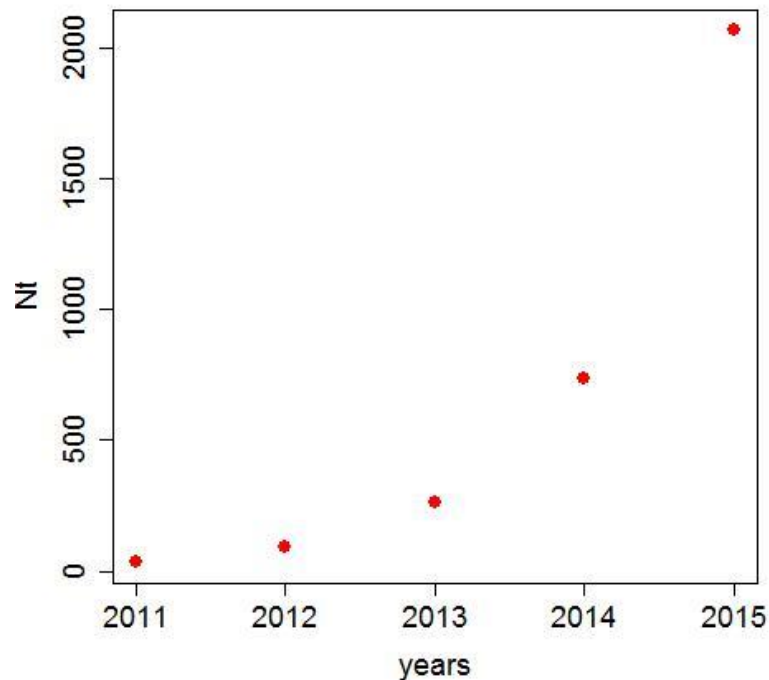
How do populations grow with different  $\lambda$ ?

$$\lambda = 2.8$$

$$\lambda = 1.8$$

$$\lambda = 3.0$$

$$\lambda = 0.7$$



$$N_t = N_0 \cdot \lambda^t$$

$$\lambda > 1$$

$$\lambda = 1$$

$$0 < \lambda < 1$$



# Continuous population growth

$$N_t = N_0 \cdot \lambda^t$$

Very small time step

$$\Delta t \quad \Delta N$$

$$\frac{dN}{dt}$$

Population growth

# Continuous population growth

$$\frac{dN}{dt} = (b - d)N$$

b: instantaneous birth rate

d: instantaneous death rate

$$\frac{dN}{dt} = rN$$

r:

Instantaneous rate of increase

Intrinsic rate of increase

What does  $r > 0$ ,  $r=0$ ,  $r<0$  mean?

# Continuous population growth

$$\frac{dN}{dt} = rN$$

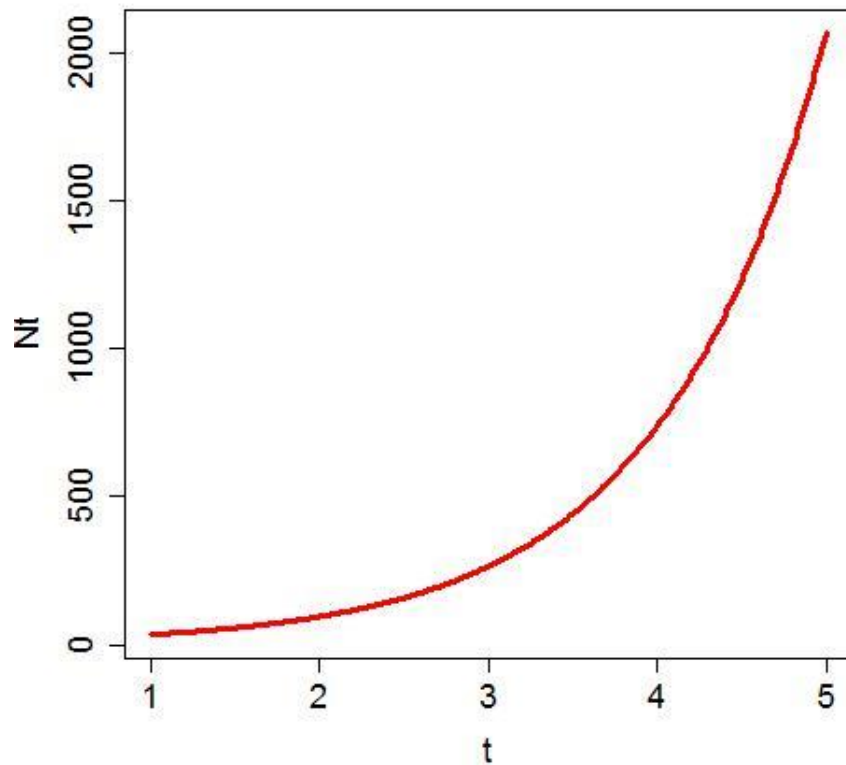
Integrated to:

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

# Exponential population growth

# Exponential growth

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

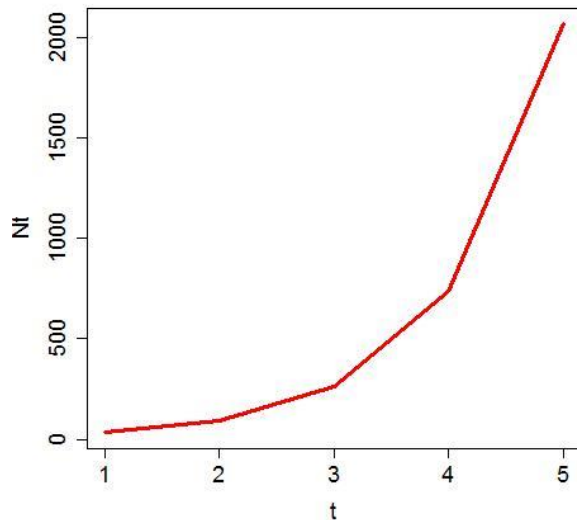


```
# Model 6, Exponential growth
t <- seq(1,5,0.01)
tn <- seq(1,length(t),1)
Nt <- rep(NA,length(t))
r <- log(2.8)
N0 <- 12
Nt[tn] <- N0*exp(r*t)
```

# Exponential growth

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

$$r = \log(\lambda)$$



```
# Model 6b, Exponential population (overlap of
# generations, constant growth)
# Finite rate of increase
t <- c(1:5)
Nt <- rep(NA, length(t))
b <- 2    # birth rate per individual
d <- 0.2  # death rate per individual
R <- b - d # per individual population growth rate
lambda <- 1 + R # Finite rate of increase
r <- log(lambda) # Intrinsic growth rate
N0 <- 12

Nt[t] <- N0*exp(r*t)
```

NOTE: although they are mathematically related, the geometric and exponential population growth models are based on different assumption

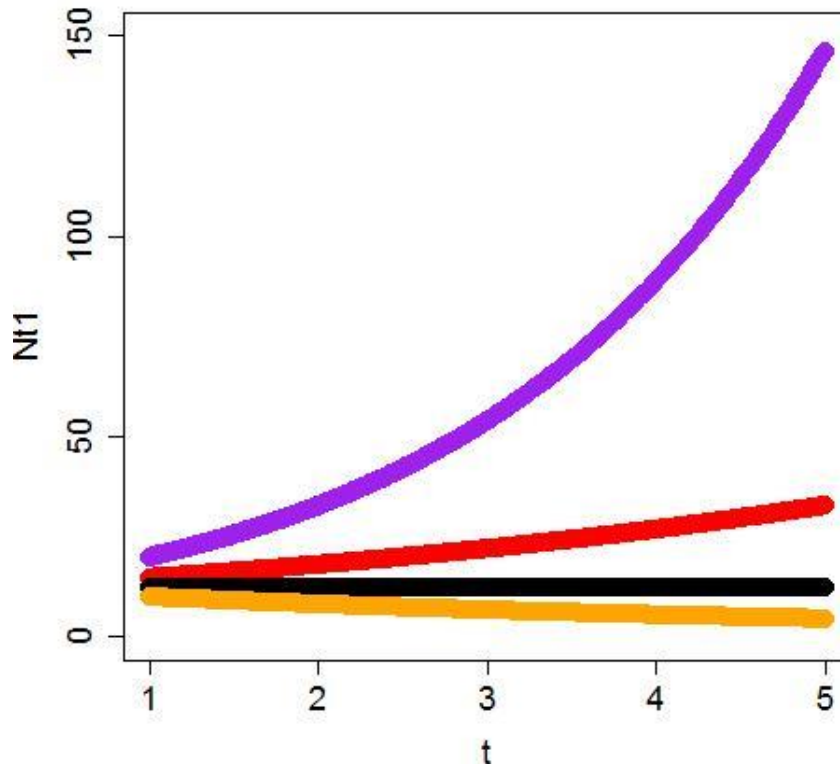
# Exponential growth

$r = 0.5$

$r = 0.2$

$r = 0$

$r = -0.2$



```
# Model 7, Exponential growth
t <- seq(1,5,0.01)
tn <- seq(1,length(t),1)
Nt1 <- rep(NA,length(t))
Nt2 <- rep(NA,length(t))
Nt3 <- rep(NA,length(t))
Nt4 <- rep(NA,length(t))
r1 <- 0.5
r2 <- 0.2
r3 <- 0
r4 <- -0.2
N0 <- 12
Nt1[tn] <- N0*exp(r1*t)
Nt2[tn] <- N0*exp(r2*t)
Nt3[tn] <- N0*exp(r3*t)
Nt4[tn] <- N0*exp(r4*t)
```

# Population doubling time

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

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

$$r = 0.4$$

$$t_{double} = 1.732868$$

Examples of exponential  
population growth?