

# Spatial Ecology

*“Populační ekologie živočichů“*

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**Spatial ecology** - describes changes in spatial pattern over time

- ▶ processes - colonisation / immigration and local extinction / emigration
- ▶ local populations are subject to continuous colonisation and extinction
- ▶ wildlife populations are fragmented

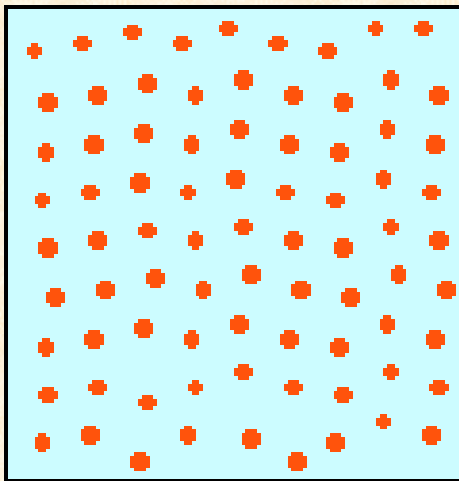
Two approaches:

- ▶ landscape ecology - focus on communities at large geographic scale
- ▶ metapopulation ecology - focus on metapopulations

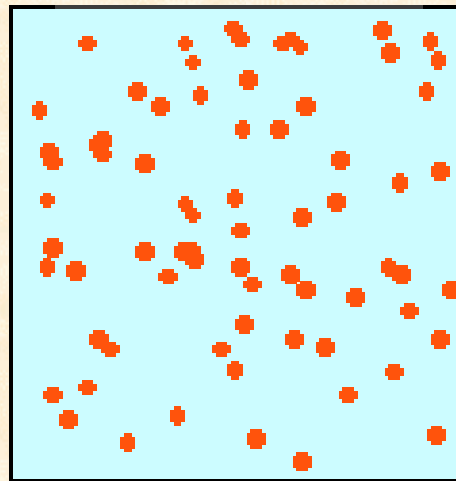
**Metapopulation** - a population consisting of many local populations (sub-populations) connected by migrating individuals with discrete breeding opportunities (not patchy populations)

# Distribution of individuals

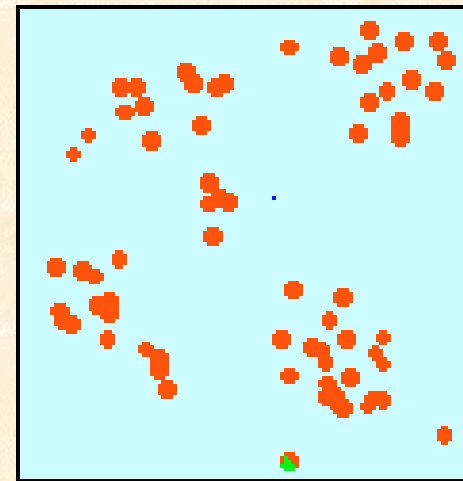
- ▶ population density changes also in space
- ▶ for migratory animals (salmon) seasonal movement is the dominant cause of population change
- ▶ movement of individuals between patches can be density-dependent
- ▶ distribution of individuals have three basic models:



Regular



Random



Aggregated

- ▶ most populations in nature are aggregated (clumped)



# Regular distribution

- ▶ regular distribution is described by hypothetical uniform distribution

$$P(x) = \frac{1}{n}$$

$n$  .. is number of samples

$x$  .. is category of counts (0, 1, 2, 3, 4, ...)

- ▶ all samples have similar probability

- ▶ mean:  $\mu = \frac{1}{2}(n + 1)$

- ▶ variance:  $\sigma^2 = \frac{1}{12}(n^2 - 1)$

- ▶ for regular distribution:  $\mu > \sigma^2$

# Random distribution

- ▶ random distribution is described by hypothetical Poisson distribution

$$P(x) = \frac{\mu^x e^{-\mu}}{x!}$$

$\mu$  .. is expected value of individuals

$x$  .. is category of counts (0, 1, 2, 3, 4, ...)

- ▶ probability of  $x$  individuals at a given area usually decreases with  $x$
- ▶ observed and expected frequencies are compared using  $\chi^2$  statistics

- ▶ for random distribution:  $\mu = \sigma^2$

# Aggregated distribution

- ▶ aggregated distribution is described by hypothetical negative binomial distribution

$$P(x) = \left(1 - \frac{\mu}{k}\right)^{-k} \frac{(k+x-1)!}{x!(k-1)!} \left(\frac{\mu}{\mu+k}\right)^x$$

$\mu$  .. is expected value of individuals

$x$  .. is category of counts (0, 1, 2, 3, 4, ...)

$k$  .. degree of clumping, the smaller  $k$  ( $\rightarrow 0$ ) the greater degree of clumping

- ▶ approximate value of  $k$ :
- ▶ exact value is estimated iteratively
- ▶ for aggregated:  $\mu < \sigma^2$

$$k \approx \frac{\mu^2}{\sigma^2 - \mu}$$

## Coefficient of dispersion (CD)

CD < 1 ... uniform distribution

CD = 1 ... random distribution

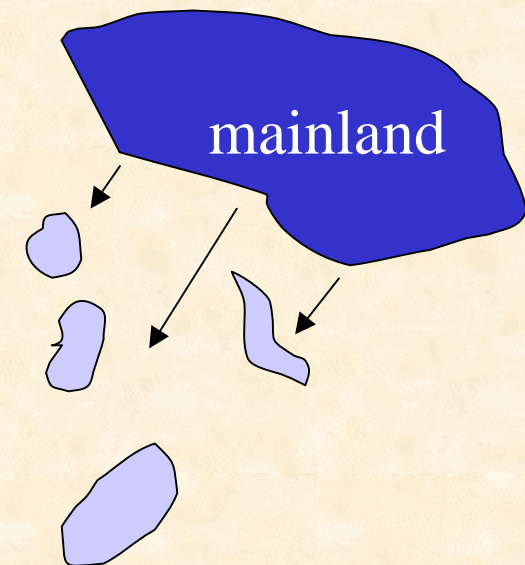
CD > 1 ... aggregated distribution

$$CD = \frac{s^2}{\bar{x}}$$



# Landscape ecology

- ▶ first model developed by MacArthur and Wilson (1967)
- ▶ the theory:
  - does not predict stable populations
  - there is ongoing colonisation and stochastic extinction
  - species composition is continually changing but the total number of species is constant
  - colonisation-extinction equilibrium
  - mainland serves as continuous source of migrants



# Species-area relationship

- ▶ larger islands/areas support more species
- ▶ Darlington's rule = tenfold increase in area result in double increase of species



$S$  .. number of species

$A$  .. island area

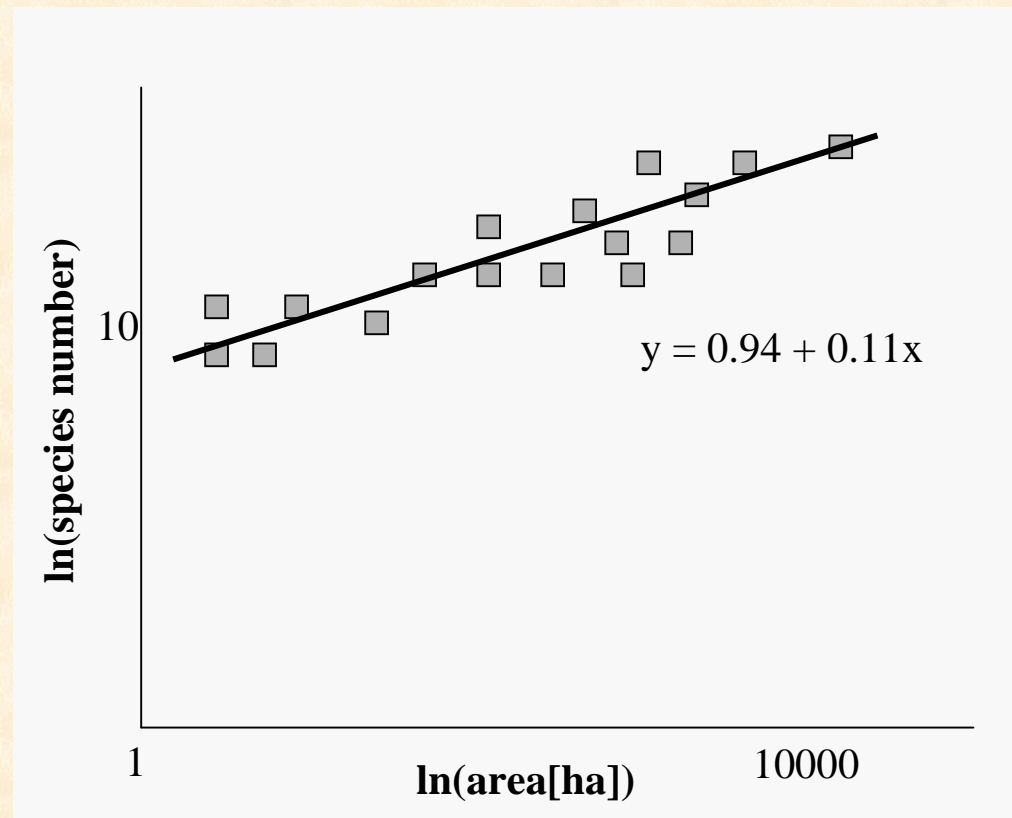
$$S = cA^z$$

$c, z$  .. constants

$$\ln(S) = \ln(c) + z \ln(A)$$

- ▶ larger area contain more habitat types
- ▶ larger habitats support larger populations (lower probability of extinction)

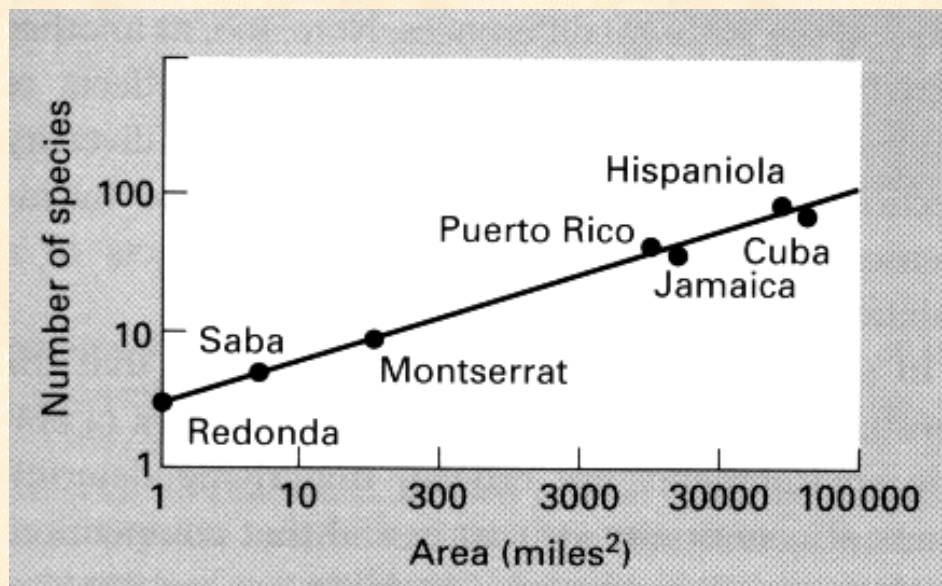
Specie-area relationship for breeding land-birds of the West Indies





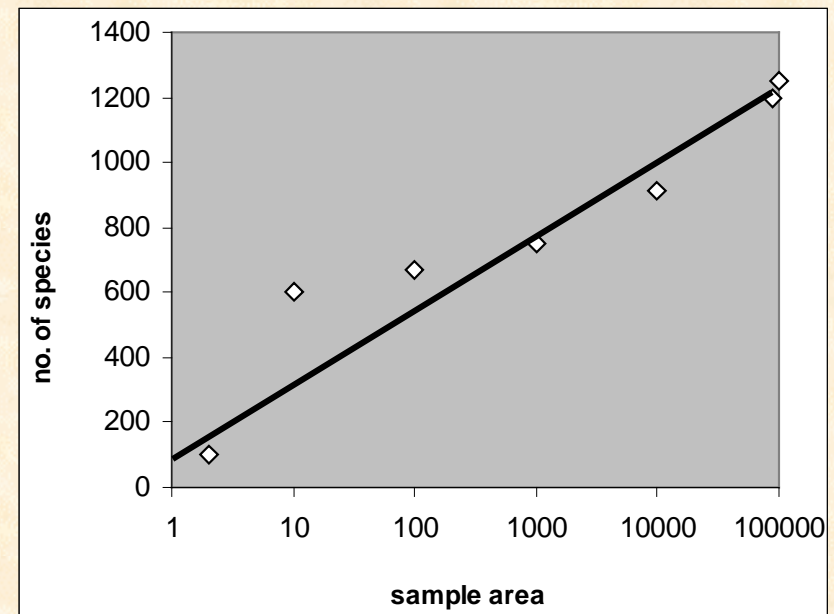
- ▶ slope of the regression line for islands ranges between 0.24-0.34 for ants, birds, plants, etc.
- ▶ species diversity is a function of sampled size and habitat diversity
- ▶ slope of linear regression ranges for inland between 0.12-0.17
- ▶ there is exchange of organisms with surrounding areas, not isolated as islands

Number of amphibians & reptiles on West Indies islands



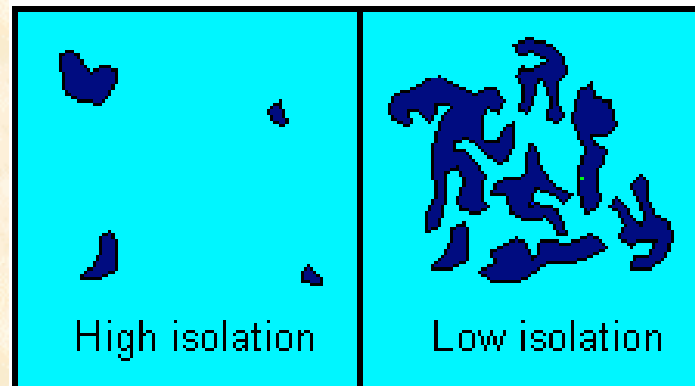
MacArthur & Wilson (1967)

Number of plant species found in sampled areas of England



# Metapopulation ecology

- ▶ Levins (1969) distinguished between dynamics of a single population and a set of local populations which interact via individuals moving among populations
- ▶ Hanski (1997) developed the theory
- ▶ the degree of isolation may vary depending on the distance among patches



- ▶ unlike growth models that focus on population size, metapopulation models concern persistence of a population - ignore fate of a single sub-population and focus on fraction of sub-population sites occupied

# Levins model

$p$  .. proportion of patches occupied

$m$  .. colonisation rate

$e$  .. extinction rate

$$\frac{dp}{dt} = mp(1-p) - ep$$

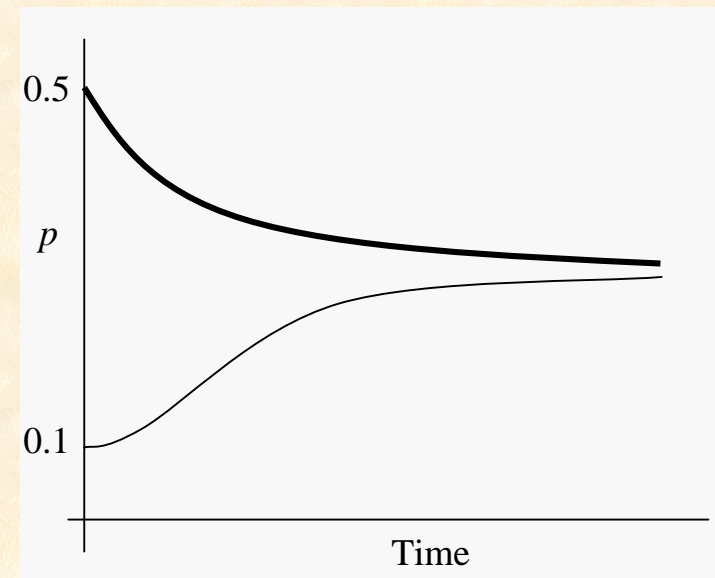
## ▶ assumptions

- sub-populations are identical in size, distance, resources, etc.
- extinction and colonisation are independent of  $p$
- many patches are available

## ▶ equilibrium is found for $dp/dt = 0$

$$p^* = \frac{m - e}{m} = 1 - \frac{e}{m}$$

- sub-populations will persist only if colonisation is larger than extinction
- all patches can not be occupied





# Hanski model - „core-satellite“

$p$  .. proportion of patches occupied

$c$  .. external colonisation rate

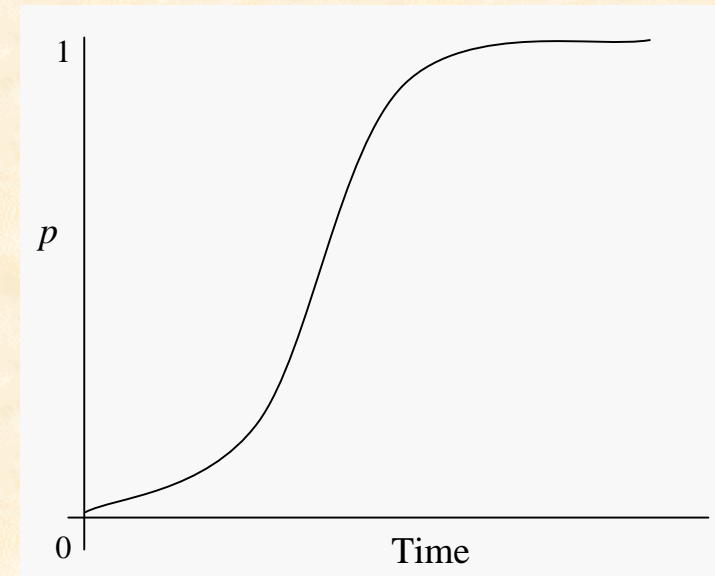
$e$  .. extinction rate

$$\frac{dp}{dt} = cp(1-p) - ep(1-p)$$

- ▶  $e$  decreases with increasing  $p$  ..  $ep(1-p)$ 
  - rescue effect - re-colonisation of sites on verge of extinction
- ▶ equilibrium is found for  $dp/dt = 0$

$$0 = (c - e)p(1 - p)$$

- if  $c > e$  .. all sites will be occupied - stable equilibrium
- if  $c < e$  .. extinction - stable equilibrium
- if  $c = e$  .. stable equilibrium



# Example 20



In a field the abundance of spiders was studied by means of 20 pitfall traps. The following counts were recorded:

0, 0, 1, 5, 7, 0, 1, 1, 4, 1, 0, 0, 2, 0, 0, 3, 1, 8, 1, 1

1. Is the distribution of spiders in the field random or aggregated?
2. If aggregated, what is the coefficient of dispersion ( $CD$ ) and the degree of aggregation ( $k$ )?

$$X^2 = \sum_{i=1}^I \frac{(x_i - \bar{x})^2}{\bar{x}}$$

```
ab<-c(0, 0, 1, 5, 7, 0, 1, 1, 4, 1, 0, 0, 2, 0, 0, 3, 1, 8, 1, 1)
table(ab)
hist(ab)

mean(ab)

chi<-sum((ab-1.8)^2/1.8);chi
1-pchisq(60.67,19)

chisq.test(ab)

var(ab)
CD<-var(ab)/mean(ab); CD

k<-mean(ab)^2/(var(ab)-mean(ab)); k

library(MASS)
fitdistr(ab,"negative binomial")
```



# Example 21

A new protected area, 48 700 ha large, is going to be established. You need to know expected number of mammal species that occur in this new area before species inventory will be performed.

1. Use information from surrounding areas to estimate the expected species richness.

Area [ha]	Species
224	24
740	39
1720	45
4304	56
10806	71
34931	80

2. The minimum number of species that a protected area must have is 90. How large you expect the new protected area must be?

```
area<-c(224, 740, 1720, 4304, 10806, 34931)
spec<-c(24, 39, 45, 56, 71, 80)
plot(area,spec)
plot(log(area),log(spec))

lm(log(spec)~log(area))

exp(2.0211+0.2352*log(48700))
```

# Example 22

There are two sub-populations of deer. One has 100 and the other 5 individuals. The first one has exploited its resources so their finite rate of population increase ( $\lambda_1$ ) is 0.8. The other has a lot of resources, therefore their  $\lambda_2 = 1.2$ . There is a possible rate of exchange ( $d$ ) between sub-populations.

1. Use discrete density-independent models to simulate fate of populations that are not connected, i.e.  $d = 0$ .
2. Simulate the dynamics of the two sub-populations for 20 years with various levels of exchange,  $d = 0.1$  to 1.

$$N_{1,t+1} = \lambda_1 N_{1,t} (1 - d) + d N_{2,t}$$

$$N_{2,t+1} = \lambda_2 N_{2,t} (1 - d) + d N_{1,t}$$



```
N12<-data.frame(N1<-numeric(1:20),N2<-numeric(1:20))  
N12[,1]<-100  
N12[,2]<-5
```

```
d=0  
for(t in 1:20) N12[t+1,]<-{  
N1<-0.8*((1-d)*N12[t,1]+d*N12[t,2])  
N2<-1.2*((1-d)*N12[t,2]+d*N12[t,1])  
c(N1,N2)}  
matplot(N12, type="l",lty=1:2)
```

```
d=0.2  
for(t in 1:20) N12[t+1,]<-{  
N1<-0.8*((1-d)*N12[t,1]+d*N12[t,2])  
N2<-1.2*((1-d)*N12[t,2]+d*N12[t,1])  
c(N1,N2)}  
matplot(N12, type="l",lty=1:2)
```

```
d=0.8  
for(t in 1:20) N12[t+1,]<-{  
N1<-0.8*((1-d)*N12[t,1]+d*N12[t,2])  
N2<-1.2*((1-d)*N12[t,2]+d*N12[t,1])  
c(N1,N2)}  
matplot(N12, type="l",lty=1:2)
```