Predation

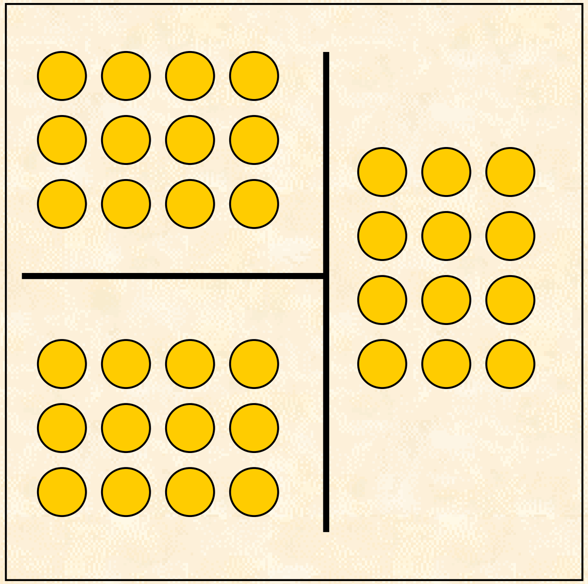
"Populační ekologie živočichů"

Stano Pekár

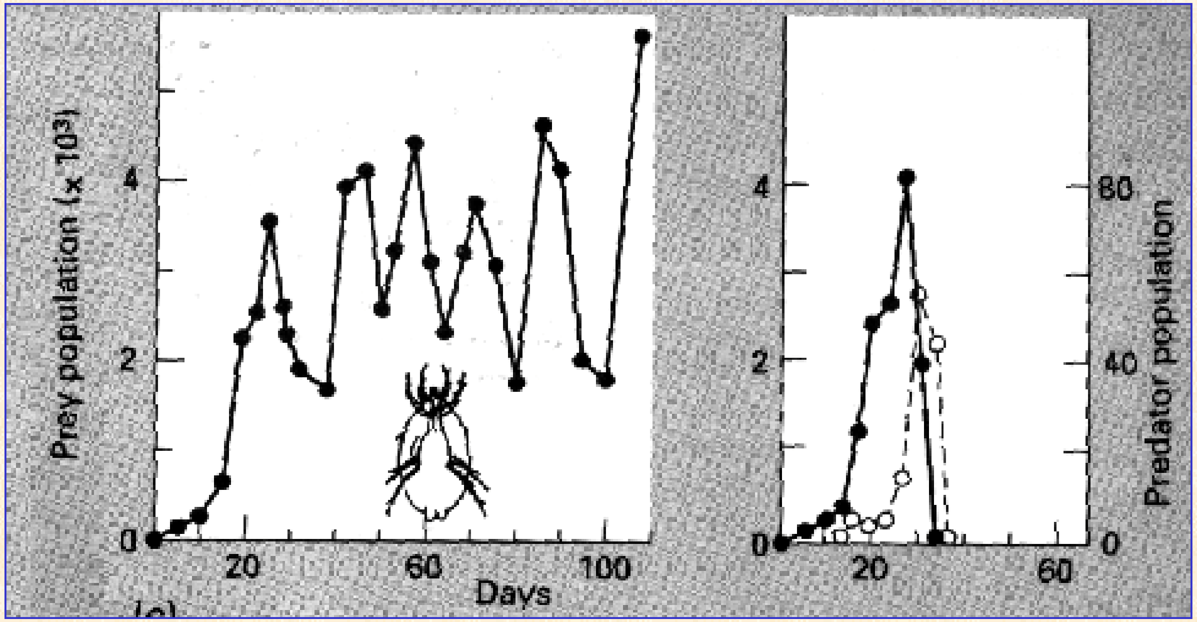
"Hide-and-seek"

- instead of concentration on profitable patches perspective predators and prey may play " hide-and-seek"
- Huffaker (1958): *Typhlodromus* fed upon *Eotetranychus* that fed upon oranges
  - *Eotetranychus* maintained fluctuating density
  - addition of *Typhlodromus* led to extinction of both

Experimental setup



Eotetranychus population dynamic   Predator-prey dynamic



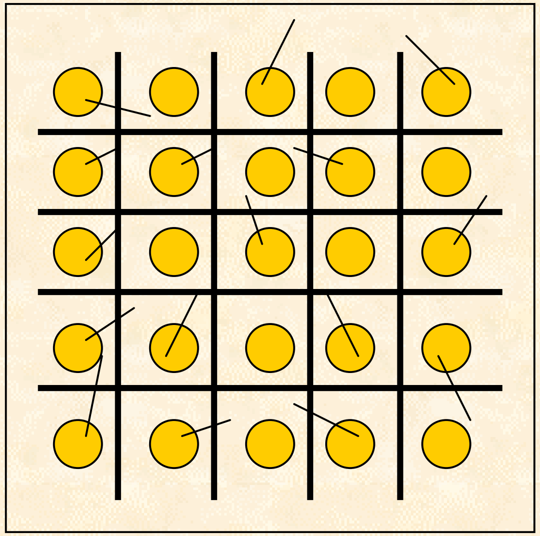
- making environment patchy

- by placing Vaseline barriers
- facilitating dispersal by adding sticks

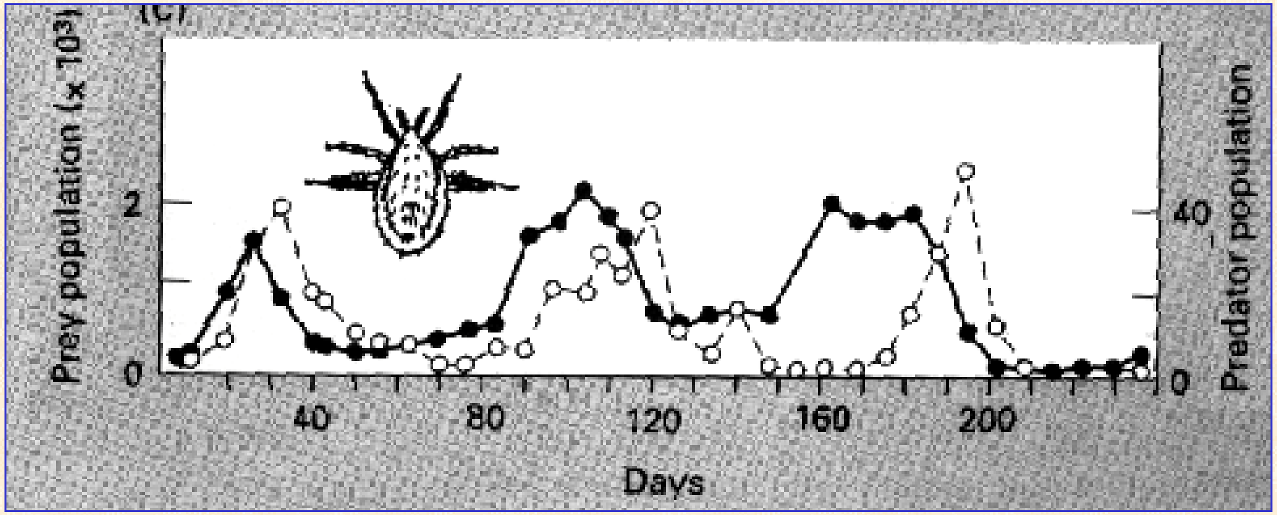
- each patch was unstable but whole cosmos was stable

- patch with prey only → rapid increase of prey
- patches with predators only → rapid death of predator
- patches with both → predator consumed prey

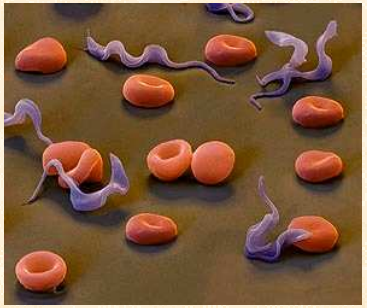
Altered experimental setup



Sustained oscillations of the predator-prey system



Host-pathogen/parasite model



- microparasites undergo population growth within host
- epidemiology

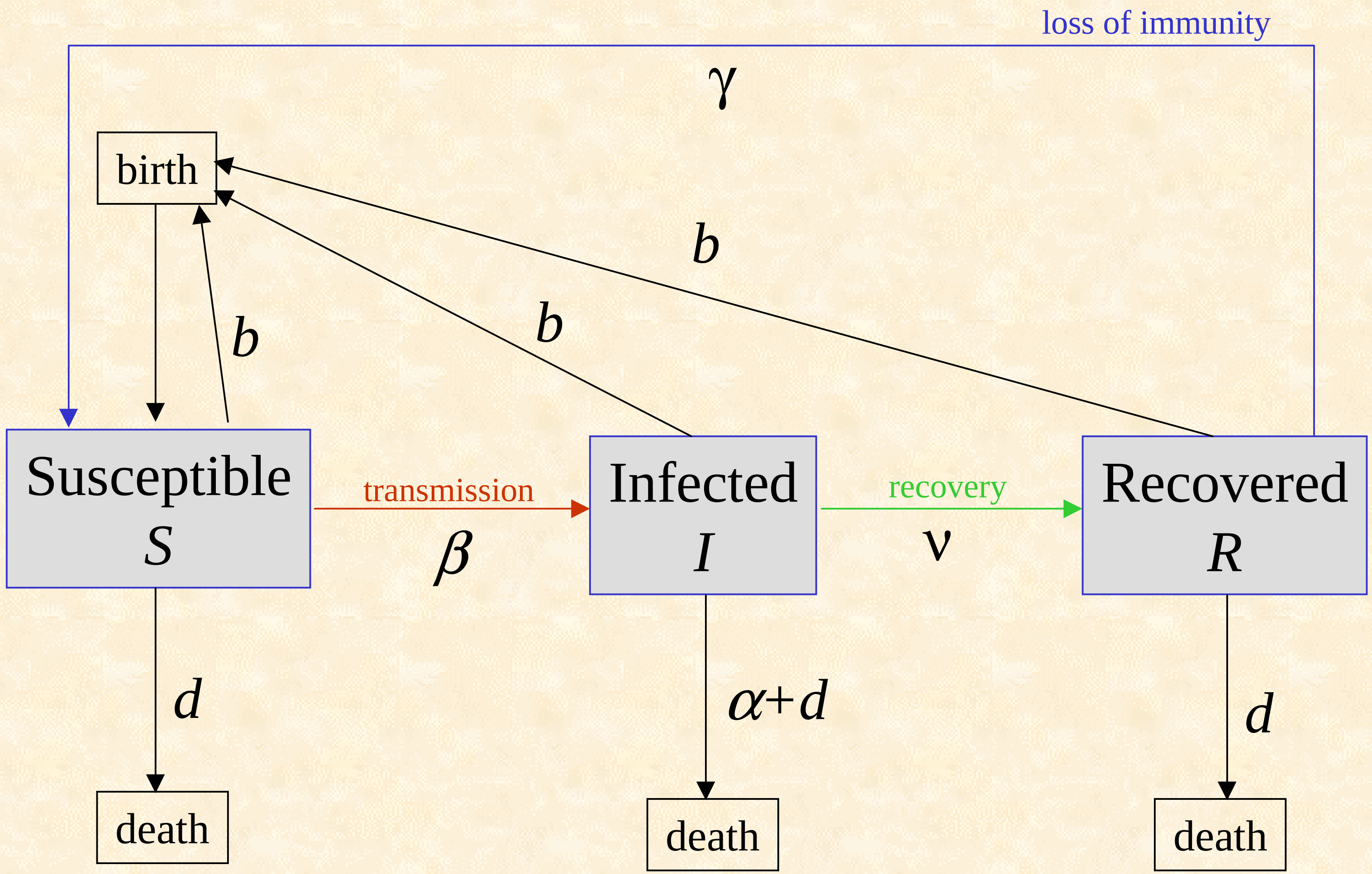
- predicts rates of disease spread
- predicts expected level of infection

- used to simulate spread of a disease (viruses, bacteria) and parasites in the human population or in the biological control
- model suggested by Kermack & McKendrick (1927), later developed by Anderson & May (1980, 1981)

- 3-component system: susceptible (S), infected (I) and recovered/immune (R) individuals
- systems may include vectors (V) and pathogens (P)

- malaria is transmitted by mosquitoes, hosts become infected only when they have contact with the vector
- the number of vectors carrying the pathogens is important
- such system is further composed of uninfected and infected vectors

- recovered hosts may have long-life immunity
- transmission might be vertical, horizontal or both



$N = S + I + R$ N .. total population of host

SIR model

b .. host birth rate
=1/host life-span
d .. host mortality due to other causes
α .. disease-induced mortality
β .. transmission rate
γ .. rate of loosing immunity
= 1/disease duration
ν .. recovery rate of infected hosts

$$\frac{dS}{dt} = bN - dS - \beta SI + \gamma R$$

$$\frac{dI}{dt} = \beta SI - (d + \alpha + \nu)I$$

$$\frac{dR}{dt} = \nu I - (d + \gamma)R$$

- βS.. density-dependent transmission function
- R = dead + resistant individuals
- prevalence =1/N

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$$

$$\frac{dN}{dt} = rN - \alpha I$$

where $r = b - d$

Disease outbreaks

- outbreak (epidemics) will occur if $S > \dfrac{\gamma}{\beta}$ i.e. when density is high

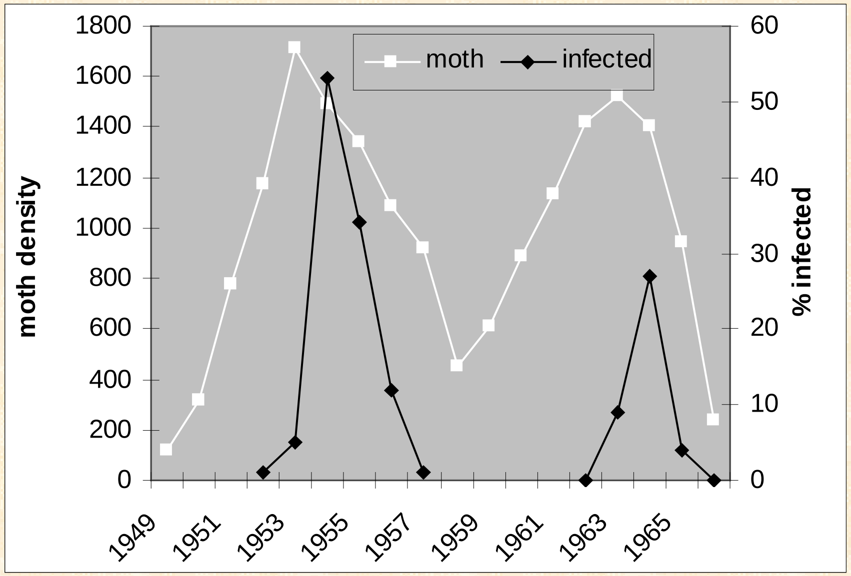
- making the population size small will halt the spread

- vaccination of *S* will stop disease spread if $S < \dfrac{\gamma}{\beta}$

- fast biocontrol effect is achieved only with viruses with high β

- low host population is achieved with pathogens with lower β

Population dynamic of a moth and the associated granulosis virus.



Example 18

Develop an optimal foraging model for a predator (shrew) that minimises time for prey capture - it attempts to acquire most food (worms or beetles) in the shortest time. Find under which conditions his foraging strategy is optimal if you know that handling time of a worm is 10 s, handling time of a beetle is 90 s, abundance of worms is 0.005-0.03 per sec and abundance of beetles is 0.0025-0.06 per sec.

a_w .. abundance of worms per second
a_b .. abundance of beetles per second
T_s .. searching time
T_h .. handling time
p .. probability of being a prey
t_w .. handling time of a single worm = 10
t_a .. handling time of a single beetle = 90

Shrew moves through a habitat with both worms and beetles. The total foraging time (T) = searching + handling time

$$T = T_s + T_h$$

Searching time: the more prey, the shorter time to find it:

$$T_s = \frac{1}{a_w + a_b}$$

The probability that shrew encounters a worm is $p_w = \frac{a_w}{a_w + a_b}$

Handling time for worms is $T_h = \frac{a_w}{a_w + a_b} \times t_w$

and for beetles $T_h = \frac{a_b}{a_w + a_b} \times t_b$

The average time to find and capture a prey is

$$T = \frac{1}{a_w + a_b} + \frac{a_w}{a_w + a_b} \times t_w + \frac{a_b}{a_w + a_b} \times t_b$$

```
aw<-seq(0.005,0.03,0.001)
ab<-aw
t1<-1/(aw+ab)+10*aw/(aw+ab)+90*ab/(aw+ab)
plot(aw,t1)

ab<-0.5*aw
t2<-1/(aw+ab)+10*aw/(aw+ab)+90*ab/(aw+ab)
lines(aw,t2)

ab<-2*aw
t3<-1/(aw+ab)+10*aw/(aw+ab)+90*ab/(aw+ab)
lines(aw,t3,lty=2)
```

Example 19

Three diseases has occurred in a population: measles, cholera and mononucleosis. You know values of the following parameters:

	b	d	alpha	beta	gamma	v
measles	0.01	0.01	0.02	0.01	0.01	0.75
cholera	0.01	0.01	0.03	0.05	0.1	0.8
mononucleosis	0.01	0.01	0.25	0.05	0.01	0.2

Use the SIR model with 999 susceptible and 1 infected individual at the start and determine:

1. Which disease results in epidemics (more than 50% infected)?
2. Will any of the diseases persist in a population?
3. If so what proportion of population will be infected?
4. When the epidemics will reoccur?

Use POPULUS Infectious microparasitic disease model with density-dependent transmission.