Excercise 5

You observe a population decrease in a duck species. You perform a life-history study with post-breeding census and find that duck has birth-pulse breeding. You obtain the following data:

x	lx	mx	mortality
0	1	0	racoons
1	0.2	2	foxes
2	0.1	3	parasite
3	0.03	5	virus
4	0.002	1	old age
5	0		

▸ Make simple population projections in POPULUS.
▸ Create transition matrix in R and find stable class distribution and reproductive values.
▸ Perform sensitivity analysis to identify important processes.
▸ Suggest a conservation plan.

```
A<-matrix(c(0.4,1.5,1.5,0.07,0,
0.2,0,0,0,0,
0,0.5,0,0,0,
0,0,0.3,0,0,
0,0,0,0.07,0),nrow=5,byrow=T);A

L<-eigen(A)
L1<-max(Re(L$values))
w<-Re(L$vectors[,1]);w
scd<-w/sum(w);scd

M<-eigen(t(A));M
v<-Re(M$vectors[,1]);v
RV<-v/v[1];RV

s<-v%*%t(w)
ss<-s/as.numeric(v%*%w);ss

e<-ss*(A/L1);e
```

Excercise 6

A mouse species has spread dramatically. You perform a life-history study and find that it breeds continuously. So you distinguish age classes based upon 3-months intervals. You obtain the following data:

x	lx	mx
0	1	0
1	0.8	5
2	0.5	12
3	0.3	4

▸ Estimate R_0 and T.

▸ Predict how the population size would change in another 10 years using initial population structure (2, 30, 10, 5) using transition matrix from POPULUS.

▸ How will r change if you subsequently halve each age-specific survival?

▸ Suggest a management plan to control mouse population.

```
x<-c(0,1,2,3)
lx<-c(1,0.8,0.5,0.3)
mx<-c(0,5,12,4)
R0<-sum(lx*mx);R0

T<-sum(x*lx*mx)/R0;T

A<-matrix(c(6.15,6.51,1.8,0,
0.72,0,0,0,
0,0.62,0,0,
0,0,0.37,0),nrow=4,byrow=T);A

L<-eigen(A); r<-log(max(Re(L$values))); r

N0<-c(2,30,10,5)
N1<-A%*%N0;N1

years<-10
Nt<-matrix(0,nrow=nrow(A),ncol=years+1)
Nt[,1]<-N0
for(i in 1:years) Nt[,i+1]<-A%*%Nt[,i]
matplot(0:years,t(Nt),type="l")
legend(2,4e+9,c(1:4),lty=1:4,col=1:4)
```
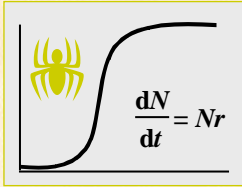
```
A1<-replace(A,c(1,2),c(3.07,0.36))
L1<-eigen(A1); log(max(Re(L1$values)))

A2<-replace(A,c(5,7),c(3.25,0.31))
L2<-eigen(A2); log(max(Re(L2$values)))

A3<-replace(A,c(9,12),c(0.9,0.18))
L3<-eigen(A3); log(max(Re(L3$values)))
```

$$\frac{\mathrm{d}N}{\mathrm{d}t} = Nr$$

Degree-day Models

„Populační ekologie živočichů"

Stano Pekár

Linear model

▸ model is based on the assumption that development rate is a linear function of temperature

▸ valid for the region of moderate temperatures (15-25°)

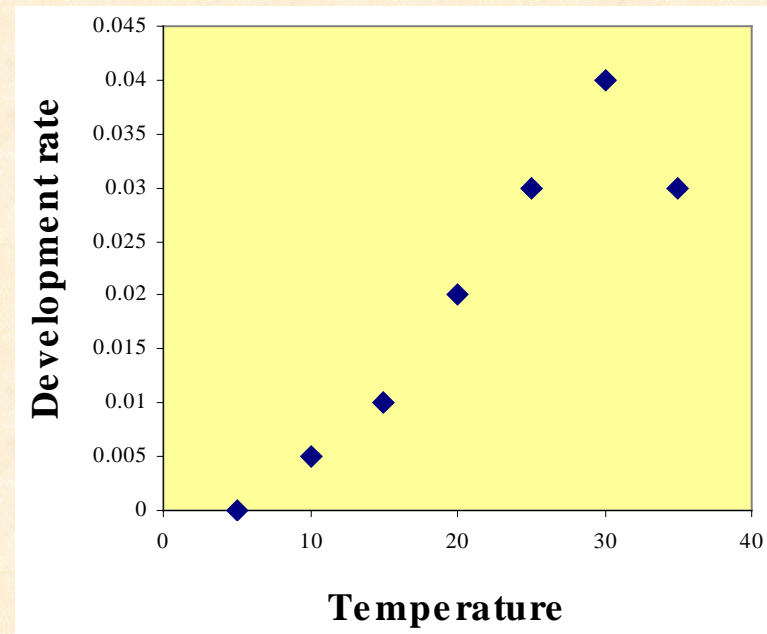▸ at low temperatures organisms die due to coldness, and at high temperatures organisms die due to overheating

T .. <u>development time</u> (days)
v .. <u>rate of development</u> = $1/T$
t_{min} .. <u>lower temperature limit</u>
.. temperature at which development rate = 0

ET .. <u>effective temperature</u> .. developmental temperature = $t - t_{min}$
S .. <u>degree-days</u> .. number of days required to complete development
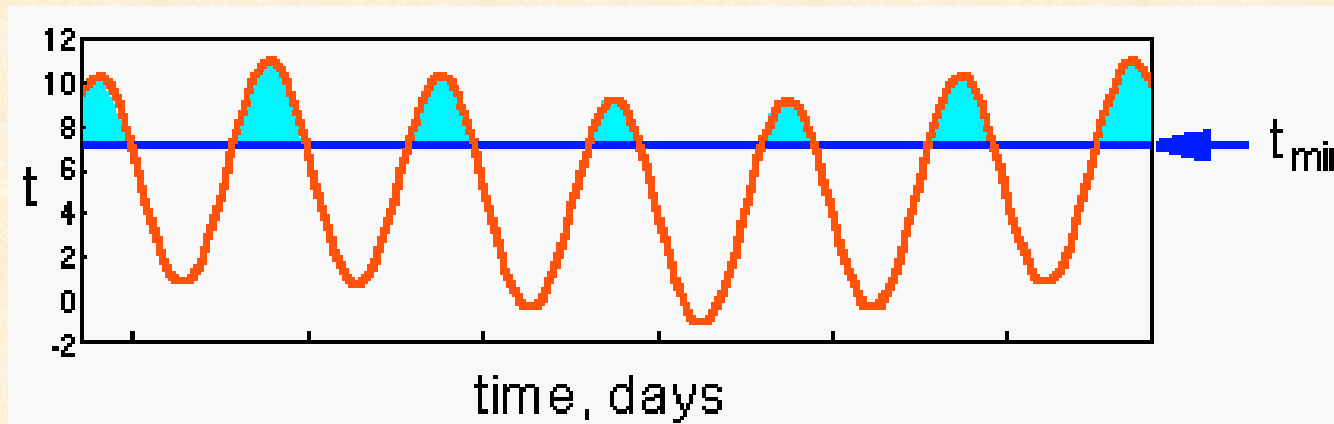.. do not depend on temperature = $T*ET$

t_{min} and *S* can be estimated from the regression line of $v = a + b$

t_{min} :
$$a + bt_{min} = 0 \implies \boxed{t_{min} = -\frac{a}{b}}$$

S :
$$S = T(t - t_{min}) = T\left(t + \frac{a}{b}\right)$$

$$T = \frac{1}{v} = \frac{1}{a + bt} \implies S = \frac{t + a/b}{a + bt} \implies \boxed{S = \frac{1}{b}}$$

▸ accumulated degree-days (S) are equal to area under temperature curve restricted to the interval between current temperature and t_{min}

Non-linear models

▸ for temperatures between t_{min} and t_{max} (upper threshold)
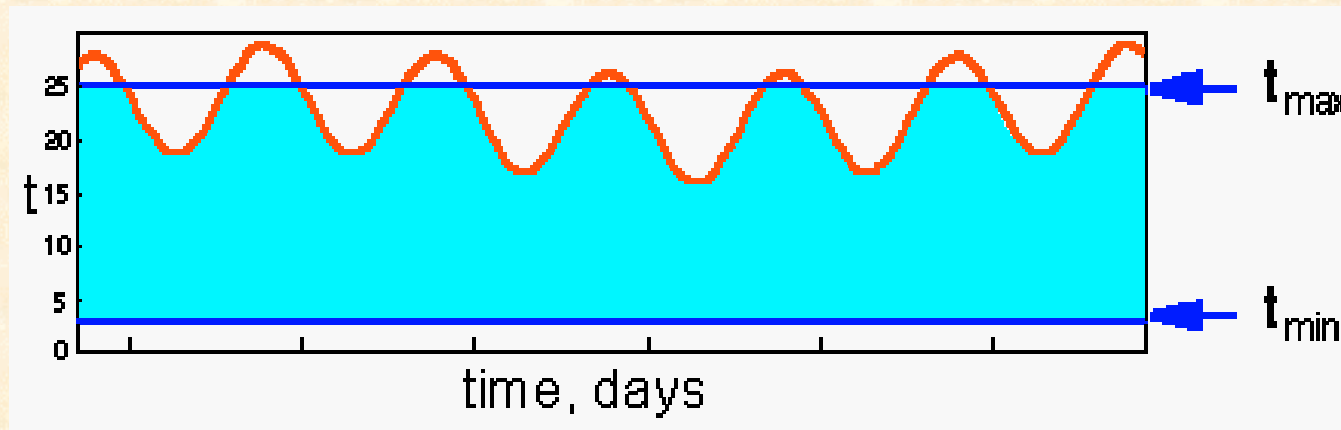
▸ several different non-linear models (Briere, Lactin, etc.)

▸ allow to estimate t_{opt} (optimum temperature)

▸ easy to interpret for experiments with constant temperature

▸ instead of using average temperature, use actual temperature because below and above *ET* model is non-linear

Briere et al. (1999)

$$v = a \times t \times (t - t_{min}) \times \sqrt{t_{max} - t}$$

v .. rate of development $(=1/T)$
t .. experimental temperature
t_{min} .. low temperature threshold
t_{max} .. upper temperature threshold

Optimum temperature:

$$t_{opt} = \frac{4t_{max} + 3t_{min} + \sqrt{16t_{max}^2 + 9t_{min}^2 - 16t_{min}t_{max}}}{10}$$

▸ parameters are estimated using non-linear regression

Lactin et al. (1995)

$$v = e^{\rho t} - e^{(\rho t_m - \frac{t_m - t}{\Delta})} + \lambda$$

v .. rate of development
t .. experimental temperature
t_m, Δ, ρ, λ .. constants

t_{max} and t_{min} can be estimated from the formula:
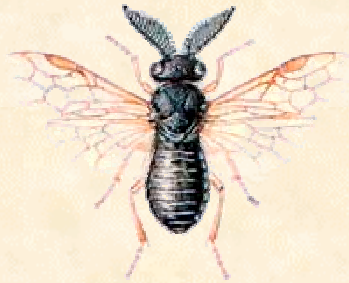
$$0 = e^{\rho t} - e^{(\rho t_m - \frac{t_m - t}{\Delta})} + \lambda$$

t_{opt} can be estimated from the first derivative:

$$0 = \rho e^{\rho \times T} - \left(\rho + \frac{1}{\Delta} \right) \times e^{(\rho T_m - \frac{T_m - T}{\Delta})}$$

Excercise 7

In the laboratory the development of *Diprion pini* was studied. Seven temperatures were used. For each temperature the development time (T) of the complete development were recorded:

t (°C)	T
5	-
10	200
15	100
20	60
25	40
30	30
35	35

Estimate the minimum development temperature (t_{min}) and the degree-days (S) using the linear model.

```
t<-c(5,10,15,20,25,30,35)
T<-c(0,200,100,60,40,30,35)
v<-1/T
m<-lm(v~t,subset=2:6)
m

abline(m)

0.010667/0.001433
1/0.001433
```

A study on aphids, *Myzus persicae,* revealed that $t_{min} = 10$ and $S = 100$. The aphids just laid eggs. Average day temperatures during the following two weeks were as follows:

15, 18, 25, 23, 24, 18, 17, 15, 18, 15, 22, 25, 26, 21.

Estimate on which day the development of aphids was complete?

```
t<-c(15, 18, 25, 23, 24, 18, 17, 15, 18, 15, 22, 25, 26, 21)
ET<-t-10
sum(ET)
sum(ET[1:10])
sum(ET[1:11])
```

Excercise 9

Effect of temperature on the development of *Nephus includens* was studied in the laboratory using a range of temperatures.

t	T
18	23.5
20	18.5
22	13
25	7.3
28	5.5
30	5
32	10.9

Use Briere's and Lactin's model to find models of development against temperature and to estimate optimum temperature.
Plot the estimated models to the data.

```
t<-c(18,20,22,25,28,30,32)
T<-c(23.5,18.5,13,7.3,5.5,5,10.9)
v<-1/T

m1<-nls(v~exp(rho*t)-exp(rho*Tm-(Tm-t)/delta)+lambda,
start=c(rho=0,Tm=30,delta=1,lambda=0))
summary(m1)

library(rootSolve)
topt1<-uniroot(function(x) 0.01*exp(0.01*x)-
(0.01+1/0.7)*exp(0.01*33.7-(33.7-x)/0.7),lower=0,upper=40); topt1

x<-seq(15,40,0.1)
plot(t,v,xlim=c(10,35),ylim=c(0,0.25))
lines(x,predict(m1,list(t=x)))

m2<-nls(v~a*t*(t-tmin)*sqrt(tmax-t), start=c(a=0.1,tmin=10,tmax=35))
summary(m2)
topt2<-(4*32.6+3*17+sqrt(16*32.6^2+9*17^2-16*32.6*17))/10; topt2
lines(x,predict(m2,list(t=x)),lty=2)
```