Nonlinear models

Bayesian statistics 8 – dynamic and nonlinear model fitting

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Things that we learned the last time

- logistic regression with $y_i \sim \mathcal{B}(n, p_i)$ with $\text{logit}(p_i) = \log(\frac{p_i}{1-p_i}) = a + bx_i$ or $\gamma(x_i - \mu_x)$ which is equivalent to $p_i = \text{logistic}(a + bx_i) = \frac{\exp(a+bx_i)}{1+\exp(a+bx_i)} = \frac{1}{1+\exp(-(a+bx_i))}$

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- "logistic ANOVA" $p_i = \text{logistic}(\alpha + \beta_1 x_{1i} + \beta_2 x_{2i} + \beta_3 x_{3i})$. Here the logistic function maps $(-\infty, +\infty) \to [0, 1]$.

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- "logistic ANOVA" $p_i = \text{logistic}(\alpha + \beta_1 x_{1i} + \beta_2 x_{2i} + \beta_3 x_{3i})$. Here the logistic function maps $(-\infty, +\infty) \to [0, 1]$.
- We can also want to use the logistic function to *model a known curve*, $y_i = f(x_i) + \epsilon_i$ or $y_i = f(t_i) + \epsilon_i$

Organism growth basics: von Bertalanffy

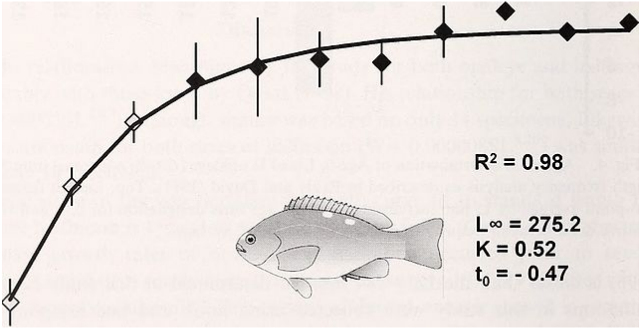

Figure 1: Von Bertalanffy growth curve fit to Girella nigricans

$$L(t) = L_\infty(1 - \exp(-k(t_i - t_0))) + \epsilon_i$$

Connection to dynamics

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We'll do for practical another example of organismal growth, Gompertz growth (Winsor PNAS 1932).

Dynamics

$$\frac{d\ln(L)}{dt} = k(\ln(L_\infty) - \ln(L))$$

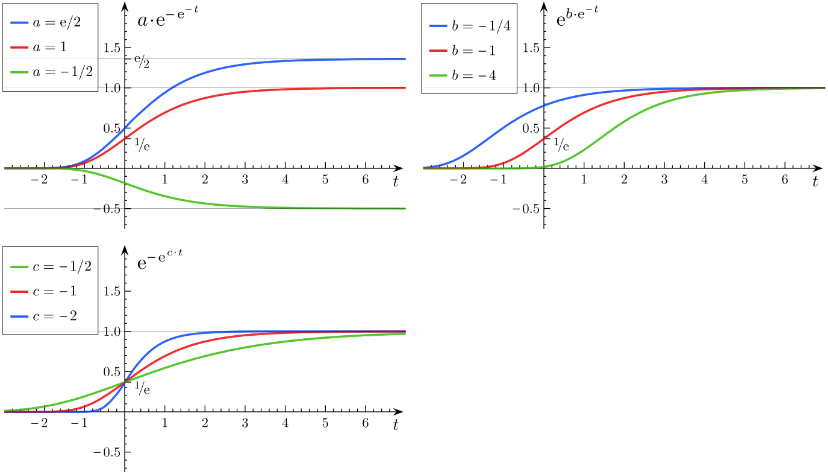
Solution

$$L(t) = ae^{-e^{b-ct}}$$

where $a = L_\infty e^1$, $b = kt_0$ and $c = k$.

Trick: note $l = \ln(L)$, solve von Bertalanffy for l, transform back.

The Gompertz growth curve is more logistic-like



Mathematical cousins of von Bertalanffy: modelling *saturation*

Monod function (microbiology) aka Michalis-Menten (chemistry) aka Holling type II (ecology) aka ...

$$f(x) = \frac{ax}{b+x}$$

Another example of connection to dynamics: logistic population growth

$N =$ population size (microbes, humans, wild boars, plants,...)

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right)$$

And the solution is...

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And the solution is...

$$N(t) = \frac{N_0 e^{rt}}{1 + N_0(e^{rt} - 1)/K}$$

If we use $t = 1, 2, 3, ...$

$$N_1 = \frac{N_0 e^{r}}{1 + N_0(e^{r} - 1)/K}, N_2 = \frac{N_1 e^{r}}{1 + N_1(e^{r} - 1)/K}, ...$$

aka Beverton-Holt model.

Two kinds of "noise" or stochasticity

Observational noise

$$y_{t+1} = N_{t+1} + \epsilon_t,\ N_t = \frac{N_t e^r}{1 + N_t(e^r - 1)/K}\ \epsilon_t \sim \mathcal{N}(0, \sigma^2) \text{ i.i.d}$$

- The effect of ϵ_t does not accumulate. ϵ_1 does not affect N_8.

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- The effect of ϵ_t does accumulate. ϵ_1 *does* affect N_8.
- *autocorrelation* between N_t values. This is a *time series* model
- Of course in real life you can have both (and sometimes it is hard to distinguish between the two)

Transforming this into a model we can fit

We need to have $y_t \sim \mathcal{D}([\text{something}])$ to be able to fit a model in jags – the data must be observed. Let's take $y_t = \ln(N_t)$. Then the previous model writes

$$y_{t+1} = y_t + r + \epsilon_t - \ln(1 + \alpha N_t),\ \epsilon_t \sim \mathcal{N}(0, \sigma^2) \text{ i.i.d}$$

with $\alpha = (e^r - 1)/K$.

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This equivalent to

$$y_{t+1} = f(y_t) + \epsilon_t\ \epsilon_t \sim \mathcal{N}(0, \sigma^2) \text{ i.i.d}$$

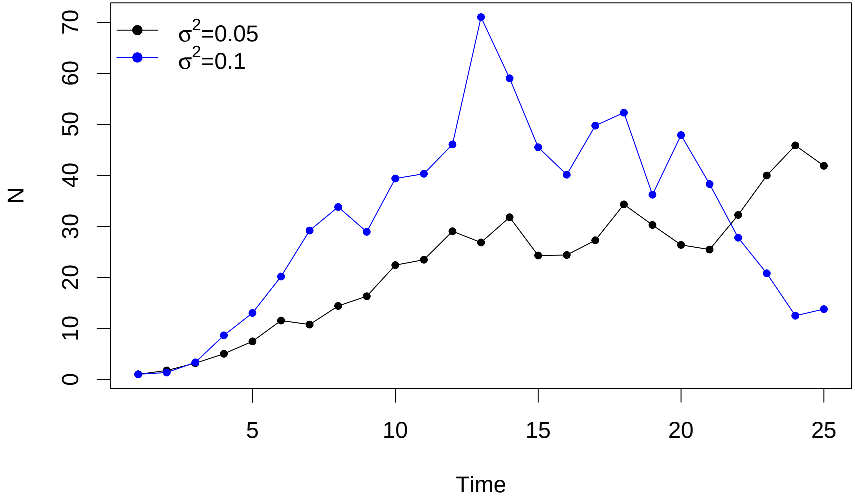
or again $y_{t+1} | y_t \sim \mathcal{N}(f(y_t), \sigma^2)$. We have our distribution!

Fitting the logistic model in discrete-time with process noise I

(you can fit the observational noise model with the solution $N(t)$ – you can't fit the process noise model solution, you have to fit the *dynamics*)

```
r=0.5
alpha=0.02
tmax=25
R=exp(r)
K=(exp(r)-1)/alpha
N_BH=N_BH1=rep(NA,tmax)
N_BH[1]=N_BH1[1]=1
for (t in 1:(tmax-1)){N_BH[t+1] =
  (exp(r+rnorm(1,0,sqrt(0.05))))*N_BH[t]/(1+alpha*N_BH[t])}
for (t in 1:(tmax-1)){N_BH1[t+1] =
  (exp(r+rnorm(1,0,sqrt(0.1))))*N_BH1[t]/(1+alpha*N_BH1[t])}
###
par(pch=20,cex=1.5)
plot(1:tmax,N_BH,type="o",ylim=range(c(N_BH,N_BH1)),xlab="Time",ylab="N")
lines(1:tmax,N_BH1,type="o",col="blue")
legend("topleft",c(expression(paste(sigma^"2","=0.05",sep="")),
                   expression(paste(sigma^"2","=0.1",sep=""))),
       col=c("black","blue"),lty=1,pch=16,bty="n")
```

Fitting the logistic model in discrete-time with process noise II



Let's fit the model

```
logistic.data <- list(logN = log(N_BH), tmax=tmax)

cat(file="logistic.growth.txt","
model {
  r ~ dnorm(2, 0.01) ## prior on r
  alpha ~ dlnorm(1, 0.01)  ## prior on alpha
  K <-(exp(r)-1)/alpha

  sigma ~ dunif(0.01,2)
  tau<-pow(sigma,-2)

  logN[1] ~ dnorm(0,1)
  N[1] <-exp(logN[1])

  #Likelihood
  for (t in 1:(tmax-1)){
  logNpred[t] <- logN[t]+ r - log(1 + alpha*N[t])
  logN[t+1] ~ dnorm(logNpred[t],tau)
  N[t+1] <- exp(logN[t+1])
  }

}
")
```

Running the model I

```r
# Inits function
inits <- function(){list(r = rnorm(1, 0, 1),
                         alpha = rlnorm(1,0,1))}

# Parameters to estimate
params <- c("r","alpha","K","sigma")

# MCMC settings
nc <- 3  ;  ni <- 2000  ;  nb <- 1000  ;  nt <- 2

# Call JAGS, check convergence and summarize posteriors
out <- jags(logistic.data, inits, params, "logistic.growth.txt", n.thin = nt,
            n.chains = nc, n.burnin = nb, n.iter = ni)
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 25
##    Unobserved stochastic nodes: 3
##    Total graph size: 183
##
## Initializing model
```

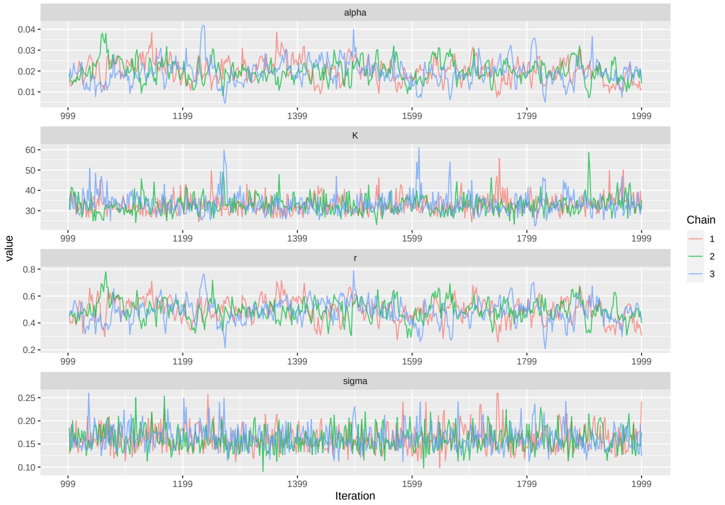
Running the model II

```
print(out, dig = 3)      # Bayesian analysis
```

```
## Inference for Bugs model at "logistic.growth.txt", fit using jags,
##  3 chains, each with 2000 iterations (first 1000 discarded), n.thin = 2
##  n.sims = 1500 iterations saved
##          mu.vect sd.vect    2.5%     25%     50%     75%   97.5% Rhat n.eff
## K         33.062   4.476  26.423  30.184  32.414  35.219  43.683 1.005  1400
## alpha      0.020   0.005   0.010   0.016   0.020   0.023   0.031 1.012   340
## r          0.492   0.081   0.329   0.440   0.492   0.544   0.649 1.010   320
## sigma      0.162   0.025   0.122   0.144   0.159   0.177   0.214 1.002   810
## deviance -18.968   2.751 -22.101 -20.989 -19.679 -17.665 -11.570 1.004  1200
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 3.8 and DIC = -15.2
## DIC is an estimate of expected predictive error (lower deviance is better).
```

Showing traceplots

```
S<-ggs(as.mcmc(out)) #R2jags
S<-filter(S,Parameter != "deviance")
ggs_traceplot(S)
```



Showing correlations (r,K) and (r,α)

```
ggs_pairs(S)
```