

Autoregressive models and simulation

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Topics

- semi-simple autoregressive models
- tips for statistical computing
- parametric bootstrapping
- the geometry of optimization
- the geometry of statistical inference

Semi-simple AR models

Brian Dennis and Taper (1994; B. Dennis et al. 2006)

```
library("ggplot2")  
theme_set(theme_bw())
```

The basic Ricker model of population dynamics:

$$N_{t+1} = N_t \exp(a + bN_t + \sigma Z_t)$$
$$Z_t \sim N(0, 1)$$

Makes ecological sense (usually expressed in ecology as $N_{t+1} = rN_t \exp(-cN_t)$). Z_t incorporates *process error*. Log-transforming makes it into a *linear autoregressive* model (linearity in the *parameters* a, b).

$$X_{t+1} = X_t + a + b e^{X_t} + \sigma Z_t$$

$a = 0, b = 0$	zero-drift Brownian motion
$a \neq 0, b = 0$	Brownian motion with drift (exp growth/decay)
$a \neq 0, b \neq 0$	density-dependent growth
$a \neq 0, b < 0$	regulation

Data from Dennis and Taper (Yellowstone grizzlies):

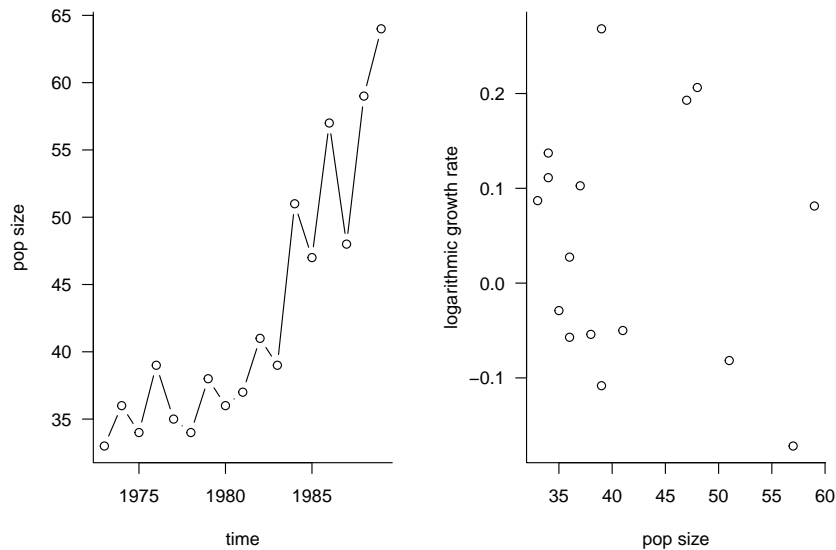
```
grizzly <- data.frame(n = c(33, 36, 34, 39, 35,  
  34, 38, 36, 37, 41, 39, 51, 47, 57, 48, 59,  
  64), t = 1973:1989)
```

Lagging variables in R is a little bit clunky; we have to drop the first and last elements respectively. `head(x, -1)` is an alternative to `x[-n]`. `lag()` doesn't work the way you think it does (!)

```
r <- log(grizzly$n[-1]/grizzly$n[-length(grizzly$n)])
```

Look at the data:

```
par(las = 1, bty = "l", mfrow = c(1, 2))
plot(n ~ t, data = grizzly, type = "b", xlab = "time",
     ylab = "pop size")
plot(grizzly$n[-length(grizzly$n)], r, xlab = "pop size",
     ylab = "logarithmic growth rate")
```



Transform data and fit:

```
## R tip: use with() to simplify extraction
## from data frames -- **never** attach()
dd <- with(grizzly, data.frame(xlag1 = log(n[-length(n)]),
                              x = log(n[-1]))))
m2 <- lm(x ~ offset(xlag1) + exp(xlag1), data = dd)
## equivalently: lm(x-xlag1~exp(xlag1),data=dd)
## (offset may be easier to read)
s2 <- sigma(m2)^2
var.unbiased <- function(m) sigma(m)^2 * df.residual(m)/nobs(m)
## D&T use MLE rather than unbiased estimate of
## variance parameters
c(coef(m2), var = var.unbiased(m2))

## (Intercept)    exp(xlag1)          var
## 0.141462270 -0.002411176  0.014524403

## test statistic
coef(summary(m2))[2, "t value"]
```

```
## [1] -0.6041122

## R tip: use update() when possible to
## simplify code
m1 <- update(m2, . ~ offset(xlag1))
c(coef(m1), var.unbiased(m1))

## (Intercept)
## 0.04139847 0.01490303
```

Parametric bootstrapping:

- for *confidence intervals*: simulate from the full model and record values. Compute quantiles.
- for *hypothesis tests*: simulate from the null model; fit the null model and the full model

Simulation

I thought I could use the `simulate()` method in R, but as it turns out I can't:

```
## simulate new data, add starting value
simfun <- function(fit, x0 = log(grizzly$n[1])) {
  cc <- coef(fit)
  a <- coef(fit)[1]
  b <- if (length(cc) == 2)
    coef(fit)[2] else 0
  sigma <- sqrt(var.unbiased(fit))
  res <- c(x0, numeric(nobs(fit) + 1))
  for (i in 2:length(res)) {
    res[i] <- res[i - 1] + a + b * exp(res[i -
      1]) + rnorm(1, sd = sigma)
  }
  res
}
```

Test simulation function:

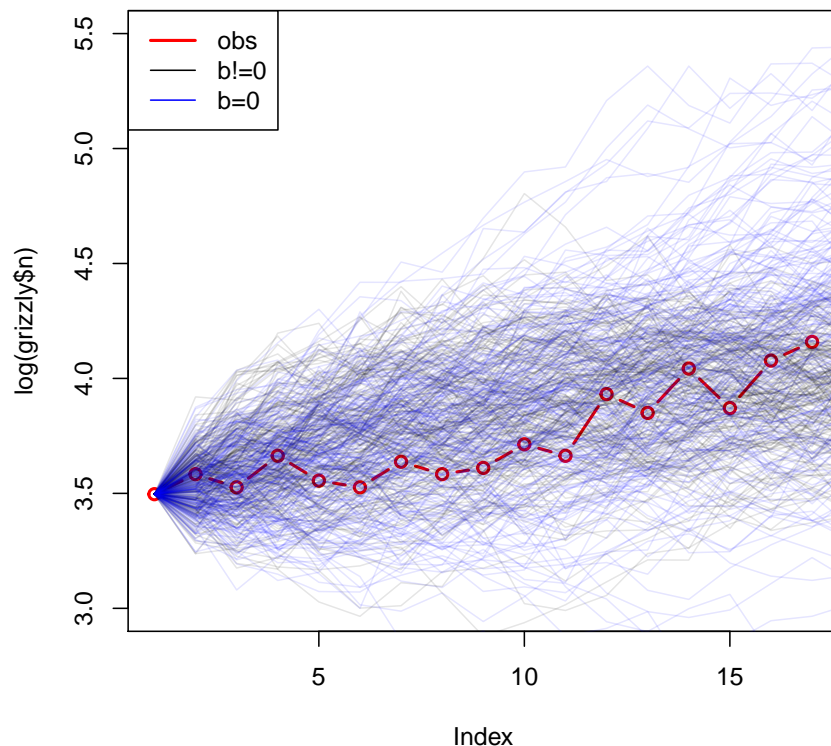
```
sim2 <- replicate(200, simfun(m2))
sim1 <- replicate(200, simfun(m1))

plot(log(grizzly$n), type = "b", ylim = c(3, 5.5),
     lwd = 2, col = 2)
matlines(sim2, col = adjustcolor("black", alpha = 0.1),
     lty = 1)
matlines(sim1, col = adjustcolor("blue", alpha = 0.1),
```

```

lty = 1)
legend("topleft", lty = 1, col = c("red", "black",
  "blue"), lwd = c(2, 1, 1), c("obs", "b!=0",
  "b=0"))

```



```

## re-fit model with new data
fitfun <- function(x, orig_fit) {
  dd <- data.frame(xlag1 = x[-length(x)], x = x[-1])
  update(orig_fit, data = dd)
}
## test:
all.equal(fitfun(log(grizzly$n), m2), m2)

## [1] TRUE

## summarize output
sumfun <- function(fit) {
  c(coef(fit), var = sigma(fit)^2 * df.residual(fit)/nobs(fit))
}
## combine all of that stuff
bootfun <- function(fit) {
  sumfun(fitfun(simfun(fit), fit))
}

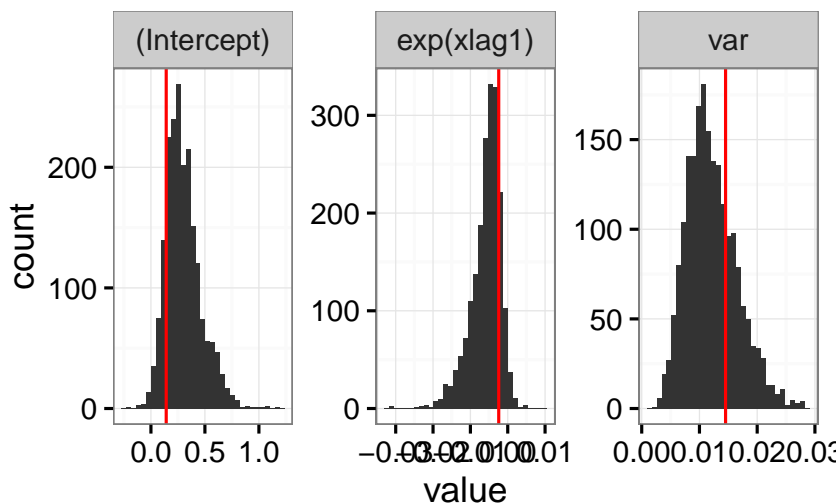
```

```

set.seed(101)
v <- t(replicate(2000, bootfun(m2)))
library("ggplot2")
theme_set(theme_bw())
library("reshape2")
mv <- melt(v)
obsvals <- data.frame(Var2 = c("(Intercept)",
  "exp(xlag1)", "var"), value = sumfun(m2))
ggplot(mv, aes(value)) + facet_wrap(~Var2, scale = "free") +
  geom_histogram() + geom_vline(data = obsvals,
  colour = "red", aes(xintercept = value))

## 'stat_bin()' using 'bins = 30'. Pick
## better value with 'binwidth'.

```



```

## compare estimates
t(apply(v, 2, quantile, c(0.025, 0.975)))

##              2.5%      97.5%
## (Intercept)  0.043354116 6.757800e-01
## exp(xlag1)   -0.016377337 5.957045e-05
## var          0.005109054 2.192644e-02

confint(m2)

##              2.5 %      97.5 %
## (Intercept) -0.2204499 0.50337446
## exp(xlag1)  -0.0109716 0.00614925

```

Should draw a picture ...

Geometry of optimization (Press et al. 1994)

- need to find point estimate (best parameters), or get close
- frequentist MLE, Bayesian maximum *a posteriori* (mode of posterior distribution)
- geometric analogies; hill-climbing
- simplest cases: use derivatives
 - Newton-Raphson (good in theory, but fragile)
 - conjugate gradients (method="CG" in R optim)
 - quasi-Newton (method="BFGS" in R optim)
- derivatives can be expensive, fragile
 - Nelder-Mead (method="Nelder-Mead")
 - BOBYQA (nloptr package)
- *complications*: noisy surfaces
 - stochastic *global* optimizers: simulated annealing, genetic algorithms, differential evolution
- *complications*: multiple peaks
 - repeated starts
 - stochastic global optimization
- similar geometric issues apply to MCMC

Geometry of inference (Bolker 2008, ch. 6-7)

- Wald intervals: quadratic
- profile confidence intervals
- marginal intervals

References

- Bolker, Benjamin M. 2008. *Ecological Models and Data in R*. Princeton, NJ: Princeton University Press.
- Dennis, B., J. M Ponciano, S. R Lele, M. L Taper, and D. F Staples. 2006. "Estimating Density Dependence, Process Noise, and Observation Error." *Ecological Monographs* 76 (3): 323–41.
- Dennis, Brian, and Mark L. Taper. 1994. "Density Dependence in Time Series Observations of Natural Populations: Estimation and Testing." *Ecological Monographs* 64 (2): 205–24. doi:10.2307/2937041.
- Press, William H., Saul A. Teukolsky, William T. Vetterling, and Brian P. Flannery. 1994. *Numerical Recipes in C: The Art of Scientific Computing*. Cambridge University Press. <http://www.nr.com/oldverswitcher.html>.