

## 1. Serial correlation simulation (25 points)

Examine and load the function `ARcorSim()` from the file `ARcorSim.R`. Use this function along with `summary()` to calculate the power for `nsim=1000`, `n=25`, and  $\beta_1 = 0$  over the set of “ar” values of 0, 0.2, 0.4, and 0.8 for both  $\beta_0 = 0$  and  $\beta_0 = 0.2$ . Turn in a plot with power on the y-axis, “ar” on the x-axis, and separate curves for the two intercept values. Use `text()` to label the curves.

```
# Get simulation class functions and simulator function
source("http://www.stat.cmu.edu/~hseltman/402/R/SimClass.R")
source("http://www.stat.cmu.edu/~hseltman/402/R/ARcorSim.R")

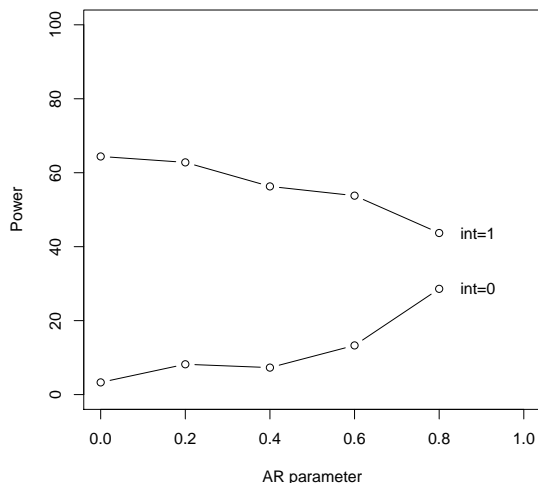
# The efficient way to make multiple calls to ARcorSim (for
# each ‘‘ar’’ value) is to make a ‘‘wrapper’’ function and
# use sapply(). The wrapper places the variable (ar) in
# the first argument position because the apply functions
# send data to that position of the specified function.
# (It’s OK to use a for loop here, but for serious large-scale
# work, its worth learning apply().)
cs=function(ar, beta0=0)
  return(summary(ARcorSim(nsim=1000, n=25, b=c(beta0,0), ar=ar))$power[1]*100)

ars=seq(0,0.8,0.2) # desired values of ‘‘ar’’
# Power values when beta0=0:
p0=sapply(ars, cs)
# Power values when beta0=0.2
p1=sapply(ars, cs, beta0=0.2)

# Create the plot:
plot(ars, p0, type="b", xlab="AR parameter", ylab="Power",
      xlim=c(0,1), ylim=c(0,100),
      main="Robustness of Intercept Estimate with Autocorrelated Error")
lines(ars, p1, type="b")
text(0.85, p0[length(ars)], "int=0", adj=0)
text(0.85, p1[length(ars)], "int=0.2", adj=0)

# Store the plot in a file:
dev.copy(pdf,"HW2Pr1.pdf"); dev.off()
```

**Robustness of Intercept Estimate with Autocorrelated Error**



Also turn in a brief statement of what you can learn about the robustness of regression analysis for estimation of the intercept under violation of the independent errors assumption through serial ar1 correlation.

When  $\beta_0 = 0$  we can see that the type-1 error rate is correct (5%) when there is no serial correlation, but rises considerably as the correlation rises. When  $\beta_0 = 0.2$  we can see that increasing correlation also has the problem of reducing the power to detect a non-zero value of the intercept.

## 2. Power study (25 points)

A proposed experiment is designed to estimate the slope of the relationship between the explanatory variable “amount of fertilizer” and the outcome “plant growth”. A reliable estimate of the error variance is  $\sigma^2 = 64$ . A reliable estimate of the intercept is  $\beta_0 = 120$ . (These estimates come from previous research reports.) The minimum meaningful slope is  $\beta_1 = 0.5$ . A total of 30 plants will be used, and we need to choose between two ways of selecting what fertilizer levels to use for these 30 plants. Using 1000 simulations each, calculate and turn in the power for

- (a) half the plants at each of two fertilizer levels of 0 and and 9 vs.
- (b) 3 plants each at fertilizer levels 0 through 9 at each whole number.

Turn in your R code, too.

```
# Make a function to simulate a single dataset
# and return the p-value for the slope.
# I chose the approach of using the passed (first)
# argument to specify which ‘x’ pattern I want.
```

```

# It's also OK to write two functions or use
# a later function argument, because this is
# constant for each apply().
#
# Remember that rnorm() uses sd, not variance.
#
doOne=function(wideSpacing=TRUE) {
  if (wideSpacing) {
    x=rep(c(0,9), each=15)
  } else {
    x=rep(0:9, each=3)
  }
  y = 120 + 0.5*x + rnorm(30,0,8)
  return(coef(summary(lm(y~x)))[2, "Pr(>|t|)"])
}

cat("Wide power:", mean(sapply(rep(T,1000), doOne)<=0.05), "\n")
# Wide power: 0.305
cat("Spread power:", mean(sapply(rep(F,1000), doOne)<=0.05), "\n")
# Spread power: 0.162

```

Surprisingly to many people, putting all your eggs in two baskets (to paraphrase an old saying) is best. Spreading the x values between the extremes reduces power.

Bonus question: What advantage is there to using all ten levels of fertilizer?

In the real world, using only two values for “x” is usually bad practice unless you are 110% certain that the relationship is linear. We usually spread the values out to allow informal (residual vs. fit plot) or formal (add  $x^2$ ) testing of linearity.

### 3. Arm strength study (25 points)

A study was designed to see if people who identify as “ambidextrous” have stronger left or right arms. The apparatus can only compare arms, and cannot make a quantitative measurement for either arm. The results are that 20 subjects were stronger on the right, 5 were equal, and 27 were stronger on the left. Compute a p-value for the null hypothesis that either arm is equally likely to be stronger. Show your work.

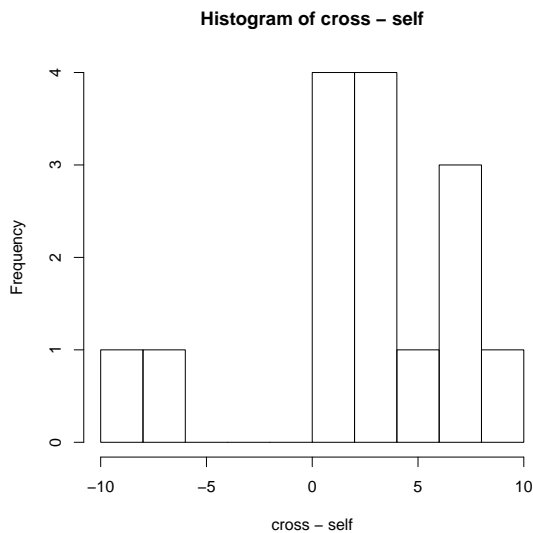
We throw away the ties, and want to use the normal approximation to the binomial(20+27,p) distribution to see if  $Y=20$  (or 27) is consistent with  $p = 0.5$ .  $E(Y|p = 0.5) = 47/2 = 23.5$ .  $\text{Var}(Y) = 47/4 = 11.75$ .  $Z = \frac{20-23.5}{\sqrt{11.75}} = -3.5/3.43 = -1.02$ .

$p.\text{value}=2*\text{pnorm}(-1.02)=0.307$

(We never need more than 3 significant figures for a p-value.)

4. Do Sleuth problem 28 on page 107 (25 points)

```
darwin = read.table("Darwin.dat", header=TRUE)
with(darwin, hist(cross-self, breaks=10))
dev.copy(pdf,"HW2Pr4.pdf"); dev.off()
with(darwin, t.test(cross,self,paired=T))
#      Paired t-test
#t = 2.148, df = 14, p-value = 0.0497
#alternative hypothesis: true difference in means is not equal to 0
#95 percent confidence interval:
# 0.003899165 5.229434169
#sample estimates:
#mean of the differences
#           2.616667
with(darwin, wilcox.test(cross,self,paired=T))
#      Wilcoxon signed rank test
#V = 96, p-value = 0.04126
#alternative hypothesis: true location shift is not equal to 0
```



(a) See above plot

(b)  $p=0.0497$

(c) 95% CI =  $[0.00390, 5.229]$  (again, don't give meaningless extra significant figures!!!)

(d) There does appear to be possible non-normality, in which case the non-parametric approach would be safer.

(e)  $p=0.0413$

Comment: the p-values are extremely similar, probably because that data really are consistent with normality.