The Virtual Ecologist

NRES 746

Fall 2021

For those wishing to follow along with the R-based demo in class, click here for the companion R-script for this lecture.

NOTE: some of this demo borrows from Hadley Wickham's presentation: Simulation

Why simulate 'fake data'?

- Formalize your understanding of the data generating process (make your assumptions *explicit*)
  - if you can tell a computer how to do it, you REALLY understand it!
  - it forces you to confront any underlying assumptions head-on
  - it allows you to better understand the implications of your hypotheses (every model you build is essentially a hypothesis)
- Assess how sampling methods potentially affect information recovery
  - Power Analysis! (how likely am I to pick up important signals from this sampling design?)

  - Sampling design! (what sampling design(s) will most effectively allow me to address my research question?)

  - Generate sampling distributions (e.g., CLT exercise, brute force t-test)
- Assess goodness of fit (could your data have been produced by this model?)

- Test whether model-fitting algorithms and statistical tests do what you think they should (e.g., estimate parameters correctly)! (test for bias, precision, etc.)
- Simulating a massive number of replicate datasets under a range of hypotheses provides the basis for performing Approximate Bayesian Computation, which is a brute-force inference method commonly used by geneticists.
- Build up and intuition and proficiency for building data-generating models and get ready for the next lecture (likelihood functions!)

We have simulated data already (e.g., CLT, brute-force t-test)! Even bootstrapping is a form of data simulation…

Random number generators (sample "data" from known distributions)

```r
###########
# Random number generators (a key component of data simulation models- but usually not the whole story)

runif(1,0,25)    # draw random numbers from various probability distributions
rpois(1,3.4)
rnorm(1,22,5.4)
```

First argument: n, number of random draws you want

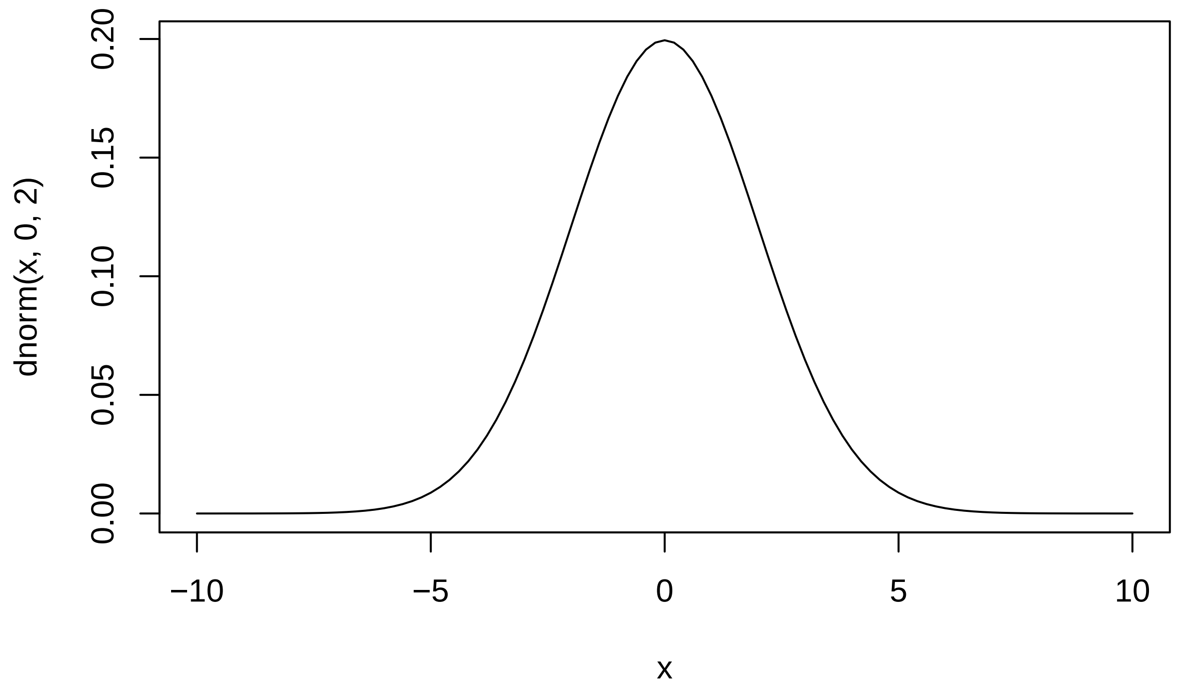
Subsequent arguments: **parameters** of the distribution

- Always check that the distribution is parameterized the way you expect (e.g., that the normal distribution is parameterized with a mean and standard deviation) – especially if you leave out the argument name in the random-number-generation functions!)

Short exercise #1:

- Generate 50 samples from $N(10, 5)$
- Generate 1000 numbers from $Poisson(50)$
- Generate 10 numbers from $Beta(0.1, 0.1)$

```
#############
# Short exercise:

# Generate 50 samples from Normal(mean=10,sd=5)


# Generate 1000 samples from Poisson(mean=50)


# Generate 10 samples from Beta(shape1=0.1,shape2=0.1)


# Try some other distributions and parameters.  NOTE: you can visualize probability densities easily us

curve(dnorm(x,0,2),-10,10)
```



```
# What happens when you try to use a discrete distribution?
```

Building a data simulation model

For our purposes, a **simulation model** is any fully specified, (usually) stochastic, data-generating process that has been programmed into a computer.

Your data simulation model could be as simple as the random numbers you were just generating. For example, we could make a (strong) assumption that our sample data were independently generated from a random Poisson process with constant mean (λ).

In general, our simulation models will comprise both **deterministic** and **stochastic** components.

For example, the data generating model underlying ordinary linear regression consists of a *deterministic component* ($y = ax + b$) and a *stochastic component* (the residual error is independently drawn from a normal distribution).

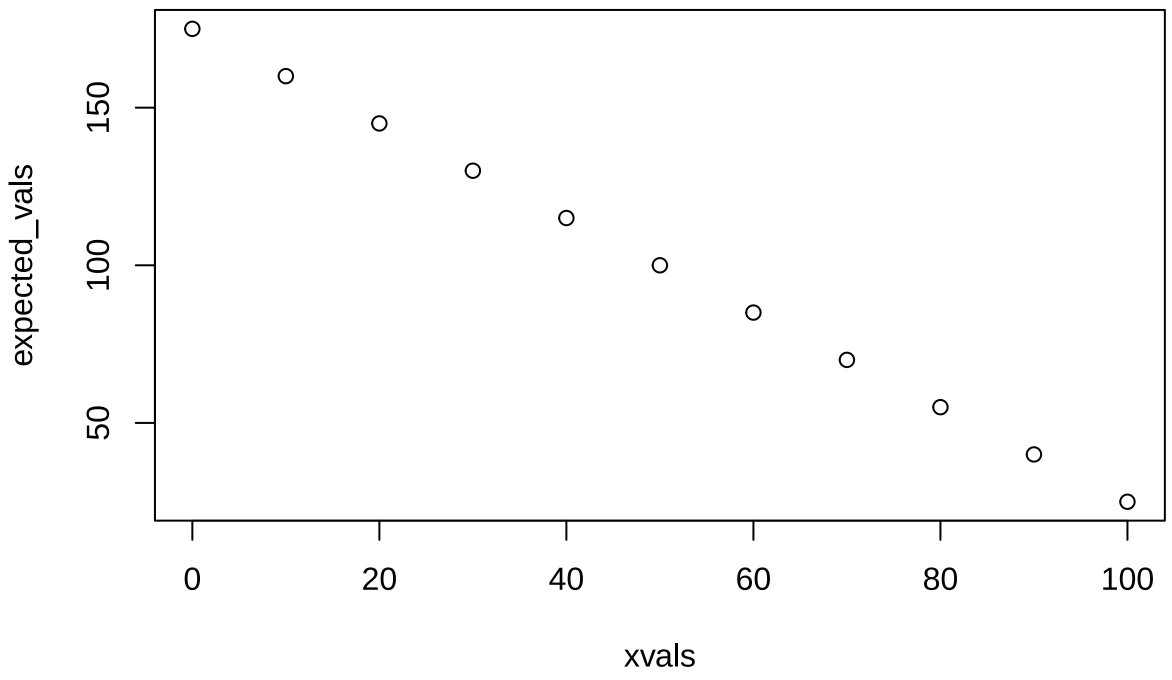
decomposing ordinary linear regression:

First, let's look at the **deterministic component**. The deterministic component maps covariate (predictor variable, or independent variable) values to an expected response. It is deterministic because the answer will be the same every time, given any specific input (covariate) value(s).

```
############
# SIMULATE DATA GENERATION: decompose into deterministic and stochastic components

##########
# Deterministic component: define function for transforming a predictor variable into an expected respo

    # Arguments:
      # x: vector of covariate values
      # a: the intercept of a linear relationship mapping the covariate to an expected response
      # b: the slope of a linear relationship mapping the covariate to an expected response

deterministic_component <- function(x,a,b){
  linear <- a + b*x   # specify a deterministic, linear functional form
  return(linear)
}

xvals = seq(0,100,10)  # define the values of a hypothetical predictor variable (e.g., tree girth)

expected_vals <- deterministic_component(xvals,175,-1.5)   # use the deterministic component to determi
expected_vals
```

```
##  [1] 175 160 145 130 115 100  85  70  55  40  25
```

```
plot(xvals,expected_vals)   # plot out the relationship
```

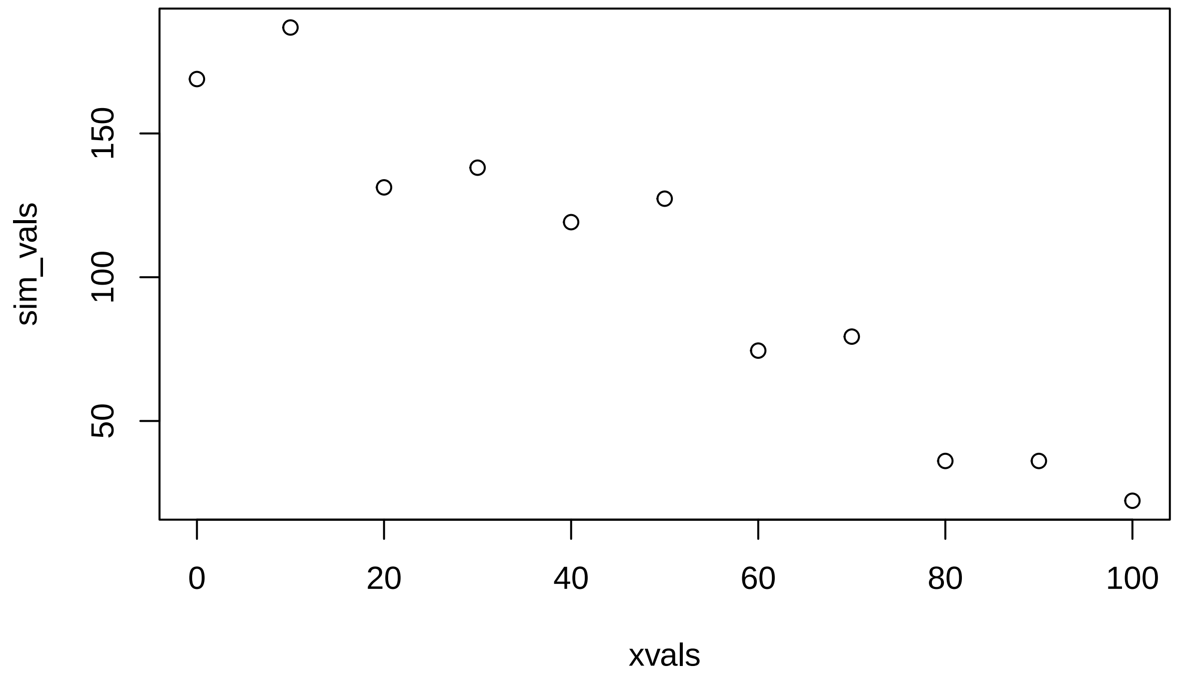


```
# plot(xvals,expected_vals,type="l")    # alternatively, plot as a line
```

Now, let's look at the **stochastic component** (also known as the "noise"). Recall that a normal distribution is defined by a mean and a variance (or standard deviation). We can consider the deterministic component as representing the **mean** (expected) value of the response for any given value(s) of relevant covariates. Therefore, if we assume the "noise" is normally distributed, all we need to generate stochastic data for any given covariate value(s) is a **variance**, or standard deviation (the mean is already defined).

```
##########
# Stochastic component: define a function for transforming an expected (deterministic) response and add

    # Arguments:
      # x: vector of expected responses
      # variance: variance of the "noise" component of your data simulation model
stochastic_component <- function(x,variance){
  sd <- sqrt(variance)       # convert variance to standard deviation
  stochvals <- rnorm(length(x),x,sd)       # add a layer of "noise" on top of the expected response val
  return(stochvals)
}

           # alternative: add the "residuals" onto the expected values.
# stochastic_component <- function(x,variance){
#   sd <- sqrt(variance)       # convert variance to standard deviation
#   stochvals <- rnorm(length(x),0,sd)       # generate the 'residuals'
#   return(x+stochvals)             # add a layer of "noise" on top of the expected response values
# }
```

```
    ### Simulate stochastic data!!
sim_vals <- stochastic_component(expected_vals,variance=500)   # try it- run the function to add noise

plot(xvals,sim_vals)     # plot it- it should look much more "noisy" now!
```



```
# ALTERNATIVELY:

sim_vals <- stochastic_component(deterministic_component(xvals,175,-1.5),500)    # stochastic "shell" s
```

You can think of the deterministic component as the **"signal"** and the stochastic component as the **"noise"**. Most data-generating processes that we will consider have both components!

Much of statistics and machine learning involves trying to tease apart these components– i.e., to detect signals from 'noisy' data. This is especially true - and difficult - in the age of big data

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Replication!

Okay, we've now generated our first random data set!

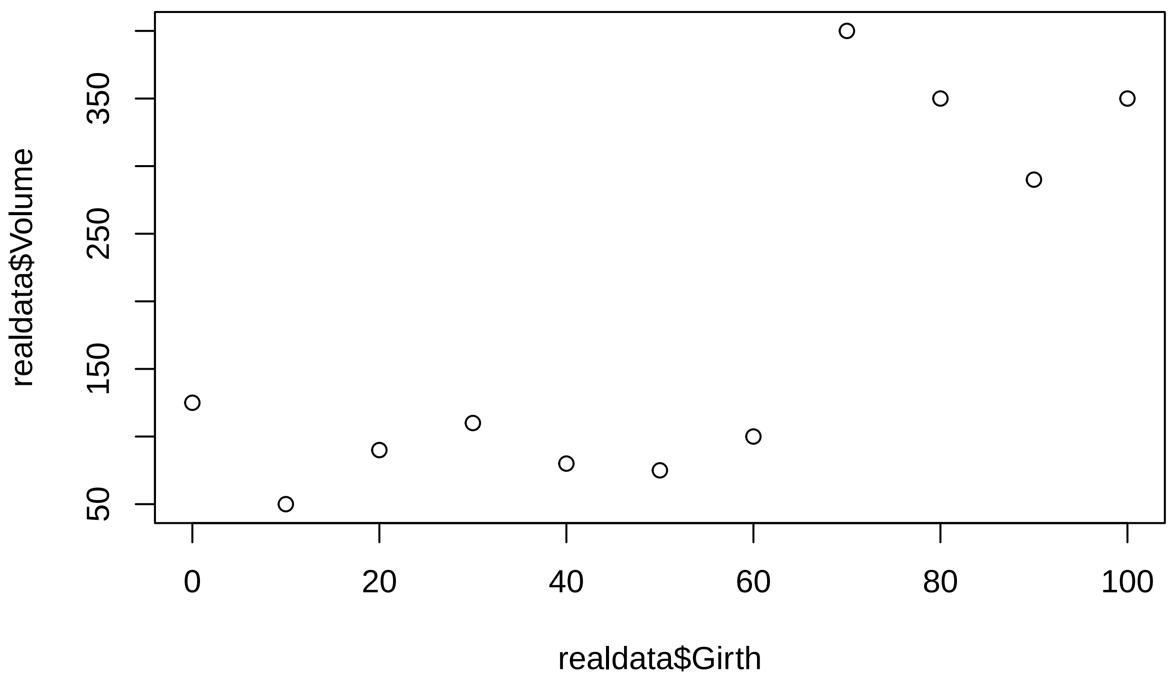
But wherever there is randomness (stochasticity), we can get different results every time (that's what it means to be random!). In such cases, a single output of the data generating model by itself has little meaning. However, we can extract a great deal of meaning if we run lots of replicates. The distribution ('cloud') of replicates becomes the real result!

Goodness-of-fit

For example, let's run a goodness-of-fit test. A goodness-of-fit test asks the question: can this model plausibly generate the observed data?

For example, consider a set of "real" data:

```
############
# Goodness-of-fit test!

    # Does the data fall into the range of plausble data produced by this fully specified model?

############
# Imagine you have the following "real" data (e.g., tree volumes).

realdata <- data.frame(Volume=c(125,50,90,110,80,75,100,400,350,290,350),Girth=xvals)
plot(realdata$Girth,realdata$Volume)
```



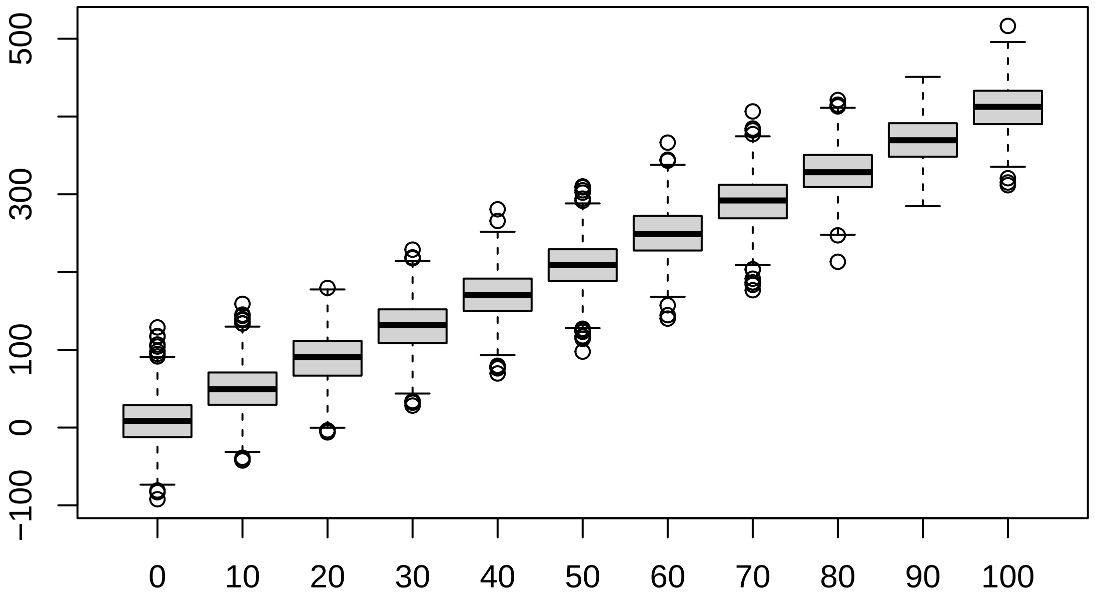
The following parameters together fully specify a data-generating model that we hypothesize is the model that generated our data. Is this fully specified linear regression model a good fit to our data?

```
intercept (a) = 10         # these parameters together specify a model that could have generated our da
slope (b) = 4
variance(var) = 1000
```

We can evaluate this question by brute force programming. And we will, because we love brute-force programming!

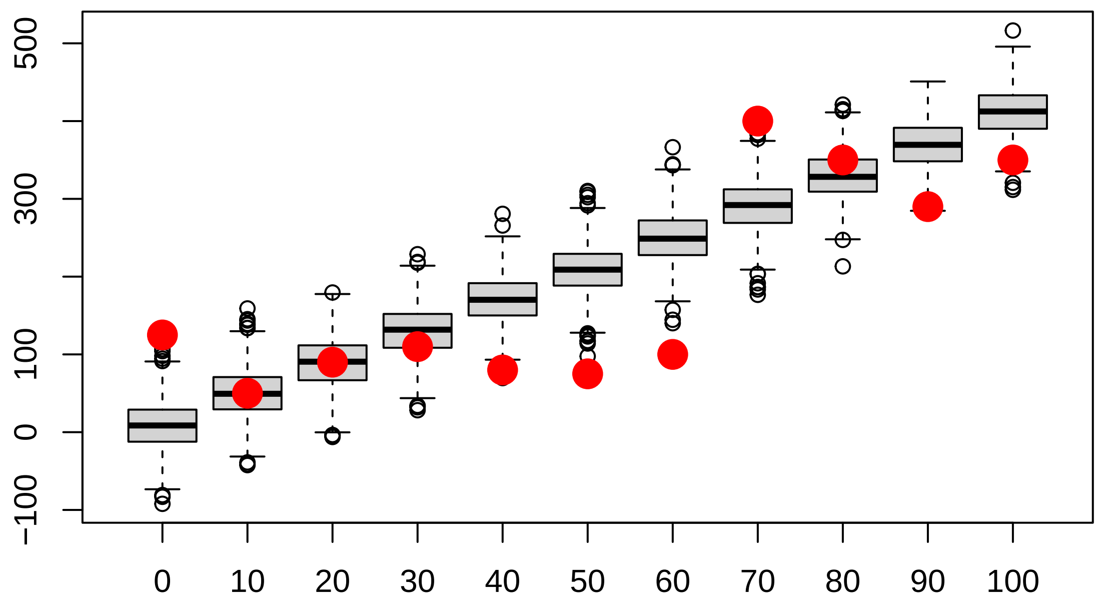
First we specify the data generating model. Then we simulate multiple datasets under this model that are comparable to our observed dataset (same sample size). Then we evaluate (visually for now) whether our data generating model is capable of generating our observed data.

```
#############
# Let's simulate many datasets from our hypothesized data generating model (intercept=10,slope=4,varian

reps <- 1000    # specify number of replicate datasets to generate
samplesize <- nrow(realdata)    # define the number of data points we should generate for each simulati
simresults <- array(0,dim=c(samplesize,reps))   # initialize a storage array for results
for(i in 1:reps){       # for each independent simulation "experiment":
  exp_vals <- deterministic_component(realdata$Girth,a=10,b=4)          # simulate the expected tree vo
  sim_vals <- stochastic_component(exp_vals,1000)  # add stochastic noise
  simresults[,i] <- sim_vals   # store the simulated data for later
}

    # now make a boxplot of the results
boxplot(t(simresults),xaxt="n")    # (repeat) make a boxplot of the simulation results
axis(1,at=c(1:samplesize),labels=realdata$Girth)                          # add x axis labels
```



Now let's overlay the "real" data. This gives us a visual goodness-of-fit test!

```
#########
# Now overlay the "real" data
    # how well does the model fit the data?

boxplot(lapply(1:nrow(simresults), function(i) simresults[i,]),xaxt="n")    # (repeat) make a boxplot o
axis(1,at=c(1:samplesize),labels=realdata$Girth)                          # add x axis labels
points(c(1:samplesize),realdata$Volume,pch=20,cex=3,col="red",xaxt="n")     # this time, overlay the "r
```

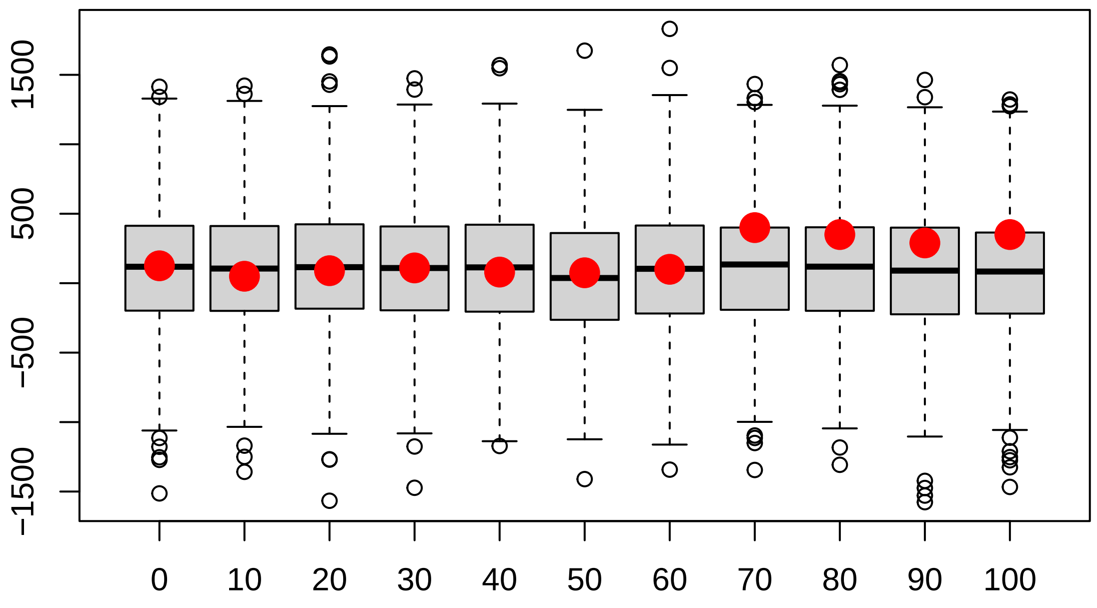


How well does this model fit the data?

Is this particular model likely to produce these data? (we will revisit this concept more quantitatively when we get to likelihood-based model fitting!)

What about if we try an intercept-only null model with expected Volume of 100 and variance of 200000 ? What happens now?

```
#############
# Let's simulate many datasets from our hypothesized data generating model (intercept=100,slope=0,varia

reps <- 1000     # specify number of replicate datasets to generate
samplesize <- nrow(realdata)     # define the number of data points we should generate for each simulati
simresults <- array(0,dim=c(samplesize,reps))    # initialize a storage array for results
for(i in 1:reps){        # for each independent simulation "experiment":
  exp_vals <- deterministic_component(realdata$Girth,a=100,b=0)           # simulate the expected tree v
  sim_vals <- stochastic_component(exp_vals,200000)  # add stochastic noise
  simresults[,i] <- sim_vals    # store the simulated data for later
}

    # now make a boxplot of the results
boxplot(lapply(1:nrow(simresults), function(i) simresults[i,]),xaxt="n")     # (repeat) make a boxplot o
axis(1,at=c(1:samplesize),labels=realdata$Girth)                           # add x axis labels
points(c(1:samplesize),realdata$Volume,pch=20,cex=3,col="red",xaxt="n")      # this time, overlay the "r
```



Could this model have generated the data?

Is this model **likely** to be the model that generated the data? What's your intuition?

Is this model **useful**?

Generating *sampling distributions* (i.e., simulate the distribution of test statistics under a null hypothesis)

A null hypothesis can usually be expressed as a data-generating model.

If so, you should be able to generate sampling distributions of any test statistic under your null distribution.

For example, the 'brute force' z-test from the first lecture!

NOTE: Frequentist statistical tests are based on a single sample that is one of an theoretically infinite number of potential samples. The interpretation of the results is implicitly based on the idea of sample replication (e.g., "if the null hypothesis were true, and the experiment were *replicated* lots and lots of times, results as or more extreme as the observed results could be expected from x% of replicates")

Power analysis!! (can my sampling design detect the "signal"?)

When designing experiments or field monitoring protocols, we often ask questions like:

- What sample size do I need to be able to address my research questions?
- What is the smallest effect size I can reliably detect with my sampling design?
- What sources of sampling or measurement error should I make the greatest effort to minimize?

In such cases, probably the most straightforward (yet not always the most efficient) way to address these questions is to simulate data under various sampling strategies and signal/noise ratios, and see how well we can recover the “true” signal through the noise!

Power analysis, example

Imagine we are designing a monitoring program for a population of an at-risk species, and we want to have *at least a 75% chance of detecting a decline in abundance of 25% or more over a 25 year period*. Let’s assume that we are using visual counts, and that the probability of encountering each member of the population is 2% per person-day. The most recent population estimate was 1000: here we will assume that is known with certainty.

What we know:

- A single surveyor has a 2% chance of detecting each animal in the population in a single day of surveying

- The initial abundance is 1000

- We want to be able to detect a decline as small as 25% over 25 years with at least 75% probability.

First, let’s set the groundwork by making some helper functions (break the problem into smaller chunks).

This function takes the true number in the population and returns the observed number:

```
################
# Power analysis example: designing a monitoring program for a rare species


   ### first, let's develop some helper functions:

########
# function for computing the number of observed/detected animals in a single survey

    # Arguments:
      # TrueN: true population abundance
      # surveyors: number of survey participants each day
      # days: survey duration, in days

NumObserved <- function(TrueN=1000,surveyors=1,days=3){
  probPerPersonDay <- 0.02      # define the probability of detection per animal per person-day [hard-c
  probPerDay <- 1-(1-probPerPersonDay)^surveyors      # define the probability of detection per animal
  probPerSurvey <- 1-(1-probPerDay)^days       # define the probability of detection per animal for the
  nobs <- rbinom(1,size=TrueN,prob=probPerSurvey)     # simulate the number of animals detected!
  return(nobs)
}
NumObserved(TrueN=500,surveyors=2,days=7)   # test the new function
```

```
## [1] 149
```

This function gives us the current-year abundance using last year’s abundance and trend information

```
#########
# function for computing expected abundance dynamics of a declining population (deterministic component

    # Arguments:
      # LastYearAbund: true population abundance in the previous year
      # trend: proportional change in population size from last year

ThisYearAbund <- function(LastYearAbund=1000,trend=-0.03){
```

```r
  CurAbund <- LastYearAbund + trend*LastYearAbund    # compute abundance this year
  CurAbund <- floor(CurAbund)  # can't have fractional individuals!
  return(CurAbund)
}
ThisYearAbund(LastYearAbund=500,trend=-0.03)    # test the new function
```

```
## [1] 485
```

```r
# NOTE: we could introduce stochastic population dynamics (or density dependence, etc!) for a more real
```

This function will simulate a single dataset (time series of observations over a given number of years)!

```r
########
# develop a function for simulating monitoring data from a declining population

    # Arguments:
      # initabund: true initial population abundance
      # trend: proportional change in population size from last year
      # years: duration of simulation
      # observers: number of survey participants each day
      # days: survey duration, in days
      # survint: survey interval, in years (e.g., 2 means surveys are conducted every other year)

SimulateMonitoringData <- function(initabund=1000,trend=-0.03,years=25,observers=1,days=3,survint=2){
  prevabund <- initabund        # initialize "previous-year abundance" at initial abundance
  detected <- numeric(years)    # set up storage variable
  for(y in 1:years){            # for each year of the simulation:
    thisAbund <- ThisYearAbund(prevabund,trend)             # compute the current abundance on the basi
    detected[y] <- NumObserved(thisAbund,observers,days)     # sample the current population using this
    prevabund <- thisAbund   # set this years abundance as the previous years abundance (to set up the 
  }
  surveyed <- c(1:years)%%survint==0    # which years were surveys actually performed?
  detected[!surveyed] <- NA            # if the survey is not performed that year, return a missing val
  return(detected)       # return the number of individuals detected
}

SimulateMonitoringData(initabund=1000,trend=-0.03,years=25,observers=1,days=3,survint=2)    # test the 
```

```
##  [1] NA 60 NA 46 NA 54 NA 44 NA 33 NA 30 NA 28 NA 39 NA 32 NA 40 NA 28 NA 25 NA
```

Note that we are using NA to indicate years where no survey was conducted. A zero value would mean something very different than an NA.

Now we can develop a function for determining if a decline was in fact detected by the method:

```r
#########
# finally, develop a function for assessing whether or not a decline was detected:

    # Arguments:
      # monitoringData: simulated results from a long-term monitoring study
      # alpha: define acceptable type-I error rate (false positive rate)

IsDecline <- function(monitoringData,alpha=0.05){
  time <- 1:length(monitoringData)      # vector of survey years
  model <- lm(monitoringData~time)    # for now, let's use ordinary linear regression (perform linear r
  p_value <- summary(model)$coefficients["time","Pr(>|t|)"]      # extract the p-value
  isdecline <- ifelse(summary(model)$coefficients["time","Estimate"]<0,TRUE,FALSE)     # determine if t
  sig_decline <- ifelse((p_value<=alpha)&(isdecline),TRUE,FALSE)    # if declining and significant tren
  return(sig_decline)
}

IsDecline(monitoringData=c(10,20,NA,15,1),alpha=0.05)    # test the function
```

```
## [1] FALSE
```

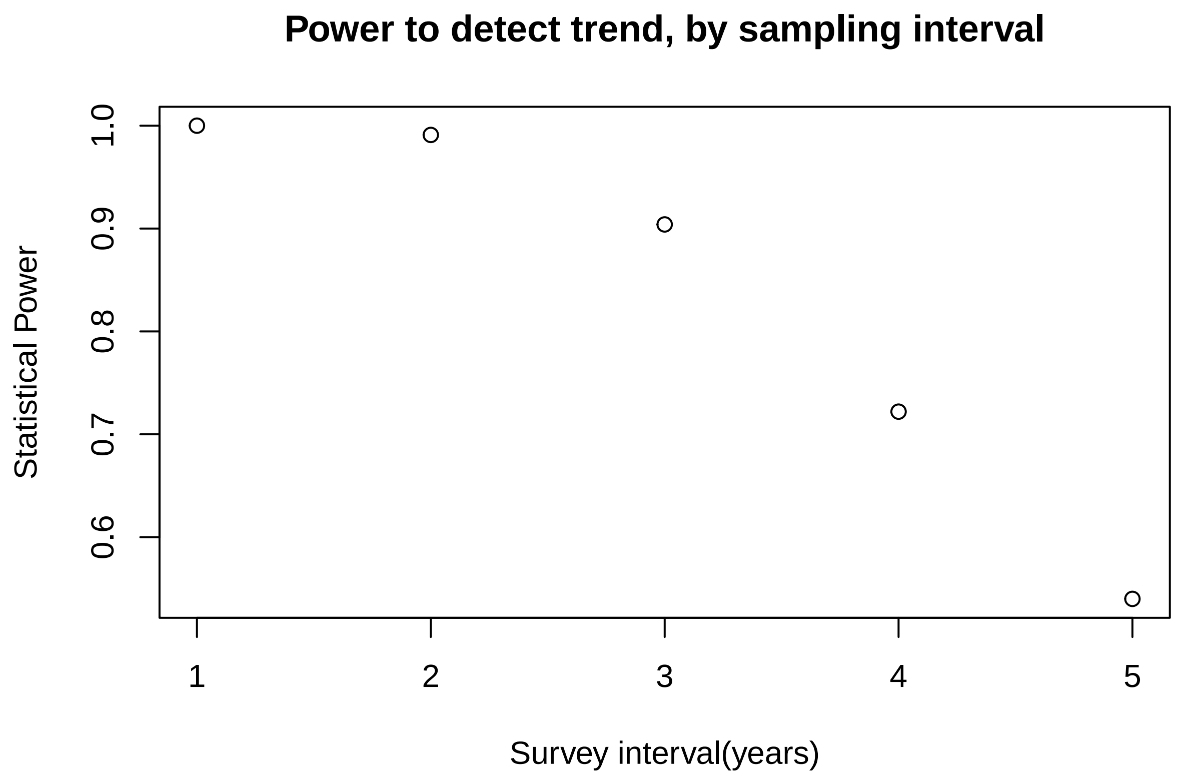
Now we can develop a "power" function that gives us the statistical power for given monitoring scenarios...

This is part of this week's lab assignment!

```
###########
# Lab exercise: develop a "power" function to return the statistical power to detect a decline under al

nreps <- 10000      # set number of replicate monitoring "experiments"
initabund <- 1000    # set initial population abundance.

GetPower <- function(nreps=nreps,initabund=initabund,trend=-0.03,years=25,observers=1,days=3,survint=2,a
     # fill this in!
  return(Power)
}
```

```
## The statistical power to detect a decline for the default parameters is: 0.375
```

And we can evaluate what types of monitoring programs might be acceptable:



–go to next lecture–