# Simulations Encore: More Uses for Simulations

*36-350*

*24 November 2014*

## Agenda

- Simulations instead of probability calculations
- Simulations as models
- Building simulations
  - Live coding of a simulation model under the direction of the class

## Previously

- Drawing independent random variables
- Making random variables dependent on each other
- Using Monte Carlo to short-cut integration

## vs. Probability Calculations

- Monte Carlo:
$$\int g(x)p(x)dx \approx \frac{1}{n}\sum_{i=1}^{n} g(X_i) \text{ when } X_i \sim p$$
- Not just integrals: | Probability of anything $\approx$ how often does it happen in the simulation

## Example: Prediction Intervals

Stock returns of the Corrections Corp. of America:

```
require(pdfetch)
```

```
## Loading required package: pdfetch
```

```
# Corrections Corp. of America
CXW <- pdfetch_YAHOO("CXW",fields="adjclose",
  from=as.Date("2000-01-01",
  to=as.Date("2014-09-30")))
CXW.returns <- na.omit(as.vector(diff(log(CXW$CXW))))
```

## Example: Prediction Intervals

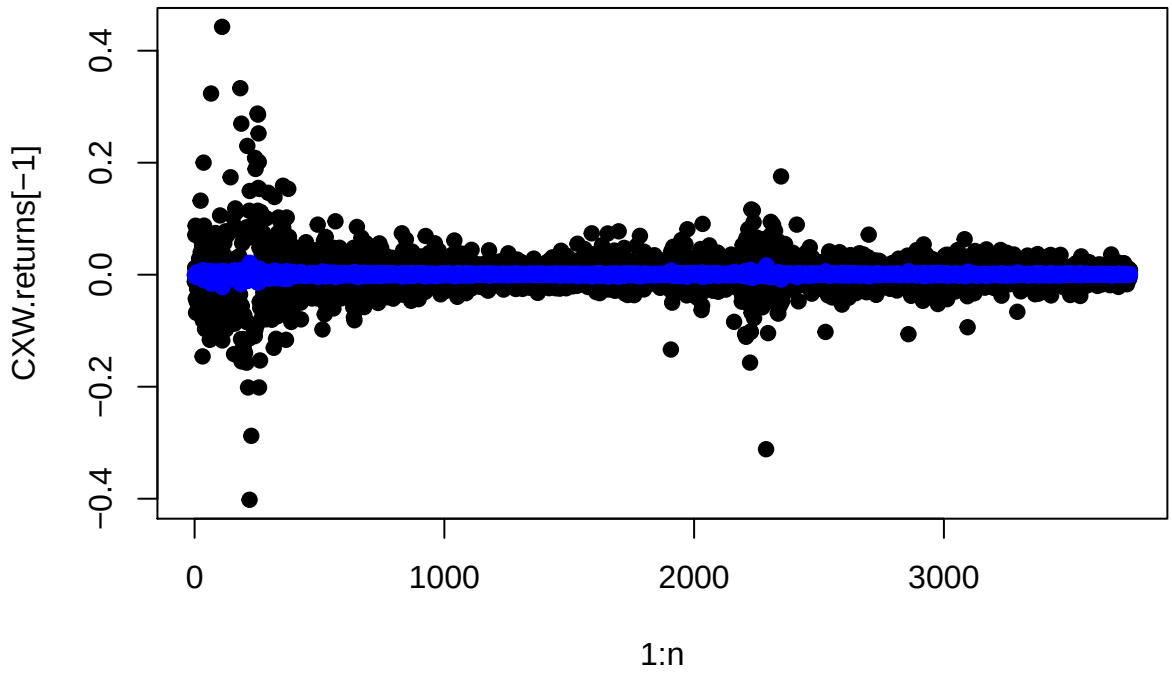
Regress tomorrow's returns on today's:

```
CXW.ar <- lm(CXW.returns[-1] ~ CXW.returns[-length(CXW.returns)])
coefficients(CXW.ar)
```

```
##                         (Intercept) CXW.returns[-length(CXW.returns)]
##                           0.0005609                         -0.0515824
```

## Example: Prediction Intervals

```
n <- length(CXW.returns)-1
plot(1:n, CXW.returns[-1],pch=19)
points(1:n, fitted(CXW.ar), col="blue",pch=19)
```




## Example: Prediction Intervals

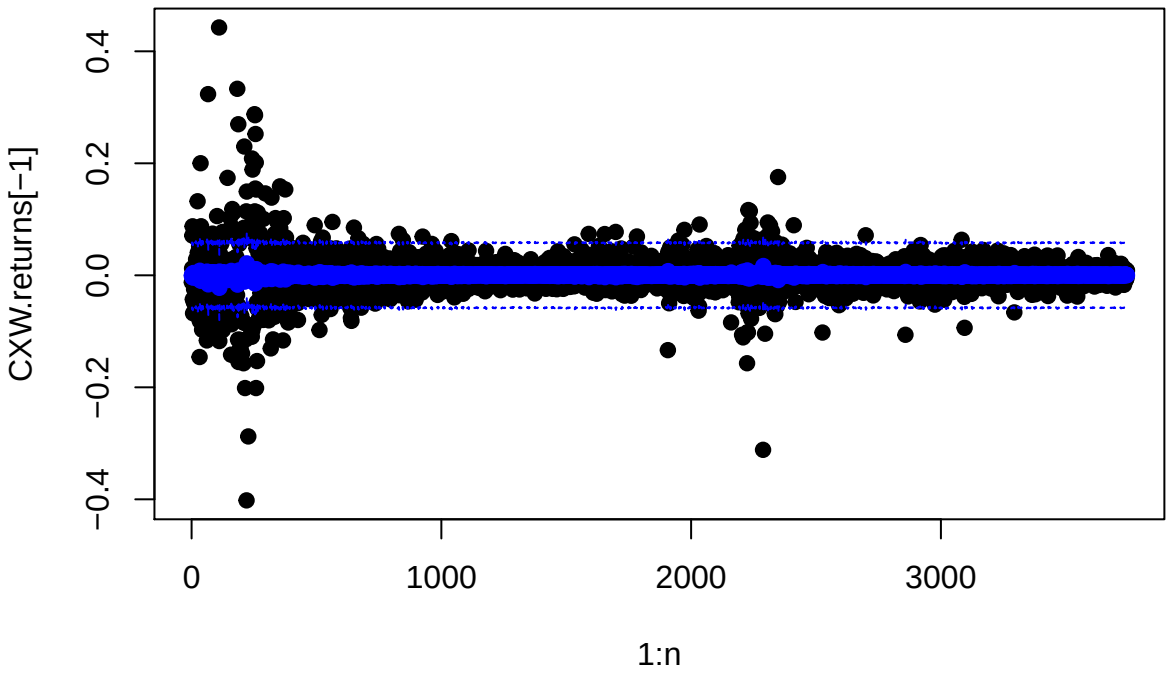
Could work out prediction intervals from theory, if they were Gaussian . . . or just simulate

```
prediction.interval <- function(model, confidence=0.95, n=1e3) {
  residuals <- residuals(model)
  sim <- sample(residuals, size=n, replace=TRUE)
  lower.limit <- (1-confidence)/2
  upper.limit <- 1-lower.limit
  return(quantile(sim, c(lower.limit, upper.limit)))
}
(CXW.interval95 <- prediction.interval(CXW.ar))
```

```
##    2.5%   97.5%
## -0.0585  0.0576
```

## Example: Prediction Intervals

```
plot(1:n, CXW.returns[-1],pch=19)
points(1:n, fitted(CXW.ar), col="blue",pch=19)
lines(1:n, fitted(CXW.ar)+CXW.interval95[1], lty="dashed", col="blue")
lines(1:n, fitted(CXW.ar)+CXW.interval95[2], lty="dashed", col="blue")
```




## Example: Prediction Intervals

(This example is slightly defective since it doesn't include parameter uncertainty; we'll cover that in 402 when we do bootstrapping)

## Simulations as Models

- Sometimes the only convenient way to specify the statistical model is as a simulation
- Lots of details, no simplifying math
- Running the simulation is then how we see what the model does at given parameters
- Fit by matching simulation output to data

## Example: Antibiotics Again

- Doctors have either adopted or they haven't
- Every day, two random doctors meet
- If one has adopted but the other hasn't, the hold-out adopts with probability $p$
- Look at number of adoptions over time

This was originally a model of disease spread, but now the "disease" is adopting a new drug

[Break for live coding under the direction of the class]

## Example: Antibiotics Again

Code written by section 1:

```
sim_doctors_1 <- function(num.doctors, num.days, initial_doctors, p) {
  # Remember to set up all_doctors
  all_doctors <- 1:num.doctors
  # Remember to set up has_adopted as binary vector
  has_adopted <- matrix(0,nrow=num.doctors,ncol=num.days)
  # Set some doctors to have initially adopted
    # initial_doctors are indices of doctors who are using as of day 1
  has_adopted[initial_doctors,1:num.days] <- 1
  for (today in 1:num.days) {
    # pull two random doctors
    todays_doctors <- sample(all_doctors,size=2,replace=FALSE)
    # check that one has adopted and the other hasn't
    if(sum(has_adopted[todays_doctors,today])==1) {
      # make the non-adopter adopt with probability p
      which_of_todays <- which(has_adopted[todays_doctors,today]==0)
      receiver <- todays_doctors[which_of_todays]
      has_adopted[receiver,today:num.days] <- rbinom(n=1,size=1,prob=p)
    }
  }
  return(has_adopted)
}
```

## Example: Antibiotics Again

Code written by section 2:

```
sim_doctors_2 <- function(num.doctors,num.meetings,starting_adopters, prob) {
  # vector to keep track of which doctors have adopted
  has_adopted <- rep(FALSE, num.doctors)
  # Set some to have adopted initially
  has_adopted[1:round(starting_adopters*num.doctors)] <- TRUE
  # matrix to keep track of adoptions over time
  adoptions_vs_time <- matrix(FALSE,nrow=num.doctors,ncol=num.meetings)
  for (meeting in 1:num.meetings) {
    # select 2 doctors at random
    meeting_pair <- sample(1:num.doctors,size=2)
    # check whether exactly one selected doctor has adopted
    if(has_adopted[meeting_pair[1]] != has_adopted[meeting_pair[2]]) {
      # With probability prob., update the vector of adopters
      if(rbinom(n=1,size=1,prob=prob)) { has_adopted[meeting_pair] <- TRUE }
    }
    # update adoptions_vs_time matrix
    adoptions_vs_time[,meeting] <- has_adopted
```

```
  }
  return(adoptions_vs_time)
}
```

## Example: Antibiotics Again

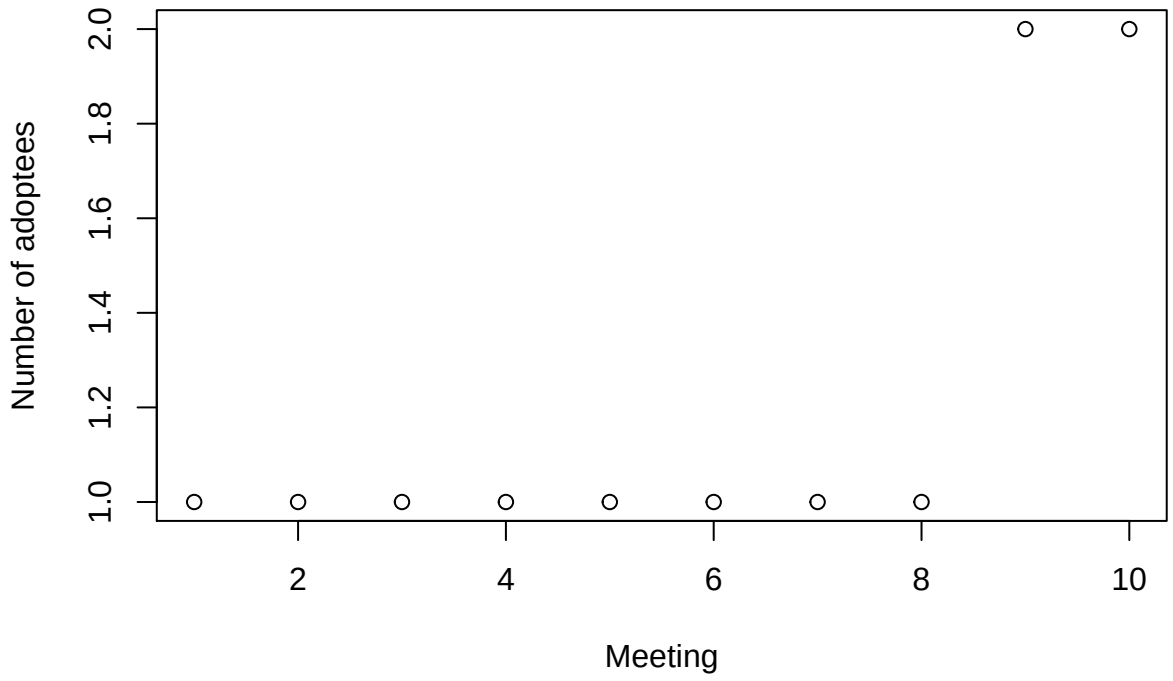
```
sim2 <- sim_doctors_2(num.doctors=10,num.meetings=10,starting_adopters=0.1,prob=1.0)
dim(sim2)
```

```
## [1] 10 10
```

- Start small for debugging
- Making transmission always successful lets us see about updating

## Example: Antibiotics Again

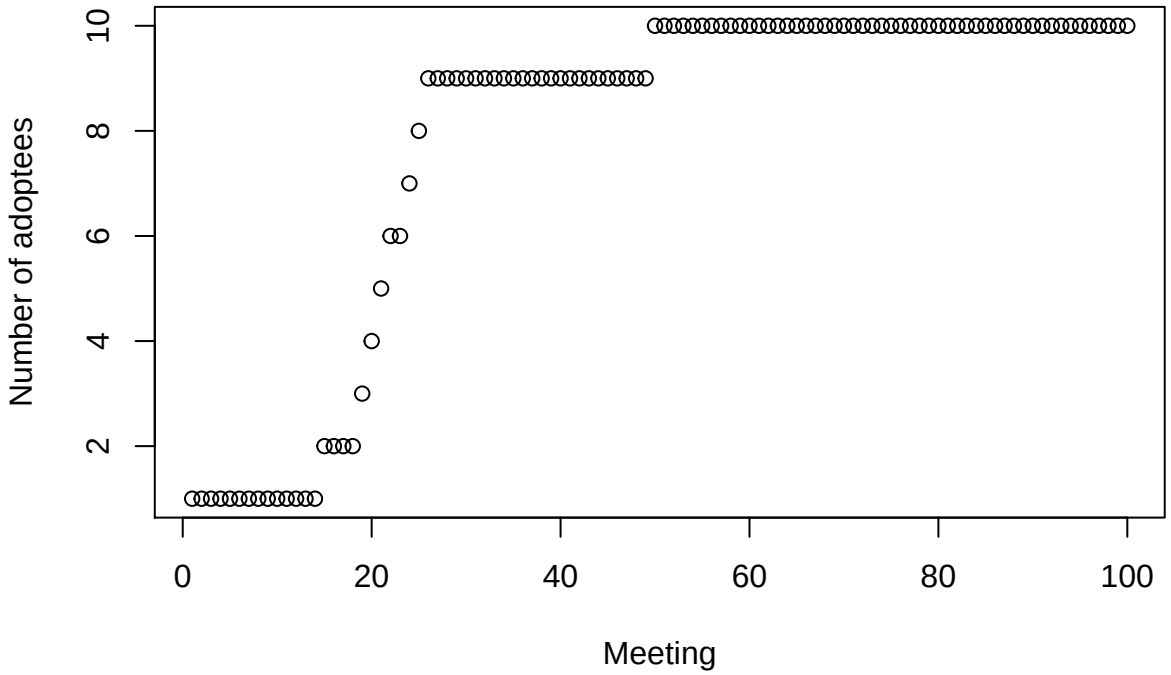
```
plot(colSums(sim2),xlab="Meeting",ylab="Number of adoptees")
```




## Example: Antibiotics Again

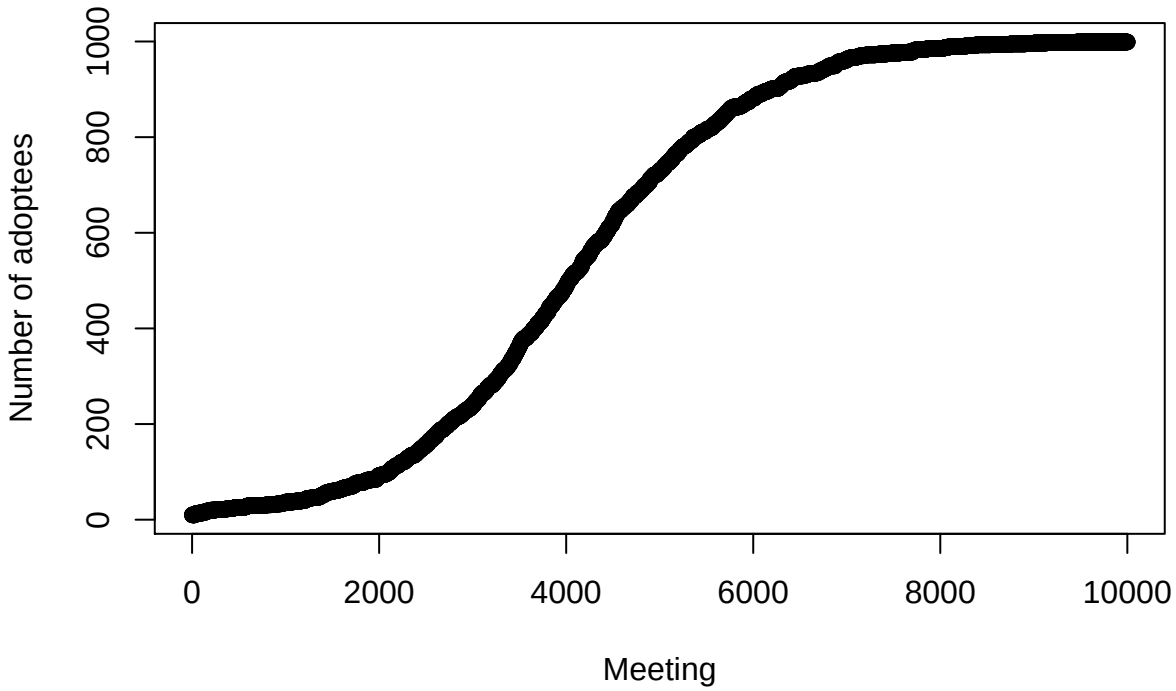
Maybe not that small? With only 10 time-steps it's pretty likely we never pick the one initial adoptee

```
sim2.1 <- sim_doctors_2(num.doctors=10,num.meetings=100,starting_adopters=0.1,prob=1.0)
plot(colSums(sim2.1),xlab="Meeting",ylab="Number of adoptees")
```




## Example: Antibiotics Again

```
sim.big <- sim_doctors_2(num.doctors=1000,num.meetings=10000,starting_adopters=0.01,prob=0.5)
plot(colSums(sim.big),xlab="Meeting",ylab="Number of adoptees")
```



Elapsed time from starting to code to final figure: 20 minutes

## Example: Antibiotics Again

- These **logistic** or **sigmoid** curves are very characteristic of actual product-adoption curves, and of a lot of epidemiology
- This is the "susceptible-infectious" (SI) model Lots of variants
  - susceptible-infectious-susceptible (SIS), susceptible-infectious-recovered (SIR)
  - multiple stages of infectiousness
  - competing infections
  - can only transmit to network neighbors, not random pairing
  - etc., etc.

## Summary

- When we don't have exact probability formulas or they don't apply, we can simulate to get arbitrarily-good approximations
- If we can describe the process of our model, we can set up a simulation of it