Introduction Introduction to Data Science Lecture 1



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Block 4 2020

Outline

- 1. Overview of this course
- 2. What is data science?
- 3. Data science workflow
- 4. Data science novelties
- 5. Statistical modeling

Course Outline



Course Road-map

This course will be broken into two parts:

- We will spend the first three weeks on *supervised learning* methods.
- Around the beginning of May, we'll begin discussing unsupervised learning methods.

Course Structure

- For the first three weeks:
 - Two plenary lecture sessions per week
 - These lectures will be streamed via Zoom.
 - Hopefully, the live-stream will be recorded and posted to Canvas for students with time-zone difficulties.
 - Two lab meetings per week
 - I will pre-record a demonstration lecture and post the video to Canvas.
 - During the scheduled lab session, I will be available for questions via Zoom.
- For the final four weeks:
 - o One plenary lecture session per week
 - One lab meeting per week
 - Kim will flesh-out the details at a later date.

Grading & Evaluation

- You will complete two group assignments.
 - One on supervised learning
 - One on unsupervised learning
- The course is rounded-off with a written final exam.
- Your course grade will be a weighted average of the grades you receive for the group assignments and your exam grade.
 - The assignments will contribute 40% to your grade.
 - The exam will contributed 60% to your grade.
 - The three grades *can* compensate one another.

DEFINING DATA SCIENCE



At the very least, "data science" is a buzzword.

- It's also a job
 - You can certainly be hired as a data scientist.



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- It's also a job
 - You can certainly be hired as a data scientist.

In a strict sense, "data science" is almost certainly a misnomer.

• Data science is not the science of data.



A mixture of skills and a merger of disciplines:

- Statistics
- Computer science
- Mathematics
- Programming
- Data processing
- Data visualization
- Communication
- Substantive expertise

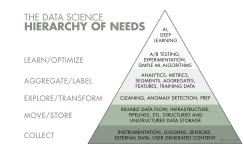
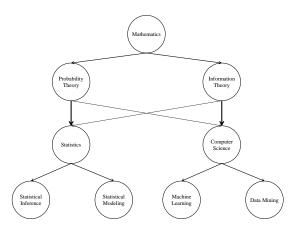


Figure source: https://hackernoon.com/the-ai-hierarchy-of-needs-18f111fcc007

Aside: Confusing Nomenclature

When you start studying this stuff, you will encounter a dizzying array of terms that all seem to describe the same things. Here's why:



A focus on practical problem solving

- Data analysis should create value.
 - We're trying to extract knowledge from data.
 - Start with a question and use data to answer it.
 - Don't start with data and generate answerable questions.
- Use appropriately complex methods.
 - Don't waste resources on complex analyses when simpler analyses will solve your problem equally well.
 - Don't settle for bad answers just because good answers will require complex/difficult analyses.
- Don't ask if you can; ask if you should.
 - Why are you doing a particular analysis?
 - All analytic decisions should be justified.

A strong focus on pragmatism and skepticism

- Don't be tied to a "pet method".
- Embrace exploratory methods.
 - Don't overgeneralize exploratory findings.
- · Treat neither data nor theory as sacred.
 - Don't sanctify theory in the face of (definitively) contradictory data.
 - Don't blithely let data overrule well-supported theory.
- Trust no one.
 - Not data, other people, or yourself
 - Check and double check
- Don't assume what can be tested.
- When in doubt, err on the side of conservative inference.
- Document everything!

A fast-paced, curious, open-minded attitude

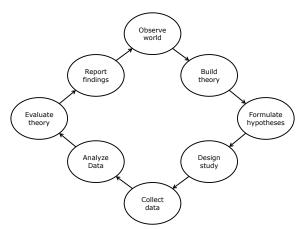
- Iterate quickly, fail quickly
- Never stop learning.
 - · Learn and use new methods
 - Always remain open to new ideas/approaches.
- Don't be afraid to tackle new problems.
 - Generalize and extend what you know.
 - Don't stagnate.
- Show an appropriate degree of humility.
 - You don't know everything.
 - Embrace and correct your ignorance.
 - Ask questions.
 - · Communicate. Don't just talk.

DATA SCIENCE WORKFLOW



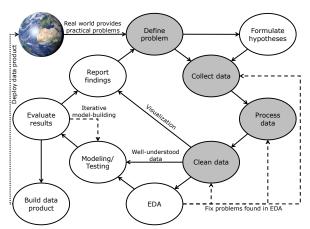
Research Cycle

The following is a representation of the *Research Cycle* used for empirical research in most of the sciences.



Data Science Cycle

The *Data Science Cycle* represented here was adapted from O'Neil and Schutt (2014).



DATA SCIENCE NOVELTIES



Novel Data Structures

In the social and behavioral sciences, we are accustomed to analyzing small, rectangular datasets.

- Rows represent observational units.
- Columns represent variables.

Data science applications deal with much more diverse forms of data.

- Relational databases
- Data streams
- Web logs

- Sensor data
- Image data
- Unstructured text

These datasets are often much larger and less structured that those traditionally analyzed in the social and behavioral sciences.

Parallel Processing/Distributed Computing

When dealing with large amounts of (distributed) data, we should move the data as little as possible.

- We can analyze distributed data in situ without moving them to a central computer.
 - Distributed computing

When executing long-running jobs, we should try to split the calculations into smaller pieces that can be executed simultaneously.

Parallel processing

Parallel processing comes in two flavors:

- Embarrassingly Parallel
- Multi-threading

Parallel Processing Technologies

We can distribute embarrassingly parallel jobs directly.

No real need for clever task partitioning

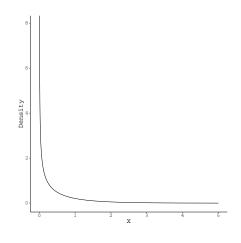
We must break multi-threaded jobs into independent subtasks.

- Several technologies can facilitate multi-threading.
 - Small-scale:
 - Message Passing Interface (MPI)
 - Open Multi Processing (OpenMP)
 - Large-scale:
 - Google's MapReduce algorithm
 - Apache Hadoop
 - Apache Spark

Some software can use parallel processing behind-the-scenes.

Run a Monte Carlo simulation to test the central limit theorem.

- Population model:
 - $x_p \sim \Gamma(0.5, 1.0)$
- Parameters:
 - $P \in \{1, 2, \dots, 50\}$
 - $0 N \in \{5, 10, \dots, 100\}$
- Mean score for the nth row:
 - $\bar{x}_n = P^{-1} \sum_{p=1}^P x_{np}$
- Outcome:
 - KS statistic testing if \bar{x}_n is normally distributed



First, we'll define a function to run one replication of the simulation:

```
## Run one replication of the simulation:
doRep <- function(rp, conds) {</pre>
    res <- rep(NA, nrow(conds))
    for(i in 1 : nrow(conds)) { # Loop through conditions
        ## Compute a mean score from p variables:
        x <- rowMeans(
            replicate (conds[i, "p"],
                      rgamma (conds[i, "n"], 0.5, 1)
        ## Calculate the KS statistic:
        res[i] <- ks.test(x, "pnorm", mean(x), sd(x))$stat
    cbind(conds, res) # Return the results
```

Then, we prepare the environment:

```
library(parallel) # We'll need this for parallel processing
library(lattice) # We'll use this for plotting

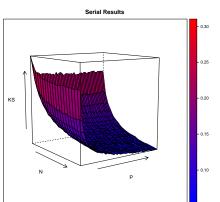
## Define simulation conditions:
nVec <- seq(5, 100, 5)
pVec <- 1 : 50
conds <- expand.grid(n = nVec, p = pVec)

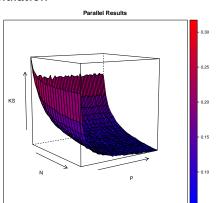
## How many replications?
nReps <- 500</pre>
```

We'll run the simulation in two ways:

```
# Run 'nReps' replications in a loop:
t1 <- system.time(
   out1 <- list()
   for(rp in 1 : nReps)
        out1[[rp]] <- doRep(rp, conds = conds)
## Run 'nReps' replications in parallel using mclapply():
t2 <- system.time(
   out 2 \leftarrow mclapply(X) = 1 : nReps,
                     FUN = doRep,
                     conds = conds,
                     mc.cores = 2)
```

We can visualize the results of our simulation:





Finally, we'll compare the computational speed of the parallel and serial approaches:

```
## Serial version:
t1

## user system elapsed
## 557.867   0.004 558.187

## Parallel version:
t2

## user system elapsed
## 271.906   0.128 276.540
```

Running the program in parallel substantially speeds computation.

• The parallel version is 2.02 times faster than the serial version.

Computationally Efficient Algorithms

In general, there will be many ways to estimate a given model.

 When dealing with large data structures, choosing a computationally efficient approach is important.

There will usually be a trade-off between memory efficiency and computational efficiency.

• We can compute faster by storing the result of initial calculations, but doing so entails higher memory usage.

Certain data structures should be analyzed with specialized computational techniques.

- Data streams → online learning, batch processing
- Distributed data → distributed computing

Online Learning Example

Suppose we want to estimate the mean of *X*.

• Traditional approach:

$$\bar{X} = N^{-1} \sum_{n=1}^{N} x_n$$

Maybe, we don't want to keep all of *X* in memory.

Online updating:

$$\bar{X}_n = \frac{(n-1)\bar{X}_{n-1} + x_n}{n}$$

```
## Generate some data:
x < - runif(10000)
## Traditional estimation:
m0 <- sum(x) / length(x)
## Online updating:
m1 < - x[1]
for(n in 2 : length(x))
    m1 < -((n - 1) * m1 + x[n]) / n
## Compare results:
m0; m1
## [1] 0.4995201
   [1] 0.4995201
```

STATISTICAL MODELING

Statistical Reasoning

Statistics and data science are used to answer questions about hypothetical populations.

- Do men have higher job satisfaction than women?
- Can I predict your voting behavior?
- Can I detect groups of people who share similar attitudes towards climate change?

To answer these questions, we need to use statistical reasoning.

 The foundation of all good statistical analyses is a deliberate, careful, and thorough consideration of uncertainty.

Statistical Reasoning

If I measure a mean satisfaction rating for men of 5.6 and a mean satisfaction rating for women of 5.1, does that imply higher job satisfaction for men?

- Maybe...
- If the satisfaction ratings are highly variable, with respect to the size
 of the mean difference, we may not care much about the observed
 mean difference.
- The *observed* mean difference may not represent a *true* mean difference in the population.

The purpose of statistics is to systematize the way that we account for uncertainty when making data-based decisions.

Statistical Modeling

To implement this "statistical reasoning," we could use two different approaches: *statistical testing* or *statistical modeling*.

- In experimental contexts, real-world "messiness" is controlled through random assignment, and statistical testing is a sufficient method of knowledge generation.
- Apart from A/B testing, data scientists rarely have the luxury of being able to conduct experiments.
- Data scientists work with messy observational data and often don't have questions that lend themselves to straight-forward testing.

Data scientists need statistical modeling.

Statistical Modeling

Modelers attempt to build a mathematical representation of the (interesting aspects) of a data distribution.

- The model succinctly describes whatever system is being analyzed.
- Beginning with a model ensures that we are learning the important features of a distribution.
- The modeling approach is especially important in messy data science applications.

Two Modeling Traditions

Breiman (2001) defines two cultures of statistical modeling:

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Data scientists use both types of models.

- Both types of model have strengths and weaknesses.
 - Data models tend to support a priori hypothesis testing more easily.
 - Data models also tend to provide more interpretable results.
 - Algorithmic models can't be beat for pure power.



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 - Algorithmic models can't be beat for pure power.
- Algorithmic models are currently preferred in cutting edge prediction/classification applications.
- Many models can be viewed as data models or algorithmic models, depending on how they're used.

Characteristics of Models

Data models share several core features:

- Data models are built from probability distributions.
 - Data models are modular.
- Data models encode our hypothesized understanding of the system we're exploring.
 - Data models are constructed in a "top-down", theory-driven way.



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Algorithmic models are distinct from data models in several ways:

- Algorithmic models do not have to be built from probability distributions.
 - Often, they are based on a set of decision rules (i.e., an algorithm).
- Algorithmic models begin with an objective (i.e., a problem to solve) and seek the optimal solution, given the data.
 - They are built in a "bottom-up", data-driven way.

Suppose we believe the following:

- 1. BMI is positively associated with disease progression in diabetic patients after controlling for age and average blood pressure.
- After controlling for age and average blood pressure, the effect of BMI on disease progression is different for men and women.

We can represent these beliefs with a moderated regression model:

$$Y_{prog} = \beta_0 + \beta_1 X_{BMI} + \beta_2 X_{sex} + \beta_3 X_{age} + \beta_4 X_{BP} + \beta_5 X_{BMI} X_{sex} + \varepsilon$$

We can use R to fit our model to some patient data:

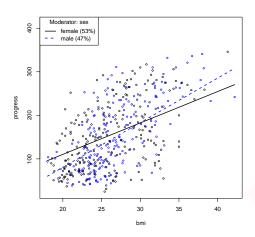
```
library (rockchalk)
##
## Attaching package: 'rockchalk'
  The following object is masked from 'package:plyr':
##
## summarize
## Load the data:
dataDir <- "../data/"
dDat <- readRDS(paste0(dataDir, "diabetes.rds"))</pre>
## Fit the regression model:
fit <- lm(progress ~ bmi * sex + age + bp, data = dDat)
```

```
partSummary(fit, -c(1, 2))
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -174.7986 27.0004 -6.474 2.58e-10
## bmi
            7.2106 0.8922 8.082 6.34e-15
## sexmale -90.1718 35.1134 -2.568 0.0106
            0.1691 0.2322 0.728 0.4670
## age
## bp
             1.4032 0.2385 5.884 7.97e-09
## bmi:sexmale 3.0257 1.3090 2.311 0.0213
##
## Residual standard error: 59.68 on 436 degrees of freedom
## Multiple R-squared: 0.4075, Adjusted R-squared: 0.4007
## F-statistic: 59.98 on 5 and 436 DF, p-value: < 2.2e-16
```

We can do a simple slopes analysis to test the group-specific effects of BMI on disease progression:

```
psOut <- plotSlopes(fit, plotx = "bmi", modx = "sex")
tsOut <- testSlopes(psOut)</pre>
```

We can also visualize the simple slopes:



Suppose we want to find the best predictors of disease progression among the variables contained in our dataset:

- Age
- BMI
- Blood Pressure
- Blood Glucose
- Sex

- Total Cholesterol
- LDL Cholesterol
- HDL Cholesterol
- Triglycerides
- Lamorigine

We could try best-subset selection.

- Fit a series of regression models wherein disease progression is predicted by all possible subsets of X variables.
- Choose the set of X variables that minimizes the prediction error.

```
library(leaps)
## Save the predictor variables' names:
xNames <- grep (pattern = "progress",
               x = colnames(dDat),
               invert = TRUE,
               value = TRUE)
## Train the models:
fit <- regsubsets(x = progress ~ .,
                  data = dDat,
                  nvmax = ncol(dDat) - 1
## Summarize the results:
sum <- summary(fit)</pre>
```

```
sum$outmat
##
                       bmi bp tc ldl hdl tch ltg glu sexmale
##
                                  11 11
                                      11
                                          11 11
                                                11 11
                                            - 11
                                            ***
## 5
                            11 ... 11
                                  11 11
                                       11 11 11 11 11
                                                    11
                                                        11 ... 11
                                  11 ... 11
                                       11 11 11 11 11
                                                    - 11
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## 7
                                  "<sub>+</sub>" "<sub>+</sub>" " "
                                                  II 🗼 II
                                  "*" "*" "*" "*" "*" "*"
## 9
                       "4" "4" "4" "4" "4" "4" "4" "4" "4"
## 10
```

```
## Variables selected by BIC:
xNames[with(sum, which[which.min(bic), -1])]
## [1] "bmi" "bp" "hdl" "ltg" "sex"
## Variables selected by Adjusted R^2:
xNames[with(sum, which[which.max(adjr2), -1])]
## [1] "bmi" "bp" "tc" "ldl" "tch" "ltg" "glu" "sex"
## Variables selected by Mallow's Cp:
xNames[with(sum, which[which.min(cp), -1])]
## [1] "bmi" "bp" "tc" "ldl" "ltg" "sex"
```

The results seem to be highly sensitive to the error measure. What should we do?

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- We could pick our favorite error measure and use its results.
- We could throw our hands up in defeat and quit.
- We could look at the results and pick the answer we like best.
 - The previous two suggestions are sub-optimal, but this one is actually unethical. Don't do this!

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If we think like a data scientist and get creative, we don't need to settle for these ambiguous results.

- We could implement a more robust method of calculating prediction error like *K-fold cross validation*.
- We can use resampling methods to quantify uncertainty in the variable selection process.

```
bic \leftarrow r2 \leftarrow cp \leftarrow matrix (NA, 100, ncol(dDat) - 1)
for (rp in 1 : 100) {
    ## Resample the data:
    tmp <- dDat[sample(1 : nrow(dDat), nrow(dDat), TRUE), ]</pre>
    ## Train the models:
    fit <- regsubsets(x = progress ~ .,
                        data = tmp,
                        nvmax = ncol(tmp) - 1
    sum <- summary(fit)</pre>
    ## Save the optimal selections:
    bic[rp, ] <- with(sum, which[which.min(bic), -1])
    r2[rp, ] <- with(sum, which[which.max(adjr2), -1])
    cp[rp, ] \leftarrow with(sum, which[which.min(cp), -1])
```

```
colMeans (bic)
##
   age bmi bp tc ldl hdl tch
##
   0.02 1.00 0.99 0.59
                          0.21
                               0.42 0.22
##
  ltg glu sexmale
##
   1.00 0.10 0.87
colMeans(r2)
##
   age bmi bp tc ldl hdl tch
   0.28 1.00 1.00 0.94 0.71
##
                               0.32 0.57
##
  ltg glu sexmale
##
   1.00 0.55 1.00
colMeans(cp)
##
   age bmi
                    tc ldl hdl tch
              bp
##
    0.10 1.00 0.99 0.91
                          0.57
                               0.26 0.45
##
   ltg glu sexmale
##
    1.00 0.37 1.00
```

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```
## Find the best subset via majority vote:
votes <- colMeans(rbind(bic, r2, cp)); round(votes, 3)</pre>
## age bmi bp tc ldl hdl tch
## 0.133 1.000 0.993 0.813 0.497 0.333 0.413
## ltg glu sexmale
## 1.000 0.340 0.957
preds <- xNames[votes > 0.5]; preds
## [1] "bmi" "bp" "tc" "ltg" "sex"
## Fit the winning model to the original data:
form <- paste0("progress ~ ",
             paste(preds, collapse = " + ")
fit <- lm(form, data = dDat)</pre>
```

```
partSummary(fit, -c(1, 2))
## Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -335.11146 25.68289 -13.048 < 2e-16
## bmi
      6.47376 0.68565 9.442 < 2e-16
             1.05016 0.21789 4.820 1.99e-06
## bp
## tc -0.29836 0.08833 -3.378 0.000796
## ltg
            60.36010 6.49158 9.298 < 2e-16
## sexmale -14.14306 5.40833 -2.615 0.009231
##
## Residual standard error: 54.83 on 436 degrees of freedom
## Multiple R-squared: 0.4999, Adjusted R-squared: 0.4941
## F-statistic: 87.15 on 5 and 436 DF, p-value: < 2.2e-16
```

Data Science for the Social and Behavioral Sciences

Social and behavioral scientists specialize in the types of problems for which a data science approach is most beneficial.

- · Social systems are messy, noisy, and chaotic.
- Social systems are usually complex systems.
- Social scientific constructs tend to be difficult to measure.
- · Human behavior produces a lot of data.
- Many layers of uncertainty open the door for a host of poor/unethical research practices.

References

- Breiman, L. (2001). Statistical modeling: The two cultures (with comments and a rejoinder by the author). *Statistical Science*, *16*(3), 199–231.
- O'Neil, C., & Schutt, R. (2014). *Doing data science: Straight talk from the frontline*. Sebastopol, CA: O'Reilly Media, Inc.