Expectations and Skills for Undergraduate Students Doing Research in Statistics and Data Science

Jo Hardin
Pomona College

jo.hardin@pomona.edu
@jo_hardin47
Github: hardin47

High-Impact Educational Practices

A Brief Overview

Excerpt from High-Impact Educational Practices: What They Are, Who Has Access to Them, and Why They Matter, by George D. Kuh (AAC&U, 2008)

Chart of High-Impact Practices (pdf)

High-Impact Educational Practices: A Brief Overview

The following teaching and learning practices have been widely tested and have been shown to be beneficial for college students from many backgrounds. These practices take many different forms, depending on learner characteristics and on institutional priorities and contexts.

Undergraduate Research

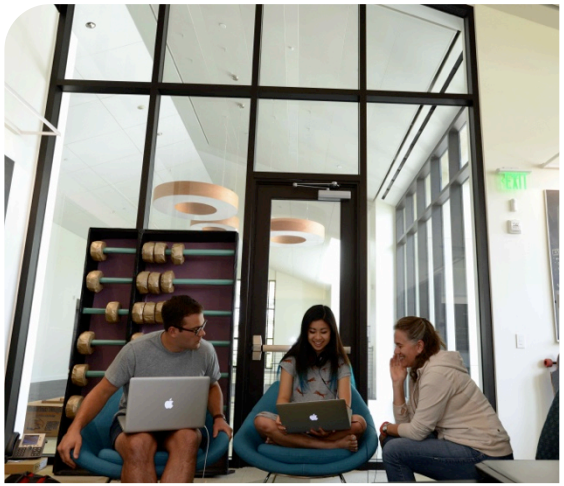
- Statistics curriculum guidelines
- Data science curriculum guidelines
- GAISE recommendations

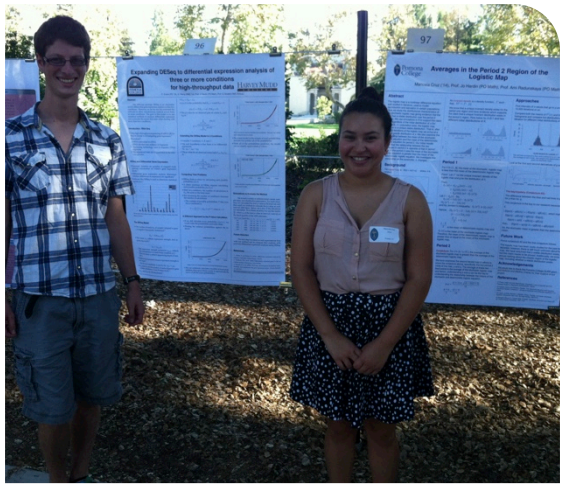
Needed skills for successful undergrad research

- Make an argument
- Engage with theory
- Work independently
- Wrangle data

My background

- Research with ~4 students / summer
- Senior thesis projects ~4 students / year
- 12 peer-reviewed pubs w/undergrads, 1 submitted





Make an Argument

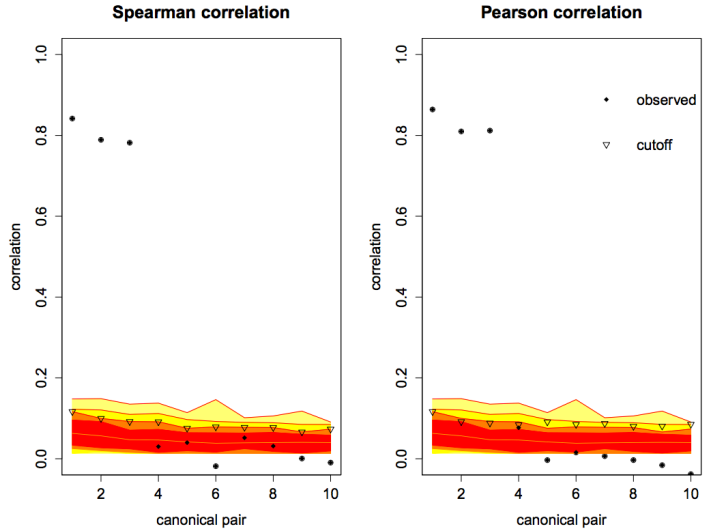
- Theoretical
- Simulation
- Literature

In the Classroom

- Hypothesis test using mean and median to demonstrate two different approaches to the same scientific hypothesis
- Simulation studies (e.g., bootstrap confidence intervals)
- How do we know that? How can we argue that result is better than the other?

Make an Argument

- As compared to what?
- Permutation test for cutoff
- Simulation analysis to demonstrate FP& FN rates



Stat Appl Genet Mol Biol. 2016 Apr;15(2):123-38. doi: 10.1515/sagmb-2014-0081.

Resistant multiple sparse canonical correlation.

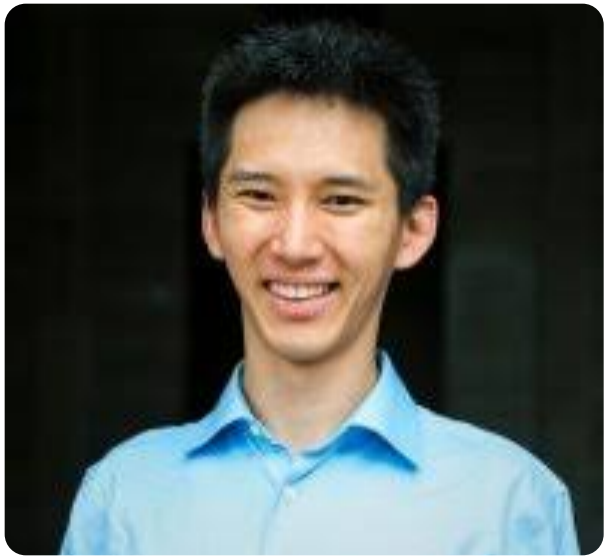
Coleman J, Replogle J, Chandler G, Hardin J.

Engage with Theory

- Connect theoretical ideas to core principles in statistics

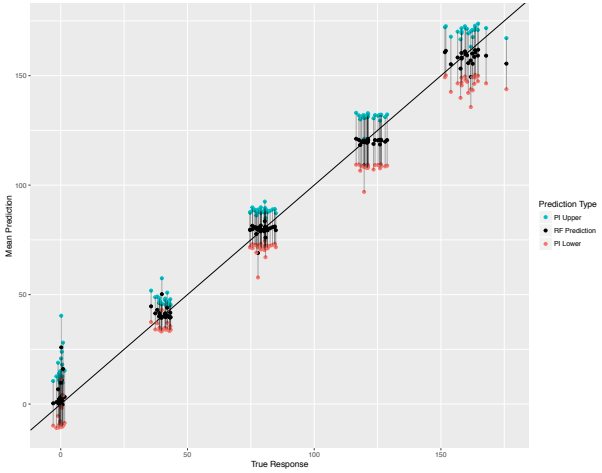
In the Classroom

- Moment generating function: **why** do they uniquely determine a distribution?
- Simulate theoretical results for visualization of the process.



Engage with Theory

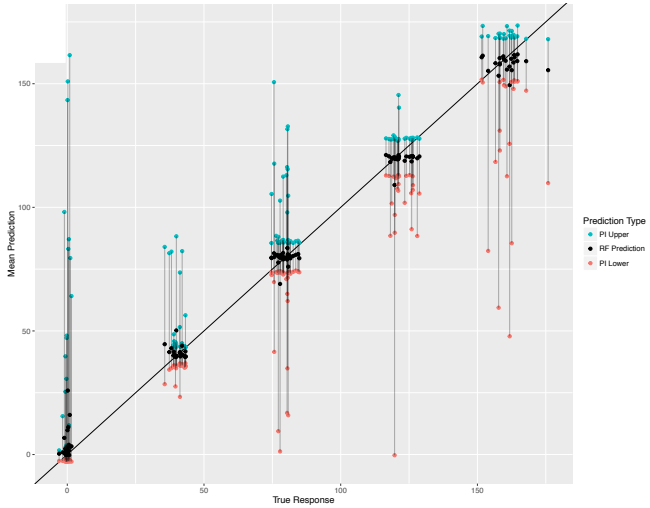
- June 2016 – July 2017
- Kept coming back to his knowledge of prediction intervals for SLR (MSE)
- Organization was impeccable



Constructing Prediction Intervals for Random Forests

Author:
Benjamin Lu

Advisor:
Dr. Jo Hardin



Work Independently

- What did you do?
- Why did you do it?
- What is the next step?
- What do I still not understand?

In the Classroom

- Independent projects (peer assessment!)
- Reflect on assignments (quickly or in detail)

HHMI PROJECT WITH DR. JO HARDIN & DR. DAN STOEBEL, SUMMER 2017

SEARCH

Share

June 27, 2017

—

today

1) Met with Dr. Hardin and Dr. Stoebel. Here is the plan:

• We are concerned about the unequal proportions of reads for each gene region across the different samples
• We are concerned about the top 25% (or less) of genes dominating the read counts, with very low counts for 75% of genes. This is a phenomenon consistent across all regions. We're also curious about the spread of raw counts within each sample.
-- Dominant genes affecting size factors? And the rank of size factors changing across different regions.
• I need to investigate the correlations between replicates within each sample, both Pearson and Spearman.

Moving forward

1) technical paper, Rmd file (2 pages) for Jonathan describing, put on github
• concerns about a few genes dominating the read counts in each region and overall and a summary of the most dominant genes
• the distribution of raw reads by sample (box plots)
• unequal proportions of raw counts by "region" across samples
• correlation coefficients between replicates
• comparing our data set with the CodY data set
2) Clustering Analysis!
• Madison reads papers and educates self on process, does a series of exploratory clustering analysis on new data
• Perform clustering analyses on data filtering out counts <~10 and >~100,000 or something, and disregarding rRNA/AS_rRNA and tRNA/AS_tRNA counts?
3) If time, investigate Optimal Sequencing Depth

Working Independently

- Madison's daily blog
- Use Google Doc to reflect (automatic updates back to you!)

questions

1) Are the high count genes in our DE 0%vs190% regulon?
2) The correlations between the replicates of each sample are pretty good...even the spearman (.75 - .95). What do we think about that and what further analysis could I do? (Maybe I could look at distances by gene specifically, so I'm not just looking an aggregate figure).
3) Could large counts really be affecting size factors? I'm confused about that because I thought the median method helped disregard outliers in the creation of size factors (see blog post 6/23). The question: are size factors really systematically being pulled around by the inclusion of IGR, or not, for example?
4) How could analyzing dispersions help our analysis?

todo

1) Look at replicate distances across Geneid
2) How could large counts be affecting size factors? Or including different gene regions be affecting size factors?
3) Look up information about dispersion and try to understand this better. Also read R with Convincing!
4) Work through clustering analysis resources Dr. Hardin sent me!
5) Revise technical paper for Jonathan with feedback!

Wrangle Data

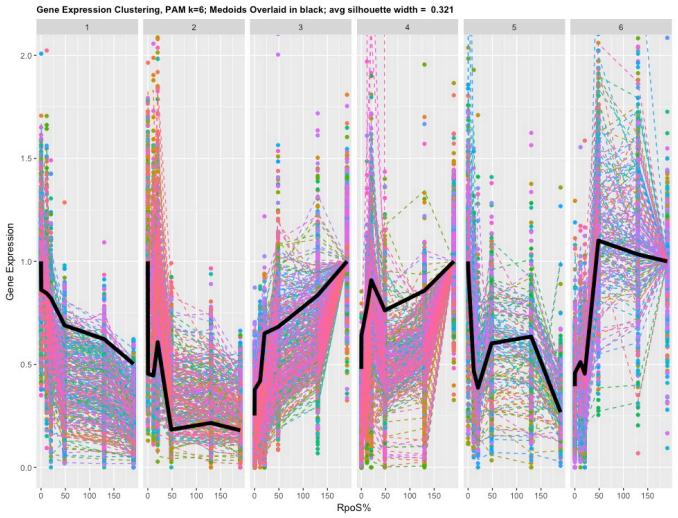
- Data Science
- Statistics
- Theoretical

In the Classroom

- Practice, practice, practice
- Learn how to problem solve independently.
- Data wrangling should happen in every class at every level.

Data Wrangling

- dplyr
- ggplot
- grep



- DataCamp
- Madison found a potentially important intergenic region

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The genome-wide transcriptional response to varying RpoS levels in *Escherichia coli* K-12.

Garrett T. Wong[1], Richard P. Bonocora[3], Alicia N. Schep[1], Suzannah M. Beeler[1], Anna J. Lee Fong[1], Lauren M. Shull[1], Lakshmi E. Batachari[1], Moira Dillon[1], Ciaran Evans[8], Carla J. Becker[1], Eliot C. Bush[1], Johanna Hardin[8], Joseph T. Wade[3,10#] and Daniel M. Stoebel[1#]

What else?

- Become a part of the larger community (e.g., quo() function in dplyr v 0.7.1, June 22, 2017)
- Use Git & GitHub (http://happygitwithr.com/)
- Bring your love of research to the classroom to generate excitement.

Thank you!

Jo Hardin
Pomona College

jo.hardin@pomona.edu
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