

# Michael Sekula

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## EDUCATION

- Doctor of Philosophy in Biostatistics** May 2020  
University of Louisville, Louisville, KY  
Dissertation: “Novel Bayesian methodology for the analysis of single-cell RNA-sequencing data”
- Master of Science in Biostatistics** May 2015  
University of Louisville, Louisville, KY  
Thesis: “optCluster: An R package for determining the optimal clustering algorithm and optimal number of clusters”
- Bachelor of Science in Mathematics Education** May 2010  
Saginaw Valley State University, University Center, MI  
Minor in Physics  
*Summa Cum Laude*

## PROFESSIONAL EXPERIENCE

- Assistant Professor** June 2020 – Present  
Department of Bioinformatics and Biostatistics  
University of Louisville, Louisville, KY
- Graduate Student Instructor** Aug. 2017 – May 2020  
Department of Bioinformatics and Biostatistics  
University of Louisville, Louisville, KY
- Science Teacher** Aug. 2010 – June 2013  
Pleasure Ridge Park High School  
Jefferson County Public Schools, Louisville, KY

## HONORS & AWARDS

- School of Public Health and Information Sciences Dean’s Award, 2020  
Graduate Dean’s Citation, 2020  
University of Louisville Faculty Favorite Nominee, 2019  
Best Student Presentation in Complex Modeling Techniques Session, Kentucky American Statistical Association Chapter, 2019  
Boyd Harshbarger Travel Award, Southern Regional Council on Statistics, 2018, 2019  
Best Student Presentation in Biostatistics Session, Kentucky American Statistical Association Chapter, 2018  
President of University of Louisville Biostatistics Club, 2016 – 2017  
University Fellowship, University of Louisville, 2015 – 2017  
ETS Recognition of Excellence for Mathematics: Content Knowledge, 2010  
Outstanding Senior in Mathematics Education, 2010

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## PROFESSIONAL MEMBERSHIPS

American Statistical Association  
Delta Omega, Beta Pi Chapter

## TEACHING

*University of Louisville*

PHUN 301: Quantitative Public Health <i>Substantially revised course</i>	2017
PHST 301: Quantitative Methods in Public Health <i>Previously PHUN 301 until 2018 Developed new hybrid implementation (2020)</i>	2018 – Present
PHST 302: Intermediate Statistical Analysis <i>Developed new course</i>	2019

## METHODOLOGICAL PUBLICATIONS

**Sekula, M.**, Gaskins, J., and Datta, S. A sparse Bayesian factor model for the construction of gene co-expression networks from single-cell RNA sequencing count data. (*Submitted for consideration of publication*)

**Sekula, M.**, Gaskins, J., and Datta, S. (2019). Detection of differentially expressed genes in discrete single-cell RNA sequencing data using a hurdle model with correlated random effects. *Biometrics*, 75(4), 1051-1062.

**Sekula, M.**, Datta, S., and Datta, S. (2017). optCluster: An R Package for Determining the Optimal Clustering Algorithm. *Bioinformatics*, 13(3), 101.

## COLLABORATIVE PUBLICATIONS

Gupta, A., Meriwether, K., Tuller, M., **Sekula, M.**, Gaskins, J., Stewart, J.R., Hobson, D., Cardenas-Trowers, O., Francis, S. (2020). Candy cane compared with boot stirrups in vaginal surgery: A randomized controlled trial. (*Recently accepted for publication in Obstetrics & Gynecology*)

## SOFTWARE PACKAGES

scREhurdle ([available on GitHub](#))  
hbfm ([available on GitHub](#))  
optCluster ([available on CRAN](#))

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PRESENTATIONS

“A sparse Bayesian factor model for the construction of gene co-expression networks from discrete single-cell RNA sequencing data”. Bioinformatics and Biostatistics Seminar Series. University of Louisville, Louisville, KY. September 6, 2019.

“A sparse Bayesian factor model for the construction of gene co-expression networks from discrete single-cell RNA sequencing data”. Poster session presented at the Southern Regional Council on Statistics Summer Conference. General Butler State Resort Park, KY. June 3, 2019.

“A sparse Bayesian factor model for the construction of gene regulatory networks from discrete single-cell RNA sequencing data”. Kentucky American Statistical Association Chapter Meeting. University of Louisville, Louisville, KY. April 4, 2019.

“A correlated random effects hurdle model for detecting differentially expressed genes in discrete single-cell RNA sequencing data”. Contributed paper session at East North American Region (ENAR). Philadelphia, PA. March 26, 2019.

“A correlated random effects hurdle model for detecting differentially expressed genes in discrete single-cell RNA sequencing data”. Contributed paper session at Joint Statistical Meetings (JSM). Vancouver, British Columbia, Canada. July 30, 2018.

“Detection of differentially expressed genes in discrete single-cell RNA sequencing data using a hurdle model with correlated random effects”. Poster session presented at the Southern Regional Council on Statistics Summer Conference. Virginia Beach, VA. June 5, 2018.

“Advanced R programming”. University of Louisville Biostatistics Club Seminar. University of Louisville, Louisville, KY. April 6, 2018.

“A correlated random effects hurdle model for differential gene expression analysis of discrete single-cell RNA sequencing data”. Kentucky American Statistical Association Chapter Meeting. University of Louisville, Louisville, KY. March 2, 2018.

“Hurdle model with correlated random effects for differential expression of single-cell RNA sequencing data”. Bioinformatics and Biostatistics Seminar Series. University of Louisville, Louisville, KY. October 27, 2017.

“Writing and building R packages”. Advanced Statistical Computing Course. Department of Bioinformatics and Biostatistics. University of Louisville, Louisville, KY. November 22 & 29, 2016.

“S4 objects and R packages”. Advanced Statistical Computing Course. Department of Bioinformatics and Biostatistics. University of Louisville, Louisville, KY. October 27 & 29, 2015.