

Michael Sekula

Curriculum Vitae

Date: 1/18/24

CONTACT INFORMATION

485 E. Gray St.
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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 AND EMPLOYMENT

Assistant Professor (Tenure-track) Oct. 2022 – Present
Department of Bioinformatics and Biostatistics
University of Louisville, Louisville, KY

Assistant Professor (Term) June 2020 – Oct. 2022
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

- University of Louisville Faculty Favorite Nominee, 2022, 2021, 2019

- School of Public Health and Information Sciences Dean's Award, University of Louisville, 2020
- Graduate Dean's Citation, University of Louisville, 2020
- Best Student Presentation in Complex Modeling Techniques Session, Kentucky American Statistical Association Chapter, 2019
- Boyd Harshbarger Travel Award, Southern Regional Council on Statistics, 2019, 2018
- 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, Saginaw Valley State University, 2010

PROFESSIONAL MEMBERSHIPS

- American Statistical Association (ASA)
- Delta Omega Honor Society, Beta Pi Chapter
- Kentucky Academy of Science

TEACHING

University of Louisville

PHST 200: Reasoning with Data in Daily Life

- 2021 – Spring (*Developed new course*), Fall
- 2022 – Spring, Fall
- 2023 – Spring, Fall (*Co-instructor - 50% of lectures*)
- 2024 – Spring (*Co-instructor - 50% of lectures*)

PHST 301: Quantitative Methods in Public Health

- 2018 – Fall (*Previously PHUN 301 until Fall 2018*)
- 2019 – Fall
- 2020 – Fall (*Developed new hybrid/online course implementation*)
- 2021 – Spring, Summer, Fall

PHST 302: Intermediate Statistical Analysis

- 2019 – Spring (*Developed new course*)
- 2021 – Spring (*Co-instructor - 50% of lectures*)

PHST 602: Biostatistics Seminar

- 2022 – Spring, Fall
- 2023 – Spring, Fall
- 2024 – Spring (*Co-instructor - 50% of lectures*)

PHST 703: Biostatistical Consulting Practicum

- 2022 – Summer (*2 students*)

PHST 710: Advanced Statistical Computing I

- 2023 – Fall (*Co-instructor - 50% of lectures*)

PHST 750: Statistics for Bioinformatics

- 2024 – Spring (*Co-instructor - 50% of lectures*)

PHUN 301: Quantitative Public Health

- 2017 – Fall (*Substantially revised course*)

STUDENT MENTORING

PhD students for whom I serve(d) as a committee member:

Irina Kondaurova, Biostatistics (TBD) TBD

Yasin Parh, Biostatistics (Expected 2024-2025) TBD

Anish Mukherjee, Biostatistics (Expected Spring/Summer 2024) TBD

Farhin Rahman, Biostatistics (Summer 2023). “Statistical Inference on Lung Cancer Screening Using the National Lung Screening Trial Data”

Sagnik Bhadury, Biostatistics (Fall 2022). “Bayesian Methods for Graphical Models with Neighborhood Selection”

Siddhesh Kulkarni, Biostatistics (Summer 2022). “Bayesian Methodologies for Constrained Spaces”

MS students for whom I serve(d) as a committee member:

Colin Jones, Oral Biology (Spring 2023). “Kentucky Dentist Attitudes towards Medicaid: Participation Considered via Stages of Change Algorithm”

RESEARCH FUNDING

Currently Funded Grants

| | |
|-----------------|--|
| Title: | Quantifying Medicaid Policies Aimed at Increasing Health Equity: A Comparative Study Over Time |
| Funding Agency: | Kentucky Cabinet for Health and Family Services – State University Partnership Program |
| Role: | PI |
| Effort: | 30% |
| Duration: | 07/01/2023 - 06/30/2024 |
| Total Costs: | \$262,812 |
| Direct Costs: | \$137,668 |

Description: The objective of this research is to determine, in context of health policy ecosystem, which policies, policy elements, or combination policy and elements were most effective in promoting health equity during the SARS-CoV-2 Public Health Emergency period.

Title: Functional Microbiomics, Inflammation and Pathogenicity – ADMIN CORE

Funding Agency: National Institutes of Health – National Institute of General Medical Sciences (NIH-NIGMS)

PI: R. Lamont

Role: Bioinformatician

Effort: 10%

Duration: 03/01/23 – 02/29/28

Description: The purpose of the Administrative Core is to provide a formal governance structure for the administrative, fiscal and scientific oversight of this Phase 2 COBRE.

Previously Funded Grants

Title: Functional Microbiomics, Inflammation and Pathogenicity – ADMIN CORE

Funding Agency: National Institutes of Health – National Institute of General Medical Sciences (NIH-NIGMS)

PI: R. Lamont

Role: Bioinformatician

Effort: 10%

Duration: 09/01/22 – 02/28/23

Total Costs: \$1,085,951

Direct Costs: \$705,162

Description: The Administrative Core will provide overall governance and will ensure that the COBRE projects and cores in Functional Microbiomics, Inflammation and Pathogenicity work together in a cohesive and coordinated manner.

Title: Identifying and Removing Barriers to Treatment of Hepatitis C Infection in Kentucky Medicaid

Funding Agency: Kentucky Cabinet for Health and Family Services – State University Partnership Program

PI: B. Little

Role: Co-investigator

Effort: 15%

Duration: 07/01/2020 - 06/30/2022

Total Costs: \$391,787

Direct Costs: \$262,843

Description: The overarching goal of this study is to perform population health analyses aimed at identification of patients with hepatitis C virus and decreasing barriers to treatment for Kentucky Medicaid beneficiaries.

Funded Contract Work

| | |
|----------------|---|
| Funding Group: | University of Louisville School of Dentistry |
| Effort: | 40% |
| Duration: | January 2022 - Present |
| Description: | Collaborative support in the planning, design, and statistical analysis of research projects within the school. Prepare statistical write-ups for training, protocols, proposals, grants, and publications. Provide mentorship and statistical support to residents during their thesis project work. |

SERVICE ACTIVITIES (INTRAMURAL)

- SPHIS Teaching Faculty Learning Community, 2018 - 2021
- SPHIS Faculty Council, July 2021 – June 2023
- Biostatistics PhD Comprehensive Exam Committee, 2021 - Present
- Course Director – PPH 523, Fall 2021, Fall 2022, Fall 2023

SERVICE ACTIVITIES (EXTRAMURAL)

- Judge, American Statistical Association – Kentucky Chapter Spring Meeting, 2021
- Journal Referee
 - BMC Bioinformatics (2023)
 - BMC Medical Research Methodology (2021)
 - Briefings in Bioinformatics (2022)
 - Computational Statistics & Data Analysis (2020)
 - Journal of Statistical Computation and Simulation (2020)
 - Statistics in Medicine (2022, 2023)

METHODOLOGICAL PUBLICATIONS (PEER-REVIEWED JOURNALS)

1. Wu, D., Gaskins, J.T., **Sekula, M.**, Datta, S. (2023). Inferring Cell–Cell Communications from Spatially Resolved Transcriptomics Data Using a Bayesian Tweedie Model. *Genes*, 14(7):1368.
2. **Sekula, M.**, Gaskins, J., Datta, S. (2022). Single-cell differential network analysis with sparse Bayesian factor models. *Frontiers in Genetics*, 12, 810816.
3. **Sekula, M.**, Gaskins, J., Datta, S. (2020). A sparse Bayesian factor model for the construction of gene co-expression networks from single-cell RNA sequencing count data. *BMC Bioinformatics*, 21, 361.
4. **Sekula, M.**, Gaskins, J., 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.

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

COLLABORATIVE PUBLICATIONS (PEER-REVIEWED JOURNALS)

1. Patel, B., Rose, J., Nash, J., **Sekula, M.**, Gioia, C., Deguchi, T., Gudhimella, S., Gandhi, V. (2024). Variability associated with maxillary infrazygomatic crest and palatal bone width, height, and angulation in subjects with different vertical facial growth types: a retrospective cone-beam computed tomography study. *The Angle Orthodontist*. 10.2319/062023-430.1.
2. Tan, J., Lamont, G., **Sekula, M.**, Hong, H., Sloan, L., Scott, D.A. (2024). The transcriptomic response to cannabidiol of *Treponema denticola*, a phytocannabinoid-resistant periodontal pathogen. *Journal of Clinical Periodontology*. Feb;51(2):222-232. doi: 10.1111/jcpe.13892. Epub 2023 Dec 17. PMID: 38105008.
3. Fischer, K., Metz, M., **Sekula, M.**, Katwal, D., Hannigan, D., Williams, T. (2023). Effect of Educational Intervention on CAD/CAM Technology to Preclinical Dental Students. *European Journal of Dental Education*. DOI: 10.1111/eje.12953.
4. Ramage, A., Lopez, B., Fischer, K., **Sekula, M.**, Santaella, G., Scarfe, W., Brasil, D., de Oliveria-Santos, C. (2023). Filtered Back Projection vs. Iterative Reconstruction for CBCT: Effects on Image Noise and Processing Time. *Dentomaxillofacial Radiology*. 52(8), 20230109. DOI:10.1259/dmfr.20230109
5. Shah, B., Dukka, H., Alhachache, S., Hill, M., Cheng, G. L., **Sekula, M.** (2023). Analysis of risk factors for early crestal bone loss in osseointegrated, submerged implants prior to restoration. *Journal of Periodontology*, 1-9. <https://doi.org/10.1002/JPER.23-0161>
6. Gupta, A., Meriwether, K., Tuller, M., **Sekula, M.**, Gaskins, J., Stewart, J.R., Hobson, D., Cardenas-Trowers, O., and Francis, S. (2020). Candy cane compared with boot stirrups in vaginal surgery: A randomized controlled trial. *Obstetrics & Gynecology*, 136(2), 333-341.

SOFTWARE PACKAGES

- scSFMnet ([available on GitHub](#))
- scREhurdle ([available on GitHub](#))
- hbfm ([available on GitHub](#))
- optCluster ([available on GitHub](#))

PRESENTATIONS

1. “Detection of differentially expressed genes in discrete single-cell RNA sequencing data using a hurdle model with correlated random effects” Bioinformatics and

- Biostatistics Seminar Series. University of Louisville, Louisville, KY. March 3, 2023.
2. “Single-cell differential network analysis with sparse Bayesian factor models”. Bioinformatics and Biostatistics Seminar Series. University of Louisville, Louisville, KY. January 21, 2022.
 3. “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.
 4. “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.
 5. “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.
 6. “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.
 7. “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.
 8. “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.
 9. “Advanced R programming”. University of Louisville Biostatistics Club Seminar. University of Louisville, Louisville, KY. April 6, 2018.
 10. “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.
 11. “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.