Katerina Kechris

CURRENT POSITION

Department of Biostatistics and Informatics 2006-present
Colorado School of Public Health, University of Colorado Anschutz Medical Campus
Professor with tenure (2018-present)
Associate Professor with tenure (2012-2018)
Assistant Professor (2006-2012)

Affiliations

Computational Bioscience Program (Core Faculty) 2006-present
School of Medicine, University of Colorado Anschutz Medical Campus
Program in Integrative and Systems Biology (Training Faculty) 2012-present
College of Liberal Arts and Sciences, University of Colorado Denver
Interdisciplinary Quantitative Biology Program (Training Faculty) 2012-present
BioFrontiers Institute, University of Colorado Boulder (Affiliate Member) 2014-present
University of Colorado Boulder
Human Medical Genetics and Genomics Program (Training Faculty) 2014-present
School of Medicine, University of Colorado Anschutz Medical Campus
Biomedical Science Program (Training Faculty) 2015-present
School of Medicine, University of Colorado Anschutz Medical Campus
Division of Biomedical Informatics and Personalized Medicine (Secondary Faculty) 2016-present
Colorado Center for Personalized Medicine (Member)
School of Medicine, University of Colorado Anschutz Medical Campus
Center for Innovative Design and Analysis (Associate Director of Data Science) 2021-present
University of Colorado Anschutz Medical Campus

Contact Information

Department of Biostatistics and Informatics
Colorado School of Public Health
University of Colorado Anschutz Medical Campus
13001 E. 17th Place B-119
Aurora, CO 80045

Legal Name: Katherina Kechris-Mays
Phone: (303) 724-4363
Fax: (303) 724-4489
katerina.kechris@ucdenver.edu
http://csph.ucdenver.edu/Sites/Kechris/

EDUCATION

B.S., Applied Mathematics 1997
University of California Los Angeles
Summa cum laude

M.A., Statistics 1999
University of California Berkeley

Ph.D., Statistics 2003
National Science Foundation Graduate Research Fellowship
University of California Berkeley
Dissertation: "Statistical Methods for Discovering Features in Molecular Sequences"
Committee: Peter Bickel (advisor), Terence Speed, Alexander Glazer

Post-Doctoral Fellow 2003-2005
Sloan Foundation/Department of Energy Fellowship
University of California San Francisco
Department of Biochemistry and Biophysics; Department of Epidemiology and Biostatistics
Mentors: Hao Li, Ru-Fang Yeh

PRIOR ACADEMIC APPOINTMENTS AND PROFESSIONAL POSITIONS

Research Assistant 1998
Department of Statistics, University of California Los Angeles Supervisor: Wing Wong
- Collected and analyzed data on β-hairpin turns in polypeptide sequences.

Graduate Student Researcher 1998
Department of Statistics, University of California Berkeley Supervisor: Deborah Nolan
- Studied the effects of short-term educational programs and methods for evaluating these programs.

Statistical Consultant 2000
Department of Statistics, University of California Berkeley Supervisor: Terence Speed
- Provided statistical consulting to campus researchers on subjects ranging from geology to linguistics.

Graduate Student Researcher 1998-2003
Department of Statistics, University of California Berkeley Advisor: Peter Bickel
- Developed methods for the identification of important sites in protein sequences.
- Improved model-based DNA motif finding algorithms by incorporating information content.

Collaborators: Alexander Glazer, Michael Eisen

Invited Summer Researcher 2006, 2007
Department of Statistics, University of California Berkeley

Statistical Consultant 2013
Statistical analysis of gene expression profiles for the *National Foundation for Fertility Research*

HONORS AND AWARDS

- NCAA Division I Intercollegiate Athletic Scholarship Track & Field, University of California Los Angeles 1995-1997.
- NCAA Division I All-American Track & Field 3000m 1997.
- Sherwood Prize in Mathematics Recognizing outstanding graduating seniors in mathematics. Department of Mathematics, University of California Los Angeles 1997
- Summa cum laude BS, Mathematics, University of California Los Angeles 1998
- National Science Foundation Graduate Research Fellowship 1999-2002.
- National Science Foundation VIGRE (Vertical Integration of Research and Education in the Mathematical Sciences) Fellowship Department of Statistics, University of California Berkeley 2002-2003.
- Evelyn Fix Memorial Medal and Citation Awarded to the Ph.D. student showing the greatest promise in statistical research, with preference for applications to biology and problems of health. Department of Statistics, University of California Berkeley 2003.
- Alfred P. Sloan Foundation/U.S. Department of Energy Post-Doctoral Fellowship in Computational Molecular Biology 2003-2005.
- University of Colorado Denver Nominee, Microsoft Research New Faculty Fellowship Grant 2009
- Mathematical Sciences Research Institute (MSRI) Travel Grant Workshop on Mathematical Genomics Apr 13-15, 2009.
- NIH Career Development Award (K01) 2007-2013.
- Colorado School of Public Health, Excellence in Faculty Research Award (2017)
- Fellow of the American Statistical Association (2019)
- Delta Omega Public Health Honor Society Alpha Upsilon Chapter Inductee (2020)
- Chancellor’s Teaching Recognition Award University of Colorado Anschutz Medical Campus (2020)

PROFESSIONAL SOCIETIES

- Institute of Mathematical Statistics (*Member* 2002-present)
- American Statistical Association (*Member* 2004-present)
- International Society for Computational Biology (*Member* 2004-present)
- Research Society on Alcoholism (*Member* 2008-present)
- Western North American Region of the International Biometric Society (*Member* 2016-present)
- Western North American Region of the International Biometric Society (*President Elect* 2018, *President* 2019, *Past President* 2020)
- American Statistical Association Section on Statistics in Genomics and Genetics (*Chair-Elect* 2020, *Chair* 2021, *Past Chair* 2022)

PROFESSIONAL LEADERSHIP AND SERVICE

Department/Program

- Faculty Search Committee, Computational Bioscience Program (2006)
- Seminar Co-Coordinator (2006-2008) (with J. Leiferman).
- PhD Preliminary Exam Coordinator (Computational Bioscience Program) (2007-2010)
- Faculty Search Committee, Colorado Biostatistics Consortium (2012)
- Student Recruiting Coordinator (2009-2012) Coordinating recruiting efforts by faculty at career fairs and undergraduate seminars.
- Implementation and Assessment Committee (2012-2013) Preparing departmental self-study document for external review of department.
- Colorado Biomedical Informatics Summer Training Program Committee (Computational Bioscience Program) (2013) Coordinating summer training program for undergraduates and graduate students.
- Computing Committee (2010-2014) Coordinating shared computer resources for the support of computer-intensive biostatistics methods research.
- Department Chair Search Committee, Biostatistics and Informatics (2013-2014)
- PhD Qualifying Exam Coordinator (Biostatistics) (2010-2013, 2016) Coordinating exam questions and grading.
- PhD Student Admissions Committee (Computational Bioscience Program) (2006-2011, 2014, 2016)
- Statistical Genomics Working Group Co-Organizer (with T. Fingerlin & D. Ghosh) (2014-2016)
- PhD Student Task Force Chair (2018) Developed plan to grow and enhance PhD program.
- Data Science Certificate Committee (2018)
- MS/PhD Qualifying Exam Committee (Biostatistics) (2008-present)
- Human Medical Genetics and Genomics Program Preliminary Committee (2017-2019)
- Faculty Search Committee Chair, Biostatistics and Informatics (2018-2019)
- Student Recruiting Committee (Biostatistics) (2019)
- CCTSI/Biostatistics, Epidemiology and Research Design (BERD) Education Committee (2019)
- PhD Theory Committee Chair (2019-2020) Evaluation and development of PhD theory curriculum.
- Program Review Committee Chair (Computational Bioscience Program) (2019) Review training program, organized retreat
- Post-Tenure Review Committee Chair (2020)
- Curriculum Update Committee Chair (Computational Bioscience Program) (2020)
- Center for Innovative Design and Analysis (CIDA) Executive Committee (2018-present)

Colorado School of Public Health (CSPH)

- CSPH Booth Coordinator Joint Statistical Meetings, Aug 3-7, 2008, Denver, CO
- Seminar Co-Coordinator (2008-2009) (with J. Leiferman)
- Faculty Senate (2009-2013) Representative to principal unit of CSPH faculty governance.
- Strategic Planning Committee (2013) Developing strategic plans for research and creative activities.
- Scholarship and Awards Committee (2012-2014)

- Faculty Search Committee, Epidemiology (2015)
- Behavioral Health Initiative Committee (2016-2017)
- Appointments, Promotions and Tenure (APT) Committee (2018-present)
- Gender Equity in Academia Task Force (2021-present)

Campus, University and Regional

- Executive Board, Center for Computational and Mathematical Biology, University of Colorado Denver (2011) Evaluating center for attaining research and pedagogical goals.
- Faculty Search Committee, Department of Pediatrics/Children's Hospital Research Institute (2013)
- Judge for 28th Annual Student Research Forum Presentations (2013)
- Lung Systems Biology Working Group Organizer (2013-2016) Organizing joint working group between Anschutz Medical Campus and National Jewish Health (with R. Bowler, NJH)
- Bioinformatics Faculty Search Committee (2016-2017), Department of Immunology & Microbiology
- Invited Marijuana Proficiency Testing Expert Panel (2016) Colorado Department of Public Health and Environment
- Steering Committee (2014-2018) Mini-Symposium "The Power of Informatics to Advance Health", University of Colorado Anschutz Medical Campus
- Graduate Council (2015-2019) Advises the Graduate School Dean on matters relating to development, coordination, and evaluation of graduate programs.
- Colorado Center for Personalized Medicine Translational Committee (2017-2019) To develop personalized medicine research and clinical educational opportunities
- Deep Learning and Systems Biology Working Group Organizer (2019-2020) Organizing joint working group between Anschutz Medical Campus and National Jewish Health (with R. Bowler and S. Humphries, NJH)
- University of Colorado Cancer Center Biostatistics and Bioinformatics Shared Resource Internal Advisory Board (2020-present)
- DEI Graduate Program Faculty Task Force (2021-present)
- Faculty Search Committee, Center for Health Artificial Intelligence (2021-present)
- Director Search Committee, Colorado Center for Personalized Medicine (2021-present)

Conference Organization

- Session Chair Bioinformatics Workshop, 7th Graybill Conference, Fort Collins, CO, Jun 12-15, 2007
- Session Chair Joint Statistical Meetings, Denver, CO, Aug 3-7, 2008
- Session Chair WNAR Annual Meeting, Portland, OR, Jun 14-17, 2009
- Invited Session Organizer WNAR Annual Meeting, Fort Collins, CO, Jun 17-20, 2012
- Program Committee (WNAR Representative) Joint Statistical Meetings, San Diego, CA, Jul 28-Aug 12, 2012
- Program Committee (WNAR Representative) and Session Chair Joint Statistical Meetings, Montreal, Canada, Aug 3-8, 2013
- Organizing Committee and Session Chair Program on Beyond Bioinformatics Opening Workshop, Statistical and Applied Mathematical Sciences Institute (SAMSI), Research Triangle Park, NC, Sep 8-12, 2014
- Organizing Committee and Session Chair Statistical and Computational Challenges in Omics Data Integration, SAMSI, Research Triangle Park, NC, Feb 16-17, 2015
- Session Chair and Poster Judge BioInfoSummer, Sydney, Australia, Dec 7-11, 2015
- Session Chair and Poster Judge 14th Graybill Conference sponsored by ASA Section on Statistics in Genomics and Genetics, Fort Collins, CO, Jun 5-7, 2017
- Session Chair Joint Statistical Meetings, Baltimore, MD, Jul 29-Aug 3, 2017.
- Session Chair 5th Annual Mini-Symposium: The Power of Informatics to Advance Health, Denver, CO, Apr 18, 2018
- Student Paper Competition Committee WNAR Annual Meeting, Edmonton, Canada June 24-27, 2018
- Invited Session Organizer Joint Statistical Meetings, Vancouver, Canada, Jul 28-Aug 2, 2018
- Session Chair: Oral Presentation of Student Paper Competition WNAR (Virtual), June 15, 2020
- Session Moderator: IBC (Virtual) Aug 21, 2020

- Session Organizer and Chair: Early Investigator Mentoring WNAR (Virtual), Dec 4, 2020
- Session Moderator: COPDGene Disease Progression Workshop Jan 13-14, 2021
- Organizing Committee Statistics in the Big Data Era, Simons Institute Berkeley, CA June 1-3, 2022

Professional Organizations and External Service

- Working Group Leader Program on Beyond Bioinformatics 2014-2015, SAMSI (w/ H. Zhao, Yale)
- External Advisory Committee Channing Division of Network Medicine Training Grant (T32HL007427) (2019-present)
- Budget and Finance Committee - International Biometric Society (2020-present)
- Community Advisory Board Member - Bioconductor: (2021-pesent)
- Awards Committee - Leadership Academy: For Emerging Leaders in Statistics: Committee of Presidents of Statistical Societies (COPSS) (2021-present)
- Awards Committee - WNAR: (2021-present)
- Collaborative Cohort of Cohorts for COVID-19 Research (C4R) Omics Working Group Convener: (2021-present)

CONTINUING PROFESSIONAL EDUCATION

- NSF Regional Grants Conference (2-day, Mar 2006)
- CU Women Succeeding Faculty Development Symposium (1-day, Mar 2006)
- CU Health Sciences Library Courses (PubMed, EndNote, Online Text; Jan 2007)
- NHLBI Genomics Hands-On Workshop (lab-based, 2-day, Jul 2007)
- Statistical Challenges in Proteomics (1-day course, Joint Statistical Meetings, Aug 2008)
- Jackson Laboratory Mouse Genome Informatics Workshop (2-hr, Oct 2008)
- Ethics in Research (PHCL 7605, 1 cr., Dept. of Pharmacology; Fall 2008)
- Receptors and Cell Signaling (PHCL 7606, 3 cr, Dept. of Pharmacology; Spring 2009)
- Safe Zone Training: Create safer campus environment for gender/sexual identities (2-hr, Mar 2014)
- Leadership for Innovative Team Science (LITeS): Year-long program to enhance management and leadership skills, Colorado Clinical and Translational Sciences Institute (year-long; 2014-2015)
- ASA Women in Statistics and Data Science Conference, Charlotte, NC (3-day, Oct 2016)
- Future of Bioscience Graduate & Postdoctoral Training Conference, Denver, CO (3-day, Jun 2017)
- Statistical Methods for Single-Cell RNA-Seq Analysis (half-day, Joint Statistical Meetings, Aug 2018)
- Mentoring Workshop, Graduate School CU Anschutz (4 2-hour sessions, Spring 2020)
- Colorado School of Public Health Human Resources Training: Communicating as a Leader, Leave Management Training, Performance Management (4 hours, Spring 2020)
- Equity Certificate Program (6 hours, Feb 2021)

REVIEW, REFEREE AND EDITORIAL ACTIVITIES

Associate Editor

- *BMC Bioinformatics* 2015-2019
- *Biometrics* 2019-present

NIH Study Section Regular Member

- Biodata Management and Analysis, BDMA (2019-present)

NIH Study Section *Ad Hoc* Member

- Neurological Sciences and Disorders B Study Section, NINDS (Jun 2010)
- SBIR/STTR Applications Small Business: Interdisciplinary Molecular Sciences and Training IRG, IMST (Feb 2013)
- Shared Instrumentation Grant Program (S10), ZRG1 BST-F 30 (Apr & Oct 2014)
- Biodata Management and Analysis, BDMA (Oct 2015)
- Kidney, Nutrition, Obesity & Diabetes Epidemiology, ZRG1 PSE-U (02) (Mar & Oct 2016)

- NIH Common Fund, ZRG1 MOSS-R (70) R (Dec 2017)
- R25 ZGM1TRN-7 MIRA (Mar 2018)
- Neurotoxicology and Alcohol Study Section (June 2018)
- Biodata Management and Analysis, BDMA (Oct 2018)
- Environmental Influences on Child Health Outcomes (ECHO) Opportunities and Infrastructure Fund (Feb 2019)

Grant Review Committees

- Butcher Seed Grant Reviewer, University of Colorado System (2012)
- Colorado Clinical & Translational Science Institute CO-Pilot Program Grant Reviewer (2012, 2013)
- Butcher Innovation Awards Committee Co-Chair, University of Colorado System (2016)
- Colorado Clinical & Translational Science Institute pre-K, K to R Grant Reviewer (2016, 2018-2020)

Statistical Expert, *The Plant Cell* (reviewed genomic and statistical analyses), 2009-2014

Journal and Scientific Meeting Reviewer

- 2003-2010*: Bioinformatics, Genome Research, Genome Biology, Journal of Biomedical Informatics, Proceedings of the National Academy of Sciences USA, Statistical Applications in Genetics and Molecular Biology, The 3rd International Symposium on Bio- and Medical Informatics and Cybernetics*
- 2011-2020*: Bioinformatics, BMC Bioinformatics, BMC Systems Biology, BMC Complementary and Alternative Medicine, Elsevier Major Reference Works, Frontiers in Genetics, Genome Biology, Human Genomics, Journal of the American Statistical Association, Metabolites*, *Nature Communications*, *Respiratory Research, Statistics and Its Interface*
- 2021-present: *Nature Communications*, *Metabolites, Molecules, Cell, Analytical Chemistry, European Respiratory Journal*

External Promotion and Tenure Review (2016, 2018-present)

RESEARCH RECORD - BIBLIOGRAPHY

(* students/post-docs, $^{\#}$ joint corresponding authors, ¶ authors contributed equally)

Peer-Reviewed Journals

1. P. Bickel, **K. Kechris**, P. Spector, G. Wedemayer and A. Glazer (2002) Finding 'important' sites in proteins. *Proceedings of the National Academy of Sciences, USA* 99:14764-14771.
2. **K. Kechris**, E. van Zwet, P. Bickel and M. Eisen (2004) Detecting DNA regulatory motifs by incorporating positional trends in information content. *Genome Biology* 5:R50.
3. A. Klebes*, A. Sustar, **K. Kechris**, H. Li, G. Schubiger and T. Kornberg (2005) Regulation of cellular plasticity in *Drosophila* imaginal disc cells by the Polycomb group, trithorax group and *lama* genes. *Development* 132:3753-3765.
4. E. van Zwet, **K. Kechris**, P. Bickel and M. Eisen (2005) Estimating motifs under order restrictions. *Statistical Applications in Genetics and Molecular Biology* 4(1):1.
5. **K. Kechris**, J. Lin, P. Bickel and A. Glazer (2006) Quantitative exploration of the occurrence of lateral gene transfer using nitrogen fixation genes as a case study. *Proceedings of the National Academy of Sciences, USA* 103:9584-9589.
6. S. Bhave, C. Hornbaker, T. Phang, L. Saba, R. Lapadat, **K. Kechris**, J. Gaydos, D. McGoldrick, A. Dolbey, S. Leach, B. Soriano, A. Ellington, E. Ellington, K. Jones, J. Mangion, J. Belknap, R.W. Williams, L. Hunter, P. Hoffman and B. Tabakoff (2007) The PhenoGen informatics website: Tools for analyses of complex traits. *BMC Genetics* 8:59.
7. C. Washenberger, J. Han, **K. Kechris**, B. Jha, R. Silverman and D. Barton (2007) Hepatitis C virus RNA: Dinucleotide frequencies and cleavage by RNase L. *Virus Research* 130:85-95.
8. B. Tabakoff, L. Saba**, K. Kechris**, W. Hu, S. Bhave, D. Finn, N. Grahame and P. Hoffman (2008) The genomic determinants of alcohol preference in mice. *Mammalian Genome* 19:352-65.
9. W. Hu*, L. Saba, **K. Kechris**, S. Bhave, P. Hoffman and B. Tabakoff (2008) Genomic insights into acute alcohol tolerance. *Journal of Pharmacology and Experimental Therapeutics* 326:792-800.

10. **K. Kechris** and H. Li. (2008) c-REDUCE: Incorporating sequence conservation to detect motifs that correlate with expression. *BMC Bioinformatics* 9:506.
11. **K. Kechris**¶, Y.-H. Yang¶ and R.-F. Yeh (2008) Prediction of alternatively skipped exons and splicing enhancers from exon junction arrays. *BMC Genomics* 9:551.
12. B. Tabakoff, L. Saba, M. Printz, P. Flodman, C. Hodgkinson, D. Goldman, G. Koob, H. Richardson, **K. Kechris**, R. Bell, N. Hübner, M. Heinig, M. Pravenec, J. Mangion, L. Legault, M. Dongier, K. Conigrave, J. Whitfield, J. Saunders, B. Grant, P.L. Hoffman and WHO/ISBRA Study on State and Trait Markers of Alcoholism (2009) Genetical genomic determinants of alcohol consumption in rats and humans. *BMC Biology* 7:70.
13. A.N. Glazer and **K. Kechris** (2009) Conserved amino acid sequence features in the α subunits of MoFe, VFe, and FeFe nitrogenases. *PLoS ONE* 4:e6136*.*
14. E. Siewert* and **K. Kechris** (2009) Prediction of motifs based on a repeated-measures model for integrating cross-species sequence and expression data. *Statistical Applications in Genetics and Molecular Biology* 8(1):36.
15. B. Biehs*, **K. Kechris**, S.M. Liu and T. Kornberg (2010) Hedgehog targets in the Drosophila embryo and the mechanisms that generate tissue-specific outputs of Hedgehog signaling. *Development* 137:3887-98.
16. **K. Kechris**, B. Biehs* and T. Kornberg (2010) Generalizing moving averages for tiling arrays using combined p-value statistics. *Statistical Applications in Genetics and Molecular Biology* 9(1):29.
17. B. Bennett, L.M. Saba, C.K. Hornbaker, **K. Kechris**, P. Hoffman and B. Tabakoff (2011) Genetical genomic analysis of complex phenotypes using the PhenoGen website. *Behavior Genetics* 41:625-8.
18. L.M. Saba, B. Bennett, P.L. Hoffman, K. Barcomb, T. Ishii, **K. Kechris** and B. Tabakoff (2011) A systems genetic analysis of alcohol drinking by mice, rats and men: Influence of brain GABAergic transmission. *Neuropharmacology* 60:1269-1280.
19. P. Hoffman, B. Bennett, L. Saba, S. Bhave, P. Carosone-Link, C. Hornbaker, **K. Kechris** and B. Tabakoff (2011) Using the PhenoGen website for "in silico" analysis of morphine-induced analgesia: Identifying candidate genes. *Addiction Biology* 16:393-404.
20. T.-L. Phang, W. Feng, R.A. Radcliffe and **K. Kechris** (2011) Post-processing multi-treatment time-course microarray studies using the Johnson-Neyman procedure. *Biostatistics, Bioinformatics and Biomathematics* 2:107-126.
21. D. Pollock, A.P.J de Koning, H. Kim*, T.A. Castoe, M.E.A. Churchill and **K. Kechris** (2011) Bayesian analysis of high-throughput quantitative measurement of protein-DNA interactions*. PLoS ONE* 6: e26105.
22. C. Downing, S. Flink, B.A. Rikke, M.L. Florez-McClure, S. Bhave, B. Tabakoff, T.E. Johnson and **K. Kechris** (2012) Gene expression changes in C57BL/6J and DBA/2J mice following prenatal alcohol exposure. *Alcoholism: Clinical & Experimental Research* 36:1519-29.
23. B. Pedersen, D.A. Schwartz, I.V. Yang# and **K. Kechris**# (2012) Comb-p: software for combining, analyzing, grouping, and correcting spatially correlated p-values. *Bioinformatics* 28:2986-8.
24. J. Howard, **K. Kechris**, D. Rees and A. Glazer (2013) Multiple amino acid sequence alignment of nitrogenase component 1: Insights into phylogenetics and structure-function relationships. *PLoS One* 8(9):e72751.
25. I. Baldea, G. Costin, Y. Shellman, **K. Kechris**, A. Filip, M. Cosgarea, D. Norris and S. Birlea (2013) Biphasic pro-melanogenic and pro-apoptotic effects of all-trans-retinoic acid (ATRA) on human melanocytes: Time-course study. *Journal of Dermatological Science* 72:168-76.
26. L. Vanderlinden*, L. Saba, **K. Kechris**, M. Miles, P. Hoffman and B. Tabakoff (2013) Whole brain and brain regional coexpression network interactions associated with predisposition to alcohol consumption. *PLoS One* 8:e68878
27. B.J. Carolan, Y. Kim, A.A. Williams, **K. Kechris**, S. Lutz, N. Reisdorph and R.P. Bowler (2013) The association of adiponectin with CT phenotypes in chronic obstructive pulmonary disease. *American*

Journal of Respiratory and Critical Care Medicine 88:561-6.

28. N. West, **K. Kechris** and D. Dabelea (2013) Exposure to maternal diabetes *in utero* and DNA methylation patterns in the offspring. *Immunometabolism* 1:1-9.
29. T. Bahr*, G. Hughes*, M. Edwards, C. Coldren, C. Schnell, A.L. Friedlander, K. Butterfield, **K. Kechris**[#] and R. Bowler[#] (2013) Peripheral blood mononuclear cell gene expression in chronic obstructive pulmonary disease. *American Journal of Respiratory Cell and Molecular Biology* 49:316-23.
30. N. Reisdorph, R. Stearman, **K. Kechris**, T.-L. Phang, R. Reisdorph, J. Prenni, C. Coldren, D. Erle, K. Schey, A. Nesvizhskii and M. Geraci (2013) Hands on workshops as an effective means of learning advanced technologies including genomics, proteomics, and bioinformatics. *Genomics, Proteomics & Bioinformatics* 11:368-77.
31. R. Bowler, T. Bahr, G. Hughes, S. Lutz, Y.-I. Kim, C. Coldren, N. Reisdorph and **K. Kechris** (2013) Integrative omics approach identifies Interleukin 16 as a biomarker of emphysema. *OMICS: A Journal of Integrative Biology* 17:619-26.
32. E. Siewert* and **K. Kechris** (2013) Modeling considerations for using expression data from multiple species. *Statistics in Medicine* 32:4057–4070.
33. D. Dvorkin*, B. Biehs and **K. Kechris** (2013) A graphical model method for integrating multiple sources of genome-scale data. *Statistical Applications in Genetics and Molecular Biology* 12:469-87.
34. B. Carolan, G. Hughes, J. Morrow, W. O'Neal, S. Rennard, S. Pillai, P. Belloni, D. Cockayne, A. Comellas, M. Han, C. Hersh, **K. Kechris** and R. Bowler (2014) The association of plasma biomarkers with computed tomography-assessed emphysema phenotypes. *Respiratory Research 15:127.*
35. P. Hoffman, L. Saba, S. Flink, N. Grahame, **K. Kechris** and B. Tabakoff (2014) Genetics of gene expression characterizes response to selective breeding for alcohol preference. *Genes, Brain and Behavior* 13:743-57.
36. S. De, B. Pedersen and **K. Kechris** (2014) The dilemma of choosing the ideal permutation strategy while estimating statistical significance of genome-wide enrichment. *Briefings In Bioinformatics* 15:919-28.
37. Y. Ru*¶, **K. Kechris¶**, B. Tabakoff, P. Hoffman, R.A. Radcliffe, R. Bowler, S. Rossi, G.A. Calin, L. Bemis and D. Theodorescu (2014) The multiMiR R package: Multiple databases of microRNA-target interactions with their disease and drug associations. *Nucleic Acids Research* 42:e133.
38. G. Hughes*, C. Cruickshank-Quinn, R. Reisdorph, S. Lutz, I. Petrache, N. Reisdorph, R. Bowler and **K. Kechris** (2014) MSPrep: Summarization, normalization, and diagnostics for processing of mass spectrometry based metabolomic data. *Bioinformatics* 30:133-4.
39. A. Bradford, K. Jones, **K. Kechris**, J. Chosich, M. Montague, W. Warren, M. May, Z. Al-Safi, S. Kuokkanen, S. Appt and A. Polosky (2015) Joint miRNA/mRNA expression profiling reveals changes consistent with development of dysfunctional corpus luteum after weight gain. *PLoS One* 10:e0135163.
40. N. Goldstein, M. Koster, L. Hoaglin, N. Spoelstra, **K. Kechris**, S. Robinson, W. Robinson, D. Roop, D. Norris and S. Birlea (2015) Narrow band ultraviolet B treatment for human vitiligo is associated with proliferation, migration and differentiation of melanocyte Precursors. *Journal of Investigative Dermatology* 135:2068-76.
41. N. Walter*, G. Dolganov, B. Garcia, W. Worodria, A. Andama, E. Musisi, I. Ayakaka, T. Van, M. Voskuil, B. de Jong, R. Davidson, T. Fingerlin, **K. Kechris**, *et al.* (2015) Transcriptional adaptation of drug-tolerant mycobacterium tuberculosis during treatment of human tuberculosis. *Journal of Infectious Diseases* 212:990-8.
42. B. Newell*, **Kechris K**, M. McQueen and T.E. Johnson (2015) Genetic analysis of a murine QTL for diet restriction on chromosome 15. *Age* 37(1):9740.
43. R. Bowler, S. Jacobson, C. Cruickshank, G. Hughes, C. Siska, D. Ory, I. Petrache, J. Schaffer, N. Reisdorph and **K. Kechris** (2015) Plasma sphingolipids associated with COPD phenotypes. *American*

Journal of Respiratory and Critical Care Medicine 191:275-84.

44. N. Walter*, M. Miller, J. Vasquez, …, M. Strong, **K. Kechris**, T. Fingerlin, R. Reves and M. Geraci (2016) Blood transcriptional biomarkers for active TB among US patients: A case-control study with systematic cross-classifier evaluation. *Journal of Clinical Microbiology* 54(2):274-82
45. K. Harrall*, **K. Kechris**, L. Hines, P. Hoffman, B. Tabakoff and L.M. Saba (2016) Uncovering the liver's role in immunity through RNA co-expression networks. *Mammalian Genome* 27:469-84
46. N. Walter*, B. de Jong, B. Garcia, …, T. Fingerlin, **K. Kechris**, M. Strong, M. Voskuil, J. Davis and G. Schoolnik (2016) Adaptation of *Mycobacterium tuberculosis* to impaired host immunity in HIV-infected patients. *Journal of Infectious Diseases* 214:1205-11.
47. K. Serban, S. Rezania, …, W. Hubbard, **K. Kechris**, B. Dragnea, E. Berdyshev, J. McClintock and I. Petrache (2016) Structural and functional characterization of endothelial microparticles released by cigarette smoke. *Scientific Reports* 6:31596.
48. Q. Lu*, C. Jin, J. Sun, R. Bowler, **K. Kechris**, N. Kaminski and H. Zhao (2016) Post-GWAS prioritization through data integration provides novel insights on chronic obstructive pulmonary disease. *Statistics in Biosciences* 2016:1-17.
49. W. Sun¶, **K. Kechris¶**, S. Jacobson¶, et al (2016) Common genetic polymorphisms influence blood biomarker measurements in COPD. *PLoS Genetics* 12(8):e1006011.
50. C. Siska*, R. Bowler, **K. Kechris** (2016) The discordant method: A novel approach for differential correlation. *Bioinformatics* 32(5):690-6.
51. J. Keene, S. Jacobson, **K. Kechris**, G. Kinney, ..., R. Bowler and W. O'Neal; for COPDGene and SPIROMICS Investigators. (2017) Biomarkers predictive of exacerbations in the SPIROMICS and COPDGene Cohorts. *American Journal of Respiratory and Critical Care Medicine* 195(4):473-481.
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Conference Proceedings

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Book Chapters

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2. D. Reinhold, H. Pielke-Lombardo, S. Jacobson, D. Ghosh and **K. Kechris** (2019) Pre-analytic Considerations for Mass Spectrometry-Based Untargeted Metabolomics Data. *High-Throughput Metabolomics* in *Methods in Molecular Biology* Vol 1978 D'Alessandro A. (ed) Humana, New York, NY.
3. T. Ghosh*, W. Zhang, D. Ghosh and **K. Kechris** (2020) Predictive Modeling for Metabolomics Data. *Computational Methods and Data Analysis for Metabolomics* in *Methods in Molecular Biology* Vol 2104 Li S. (ed) Humana, New York, NY.

Other Communications and Interviews

1. Measuring the Success of a SAMSI Program – My Experience at the Beyond Bioinformatics Transition Workshop, *Statistical and Applied Math Sciences Institute Blog*, Jun, 2015 https://samsiatrtp.wordpress.com/category/author-names/katerina-kechris/
2. Master’s and Doctoral Programs in Data Science and Analytics*, AMSTATNEWS* Dec, 2017
3. Discussion on ‘Statistical Contributions to Bioinformatics: Design, Modelling, Structure Learning and Integration’ by J. Morris and V. Baladandayuthapani (2017) *Statistical Modeling* 17(4-5): 327-331.

Software

1. *TFEM* - C (M. Richards)
   Detects DNA regulatory motifs by incorporating positional trends in information content.
2. *OR-MEME* - C (M. Richards)
   Detects DNA regulatory motifs by constraining the order of information content.
3. *c-Reduce* – perl/C (D. Dvorkin)
   Incorporates sequence conservation to detect motifs that correlate with expression.
4. *SULDEX* – C++ (D. Pollock Lab)
   Simultaneously analyzes binding dissociation constants for large repertoires of sequences.
5. *Comb-p* – python (B. Pedersen)
   Combines genome-wide p-values correcting for spatial correlations.
6. *lcmix* – R package: R-Forge (D. Dvorkin)
   Layered and chained mixture models for various univariate and multivariate distributions.
7. *MSPrep* – R package: Bioconductor/GitHub (G. Hughes, M. McGrath)
   Pre-processing of LC/MS metabolomic data.
8. *multiMiR* – R package: Bioconductor/GitHub (Y. Ru, M. Mulvahill, S. Mahaffey)
   Compilation of validated, predicted and drug/disease associated miRNA-target interactions.
9. *Discordant* – R package: Bioconductor/GitHub (C. Siska)
   Uses mixture models to identify differential correlation between groups

10. *HeritSeq* – R package: CRAN/GitHub (J. Shi, P. Rudra, B. Vestal, P. Russell)
    Heritability analysis for sequencing data
11. *miR-MaGiC* – Java/Snakemake: GitHub (P. Russell)
    miRNA expression quantification from small RNA-se.
12. *SmCCNet* – R package: CRAN/GitHub (W. Shi, Y. Zhuang)
    Unsupervised discovery of phenotype specific multi-omics networks.
13. *MCMSeq* – R package: GitHub (B. Vestal, C. Moore)
    Bayesian hierarchical modeling of clustered and repeated measures RNA sequencing experiments.
14. *tidyMicro*: R package - CRAN/GitHub (C. Carpenter)
    Pipeline for microbiome analysis and visualization.
15. *MaRR*: R package - Bioconductor/GitHub (T. Ghosh)
    Measures the reproducibility in high-dimensional replicate experiments.
16. *aptardi*: R package - Bioconductor/GitHub (R. Lusk)
    Alternative polyadenylation transcriptome analysis from RNA and DNA sequencing information
17. *PaIRKAT*: R package - Bioconductor/GitHub (C. Carpenter)
    Assessing relationships between pathways of metabolites and an outcome of interest

Abstracts at Scientific Meetings – Contributed Oral or Poster Presentations

1. Poster: *Finding 'Important' Sites in Proteins*. P. Bickel, A. Glazer, K. Kechris, P. Spector and G. Wedemayer
    - 5th Annual International Conference on Research in Computational Biology (RECOMB), Montreal, Canada, Apr 22-25, 2001. (International)
2. Oral: *Detecting DNA Regulatory Motifs by Incorporating Positional Trends in Information Content.* K. Kechris, E. van Zwet, P. Bickel and M. Eisen
    - International Biometric Society, Eastern North American Region Spring Meeting, Tampa, FL, Mar 30-Apr 2, 2003. (Regional)
3. Poster: *Analysis of Human Alternative Splices Predicted from Exon Junction Arrays*. K. Kechris, Y.-H. Yang and R.-F. Yeh
    - National Academy of Sciences, Sackler Colloquium on "Frontiers in Bioinformatics: Unsolved Problems and Challenges", Irvine, CA, Oct 15-17, 2004. (National)
4. Poster: *Sequence Analysis of Human Alternative Splices Predicted from Exon Junction Arrays.* K. Kechris, Y.-H. Yang and R.-F. Yeh (International)
    - 13th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Detroit, MI, Jun 25-29, 2005.
5. Poster: *Quantitative Exploration of the Occurrence of Lateral Gene Transfer Using Nitrogen Fixation Genes as a Case Study.* K. Kechris, J. Lin*, P. Bickel and A. Glazer
    - National Academy of Sciences, Sackler Colloquium on "Tapestry of Life: Lateral Transfers of Heritable Elements", Irvine, CA, Dec 11-13, 2005. (National)
6. Oral: *Statistical Methods in Bioinformatics.* K. Kechris
    - Colorado/Wyoming Chapter of the American Statistical Association Spring Meeting, Boulder, CO, Apr 21, 2006. (Regional)
7. Poster: *Incorporating Phylogenetic Conservation to Detect Motifs that Correlate with Expression.* K. Kechris and H. Li.
    - 11th Annual International Conference on Research in Computational Biology (RECOMB), San Francisco Bay Area, CA, Apr 21-25, 2007. (International)
8. Poster: *Evolution of Eukaryotic Transcription Factor Binding Sites.* K. Kechris
    - Butcher Symposium on Genetics and Biotechnology: The Future of Biomedicine in Colorado - A Workshop of the Possible, Westminster, CO, Nov 16, 2007. (Regional)
9. Oral: *Motif Prediction Based on a Phylogenetic Multivariate Model for Cross-Species Sequence and Expression Data.* K. Kechris and E. Siewert*
    - Western North American Region Annual Meeting, Portland, OR, Jun 14-17, 2009. (Regional)
10. Poster: *Bioinformatic Analysis of Regulatory Polymorphisms Associated with Alcohol Preference.* K. Kechris, L. Saba, P. Hoffman and B. Tabakoff

- 32nd Annual Research Society on Alcoholism (RSA) Scientific Conference, San Diego, CA, Jun 20-24, 2009. (National)
- Published in *Alcoholism Clinical and Experimental 33(6): 79A*

11. Poster: *Genome-wide Prediction of Transcription Factor Binding Sites.* K. Kechris and E. Siewert*
    - Butcher Symposium on Genomics and Biotechnology: The Future of Biomedicine in Colorado - A Workshop of the Possible, Westminster, CO, Nov 6, 2009. (Local)
12. Poster: *Changes in Brain Expression During Selective Breeding for Alcohol Preference.* S. Flink, K. Kechris, L. Saba, N. Grahame, B. Tabakoff and P. Hoffman
    - 34th Annual Research Society on Alcoholism (RSA) Scientific Conference, Atlanta, GA, Jun 25-29, 2011. (National)
    - Published in *Alcoholism: Clinical & Experimental Research. 35:259A*
13. Oral: *Methods for Integrating Diverse Omics Data*
    - Colorado/Wyoming Chapter of the American Statistical Association Spring Meeting, Boulder, CO, Apr 19, 2013. (Regional)
14. Poster: *Computational Methods for Integrating Diverse Omics Data*. K. Kechris, C. Siska* and D. Dvorkin*
    - Butcher Symposium, Westminster, CO, Nov 1, 2013. (Local)
15. Oral: *MSPrep – Summarization, Normalization, and Diagnostics for Processing of Mass Spectrometry Based Metabolomic Data*. K. Kechris, G. Hughes*
    - 11th Annual Rocky Mountain Regional Bioinformatics Conference, Snowmass, CO, Dec 12-14, 2013. (Regional)
16. Poster: *Micro RNA in Response to Alcohol in the Selectively Bred Inbred Long and Short Sleep Mouse Strains.* K. Kechris, L. Saba, C. Larson, A. Odell, R. Dowell and R. A. Radcliffe
    - 37th Annual Research Society on Alcoholism (RSA) Scientific Conference, Bellevue, WA, Jun 21-25, 2014. (National)
    - Published in *Alcoholism: Clinical & Experimental Research. 38:2A*

Abstracts at Scientific Meetings – Contributed Poster Abstracts Selected for Oral Presentations

17. Oral: *Sequence Analysis of Human Alternative Splices Predicted from Exon Junction Arrays.* K. Kechris, Y.-H. Yang and R.-F. Yeh
    - Alternative Splicing Special Interest Group Meeting, 13th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Detroit, MI, Jun 23-24, 2005. (International)
18. Oral: *Computational Detection of Regulatory Polymorphisms for Alcohol Preference Candidate Genes.* K. Kechris, L. Saba, P. Hoffman and B. Tabakoff
    - 6th Cold Spring Harbor/Wellcome Trust Conference on Pharmacogenomics, Cold Spring Harbor, NY, Nov 19-22, 2008. (International)

Abstracts at Scientific Meetings – Invited Presentations (plenary indicates single-session)

19. Plenary: *Detecting DNA Regulatory Motifs by Incorporating Positional Trends in Information Content.* K. Kechris, E. van Zwet, P. Bickel and M. Eisen
    - 7th Purdue International Symposium on Statistics, Workshop: Bioinformatics and Microarrays, West Lafayette, IN, Jun 19-24, 2003. (National)
20. Plenary: *Sequence Analysis of Human Alternative Splices Predicted from Exon Junction Arrays.* K. Kechris, Y.-H. Yang and R.-F. Yeh
    - 3rd Annual Rocky Mountain Regional Bioinformatics Conference, Snowmass, CO, Dec 9-11, 2005. (Regional)
21. Oral: *Incorporating Sequence Conservation to Detect Motifs that Correlate with Expression.* K. Kechris and H. Li.
    - Bioinformatics Workshop, Graybill Conference VI, Fort Collins, CO, Jun 12-15, 2007. (National)
22. Plenary: *Genomic Profiles of Chronic Obstructive Pulmonary Disease: A Promising Role for Sphingolipid Metabolism and Signaling Pathways.* K. Kechris, T. Bahr, C. Coldren and R. Bowler
    - Butcher Symposium, University of Colorado BioFrontiers Institute, Westminster, CO, Nov 11, 2011. (Local)

23. Oral: *Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions*
    - Western North American Region Annual Meeting, Fort Collins, CO, Jun 17-20, 2012. (Regional)
24. Oral: *Mixtures Models for Omics Data Integration.* K. Kechris and D. Dvorkin
    - Topic Contributed Session, Joint Statistical Meetings, Boston, MA, Aug 2-7, 2014. (National)
25. Plenary: *New Directions in Data Integration using Chronic Obstructive Pulmonary Disease as a Case Study*
    - Beyond Bioinformatics Research Program, Statistical and Applied Mathematical Sciences Institute (SAMSI), Research Triangle Park, NC, May 11-13, 2015. (National)
26. Oral: *Discovering Disease Associated Molecular Interactions Using Discordant Correlation.* K. Kechris and C. Siska
    - Invited Session, Joint 24th ICSA Applied Statistics Symposium and 13th Graybill Conference, Fort Collins, CO, Jun 14-17, 2015. (National)
27. Plenary: *Epigenetic Marks of in utero Exposure to Gestational Diabetes: The Exploring Perinatal Outcomes in Children (EPOCH) Study.*
    - Precision Medicine Symposium: The Future is Now, National Jewish Health, Denver, CO, Jun 24, 2015. (Regional)
28. Oral: *Challenges and Opportunities in Metabolomic Data Analysis for Translational Research.*
    - iBRIGHT: Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine, Houston, TX, Nov 1-3, 2015. (National)
29. Plenary: *Metabolomics and Translational Research in Pulmonary Disease.*
    - BioInfoSummer 2015, Sydney, Australia, Dec 7-11, 2015. (International)
30. Oral: *Data Integration using Network Analysis and Kernel Machine Methods.*
    - Invited Session, International Biometric Society, Eastern North American Region Spring Meeting, Austin, TX, Mar 6-9 2016. (Regional)
31. Plenary: *Good (and bad) Things Come in Small Packages: microRNA and Alcoholism*
    - 3rd Annual Mini-Symposium: The Power of Informatics to Advance Health, Denver, CO, Apr 8, 2016 (Local)
32. Oral: *Accounting for Genetics in Biomarker-Disease Association Studies: Lessons Learned from Lung Disease*
    - Invited Session, Joint Statistical Meetings, Baltimore, MD, Jul 29-Aug 3, 2017. (National)
33. Plenary: *Multi-Omics Approaches in Genetic Epidemiology Studies*
    - International Genetic Epidemiology Society 26th Annual Meeting, Cambridge, UK, Sep 9–11, 2017 (International)
    - Published in *Genetic Epidemiology 41 (7), 644-644*
34. Oral: *Good (and bad) Things Come in Small Packages: miRNA Mediated Genetic Predisposition to Alcohol Related Behaviors*
    - 41st Annual Meeting of the Research Society on Alcoholism, San Diego, CA, Jun 16-20, 2018. (National)
    - Published in *Alcoholism: Clinical & Experimental Research 42:319A*
35. Oral: *Sequencing Data, Repeated Measures and Genetic Heritability*
    - Topic Contributed Session, Joint Statistical Meetings, Vancouver, Canada, Jul 28-Aug 2, 2018. (National)
36. Oral: *Network Analysis for -Omics Data Integration*
    - Invited Session, International Biometric Society, Western North American Region Annual Meeting, Portland, OR, Jun 23-26, 2019. (Regional)
37. Panel: *Women in Leadership: Challenges and Opportunities*
    - International Biometric Society, Western North American Region Annual Meeting, Portland, OR, Jun 23-26, 2019. (Regional)
38. Panel: *Training & Resources for Data Science*
    - Data Science Symposium, Colorado School of Public Health, Apr 12, 2019 (Local)
39. Plenary: *Unsupervised Learning for Studying Chronic Obstructive Pulmonary Disease*
    - CCTSI CU/CSU Summit VII: AI and Machine Learning in Biomedical Research, Aug 14, 2019. (Local)
40. Panel: *Data Science Applications*

  - Data Science Symposium, University of Colorado Denver, Aug 30, 2019. (Local)

41. Oral: *Multi-Omics Subtyping of Chronic Obstructive Pulmonary Disease Using Deep Learning Approaches*
    - Invited Session, International Biometric Society, Eastern North American Region Spring Meeting, Virtual Mar 14-17 2021. (Regional)
42. Plenary: *Multi-Omics Networks Associated with COPD*
    - GSP-TOPMed Analysis Workshop Mar 25-26, 2021 (National)
43. Oral: *Generalized Tensor Canonical Correlation Analysis for Network Inference Using Multi-Omics Data*
    - Topic Contributed Session, Joint Statistical Meetings, Aug 8-12, 2021, online (National)

Abstracts at Scientific Meetings - Presented by Co-Authors (125+, available upon request)

INVITED PRESENTATIONS: SEMINARS, PANELS, WORKSHOPS

Invited Presentations - Local

- *Pattern Discovery in Protein Sequences.*
  - Department of Statistics, University of California Berkeley, Jan 25, 2001.
- *Non-Parametric Exploration of Gene Expression Regulation in Yeast.*
  - Computational Biology and Genomics Seminar, Department of Molecular and Cell Biology, University of California Berkeley, Oct 24, 2001.
- *Detecting DNA Regulatory Motifs by Incorporating Positional Trends in Information Content.*
  - Division of Biostatistics, University of California Berkeley, Jan 23, 2003.
- *Statistical Issues in Molecular Sequence Analysis.*
  - Undergraduate Statistics Seminar, Department of Statistics, University of California Berkeley, Oct 3, 2003.
- *Detecting DNA Regulatory Motifs by Incorporating Positional Trends in Information Content.*
  - Center for Computational Biology, University of Colorado Denver, Feb 3, 2006.
- *Statistics in Bioinformatics: Selected Topics in the Analysis of Genomic Data*
  - Department of Preventive Medicine and Biometrics, University of Colorado Denver, Feb 22, 2006.
- *Finding Functional DNA Sequences Using Genome Informatics*
  - CCTSI Informatics Seminar Series, CU Anschutz, Jan 15, 2009.
- *Combined P-value Statistics for Tiling Arrays.*
  - Mathematical and Statistical Sciences, University of Colorado Denver, Mar 18, 2009.
  - Computational Bioscience Program, CU Anschutz, May 18, 2009.
- *Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions*
  - Department of Biostatistics and Informatics, CU Anschutz, Feb 29, 2012.
- *Next Generation Sequencing Data Analysis*
  - CCTSI Informatics Seminar Series, CU Anschutz, Apr 12, 2012.
- *Got Data? How to Determine whether you need Bioinformatics and/or Biostatistics Support for your Research Project*
  - CCTSI Biostatistics Seminar, CU Anschutz, Jan 21, 2014.
  - CCTSI Informatics Tools for Accelerating Clinical and Translational Research Seminar, CU Anschutz, Jan 23, 2014.
- *RNA-Seq Time Series*
  - Lung Systems Biology Working Group, NJH-CU Anschutz, Jan 27, 2014.
- *Time Series Expression Analysis Using RNA-Seq*
  - Bioinformatics Journal Club, CU Anschutz, Mar 7, 2014.
- *Integration of Omics Data: Lessons Learned from Lung Disease*
  - Human Medical Genetics and Genomics Program Seminar, CU Anschutz, Oct 30, 2014.
- *multiMiR R Package*
  - Bioinformatics Journal Club, CU Anschutz, Nov 14, 2014.

- *Review of "Impact of Regulatory Variation from RNA to Protein"*
  - Statistical Genomics Working Group, CU Anschutz, May 8, 2015.
- *Good (and Bad) Things Come in Small Packages: microRNA and Alcoholism*
  - Department of Pharmacology, CU Anschutz, Feb 29, 2016.
- *Review of "Statistics Requantitates the Central Dogma"*
  - Statistical Genomics Working Group, CU Anschutz, April 7, 2016.
  - Lung Systems Biology Working Group, NJH-CU Anschutz, Mar 21, 2016.
- *Review of "Similarity Network Fusion for Aggregating Data Types on a Genomic Scale"*
  - Network Analysis Working Group, CU Anschutz, Sep 23, 2016.
- *Accounting for Genetics in Protein Biomarker-Disease Association Studies*
  - Division of Biomedical Informatics and Personalized Medicine, CU Anschutz, Nov 16, 2016.
- *Biomarkers, Genetics and COPD*
  - Schwartz/Yang Lab Meeting, Department of Medicine, CU Anschutz, Dec 2, 2016.
- *Review of "Combined Analysis of Pleiotropy and Epistasis"*
  - Statistical Genomics Working Group, CU Anschutz, Oct 5, 2018.
- *miRNA Mediated Genetic Predisposition to Alcohol Related Behaviors*
  - Department of Integrative Biology Seminar Series, University of Colorado Denver, Apr 13, 2018.
- *Studying COPD Using Integrative Omics and Network Approaches*
  - Division of Biomedical Informatics and Personalized Medicine, CU Anschutz, May 2, 2018.
- *miRNA Mediated Genetic Predisposition to Alcohol Related Behaviors*
  - Division of Biomedical Informatics and Personalized Medicine, CU Anschutz, Feb 6, 2019.
- *Review of "Similarity Network Fusion for Aggregating Data Types on a Genomic Scale"*
  - Division of Biomedical Informatics and Personalized Medicine, CU Anschutz, May 8, 2019.
- *Big Data Seminar Series: OMICS Data*
  - Center for Innovative Design and Analysis, CU Anschutz, Nov 5, 2019.
- *Unsupervised Learning for Studying COPD: Integrative -Omics and Network Approaches*
  - Deep Learning and Systems Biology Meeting, NJH-CU Anschutz, Nov 11, 2019
- *Review of "An Integrative U method for Joint Analysis of Multi-Level Omic Data."*
  - Division of Biomedical Informatics and Personalized Medicine, CU Anschutz, Jan 7, 2020.
- *Review of "Network Propagation: A Universal Amplifier of Genetic Associations"*
  - Division of Biomedical Informatics and Personalized Medicine, CU Anschutz, Jan 13, 2021.
- *Big Data Seminar Series: OMICS Data*
  - Center for Innovative Design and Analysis, CU Anschutz, Jan 20, 2021.

Invited Presentations (Seminars) – Regional

- *Quantitative Exploration of the Occurrence of Lateral Gene Transfer Using Nitrogen Fixation Genes as a Case Study.*
  - Bioinformatics Supergroup, University of Colorado Boulder, Apr 17, 2006.
- *Finding Functional DNA Sequences Using Genome Informatics: Integrating Bioinformatics, Genomics and Genetics.*
  - First Friday Talk, Institute of Behavioral Genetics, Boulder, CO, Sep 12, 2008.
- *Introduction to Microarray Data Analysis.*
  - Institute of Behavioral Genetics, Boulder, CO, Aug 20, 2009.
- *Predicting Motifs Using Multiple Species Regression Models.*
  - Department of Statistics, Colorado State University, Fort Collins, CO, Mar 28, 2011.
- *Regulation of the Transcriptome: Integrating Data and Modeling Dependencies*
  - BioFrontiers Institute, University of Colorado Boulder, Jan 10, 2017.
- *Estimating Heritability of Genomic Traits from Sequencing Data*
  - Department of Applied Mathematics, University of Colorado Boulder, Feb 6, 2017.
- *Studying Complex Diseases Using Integrative -Omics and Network Approaches*
  - Applied Mathematics Seminar, Colorado State University, Mar 5, 2020.

Invited Presentations – National

- *Detecting DNA Regulatory Motifs by Incorporating Positional Trends in Information Content.*
  - Center for Biomolecular Science and Engineering, University of California Santa Cruz, Feb 20, 2003.
  - Department of Health Research and Policy, Stanford University, Jan 30, 2003.
  - Department of Statistics, University of California Los Angeles, Jan 28, 2003.
- *Statistical Methods in Bioinformatics: Discovering Regulatory Sequences in DNA.*
  - Department of Mathematics, Harvey Mudd College, Feb 8, 2005.
  - School of Natural Sciences, University of California Merced, Feb 22, 2005.
  - Bioinformatics Program, University of Texas El Paso, Mar 29, 2005.
  - Department of Statistics, University of California Riverside, Apr 26, 2005.
  - Beckman Research Institute, City of Hope National Medical Center, Apr 29, 2005.
- *Comparative Genomics for Motif Prediction: Integrating Multiple Species Sequence and Expression Data.*
  - Computational Biology Colloquium, University of Southern California, Apr 1, 2010.
- *Challenges of Data Integration: Within and Across Genomes*
  - Computational and Statistical Genomics Workshop, Penn State University, Oct 21-22, 2013.
- *'Omics Data Integration*
  - COPDGene Investigators Meeting, Denver, CO, Nov 14, 2013. (National)
- *Regulation of the Transcriptome: Modeling Dependencies and Integrating Multiple Data Types*
  - Department of Medical Informatics and Clinical Epidemiology, Oregon Health Sciences University, Portland, OR, Apr 14, 2014.
- *PBMC Gene Expression Module Subtypes.*
  - COPDGene Subtyping Summit, Denver, CO, Feb 26-27, 2015. (National)
- *Integration of Omics Data: Lessons Learned from Chronic Obstructive Pulmonary Disease*
  - Collaborative Studies Coordinating Center, University of North Carolina, Chapel Hill, May 14, 2015.
- *Studying COPD Using Integrative Omics and Network Approaches*
  - Theodore L. Badger Lecture Series, Channing Division of Network Medicine, Brigham and Women's Hospital, Boston, MA, Apr 24, 2018.
- *High-throughput Methods for Studying the Role of miRNA Regulation in Alcohol Related Behaviors*
  - Biostatistics Seminar Series, Fred Hutchinson Cancer Research Center, Mar 13, 2019.
- *Studying COPD Using Integrative Omics and Network Approaches*
  - Department of Biomedical Informatics, The Ohio State University, Feb 4, 2020.
- *Multi-Omics of COPD*
  - Population Architecture Using Genomics & Epidemiology (PAGE) Consortium, Virtual Nov 17, 2020.
- *Multi-Omics Studies of COPD*
  - NHLBI Trans-Omics for Precision Medicine (TOPMed) F2F Meeting, Virtual Dec 9, 2020
- *Studying Complex Diseases Using Integrative -Omics and Network Approaches*
  - Department of Biostatistics and Epidemiology, University of Massachusetts Amherst, Virtual Feb 12, 2021
- *Studying COPD Using Multi-Omics and Network Approaches*
  - Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Webinar Series, Mar 10, 2021
- *Introduction to Metabolomics Platforms and Data Analysis*
  - NIDA Center of Excellence in Omics, Systems Genetics, and the Addictome Webinar Series, Apr 9, 2021
- *Multi-Omics Subtyping of Chronic Obstructive Pulmonary Disease Using Deep Learning Approaches*
  - NHLBI Trans-Omics for Precision Medicine (TOPMed) Lung Multiomics Analyst Call, Jun 24, 2021
- *Introduction to Methylation Platforms and Data Analysis*
  - NIDA Center of Excellence in Omics, Systems Genetics, and the Addictome Webinar Series, Aug 30, 2021

Invited Workshops

Genomics and Proteomics Hands-on Workshop: From Sample Preparation to Data Analysis 2007-2010
National Jewish Health and University of Colorado Denver, School of Medicine, Denver, CO
Director: Nichole Reisdorph; Chris Coldren, Katerina Kechris and Tzu-lip Phang (Co-Directors)

- *Lecture:* Microarray Data Analysis (7 hours) and Bioinformatics (7 hours)
  Jul 18-27, 2007; Jul 23-Aug 1, 2008; Jul 8-17, 2009; Jun 23-Jul 2, 2010
- *Lecture:* Next Generation Sequencing Data Analysis; Web-based Update, Jan 26, 2012

BioInfoSummer 2015
University of Sydney and Australian Mathematical Sciences Institute, Australia, Dec 7-11, 2015
Director: Jean Yang, Nicola Armstrong, Simi Henderson
Description: The BioInfoSummer series is an introduction to bioinformatics and mathematical and computational biology. Established in 2003, BioInfoSummer is a key training event in Australia, bringing together people from all disciplines to share current research and developments in Bioinformatics.
Audience: International; undergraduate & postgraduate students, researchers and professionals (n=200)

- *Lecture:* Metabolomics Data Analysis in R (3 hours); Dec 10, 2015

New Strategies and Challenges in Lung Proteomics and Metabolomics Workshop
National Jewish Health, Denver, CO, Feb 4-5, 2016

- *Lecture:* Statistical Approaches

TEACHING RECORD

Course Development

University of Colorado Anschutz Medical Campus

- BIOS 7659/CPBS 7659 - Statistical Methods in Genomics

Responsibility: Course Developer, Sole Instructor
Description: Analysis of genomic data is becoming an integral component of biomedical research. This course will give an introduction to problems in genomics and review the pioneering statistical methods that were developed for analyzing molecular sequences and gene expression data.
Credits: 3 credits (first year offered - 2 credits)
Audience: Biostatistics MS/PhD & Computational Bioscience PhD students (n=5-15 enrollment/course)
Offered: Fall 2006, Fall 2008, Fall 2012, Spring 2015, Fall 2016, Fall 2018, Fall 2020

- BIOS 7731 - Advanced Mathematical Statistics I

Responsibility: Course Developer, Sole Instructor
Description: This course will provide the framework for understanding the formal concepts, models and assumptions for characterizing uncertainty, analyzing data, developing models, estimating model parameters, testing model hypotheses, using asymptotics and evaluating the performance of estimation and decision procedures.
Credits: 3 credits
Audience: Biostatistics PhD students (n=5-15 enrollment/course)
Offered: Fall 2007 (as MATH 6381), 2011, 2013, 2015, 2017, 2019, 2020

- BIOS 7899 - Independent Studies in Biostatistics, “R Programming”

Description: This independent study course provides an introduction to the R statistical software using a structured format with assigned readings and exercises. The class introduces R syntax and functions for graphical output, exploratory data analysis and commonly used statistical methods.
Credits: 1-3 credit(s)
Audience: Biostatistics MS/PhD & Computational Bioscience PhD students/post-doctoral fellows, computational researchers (n=1-2)
Offered: Spring & Fall 2007, Summer 2008, Fall 2009, Fall 2012, Spring 2013, Spring 2014, Summer 2014

Workshop Development

National Jewish Health and University of Colorado Anschutz Medical Campus

- Genomics and Proteomics Hands-On Workshop: From Sample Preparation to Data Analysis

Description: A hands-on workshop designed to provide a comprehensive view of proteomics, genomics, and bioinformatics to investigators who are currently utilizing, or are considering utilizing, these methods in their own research

Duration: 10-day summer workshop

Audience: National competitive process. Basic and clinical scientists, principal investigators, post-doctoral fellows, graduate students in their final year of training, "omics" core users, bioinformaticists, and others who need to be familiar with typical "omics" workflows. (n=20-25)

Guest Lectures

University of California Berkeley

- PH 256 - Applications of Statistics to Genetics and Molecular Biology
  Primary Instructor: Dr. Sandrine Dudoit, Division of Biostatistics
  Lecture: "Pattern Discovery in Protein Sequences", Nov 26, 2001

University of Colorado Boulder

- IPHY 5102 – Genomic Analysis of Physiology and Behavior
  Primary Instructor: Dr Thomas Johnson, Department of Integrative Physiology
  Lecture: "Sequence Alignment and Hidden Markov Models", Apr 2, 2013

University of Colorado Anschutz Medical Campus

- CPBS 7711 - Introduction to Bioinformatics I
  Primary Instructor: Dr. Larry Hunter, Computational Bioscience Program
  Lecture: "DNA Motif Finding", Oct 6, 2005
- PRMD 6639 - Methods in Genetics and Molecular Epidemiology
  Primary Instructor: Dr. Jill Norris, Preventive Medicine and Biometrics
  Lecture: "Introduction to Microarrays", Nov 27, 2006
- CPBS 7712 - Introduction to Bioinformatics II
  Primary Instructor: Dr. Larry Hunter, Computational Bioscience Program
  Lecture: "Reviewing Manuscripts", Mar 28, 2006
  Primary Instructor: Dr. David Pollock, Biochemistry & Molecular Genetics
  Lectures: "Motif Finding, Introduction to Probability, EM Algorithm", "Reviewing Manuscripts", Feb 22 & 27, Mar 1, May 10, 2007
- BIOS 6606 - Statistics for the Basic Sciences
  Primary Instructor: Dr. Doug Everett, National Jewish Health
  Lecture: "Analysis of Microarrays", May 5 & 9, 2007; Oct 17 & 19, 2007
- HMGP 7620 - Genomics
  Primary Instructors: Drs. David Pollock, Jim Sikela, and Mark Johnston, Biochemistry & Molecular Genetics and Pharmacology
  Lecture: "Transcription Factor Binding Site Motifs", Mar 9, 2010
- BIOS 6606 – Statistics for the Basic Sciences
  Primary Instructor: Dr. Kathleen Torkko, Pathology
  Lecture: "Ethics, Replication and Reproducible Research", Dec 6 & 8, 2016
- MOLB 7801/PHCL 7801 – Rigor and Reproducibility in Biomedical Research
  Primary Instructor: Dr. Robert Sclafani, Biochemistry & Molecular Genetics
  Lecture: "Big Data & When Things Go Bad with Non-Reproducible Research", Mar 10, 2017; Mar 9, 2018, Mar 15, 2019
- BIOS 6621/22 – Statistical Consulting I
  Primary Instructor: Dr. Gary Grunwald, Biostatistics
  Lecture: "Reproducibility: Big Data Analysis and Statistical Methods", Apr 4, 2017; Oct 10, 2018, Sep 3, 2019
- BIOS 6606 – Statistics for the Basic Sciences
  Primary Instructor: Dr. Kathleen Torkko, Pathology

Lectures: "Reproducibility: Big Data Analysis and Statistical Methods", Dec 4 & 6, 2017; Dec 6 & 8, 2018; Sep 30 & Oct 2, 2019; Sep 28 & Dec 9, 2020

- CPBS 7711 - Introduction to Bioinformatics I
  Primary Instructor: Dr. Larry Hunter, Computational Bioscience Program
  Lectures: "Reviewing Manuscripts", Oct 29 & Nov 5, 2009; Oct 20 & Nov 1, 2011; Nov 25 & Dec 3, 2013; Nov 21 & Dec 4, 2014; Nov 19 & Dec 1, 2015; "Introduction to Concepts in Statistics", Sep 26, 2013; Oct 16, 2014; Sep 10, 2015, Sep 6, 2016, Sep 12, 2017; Sep 11, 2018; "Introduction to Next Generation Sequencing", Sep 27, 2016; Sep 26, 2017, Sep 25, 2018; "Re-sampling and Simulation Based Methods" Oct 6, 2020; Oct 12, 2021; "Hackathon" Oct 13, 2020, Oct 19 2021; "Sequence Alignment" Oct 11, 2021

- CPBS 7712 - Computational Bioscience Research
  Primary Instructor: Dr. Larry Hunter, Computational Bioscience Program
  Lectures: "Kechris Lab Research", Apr 22, 27 & 29, 2010; Feb 22, 24 & Mar 1, 2011; Apr 3, 5 & 10, 2012; "Data Analysis for Gene Expression Regulation & Omics Integration", Feb 27 & Mar 4, 2014; Feb 2 & 3, 2015; Feb 16 & 18, 2016; Jan 31 & Feb 2, 2017; Mar 6 & 8, 2018, Jan 29 & 31, 2019, "Metabolomics" Mar 11, 2021; "Proteomics" Mar 16, 2021

Colorado Biomedical Informatics Summer Fellowship Program

- Lecture: "Biological Macromolecules", Jun 12, 2013; Jun 6, 2016; May 22, 2017; June 4, 2018, June 18, 2019
- Lecture: "Scientific Communication: Written", Jun 22, 2016; Jun 20, 2017; May 24, 2018, June 6, 2019

Other Teaching Activities

Tutor/Reader

Department of Mathematics, University of California Los Angeles Fall 1995-Fall 1997

Helped students on a walk-in basis for lower division calculus classes. Prepared solutions and graded homework in mathematics, statistics, and programming (C++) classes.

Teaching Assistant

Department of Statistics, University of California Berkeley

Spring 1999, Spring 2000, Spring 2001, Spring 2003

Planned and conducted discussion sections, graded exams and prepared computer lab sessions for undergraduate probability and statistics classes.

Journal Club (Supervisor)

Organized biweekly "Regulomics Reading Group" in 2006 for students and post-doctoral researchers.

Independent Studies

- BIOS 7899 - Independent Studies in Biostatistics, "Genetic Analysis Workshop", Fall 2006
  Student: Laura Saba, Biostatistics PhD student
- BIOI 7785 - Independent Studies in Bioinformatics, "Regulomics Reading Course", Fall 2006
  Student: Hyun-Min Kim, Computational Bioscience PhD student
- BIOS 6841 - Independent Studies in Biostatistics, "Statistical Methods in Genomics and R Programming", Spring 2011
  Student: Dr. Nicholas Walter, Pulmonary Sciences Fellow
- BIOS 7899 - Independent Studies in Biostatistics, "R Programming,"
  Spring 2007: Jesse Paquette, Computational Bioscience PhD student & Dr. Susan Trapp, Post-Doctoral Researcher
  Fall 2007: Mamta Jaiswal, Computational Bioscience PhD student
  Summer 2008: Robert Engle, Biostatistics PhD student
  Fall 2009: Dr. Stanca Birlea, Dermatology Instructor/Fellow & Phyllis Carosone-Link, Pharmacology Research Assistant

Fall 2012: Allison Buti, Epidemiology PhD & Matthew Mulvahill, Biostatistics MS students
Spring 2013: Melissa Leventhal, MPH student & Hannah Reed, CSPH Research Assistant
Spring 2014: Levi Bonnell & Mikaela Miller, MPH students
Summer 2014: Katherine Roberts & Rachel Blumahagen, Biostatistics MS students; Alexandra Schneider, MPH student

Mentoring

MS Thesis Advisor

1. Timothy Bahr, Biostatistics (Summer 2010-Spring 2011)
   Thesis Title: Genome-Wide Gene Expression Analysis of Peripheral Blood Mononuclear Cells in Smokers with and without COPD.
   Honors: Marvin Porter Award 2011, given yearly to outstanding MS student(s)
   Publications: 2 manuscripts ([29,31] in *BIBLIOGRAPHY)*
   Presentations: 1 conference ([19] in *ABSTRACTS*)
2. Grant Hughes, Biostatistics (Fall 2011-Spring 2013)
   Project Title: Processing of Metabolomic Data
   Publications: 4 manuscripts ([29,31,38, 43] in *BIBLIOGRAPHY)*
   Presentations: 1 conference ([33] in *ABSTRACTS*)
   Software: 1 package ([7] in *SOFTWARE*)
3. Mikaela Miller, Biostatistics (Fall 2014-Fall 2015)
   Project Title: Transcriptomics and metabolomics in mouse model of cigarette smoke exposure.
   Honors: Marvin Porter Award 2016, given yearly to outstanding MS student(s)
   Publications: 1 manuscript ([56] in *BIBLIOGRAPHY)*
   Presentations: 3 conferences ([44,45,52] in *ABSTRACTS*)
4. Yonghua Zhuang, Biostatistics (Fall 2014-Fall 2016, co-mentored with Laura Saba)
   Thesis Title: Tissue Augmented Bayesian Model for Expression Quantitative Trait Loci Analysis
   Publications: 1 manuscript ([80] in *BIBLIOGRAPHY)*
   Presentations: 1 conference ([68] in *ABSTRACTS*)
5. Elizabeth Litkowski, Biostatistics (Fall 2017-Fall 2018, co-mentored with L. Saba)
   Project Title: The Disrupted Co-Expression Network Method (DiscoNET): A Hybrid Approach to Assessing Gene Module Construction in Saline versus Ethanol Treated Recombinant Inbred Mice
   Presentations: 1 conference ([82] in *ABSTRACTS*)
   Publications: 1 manuscript ([106] in *BIBLIOGRAPHY)*
6. Gordon Kordas, Biostatistics (Fall 2018 – Summer 2019)
   Project Title: Insight into genetic regulation of miRNA in mouse brain
   Publications: 1 manuscript ([76] in *BIBLIOGRAPHY)*
   Presentations: 1 conference ([99] in *ABSTRACTS*)
7. Cuining Liu, Biostatistics (Fall 2017 – Summer 2019)
   Project Title: Cis-Regulatory Genetic Variants in the Developing Human Lung
   Honors: Nominated Alpha Upsilon Chapter, Delta Omega Honorary Society in Public Health
8. Guannan Shen, Biostatistics (Fall 2018 – Fall 2019)
   Project Title: Integrative Network Analysis of Host-transcriptome, Microbiome and Microbial Translocation Markers in Chronic HIV-1 Infection
   Publications: 2 manuscripts ([91,93] in *BIBLIOGRAPHY)*
9. Timothy Vigers, Biostatistics (Fall 2019 – Summer 2021, co-mentored with L. Vanderlinden)
   Project Title: A Mediation Approach to Discovering Causal Relationships Between the Metabolome and DNA Methylation in Type 1 Diabetes
   Publications: 3 manuscript ([105,108,110] in *BIBLIOGRAPHY)*
10. Jonathan Dekermanjian, Biostatistics (Fall 2020 – Summer 2021, co-mentored with D. Ghosh)
    Project Title: Mechanism-Aware Imputation: A Two-Step Approach in Handling Missing Values in Metabolomics
    Publications: 1 manuscript ([114] in *BIBLIOGRAPHY)*
11. Emily Cooper, Biostatistics (Spring 2021 – Fall 2022)

Project Title: Gut V gene-microbiome associations revealed by dimensionality reduction models in an age- and sex-matched HIV-1 infected and uninfected cohort
Publications: 1 manuscript ([91] in *BIBLIOGRAPHY)*

12. Sierra Niemiec, Biostatistics (Fall 2022 - present)
    Project Title: In-Utero PFAS Exposure and Accelerated Epigenetic Aging

MS Examination Committee Member (graduating year)

1. Jesse Paquette, Computational Bioscience (2008)
2. Wendy Dye, Biostatistics (2010)
3. Lauren (Kiemele) Vanderlinden, Biostatistics (2011)
4. May Alhazzani, Computer Science, University of Colorado Boulder (2014)
5. Kylie Harrall, Biostatistics (2016)
6. Rachel Blumhagan, Biostatistics (2016)
7. Justin Eagles, Biostatistics (2017)
8. Patrick Iben, Biostatistics (2019)
9. Charles Carpenter, Biostatistics (2020)

Other Degree Mentoring

1. Lucas Gillenwater, Epidemiology MPH Practicum/Capstone Preceptor (2018)
   Project Title: The Impact of Genetic Variants on Blood Metabolite Levels in a COPD Cohort
   Publications: 1 manuscript ([96] in *BIBLIOGRAPHY)*
2. Corey Cox, Biomedical Sciences and Biotechnology MPS Mentor (2018)
   Project Title: Comparison of Differential Network Analysis Tools DiffCoEx and DGCA
3. Eitan Halper-Stormberg, Medical Student Research Mentor (with Russell Bowler) (2018-2019)
   Project Title: Metabolomics Study of COPD in Plasma and BALF in the SPIROMICS Cohort
   Publications: 1 manuscript ([78] in *BIBLIOGRAPHY)*
4. William Showers, Biomedical Sciences and Biotechnology MPS Committee Member (2020)
   Project Title: Analysis of SARS-CoV-2 Mutation Over Time Reveals Increasing Prevalence of Variants in Spike Protein and SARS-CoV-2 RNA Polymerase

PhD Dissertation Advisor

1. Elizabeth Siewert, Biostatistics (Fall 2006-Spring 2010)
   Thesis Title: Prediction of Transcription Factor Binding Sites Using Information from Multiple Species.
   Honors: Strother H. Walker Award 2009 (given to outstanding PhD Biostatistics student); Maurice Davies Award 2010 (nominated by institution and awarded by CO/WY Chapter of the ASA); NIH/NLM Training Program in Biomedical Informatics Fellowship
   Publications: 2 manuscripts ([14, 32] in *BIBLIOGRAPHY)*
   Presentations: 5 conferences ([9,10,12,13,16] in *ABSTRACTS*)
   Current Position: Statistical Consultant, Statistically Speaking
2. Daniel Dvorkin, Computational Bioscience Program (Spring 2009-Summer 2013)
   Thesis Title: Graphical Model Methods for Integrating Diverse Sources of Genome-Scale Data.
   Honors: NIH/NLM Training Program in Biomedical Informatics Fellowship
   Publications: 2 manuscript ([107] in *BIBLIOGRAPHY)*
   Presentations: 7 conferences ([11,15,21,22,30,31,32] in *ABSTRACTS*)
   Software: 2 packages ([3,6] in *SOFTWARE*)
   Current Position: Bioinformatics Consultant, The Bioinformatics CRO, Inc.
3. Nicholas Walter, Epidemiology (Fall 2012-Fall 2015) [co-advisor w/ Dr. Tasha Fingerlin]
   Thesis Title: Translational Approaches to Predicting Tuberculosis Risk: From Administrative Data to Transcriptional Biomarkers.
   Publications: 3 manuscripts ([41,44,46] in *BIBLIOGRAPHY)*
   Current Position: Associate Professor, School of Medicine, CU Anschutz
4. Charlotte Siska, Computational Bioscience Program (Fall 2012-Summer 2016)
   Thesis Title: Differential Correlation in High-Throughput Data
   Honors: NIH/NLM Training Program in Biomedical Informatics Fellowship

Publications: 4 manuscripts ([43, 50, 52, 57] in *BIBLIOGRAPHY)*
Presentations: 3 conferences ([41,42,53] in *ABSTRACTS*)
Software: 1 package ([9] in *SOFTWARE*)
Current Position: Data Scientist, Twitter

5. Yonghua Zhuang, Biostatistics (current)
   Honors: NHLBI BioData Catalyst Fellow, Strother H. Walker Award 2021 (given to outstanding PhD Biostatistics student)
   Publications: 6 manuscripts ([78,79,84,96,109,112] in *BIBLIOGRAPHY)*
   Presentations: 1 conference ([68] in *ABSTRACTS*)
   Software: 1 package ([12] in *SOFTWARE*)

PhD Examination Committee Member (graduating year) *committee chair

1. Brandie Wagner, Biostatistics (2007)
2. Hyun-Min Kim, Computational Bioscience (2008)
3. Deborah Batista, Mathematical and Statistical Sciences (exam in 2009)
4. Alex Poole*, Computational Bioscience (exam in 2012)
5. Ronald Schuyler*, Computational Bioscience (2012)
6. Vijetha Vemulapalli, Computational Bioscience (2012)
7. Jaime Merlano*, Computational Bioscience (exam in 2014)
8. David Knox*, Computational Bioscience (2015)
9. Sally Peach, Molecular Biology (2016)
10. Joey Azofeifa, IQB, University of Colorado Boulder (2017)
11. Brian Vestal, Biostatistics (2017)
12. Aaron Wacholder, IQB, University of Colorado Boulder (2017)
13. Bre Stamper, Integrative Physiology, University of Colorado Boulder (temporary member)
14. Mengjie Yao, Mathematical and Statistical Sciences (temporary member)
15. Adrienne Narrowe, Integrative and Systems Biology (2018)
16. Michael Shaffer, Computational Bioscience (2018)
17. Rani Powers*, Biomedical Sciences/Computational Bioscience (2019)
18. Randi Johnson, Epidemiology (2019)
19. Stephen Pollard, Structural Biology and Biochemistry (2019)
20. Amanda Richer, Molecular Biology (2020)
21. Ryan Lusk, Pharmaceutical Sciences (2021)
22. Patrick Carry, Epidemiology (2021)
23. Kristen Wade*, Human Medical Genetics and Genomics (in progress)
24. Rutendo Sigauke*, Computational Bioscience (in progress)
25. Alexandria Jensen*, Biostatistics (in progress)
26. Teresa Buckner, Epidemiology (in progress)
27. Jennifer Harper, Computational Bioscience (in progress)

PhD Thesis Examiner

1. Kaushala Pathirannehelage, School of Mathematics and Statistics, University of Sydney (2015)
2. Yu Xiang Kevin Wang, School of Mathematics and Statistics, University of Sydney (2019)

Post-Doctoral Mentor

1. Wen “Jenny” Shi (2015-2018)
   Honors: NIH/NLM Training Program in Biomedical Informatics Fellowship
   Publications: 5 manuscripts (see [53,66,68,79,92] in *BIBLIOGRAPHY)*
   Presentations: 3 conferences ([62,74,80] in *ABSTRACTS)*
   Software: 2 packages (10,12] in *SOFTWARE*)
2. Pratyaydipta Rudra (2015-2018)
   Publications: 6 manuscripts (see [53,66,68,76,79,92] in *BIBLIOGRAPHY)*
   Presentations: 5 conferences ([57,60,65,69,76] in *ABSTRACTS)*
   Software: 1 package ([10] in *SOFTWARE*)

3. Elin Shaddox (2019-present)
4. Debmalya Nandy (2019-present)
5. Thao Vu (2020-present)
6. Souvik Seal (2020-present)

Junior Faculty/Career Award Mentor

1. Nicholas Walter, Assistant Professor, Division of Pulmonary Sciences & Critical Care Medicine
   - Mentored Co-Pilot Award, CCTSI (2013)
   microRNA Response to a Globally-Emerging Hypervirulent Mycobacterium Tuberculosis Lineage
   - Department of Veterans Affairs, Career Development Program (2013-2018)
   Blood Expression Profiles as a Biomarker for Responses to Tuberculosis Treatment
2. Kristen Boyle, Assistant Professor of Pediatrics
   - Center for Women's Health Research Junior Faculty Research Development Award (2014)
   Maternal Programming of Fetal Stem Cells
   - NIH/NIDDK K01 (2013-2015)
   Mesenchymal Stem Stells, Epigenetics, and the Developmental Programming of Insulin Resistance
3. Anne Starling, Post-doctoral Fellow, Department of Epidemiology [Current position: Assistant Professor, Department of Epidemiology, University of North Carolina]
   - NIH K99/R00 (2016-2018)
   A Mechanistic Study of Prenatal Air Pollution Exposure and Offspring Obesity Risk

Other Mentoring

High School Mentor

- Amogh Chaturvedi (Fall 2021-Spring 2022)
  Greater San Diego Science & Engineering Fair, Regeneron International Science & Engineering Fair
  Project: Multi-omics Data Integration for Early Non-invasive Pancreatic Adenocarcinoma Detection.

Undergraduate Mentor

Department of Statistics, University of California Berkeley

Advised undergraduate research assistants under the National Science Foundation VIGRE program.

- Mark Richards (Fall 2002-Spring 2003)
  Project: Information Content and DNA Regulatory Motifs.
  Software: 2 packages ([1,2] in *SOFTWARE*)
- Jason Lin (Fall 2003-Spring 2005)
  Project: Quantitative Exploration of the Occurrence of Lateral Gene Transfer.
  Publications: 1 published manuscript ([7] in *PUBLICATIONS)*

Department of Biology, Colorado College

Advised undergraduate senior research block.

- Jenna Otto (Spring 2007)
  Project: Bioinformatic Analysis of Polyserine Linkers.

Post-Baccalaureate Mentor

- Keenan Manpearl (Fall 2021-Spring 2022)
  Project: Regulatory role of miRNA in Alcohol Use Disorder Phenotypes in Rat
  Fellowship: NIH/NIGMD Building Infrastructure Leading to Diversity (BUILD) Promoting Opportunities for Diversity in Education and Research (PODER), California State University Northridge
- Sakaiza Rasolofomanana Rajery (Fall 2021-Spring 2022)
  Project: Exploratory Analysis of Factors that Contribute to Metabolomics Software Usage

Research Lab Rotation Supervisor – PhD Students

- Jesse Paquette, Computational Bioscience (Spring 2007)
  Project: Using Similarity Vectors for Gene Expression Sample Clustering and Classification.
- Charlotte Siska, Computational Bioscience (Summer 2012)
  Project: Identifying miRNA and Gene Targets Associated with Alcohol Preference.
- Kyle Smith, Computational Bioscience (Spring 2014)
  Project: Investigation of Methylation and Gene Expression Changes in HPV Infected Keratinocytes
- Rani Schwindt Powers, Biomedical Sciences/Computational Bioscience (Spring 2015)
  Project: Integrating Heterogeneous Data Sources to Predict Gene Essentiality
  Publication: 1 manuscript ([107] in *BIBLIOGRAPHY)*
- Daniel Polanco, Computational Bioscience (Spring 2016)
  Project: Integrating of Omics Data: Chronic Obstructive Pulmonary Disease Subtyping
- Kristen Wade, Human Medical Genetics and Genomics (Spring 2017)
  Project: Cross-Species Expression Quantitative Trait Loci Analysis
  Publication: 1 manuscript ([80] in *BIBLIOGRAPHY)*
- Emily Mastej, Computational Bioscience (Spring 2019)
  Project: Identifying Protein-Metabolite Networks Associated with COPD Phenotypes
  Publication: 1 manuscript ([84] in *BIBLIOGRAPHY)*
- Katherina Cortes, Computational Bioscience (Spring 2022)
  Project: Classification of COPD using Multi-Omics Data
- Erik Serrano, Biomedical Sciences/Computational Bioscience (Spring 2022)
  Project: Implementing GitHub API Pipeline into MSCAT for data enrichment

Student Research Assistant Supervisor

- Mamta Jaiswal, Computational Bioscience PhD student, Fall 2007
  Project: Phylogeny of Nitrogen Fixation Proteins and the Analysis of Polyserine Linker Proteins.
- Daniel Dvorkin, Computational Bioscience PhD student, Summer-Fall 2008*Project:* c-REDUCE Software Development.
- Stefan Sillau, Biostatistics PhD student, Fall 2008-Spring 2009
  Project: Analysis of Metagenomic Data.
- Sean Jacobson, Biostatistics MS student, Fall 2011-Spring 2012
  Project: Next Generation Sequence Data Analysis
- Junxiao Hu, Biostatistics PhD student, Fall 2014-Fall 2015
  Project Title: Meta and Network Analysis of COPD Expression Data
- Brian Vestal, Biostatistics PhD student, Fall 2014-Spring 2017
  Project: Analysis of Small RNA-Seq Data
- Michael Daniels, Biostatistics PhD student, Fall 2016-Fall 2018
  Project: Semi-supervised Learning for Hierarchical Mixture Models
- Jonathan Dekermanjian, Biostatistics MS student, Fall 2019-Spring 2021
  Project: Metabolomics Software Tool Database Development
- Max McGrath, Mathematical Sciences undergraduate student, Fall 2019-present
  Project: R Software Developer
- Weixuan Liu, Biostatistics PhD student, Fall 2019-present
  Project: miRNA-mRNA Network Analysis for Alcohol Related Behaviors
- Suneeta Godbole, Biostatistics PhD student, Fall 2020-present
  Project: Longitudinal Metabolomics Analysis in COPD
- Sierra Niemiec, Biostatistics MS student, Fall 2020-present
  Project: Environmental Influences on Child Health Outcomes: Epigenetic Analysis
- Ian Arriaga Mackenzie, Biostatistics PhD student, Fall 2021-present
  Project: Environmental Influences on Child Health Outcomes: miRNA Analysis

Professional Research Assistant Supervisor

- Stephen Flink, PhD. (Fall 2009-Summer 2010)
  Project: Analysis of Expression Data from the Brains of Mice Selected for Alcohol Preference.
- Pamela Russell, PhD. (Fall 2014-Summer 2017)
  Project: Analysis of Small RNA-Seq Data

Administrative Position

- Biostatistics MS/PhD Graduate Program Co-Director (2013-2018) (with Dr. Gary Grunwald)
  Responsible for program curriculum, course scheduling, student recruitment, admissions and orientation, management of research and teaching assistantships, mentoring, student awards and qualifying exams.
- Computational Bioscience PhD Program Associate Director (2021-present)

K-12 & Undergraduate Outreach, Professional Development

- Seminars at Local Institutions
  Using Statistics to Mine the Genome
    - Department of Mathematics and Computer Science, Colorado College, Oct 13, 2006

  Learning about Biostatistics!
    - Kappa Mu Epsilon Meeting, Colorado School of Mines, Feb 4, 2009; Oct 5, 2009
    - Undergraduate Mathematics Club, University of Denver, Feb 10, 2009

  Biostatistics Education and Research in the Colorado School of Public Health
    - Department of Statistics, Colorado State University, Jan 25, 2010
- LAB COATS (Link to Advanced Biomedical Research Career Opportunities and Training Section)
  The goal of this program is to retain undergraduates from underrepresented groups in science, and assist them with entry into graduate school and the pursuit of a career in biomedical research.
  Panelist for Pre-Collegiate Panel Discussion, Jun 25, 2009
- STEM (Science, Technology, Engineering and Math) Expo Participant: Organized booth for elementary school students on statistics/probability and the Colorado School of Public Health.
    - Ben Franklin Academy, Highlands Ranch CO, Sept 30, 2011
- Presentation to Native American Students: Discussed opportunities in Biostatistics and Public Health. Colorado School of Public Health, May 9, 2012
- Presentation on "Getting and Staying Connected": Biostatistics and Informatics Seminar, Colorado School of Public Health, Sep 22, 2015
- Presentation on "Scientific Communication: Written": Biostatistics and Informatics Seminar, Colorado School of Public Health, Nov 1, 2017
- Presentations on "Promotion 101": Biostatistics and Informatics, Colorado School of Public Health, Jan 12, 19, 26, 2018
- CV and Biosketch Workshop: Center for Innovative Design and Analysis, Feb 26, 2021

Training Grants Active

- *Title:* Computational Bioscience Program Training Grant (T15 LM009451)

Funding Agency: NIH/NLM
Summary: Our program is designed to provide graduate students and post-doctoral fellows training in both computational methods and molecular biology, an intimate familiarity with the science and technology that synthesizes the two, and the skills necessary to pioneer novel computational approaches to significant biomedical questions.
PI: Larry Hunter *Project Period:* 7/1/2007 - present
Role: Program Core Faculty, Mentor *Total Award:* $4,176,114

Training Grants Completed

- *Title:* Supplement to Molecular Biology Training Grant (PI: Robert Sclafani; 2T32GM008730-16) & Pharmacology Training Grant (PI: Andrew Thorburn, Co-PI J. David Port; 5T32GM007635-37)

Funding Agency: NIH/NIHG
Summary: In response to concerns about scientific rigor, repeatability and reproducibility in biomedical research, we propose to integrate these concepts into our current curriculum and to develop a new curriculum focused on teaching these concepts and to our graduate students.
PI: Robert Sclafani *Project Period:* 7/1/2016-6/30/2017
Role: Instructor *Total Award:* $81,261

- *Title:* Genomics and Proteomics Hands-On Workshop: From Sample Preparation to Data Analysis (T15 HL86386)

Funding Agency: NIH/NHLBI
Summary: A 10-day intensive hands-on workshop designed to provide a comprehensive view of proteomics, genomics, and bioinformatics to investigators who are currently utilizing, or are considering utilizing these methods in their own research.
PI: Nichole Reisdorph (National Jewish Health) *Project Period:* 9/1/2006 - 8/31/2010
Role: Instructor, Board of Directors *Total Award:* $568,226

RESEARCH RECORD – FUNDING

Grants Active – PI (*contact PI)

- *Title:* Multi-omic Networks Associated with COPD progression in TOPMed Cohorts (R01 HL152735)

Funding Agency: NIH/NHLBI
Summary: To help identify why only some smokers develop COPD, this proposal will integrate recently collected extensive molecular multi-omic profiles from three NHLBI cohorts to discover molecular networks that are important in both COPD diagnosis and progression, with specific focus on African Americans.
Role: multi-PI (K. Kechris-Mays*, F. Banaei-Kashani, R. Bowler, L. Lange)
Total Award: $3,088,398 *Project Period:* 4/05/2020-3/31/2024

- *Title:* Addressing Sparsity in Metabolomics Data Analysis (U01 CA235488)

Funding Agency: NIH Common Fund
Summary: We will develop novel statistical methods and software for the research community to improve the utilization of metabolomic data so that we can maximize its potential for making novel discoveries in disease etiology, diagnosis, and drug development.
Role: multi-PI (K. Kechris-Mays*, D. Ghosh) *Project Period:* 8/15/2018-8/31/2022
Total Award: $1,723,956

  - *Supplement:* U01CA235488-03S1
    Summary: We plan to extend the functionality of our metabolomics tools database to better determine the interoperability between software tools so that users can select analysis workflows, and to better identify the factors that contribute to successful software adoption.
    Total Award: $96,632 *Project Period:* 9/1/2021-8/31/2022
  - *Supplement:* U01CA235488-02S1
    Summary: We e plan to survey the landscape of publicly available metabolomics software tools, in addition to testing software installation, assessing interoperability between tools, identifying factors contributing to their impact, developing long term maintenance for the survey, and disseminating our results.
    Total Award: $86,888 *Project Period:* 9/1/2019-8/31/2020

- *Title:* Biomarker of Lung Disease in African Americans (R01 HL137995)

Funding Agency: NIH/NHLBI

Summary: There are very few studies in COPD that address risk factors and molecular pathogenesis in African Americans. This proposal will use three existing NHLBI cohorts to identify proteomic blood signatures that can identify who will be at risk for developing smoking related lung disease in African Americans.

Role: multi-PI (R. Bowler*, K. Kechris-Mays) *Project Period:* 8/15/2018-5/31/2022
Total Award: $3,179,452 *Subcontract*: $383,870

  - *Supplement:* R01HL137995-04S1
    Summary: We propose to use this supplement to address the extent of the privacy problem among diverse TOPMed cohorts and begin investigating potential solutions for the NIH to develop new policies for protection of proteomic and metabolomic data in research.
    Total Award: $177,875 *Project Period:* 8/25/2021-5/31/2023

Grants Active – co-I

- *Title:* The Early Life Exposome and Childhood Health (UG3 OD023248)

Funding Agency: NIH/Office of the Director

Summary: The overarching goal of this project is to leverage an existing, ongoing pre-birth cohort to determine the early life "exposome" across a wide range of exposures (social, lifestyle, nutritional, chemical, physical), and to conduct integrative analyses with child health outcomes that are informed by biological pathways and account for postnatal factors.

PI: D. Dabelea *Project Period:* 9/21/2016 – 8/31/2023
Role: Co-I *Total Award:* $1,244,398

- *Title:* NIDA Core "Center of Excellence" in Transcriptomics, Systems Genetics and the Addictome (P30 DA044223)

Funding Agency: NIH/NIDA

Summary: The aims of the Research Support Core are to: gather and curate genomic and transcriptomic data from previously funded NIDA research; create a tissue-specific transcriptomic map and quantify the full transcriptome; and integrate multiple omics data types (DNA, RNA, etc.) to statistically infer molecular mechanisms of transcription and translation control.

PI: L. Saba, R. Williams *Project Period:* 7/01/17-6/30/2022
Role: Co-I

- *Title:* Schistosomiasis at the Edge of Elimination: Characterizing Sources of New Infections in Residual Transmission Hotspots (R01 AI134673)

Funding Agency: NIH/NIAID

Summary: The persistence of infections in transmission hotspots is a key challenge confronting global efforts to eliminate high-impact infectious diseases, including the water-borne parasite schistosomiasis. This study uses genomic analysis and a decade-long study of schistosomiasis reemergence to determine the origins of new infections in areas where infections persist despite control efforts.

PI: E. Carlton *Project Period:* 11/23/18-10/31/2023
Role: Co-I

Grants and Fellowships Completed – PI or sub-contract PI (*contact PI)

- *Title:* SiNorm: a novel statistical methodology for normalizing signal intensities in preclinical MRI

Funding Agency: Colorado CTSA UL1 TR002535, NIH/NCATS Colorado Clinical and Translational Sciences Institute Translational Method Pilot Award

Summary: We will develop a novel signal intensity normalization procedure, SiNorm, for preclinical MRI images to adjust for miscellaneous sources of unwanted variations and implement SiNorm as an R software package.

Role: multi-PI (K. Kechris-Mays*, F. Xing) *Project Period:* 5/1/2020-4/30/2021
Total Award: $20,000

- *Title:* Genome-wide Identification of miRNAs Associated with Alcoholism Endophenotypes (R01 AA021131)

Funding Agency: NIH/NIAAA
Summary: The goals of this proposal are 1) to perform high-throughput miRNA brain expression profiling in a large panel of RI mice and 2) to develop statistical methods for identifying miRNAs and respective target mRNA expressed in the brain associated with the predisposition to alcoholism endophenotypes.
Role: PI *Project Period:* 9/15/2013-8/31/2020 (NCE)
Total Award: $1,549,431

  - *Supplement:* NLM Administrative Supplements for Informationist Services in NIH-funded Research Projects (AA021131-03S1)
    Summary: This work will increase the impact of the data generated in the parent award by submitting the data to public repositories, sharing metadata and analysis workflows to facilitate data reuse, and creating tutorials to help a wider audience utilize the data.
    Total Award: $76,658 *Project Period:* 9/1/2015-8/31/2017

- *Title*: Omics Data Integration to Identify Disease Pathways in COPD (R21 HL140376)

Funding Agency: NIH/NHBLI
Summary: We will integrate -omics datasets to identify specific pathways that can serve as novel diagnostic and therapeutic targets for chronic obstructive pulmonary disease and emphysema and for molecular subtyping of this complex and heterogeneous disease.
Role: multi-PI (K. Kechris-Mays*, R. Bowler, F. Banaei-Kashani) *Project Period:* 9/1/2017-8/31/2020 (NCE)
Total Award: $234,742

- *Title:* Integrative Genomics of Clinical Subtypes in COPDGene (R01 HL125583)

Funding Agency: NIH/NHLBI
Summary: We will use expression quantitative trait locus (eQTL) analysis to identify functional single nucleotide polymorphisms (SNPs) affecting expression of differentially expressed genes and miRNAs.
PI: C. Hersh (Brigham and Women's Hospital) *Project Period:* 9/1/2015 – 5/31/2020 (NCE)
Role: Subcontract PI/Co-I *Total Award*: $2,250,982 *Subcontract*: $262,384

- *Title:* Epigenetic Marks of In Utero Exposure to Gestational Diabetes (R01 DK100340)

Funding Agency: NIH/NIDDK
Summary: We plan to identify DNA methylation changes that are associated with *in utero* GDM exposure, followed by identification of epigenetic marks that are causal and mediate adiposity-related outcomes, and to identify DNA methylation marks (and associated gene expression changes) that persist into adolescence.
Role: multi-PI (D. Dabelea*, I. Yang, K. Kechris-Mays) *Project Period:* 7/1/2014-6/30/2019 (NCE)
Total Award: $2,002,969

- *Title:* Metabolic Profiles of COPD Phenotypes (P20 HL113445)

Funding Agency: NIH/NHLBI
Summary: The goal of this project is to use the NHLBI sponsored COPDGene cohort for an integrated metabolomics-genomics-animal model approach to identify dysregulated pathways that explain why some smokers get COPD and emphysema while others do not.
PIs: R. Bowler*, I. Petrache (National Jewish Health) and N. Reisdorph (CU Anschutz)
Role: Subcontract PI/Co-I *Project Period:* 4/15/2012-2/28/2017
Total Award: $6,006,412 *Subcontract*: $203,135

- *Title:* Genomic Regulatory Sequence Analysis for Alcohol-Related Phenotypes (K01 AA016922)

Funding Agency: NIH/NIAAA
Summary: The goal of this work is to study mammalian model systems to identify genomic regulatory sequences that contribute to transcriptional changes in alcohol-related behaviors.
Role: PI *Project Period:* 9/15/2007 – 9/14/2013
Total Award: $701,735

- *Supplement:* Genomic Regulatory Sequence Analysis for Alcohol-Related Phenotypes, American Recovery and Reinvestment Act (ARRA) Supplement (K01 AA016922-02S1)
  Summary: The goal of this study is to identify gene expression changes in the brains of mice selected for alcohol preference, a trait associated with alcoholism.
  Total Award: $36,180 *Project Period:* 8/01/2009 – 7/31/2010

- *Title:* Metabolome and Proteome Profiles of Emphysema and Airway Disease (R01 HL095432)

Funding Agency: NIH/NHLBI
Summary: The goals of this proposal are to (1) use proteomic and metabolomic approaches to identify plasma biomarkers that are associated with Chronic Obstructive Pulmonary Disease (COPD) phenotypes and (2) identify the genetic control of these biomarkers.
PI: R. Bowler (National Jewish Health) *Project Period:* 4/01/2009 - 3/31/2013
Role: Subcontract PI/Co-I *Total Award:* $1,577,488
Subcontract: $19,667

- *Title:* Genetics of Gene Expression in COPD

Funding Agency: Butcher/CU-Boulder Chancellor's Office (Butcher Seed Grant Proposals)
Summary: The goal of this study is to combine and analyze data from a genome wide association study and gene expression analysis to elucidate the mechanisms controlling gene expression in COPD.
Role: PI *Project Period:* 7/01/2010 – 6/30/2012
Total Award: $99,939

- *Title:* Using Comparative Genomics for Finding Functional Signatures of Human Non-coding Sequences and Identifying Horizontal Gene Transfer in Bacterial Genomes (R01 GM075312)

Funding Agency: NIH/NIGMS
Summary: The two major goals of this project are: 1) the development of methodology for finding functionally predictive signatures of non-coding sequences highly conserved across multiple species and 2) the development of novel approaches for detecting horizontal gene transfer.
PI: P. Bickel*, H. Huang (University of California Berkeley)
Role: Subcontract PI *Project Period:* 6/1/2005 - 5/31/2009
Total Award: $1,012,201 *Subcontract*: $14,424

- *Title:* Postdoctoral Fellowship in Computational Molecular Biology

Funding Agency: Sloan Foundation/Department of Energy **(Up to 10 yearly awards)**
Summary: The purpose of this program is to catalyze career transitions into computational molecular biology from physics, mathematics, computer science, chemistry, and related fields.
Role: Post-Doctoral Fellow *Project Period:* 10/1/2003 - 9/30/2005
Total Award: $120,000

- *Title*: Graduate Research Fellowship

Funding Agency: National Science Foundation
Summary: The program recognizes and supports outstanding graduate students in NSF-supported science, technology, engineering, and mathematics disciplines who are pursuing research-based master's and doctoral degrees at accredited United States institutions.
Role: Graduate Fellow *Project Period:* 8/1/1999 - 6/30/2002
Total Award: $51,000 + tuition and registration fees

Grants and Fellowships Completed – co-I

- *Title:* MicroRNAs and Early Life Exposures in the Developmental Origin of Asthma (R01HL125734)

Funding Agency: NIH/NHLBI
Summary: This project seeks to identify microRNAs that are associated with in utero smoke (IUS) exposure in the human lung that may be a biomarker for asthma susceptibility later in life. Identification of an integrative network of IUS exposure during human lung development, which includes genomic and

epigenetic data, may identify microRNAs and pathways for novel therapies and targeted preventive strategies for asthma.
PI: S. Sharma *Project Period:* 3/01/16-2/28/2021
Role: Co-I *Total Award:* $3,480,962

- *Title:* Islet Autoimmunity Reversion as a Model of T1D Resiliency (R21 AI142483)

Funding Agency: NIH/NIAID
Summary: The goal of this study is to examine epigenetic and gene expression biomarkers in the Diabetes Autoimmunity Study in the Young (DAISY), in order to elucidate why some individuals with islet autoimmunity develop T1D, and others lose their autoimmunity.
PI: J. Norris *Project Period:* 3/01/19-2/28/2021
Role: Co-I

- *Title:* Discovery and Validation of Biomarkers of Cardiovascular Complications in Type 1 Diabetes (R01 DK116731)

Funding Agency: NIH/NIDDK
Summary: We propose to apply a precision medicine approach to assess novel proteomic and lipidomic biomarkers of cardio-renal Type 1 diabetes complications, develop composite risk scores utilizing a combination of these biomarkers and genetic markers, and examine their specificity for vascular endpoints.
PI: J. Snell *Project Period:* 5/01/18-4/30/2021
Role: Co-I

- *Title:* Nutrigenetics & -Genomics of Vitamin D and Omega-3 Fatty Acids in T1D (R01 DK104351)

Funding Agency: NIH/NIDDK
Summary: We will measure metabolites related to vitamin D and omega-3 fatty acid pathways and explore the nutrigenetics and nutrigenomics of T1D by investigating whether vitamin D and omega-3 fatty acid intake alters gene expression, via epigenetic changes, to influence predisposition to T1D.
PI: J. Norris *Project Period:* 9/15/2014-8/31/2019
Role: Co-I *Total Award*: $2,888,613

- *Title:* Endocrine Disruptors, Epigenetic Programming and Neonatal Outcomes (R01 ES022934)

Funding Agency: NIH/NIEHS
Summary: We will evaluate exposure to endocrine disrupting chemicals during pregnancy to see if they increase the fat mass of the newborn and infant, and we will test whether the chemicals alter the DNA methylation patterns of the newborn as a possible mechanism for developmental programming of obesity and metabolic syndrome.
PIs: R. Hamman, D. Dabelea, J. Adgate *Project Period:* 9/19/2014-8/31/2019 (NCE)
Role: Co-I *Total Award*: $2,250,982

- *Title:* Identifying Parasite Reservoirs in Areas Approaching Elimination (R21 AI115288)

Funding Agency: NIH/NIAID
Summary: This research evaluates genomic tools for identifying the source of *schistosomiasis* infections in areas where officials are attempting to eliminate the disease.
PI: E. Carlton *Project Period:* 7/1/2015-6/30/2017
Role: Co-I *Total Award:* $408,589

- *Title:* RGAP: The Heritable Transcriptome and Alcoholism (R24AA013162)

Funding Agency: NIH/NIAAA
Summary: The goal of this project is to establish a national resource for systems genetic analyses of the rodent transcriptome.
PI: B. Tabakoff*, P. Hoffman, L. Saba *Project Period:* 8/01/07-6/30/17
Role: Co-I *Total Award:* $4,588,806