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Education
B.A. Statistics and Psychology, State University of New York at Buffalo, Buffalo, New York (1989)
Ph.D. Statistics, The University of Chicago, Chicago, Illinois (1994)

Professional Experience
Assistant Adjunct Professor, Department of Family & Preventive Medicine, University of California, San Diego (1994-1997)

Assistant Professor, Division of Human Cancer Genetics, Department of Molecular Virology, Immunology and Medical Genetics, The Ohio State University, Columbus, Ohio (1997-2002)

Associate Professor, Department of Biostatistics, University of North Carolina at Chapel Hill (2002-2008)

Professor, Department of Biostatistics, University of North Carolina at Chapel Hill (2008-2013)

Professor, Departments of Statistics and Biological Sciences, North Carolina State University (2013-present)

Director, Bioinformatics Research Center, North Carolina State University (2013-present)

Director, NC State NIEHS T32 Graduate Training Program in Bioinformatics (2017-present)

Honors
- Delta Omega, the Public Health Honor Society (elected 2004)
- Fellow of the American Statistical Association (elected 2011)

Professional Activities
  memberships in
- American Society of Human Genetics
- American Statistical Association
- International Society of Computational Biology
- Society of Toxicology

Journal Articles (Google Scholar *h* Index = 62)

1. Becker, LB, Han B, Meyer P, **Wright FA**, Rhodes K, Smith D, Barrett J: Racial differences in the

incidence of cardiac arrest and subsequent survival. *New England Journal of Medicine,* 329: 600-606, 1993.

2. Kong A and **Wright F**: Asymptotic theory for gene mapping. *Proceedings of the National Academy of Sciences, USA,* 91: 9705-9709, 1994.

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4. Winqvist R, Hampton G, Mannerma A, Blanco G, Alavaikko M, Kiviniemi H, Taskinen PJ, Evans G, **Wright FA**, Newsham I, Cavenee W: Loss of heterozygosity for chromosome 11 in primary human breast tumors is associated with poor survival after metastasis. *Cancer Research,* 55: 2660-2664, 1995.

5. Paulson TG, **Wright FA**, Parker BA, Russak V, Wahl GM: Microsatellite instability correlates with reduced survival and poor disease prognosis in breast cancer. *Cancer Research*, 56:4021-4026, 1996.

6. **Wright FA**: The phenotypic difference discards sibpair QTL linkage information. *American Journal of Human Genetics,* 60: 740-742, 1997.

7. **Wright FA** and Kong A: Linkage mapping in experimental crosses: the robustness of single-gene models. *Genetics,* 146: 417-425, 1997.

8. Rock CL, Flatt S, **Wright FA**, Faerber S, Newman V, Kealey S, Pierce JP: Responsiveness of carotenoids to a high-vegetable diet intervention to prevent breast cancer recurrence. *Cancer Epidemiology, Biomarkers, and Prevention*, 6: 617-623, 1997.

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12. Newman V, Rock CL, Faerber S, Flatt SW, **Wright FA**, Pierce JP: Dietary supplement use by women at risk for breast cancer recurrence. The Women's Healthy Eating and Living Study Group. *Journal of the American Dietetic Association,* 98: 285-292, 1998.

13. Rayburn K, Martinez R, Escobedo M, **Wright FA**, Farias M: Glycemic effects of various species of nopal (opuntia sp.) in type 2 diabetes mellitus. *Texas Journal of Rural Health*, 16: 68-76, 1998.

14. Hryniuk W, Frei E, **Wright FA**: A single scale for comparing dose-intensity of all chemotherapy regimens in breast cancer: Summation dose-intensity. *Journal of Clinical Oncology,* 16: 3137-3147, 1998.

15. De La Chapelle A, **Wright FA**: Linkage disequilibrium mapping in isolated populations: The example

of Finland revisited. *Proceedings of the National Academy of Sciences*, 95: 12416-12423, 1998.

16. Sadler GR, Thomas AG, Dhanjal SK, Gebrekristos B, **Wright FA**: Breast cancer screening adherence in African-American women - black cosmetologists promoting health. *Cancer,* 83: 1836-1839, 1998.

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21. Costello JF, Fruhwald MC, Smiraglia DJ, Rush LJ, Robertson GP, Gao X. **Wright FA,** Feramisco JD, Peltomaki P, Lang JC, Schuller DE, Yu L, Bloomfield CD, Caligiuri MA, Yates A, Nishikawa R, Huang H-J S, Petreilli NJ, Zhang X, O'Dorisio MS, Held WA, Cavenee WK, Plass C: Aberrant CpG island methylation has non-random and tumor type-specific patterns. *Nature Genetics,* 24:132-138, 2000.

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retina. *Toxicological Sciences*, 107:281-292, 2009.

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Additional papers as a named member of the GTEx Consortium

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Book Chapters and Books

1. Walter V, Nobel AB, Hayes DN, **Wright FA**: Identification of recurrent DNA copy number aberrations in tumors. In *Statistical Diagnostics of Cancer: Genetics and Genomics Data*, eds. Emmert-Streib F, Dehmer M. Wiley-Blackwell, 2013.

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3. National Academies of Sciences, Engineering, and Medicine, Division on Earth and Life Studies, Board on Environmental Studies and Toxicology, Committee on Incorporating 21st Century Science into Risk-Based Evaluations. *Using 21st Century Science to Improve Risk-Related Evaluations*. Washington (DC): National Academies Press (US), 2017 .

Other correspondence

1. **Wright FA** and Thomas RG: Familial melanoma and pancreatic cancer. *New England Journal of Medicine*, 334:470-471, 1996.

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1. Parmer RJ, Kailasam MT, Martinez JA, **Wright FA**, Wilson AF, O'Connor DT: Evidence suggesting that urinary kallikrein excretion is heritable in African-American families with essential hypertension. *Hypertension,* 26: 545-545, 1995.

2. **Wright FA**, O'Connor DT, Yoneda LU, Kutey G, Roberts E, Berry C, Weber J, Timberlake D, Schlager G: A genome scan for blood pressure loci in mice. *Hypertension,* 32: 25-25, 1998.

3. Graham JS, Bradley TL, Hampel H, **Wright FA**, Westman JA, Jameslink: An innovative touch-screen kiosk system for tailored cancer risk assessment and notification. *American Journal of Human Genetics*. 65: A82-82 Suppl. S, 1999.

4. Gao X, **Wright FA**: Nonparametric Disequilibrum Mapping When Haplotypes Are Available.

American Journal of Human Genetics 65: A 250-250 Suppl. S, 1999.

5. Skrivanek Z, Irwin M, Lin S, **Wright FA**: SIMPLE: A linkage program that incorporates interference. *American Journal of Human Genetics*, 65:A446-A446 Suppl. S, 1999.

6. Hoffman HM, **Wright FA**, Broide DH, Wanderer AA, Kolodner RD: Fine genetic mapping of the 1q44 locus for familial cold urticaria. *American Journal of Human Genetics* 67: (4) 308-308 Suppl, 2000.

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8. Virtaneva KI, Tamayo P, Gao X, Palatini J, Wise T, Udd B, Ashizawa T, **Wright FA**, Krahe R: Microarray-based profiling of gene expression changes in myotonic dystrophy (DM1): evidence for a global defect in RNA metabolism. *American Journal of Human Genetics* 67: 410-410 Suppl, 2000.

9. Rush LJ, Xin G, **Wright FA**, Kolitz JE, Bloomfield CD, Caligiuri MA, Plass C: DNA hypermethylation in acute myeloid leukemia (AML): Nonrandom patterns with preferential involvement of chromosome 11. *Blood* 96:501A-501A Part 1, 2000.

10. Hoffman HM, **Wright FA**, Broide DH, Wanderer AA, Kolodner RD: Genetic and physical mapping of the FCU locus on chromosome 1q44. *Cytogenetics and Cell Genetics* 92:46-46, 2001.

11. Cheng R, Ma JZ, **Wright FA**, Lin S, Gao X, Wang D, Elston RC, Li MD: Nonparametric disequilibrium mapping of functional sites using haplotypes of multiple tightly linked single-nucleotide polymorphism (SNP) markers. *American Journal of Human Genetics* 69: 520-520 1982 Suppl. 1, 2001

12. **Wright FA**, Miller BJ, Wang D, Krahe R: Pooled analysis of loss of heterozygosity in breast cancer provides comparative evidence for multiple tumor suppressors in a genomewide scan and identifies novel candidate regions. *American Journal of Human Genetics* 71: 240-240 401 Suppl. S, 2002

13. Bachinski L, **Wright FA**, Krahe R: A single shared haplotype among DM2 (CCTG)n expansion mutation carriers from different European origins indicates ancestral founder effect. *American Journal of Human Genetics* 73 (5): 2606, 2003

14. Krahe R, Hendrickson BW, Colella S, Alam R, **Wright FA**, Huff V: Genome anatomy of Wilms' Tumor: genome-wide LOH analysis reveals unique signatures and tumor subgroups. *American Journal of Human Genetics* 73:195, 2003.

15. Bachinski L, **Wright FA**, Krahe R: A single shared haplotype among DM2 (CCTG)n expansion mutation carriers from different European origins indicates ancestral founder effect. *American Journal of Human Genetics* 73: 612, 2003.

16. Yeatts JP, Kiser MM, Goss CH, Schechter MS, Konstan MW, Pace RG, **Wright FA**, Drumm ML, Knowles MR: Early clinical features of Delta F508 homozygotes defined as "severe" or "mild" for the gene modifier study of CF lung disease. *Pediatric Pulmonology* S30:273, 2007.

17. Guo XL, O'Neal WK, Yeatts JP, Swallow DM, Pace RG, Stonebraker JR, Zariwala MA, Harris A, Wright FA, Zou F, Perez-Vilar J, Knowles MR: Assessing mucin gene polymorphisms to determine their role as modifiers of different CF phenotypes. *Pediatric Pulmonology* S30:265-266, 2007.

18. Li W , Zou F, Lee S, Corey M, Sun L, **Wright FA**, Strug LJ: Analysis of population stratification in North American CF patients. Pediatric Pulmonology, *NACF Meeting Abstract* 159, 2009.

19. O'Neal WK, Guo X, Dang H, Pace RG, Stonebraker JR, Polineni D, Gallins PJ, Jones LC, Dang AT, Doerschuk CM, **Wright FA** , Harris A, Knowles MR: From genes to function: Exploring the mechanism of association between CF lung disease severity and genetic variation at chr11p13. *Pediatric Pulmonology* S34:271, 2011.

20. Wolf W, Jones LC, Gallins PJ, Pace RG, Stonebraker JR, Dang H, **Wright F**, Knowles MR, O'Neal WK: Differential gene expression identifies genetic modifiers associated with lung disease severity and age of onset of persistent pseudomonas infection in cystic fibrosis. *Am J Respir Crit Care Med*, 189:A6717, 2014.

21. Dang H, Pace RG, Stonebraker JR, Guo XL, Jones LC, Boyle MP, Chmiel J, Drumm M, Durie PR, Polineni D, Gallins PJ, **Wright FA**, O'Neal WK, Knowles MR: Correlation of inflammatory markers in human nasal epithelia in vivo informs transcriptomic studies in cystic fibrosis (CF) complementary to genomic variation studies. *Hospital*, 4:5, 2014.

22. Polineni D, Dang H, Gallins PJ, Pace RG, Stonebraker JR, Jones LC, Guo X, Boyle MP, Chmiel JF, Drumm ML, Durie PR, Wright FA, O'Neal WK, Knowles MR: In vivo human nasal epithelia inform transcriptomic studies in cystic fibrosis (CF) complementary to genomic variation studies. *Pediatric Pulmonology*, 49, p.272, 2014.

23. Polineni D, Dang H, Pace R, Stonebraker JR, Jones L, Boyle MP, Chmiel J, Durie PR, Gallins P,…, **Wright F**, O'Neal, WK: Age of onset of chronic P. Aeruginosa pulmonary infection is associated with differential gene expression in CF nasal epithelia in vivo. *Pediatric Pulmonology* (Vol. 51, pp. 244-244), 2016.

24. Polineni D, Dang H, Gallins P, Jones L, Pace RG, Stonebraker JR, Corvol H, Cutting GR, Drumm ML, Strug LJ,…, **Wright F**, Knowles MR. Nasal transcriptomic studies combined with genomic analyses identify gene networks associated with cystic fibrosis lung disease severity. *Pediatric Pulmonology* (Vol. 52, pp. S263-S264), 2017.

Teaching Activities, NCSU

Courses
- Instructor, ST 744 Categorical Data Analysis, Spring 2015 (28 students)
- Instructor, GN 495 Personal Genomics, Spring 2016 (6 students)
- Instructor, ST 590 Bioinformatics I, Fall 2016 (33 students)
- Instructor, ST 744 Categorical Data Analysis, Spring 2017 (16 students)
- Instructor, BSC 495 Personal Genomics, Spring 2018 (10 students)

Service on Doctoral Committees

- Farida Akhtari, Genetics PhD Program
- Tao Hu, Bioinformatics PhD Program and Statistics PhD Program
- Ravi Mathur, Bioinformatics PhD Program
- George Van Den Driessche, Toxicology PhD Program

Advising/mentoring, including co-advising
- Ajay Kumar, Statistics PhD program
- Bryan Ting, Bioinformatics PhD Program
- Renfei Gong, Statistics PhD program

Teaching Activities, UNC

Courses
- Instructor, BIOS 781 Statistical Methods in Human Genetics, Fall 2002 (11 students), Fall 2003 (3 students), Fall 2004 (11 students), Fall 2006 (17 students), Fall 2008 (13 students), Fall 2010 (19 students), Fall 2012 (13 students)
- Instructor, BIOS 785 Statistical Analysis of DNA Microarrays, Fall 2005 (22 students), Fall 2007 (8 students), Fall 2009 (13 students), Fall 2011 (22 students)
- Co-instructor. GNET714 Biostatistics in Bioinformatics and Computational Biology Biostatistics Module, Spring 2004 (4 students), Fall 2005 (9 students), Fall 2006 (5 students), Fall 2007 (5 students), Spring 2009, Fall 2010 (13 students)
- Guest Lecturer, BIOS 783 Statistical Methods in Quantitative Genetics, Spring 2003, Spring 2004, Spring 2006, Spring 2008, Spring 2010
- Guest Lecturer, UNC Autism Center postdoctoral training seminar, Fall 2002, Fall 2004, Fall 2006, Fall 2008, Fall 2010
- Guest lecturer, Genetics 710, Fall 2002, Fall 2004, Fall 2006
- Guest Lecturer, BIOS 740, Spring 2012

Undergraduate Mentoring, UNC Biostatistics
- Alex Vasiljev, 2010

Guidance of Master Research, UNC Biostatistics
- Benjamin Sanford, 2002
- Tania Robbins, 2004 (co-advisor)
- Zheng Zheng Tang, 2009 (co-advisor)

Service on Doctoral Committees, UNC Biostatistics
- Lily Wang, PhD, 2004
- Szu-yun Leu, PhD, 2005
- Emily Kistner, PhD, 2005
- Guoqing Diao, PhD, 2006
- Jonathan Gelfond, PhD, 2007
- Emma Huang, PhD, 2007
- Ritendranath Mitra, PhD, 2009
- Lindsey Ho, DrPH, 2010
- Chae Ryon Kang, PhD, 2011
- Yi Gong, PhD, 2011

- Min Jin Ha, PhD, 2012-2013

Service on Master's and Doctoral Committees, Other UNC Departments
- Josh Harrill, PhD, Curriculum in Toxicology, 2008
- Pam Ross, MS, Curriculum in Toxicology, 2008
- Ni Zhao, MS, Curriculum in Toxicology, 2010
- Shannon O'Shea, MS, Curriculum in Toxicology, 2010
- Daniel Gatti, PhD, Curriculum in Toxicology and Bioinformatics/Comp. Biology, 2010
- Liying Zhang, PhD, School of Pharmacy, 2011
- Daniel Rotroff, PhD, Curriculum in Toxicology , 2012-present
- Valerie Soldatow, PhD, Curriculum in Toxicology , 2013-present

Guidance of Doctoral Research, UNC Biostatistics
- Jianhua Hu, PhD, Dept of Biostatistics, 2003 (Professor of Biostatistics, MD Anderson Cancer Center)
- Andrew Sterrett, PhD, Dept of Biostatistics, 2005 (Senior Statistician, Kaiser Permanente, Denver, CO)
- William Barry, PhD, Dept of Biostatistics, 2006 (Assistant Professor, Dana Farber Cancer Institute and Harvard Medical School)
- Yu-Ling Chang, PhD, Dept of Biostatistics, 2007 (Mathematical Statistician, Food and Drug Administration)
- Arpita Ghosh, PhD, Dept of Biostatistics, 2009 (Research Scientist, Public Health Foundation of India)
- Vonn Walter, PhD Biostatistics (co-advisor), 2010 (Assistant Professor of Biochemistry and Molecular Biology, Pennsylvania State University)
- John Schwarz, PhD Biostatistics (co-advisor), 2010 (Statistical Geneticist, Monsanto)
- Seunggeun Lee, PhD Biostatistics (co-advisor), 2010 (Assistant Professor of Biostatistics, University of Michigan)
- Yihui Zhou, 2011 (Research Assistant Professor, NC State University)
- Greg Mayhew, DrPH, 2008-2013 (GeneCentric Diagnostics, Durham NC)
- Pratyaydipta Rudra, PhD, 2010-2015 (Postdoctoral Scholar, University of Colorado)

Guidance of Post-Doctoral Research
- Rong Cheng, 1998-1999 (Research Scientist, Columbia University)
- William Lemon, 1999-2001 (Director of Scientific and Computing Services, IT Enterprises)
- Daolong Wang, 2002-2004 (Senior Scientist, Syngenta, Inc)
- Jianhua Hu, 2004 (see above)
- Hanwen Huang, 2005-2009 (Assistant Professor at University of Texas Health Science Center at Houston)
- Jinze Liu, 2006-2007 (Assistant Professor of Computer Science, University of Kentucky, Lexington)
- William Barry, 2007 (see above)
- Vonn Walter, 2010-2012 (see above)
- Andrey Shabalin, 2010-2012 (Research Assistant Professor, Virginia Commonwealth University)
- Vered Madar, 2010-2013
- Kai Xia, 2011-2012 (Research Assistant Professor, UNC Department of Psychiatry)

Presentations (since 2008 only, * indicates as co-author of a presentation)

2008

Estimating Odds Ratios in Genome Scans: An Approximate Conditional Likelihood Approach. ENAR Annual Meeting, Arlington, VA, March 2008.*

Chemical Toxicity Prediction for Toxicogenomics Studies. The 47th Annual Meeting of the Society of Toxicology. Seattle, USA, March 2008.*

Fast association mapping using summation trees. 7th Annual Meeting of the Complex Traits Consortium, Montreal, Canada, June 2008.*

Extensions of Conditional Likelihood Bias Correction for Whole-Genome Scans. JSM, Denver CO, August 2008.

A Geometric Interpretation of the Permutation P-Value and Its Application. JSM, Denver CO, August, 2008.*

Estimating Risk and Controlling for Stratification in Genome-Wide Association Studies. Duke University Statistics Seminar, October 2008.

Extensions of Conditional Likelihood Bias. Adjustment for Disease Association Risk Estimates in Whole-Genome Scans. ASHG Annual Meeting, November 2008.*

No Evidence of Differential Gene Expression in Chronic Fatigue Syndrome. ASHG Annual Meeting, November 2008.*

Control of population stratification by correlation-selected principal components. ASHG Annual Meeting, November 2008.*

The Analysis of Genomic Dose-Response Data in the EPA ToxCast Program. SRA Annual Meeting, Boston, USA, December 2008*

2009

Estimating Risk and Controlling for Stratification in Genome-Wide Association Studies. NC State Department of Statistics Seminar, March 2009.
Response Profiles from Toxicogenomics Data. The 48th Annual Meeting of the Society of Toxicology, Baltimore, March 2009.*

Risk Effect Estimation for Multiple Phenotypes and Gene-environment Interaction. ENAR 2009, March 2009, San Antonio, TX.*

Dose-response pathway analysis for gene expression microarrays. Symposium on Toxicity Pathway-Based Risk Assessment: Preparing for Paradigm Change. The National Academy of Sciences, Washington DC, May 2009.

Prediction of in vivo toxicity endpoints from ToxCast Phase I data using a variety of machine learning approaches. ToxCast Data Analysis Summit. EPA Campus, Research Triangle Park, UC, USA. May 2009.

Issues of Controlling for Bias and Population Stratification in Association Studies. Glaxo-SmithKline Statistical Genetics Seminar, August 2009.

Risk Effect Estimation for Secondary Phenotypes and Gene-Environment Interaction: A Conditional Likelihood Approach. JSM, Washington, DC, August 2009.*

An Overview of the Carolina Environmental Bionformatics Center. Board of Scientific Counselors Meeting for the EPA National Center for Computational Toxicology, EPA RTP Campus, September 2009.

The Carolina Environmental Bionformatics Center. EPA Star Center Progress Review, EPA RTP Campus, October 2009.

Principal Component Score Prediction for Related and Unrelated GWA Samples. ASHG Annual Meeting, Honolulu, HI. October 2009.*

Analysis of Population Stratification in North American CF Patients. North American Cystic Fibrosis Annual Meeting, Minneapolis, Oct 2009.*

2010

Convergence and Prediction of Principal Component Scores in High-Dimensional Settings. ENAR Annual Meeting, New Orleans, March 2010.*

Robust Gene Pathway Testing. ENAR Annual Meeting, New Orleans, March 2010.*

A Multivariate Penalized Regression Method for eQTL Mapping. JSM, Vancouver, August 2010.*

Variable Selection and Shrinkage via a Conditional Likelihood-Based Penalty. JSM,Vancouver, August 2010.

Another Look At Principal Components In Genome Association Scanning. Dept. of Health Studies Statistics Seminar, University of Chicago, October 2010.

A Direct Approach To Surrogate Variable Analysis. ASHG Annual Meeting, Washington, DC, November 2010.*

Coming Full Circle: An Hypothesis-driven GWAS (GWAS-HD) with Application to Meconium Ileus in Cystic Fibrosis. ASHG Annual Meeting, Washington, DC, November 2010.*

DiNAMIC: A Method for Assessing the Statistical Significance of DNA Copy Number Aberrations. ASHG Annual Meeting, Washington, DC, November 2010.*

2011
A Multivariate Penalized Regression Method for eQTL Mapping. ENAR Annual Meeting, Miami, March 2011.*

The Interactive Decision Committee for Chemical Toxicity Data Analysis. ENAR Annual Meeting, Miami, March 2011.*

Small-Sample Differential Expression Analysis with RNA-seq Data. ENAR Annual Meeting, Miami, March 2011.

Unified Analysis of Secondary Phenotypes in Case-Control Association Studies. ENAR Annual Meeting, Miami, March 2011.*

A Powerful and Flexible Approach to the Analysis of RNA Sequence Count Data. JSM, Miami Beach, August 2011.*

Permutation-Based Expression Pathway Analysis, Without Permutation. JSM, Miami Beach, August 2011.

Genome-Wide eQTL Mapping by Iterative Multivariate Adaptive LASSO (LMAL). JSM, Miami Beach, August 2011.*

The DR Pathway Software for Expression Dose Response Pathway Analysis. Joint Research Commission, Ispra, Italy, September 2011.

The DR Pathway Software for Expression Dose Response Pathway Analysis. The European Chemicals Agency (ECHA), Helsinki, Finland, September 2011.

The DR Pathway Software for Expression Dose Response Pathway Analysis. USEPA, Washington, DC, October 2011.

Unified Analysis of Secondary Phenotypes in Case-Control Association Studies. JSM, Miami Beach, August 2011.

Permutation Based Pathway Analysis, Without Permutation. ICSA Conference, Beijing, December 2011.*

2012

Permutation-based Expression Pathway Analysis, Without Permutation. ENAR Annual Meeting, Washington DC, April 2012.

Quantitative High-Throughput Screening for Chemical Toxicity in Population-Based In Vitro Models. National Academies of Sciences Workshop on Individual Variability. Washington, DC, April 2012.

The DR Pathway Software for Expression Dose Response Pathway Analysis. CalEPA, Sacramento, CA, May 2012.

The DR Pathway Software for Expression Dose Response Pathway Analysis. CalEPA, Oakland, CA, May 2012.

Pathway Analysis Using a Score-Based Approach for RNA-Seq Data. JSM, San Diego, CA, August 2012.*

Bootstrap Testing and Inference for Recurrent DNA Copy Number Aberrations. JSM, San Diego, CA, August 2012. *

Variable Selection--Based Weighting Schemes for Rare Variants in Sequence Data. JSM, San Diego, CA, August 2012. *

Testing and Estimation of Partial Correlation Networks. JSM, San Diego, CA, August 2012. *

Some Useful Permutation Approaches You've Probably Never Used. NC State Department of Statistics, Raleigh, December 2012.

Challenges in Using eQTL Data To Dissect Complex Disease. NC State Department of Genetics, Raleigh, NC, December 2012.

2013

Some Useful Resampling Approaches You've Probably Never Used. Michigan State University Department of Statistics, East Lansing, MI, February 2013.

Fast and Robust Association Testing for High-Throughput Testing. JSM, Montreal, Canada, August 2013.

An Empirical Bayes Approach for Joint eQTL Analysis in Multiple Tissues. JSM, Montreal, Canada, August 2013.*

The Projack: A Resampling Approach for Prediction of Ranked Effect Sizes and Estimation of Normal Means . JSM, Montreal, Canada, August 2013.*

2014

False Discovery Rate Control and Group Testing for Complex Omics Data. ENAR, Baltimore, March 2014.

Extending the Projack to Complex Settings, ENAR, Baltimore, March 2014.

A Big Data to Knowledge Proposal for Genomic Analysis, Triangle Big Data Genomics Meeting, NC Biotech Center, April 2014.

A Procedure to Detect General Association Based on Distance of Ranks. JSM, Boston, August 2014.*

Heritability and Genomics of Gene Expression in Peripheral Blood. Triangle Statistical Genomics Annual Meeting, Cary NC, October 2014.

Hypothesis Testing At the Extremes: Fast and Robust Association for High-Throughput Data. National Cancer Institute Biostatistics Series, Bethesda, MD, October 2014.

Extending the Bayesian Multi-Tissue Model to High-Dimensions. GTEx Analysis Working Group Meeting, Washington DC, December 2014.

The NCSU Bioinformatics Research Center. Joint Meeting of NCSU CALS representatives and those from China Academy of Agricultural Sciences, NCSU, December 2014.

2015

Genetic Variability and Gene Expression. Society of Toxicology Annual Meeting Continuing Education Sessions, San Diego, March 2015.

Statistical Issues in Interpreting High Throughput Data. Keck Center of the National Academy of Sciences, 21st Century Approaches to Risk Assessment, Washington DC, April 2015.

Statistics and High-Throughput Biology. NCSU Bioinformatics Research Center Seminar Series, April 2015.

Update on the Multiple Hypothesis Testing Working Group. SAMSI Bioinformatics Transition Workshop, RTP. May 2015.

Obtaining Realistic Effect Size Estimates From eQTL Rna-Seq Analysis. GTEx Analysis Working Group. Chicago, July 2015.

Further Extending the Bayesian Multi-Tissue Model to High-Dimensions. GTEx Analysis Working Group. Chicago, July 2015.

The 1000 Genomes High-Throughput Screening Study. Workshop on Interindividual Variability: New Ways to Study and Implications for Decision Making. National Academy of Sciences, Washington DC, September 2015.

An Update on eQTLs, and Their Tissue-Specificity– What Have We Learned? NCSU Genetics Program seminar. October 2015.

Integrative approaches for large-scale transcriptome-wide association studies. American Society of Human Genetics Annual Meeting (co-author) Baltimore, October 2015.

Correction for Ordering Bias Using the Projack. Columbia University Biostatistics Seminar. October 2015.

2016

Corrmeta: Fast Association Analysis for eQTL and GWAS Data with Related Samples and Correlated Phenotypes (co-author), March 2016.

Genetic Variability and Gene Expression. Society of Toxicology Annual Meeting Continuing Education Sessions, New Orleans, March 2016.

Encouraging Interdisciplinarity in the Bioinformatics Research Center. ORIED Meeting on Centers and Research Institutes, Raleigh, April 2016.

2017

eQTLs, Chemical Screening, and the Kitchen Sink - The Multifaceted Roles of Bioinformatics in High-Throughput Research. SynTheSys Lunch Talks, NC State, February 2017.

How Surprising Was Trump's Victory? NCSU Statistics Special Seminar, NC State, April 2017.

Bioinformatics and Big Data. Innovation Workshop for the Plant Sciences Initiative, NC State, April 2017.

A Pipeline for TempOseq Analysis. EPA Computational Toxicology Series, Research Triangle Park, May 2017.

Computation of Ancestry Scores with Mixed Families and Unrelated Individuals. Joint Statistical Meetings, Baltimore, August 2017.

TempOseq Analysis and Probe Design. NIEHS National Toxicology Program Seminar, Research Triangle Park, October 2017.

eQTLs: What Are They Good For? Biological Sciences Retreat, November 2017.

Ongoing Research Support

1R01HG009125 01 (Wright)   09/07/2016-06/30/2019   NIH/NIEHS
Multi-tissue and network models for next-generation eQTL
The long-term objective of this research proposal is to provide a framework, and statistical and computational tools, to advance the analysis and understanding of expression quantitative trait loci (eQTL) in single and multi-tissue studies, and to elucidate the genotypic basis of differences between tissues.
Role: PI (MPI mechanism)

C000612356 (Wright)   01/31/2017-01/31/2020   RTI International
Game-Changing Research Incentive Program (GRIP)
This joint proposal from RTI and NCSU seeks to create a multi-faceted three-year Program in Genetic Discovery and Prediction (PGDP), initially organized around a demonstration and feasibility pilot for a highly ambitious effort the team calls the "1000 GWAS Project."
Role: PI

2T32ES007329 - 16A1 (Wright)   07/01/2017-06/30/2018   NIH/NIEHS
Graduate Training in Bioinformatics
This NIH Bioinformatics training program supports 5 predoctoral trainees.
Role: PI

Concawe (Wright)   06/01/2016-10/31/2018   Concawe
New Technologies to Underpin Category Approaches and Read Across in Petroleum Regulatory Programs
This project is to devise a framework for high-throughput read across by combining multiple streams of information and a comprehensive array of the biological/toxicological effects in a broad spectrum of in vitro systems.
Role: Subcontract PI

5P42ES005978-22   (Fry)   08/31/2013 – 03/31/2018   UNC/NIEHS
Elucidating Risks: From Exposure and Mechanism to Outcome – Core D
Core D provides biostatistical and bioinformatic support for the UNC-CH/NCSU Superfund Research
Program. The aims are to facilitate research by providing state-of-the-art biostatistics and bioinformatics
expertise, to develop new statistical methods, and to provide inter-disciplinary training opportunities to
graduate students, postdoctoral fellows, and faculty. Wright is subcontract PI to supervise the Biostatistics
and Bioinformatics Core.
Role: Core PI

2015-0059/1P30ES025128-01   (Smart)   04/20/2015-03/31/2020   NIH/NIEHS
Center for Human Health and the Environment
The mission of the Center for Human Health and the Environment (CHHE) is to advance understanding of
environmental impacts on human health. Through a systems biology framework integrating all levels of
biological organization, CHHE aims to elucidate the fundamental mechanisms through which environmental
exposures/stressors interface with biomolecules, pathways, the genome, and epigenome to influence
human disease.
Role: Co-Investigator

1 P42ES027704-01 (Rusyn)   09/01/2017-03/31/2022   NIH/NIEHS
Texas A&M University/NIH/NIEHS   -   Superfund Research Center
The Texas A&M University Superfund Research Center brings together a team of scientists from biomedical,
geosciences, data science and engineering disciplines to design comprehensive solutions for complex
exposure- and hazard-related challenges
Role: co-investigator, Subcontract PI

USEP   (Rusyn)   06/01/2015-05/31/2019   USEPA
Cardiotoxicity Adverse Outcome Pathway: Organotypic Culture Model and In Vitro/ In Vivo
Extrapolation for High-Throughput Hazard, Dose-Response and Variability Assessments
The central hypotheses of this proposal are that stem cell-derived cardiomyocyte cultures constitute an
effective organotypic culture model for predictive toxicity screening of environmental chemicals, and that a
population-based experimental design utilizing a panel of human iPSCs and mouse Collaborative Cross
(CC) can assess variation in toxicity to better characterize uncertainties.
Role: Co-Investigator, Subcontract PI

OPP1052983   (Yencho)   08/29/2014-08/31/2018   Gates Foundation
GTSPI: Genomic Tools for Sweetpotato Improvement
This project will develop modern genomic, genetic, and bioinformatics tools to facilitate crop improvement
and improve genetic gains in sweetpotato, an important food security and cash crop with highly recognized
potential to alleviate hunger, vitamin A deficiency, and poverty in Sub-Saharan Africa (SSA), and
predominantly grown in small plot holdings by poor women farmers. Wright is an investigator to provide
advice on the development of new tools for genomic analysis.
Role: Co-Investigator

1R21HG007840-01A1 (Zhou)   06/15/2015-04/30/2018   NIH/NHGRI
Permutation Approximations for Next Generation Association
The objective of this research proposal is to develop an entirely new approach to the analysis and summary
of genome association data. In contrast to approaches that use asymptotic parametric results, or

computationally intensive resampling, our approach uses exact permutation moments followed by a density approximation to the relevant statistics.
Role: Co-Investigator

1R01ES024471-01A1   (Smart)   06/01/2016-05/31/2021   NIH/NIEHS
Role of Long Intergenic Noncoding RNA in UVB-induced Apoptosis and Skin Cancer
The goals of this project are to define the regulation and function of lincRNA-p21 in keratinocytes and to develop mouse genetic models to define the molecular function of lincRNA-p21 in controlling keratinocyte gene expression, apoptosis and skin cancer in response to UVB radiation.
Role: Co-Investigator

2015-DN-BX-K062 (Faith)   01/01/2016-12/31/2017   DOJ
Development of a Self-Sustaining Open Access Forensic STR Sequence Diversity Database
The practice of DNA forensics is on a trajectory to adopt a revolutionary new technology called next-generation sequencing (NGS). With the implementation of NGS, laboratories will be able to analyze biological evidence at an unprecedented genetic resolution, assisting investigations and augmenting criminal casework, missing persons, paternity, cold and unsolved cases.
Role: Co-Investigator