

## **CURRICULUM VITAE**

### **Kevin R. Coombes, Ph.D.**

#### **PRESENT TITLE AND AFFILIATION**

Professor, Department of Biomedical Informatics, Wexner Medical Center, The Ohio State University, Columbus, Ohio.

#### **OFFICE ADDRESS**

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Wexner Medical Center, The Ohio State University  
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Columbus, Ohio 43210

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#### **EDUCATION**

##### **Degree-Granting Education**

Lehigh University, Bethlehem, PA, BA, 1977, Mathematics  
University of Chicago, Chicago, IL, MS, 1978, Mathematics  
University of Chicago, Chicago, IL, PHD, 1982, Mathematics

##### **Postgraduate Training**

NSF Postdoctoral Fellow, MIT, Cambridge, MA, 1982-1984

#### **EXPERIENCE/SERVICE**

##### **Academic Appointments**

Moore Instructor, Massachusetts Institute of Technology, Boston, MA, 1982-1983  
Assistant Professor, University of Oklahoma, Norman, OK, 1983-1985  
Visiting NSF Fellow, University of Chicago, Chicago, IL, 9/1984-12/1984  
Assistant Professor, University of Michigan, Ann Arbor, MI, 1985-1989  
Visiting Instructor, Massachusetts Institute of Technology, Cambridge, MA, 1/1985-5/1985  
Visiting Assistant Professor, University of Michigan, Ann Arbor, MI, 1989-1990  
Associate Professor, University of Maryland, College Park, MD, 1989-1999  
Associate Professor, Chief,, Biostatistics and Applied Mathematics, The University of Texas M. D. Anderson Cancer Center, Houston, TX, 1999-2006  
Associate Professor, Department of Bioinformatics and Computational Biology, Division of Quantitative Sciences, The University of Texas M.D. Anderson Cancer Center, Houston, TX, 2006-2009  
Professor, Department of Bioinformatics and Computational Biology, Division of Quantitative Sciences, The University of Texas MD Anderson Cancer Center, Houston, TX, 2009-2013  
Professor, Department of Biomedical Informatics, Wexner Medical Center, The Ohio State University, Columbus, OH, 2013-present

**Administrative Appointments/Responsibilities**

Deputy Department Chair, Department of Bioinformatics and Computational Biology, Division of Quantitative Sciences, The University of Texas MD Anderson Cancer Center, Houston, TX, 9/2009-12/2010

**Institutional Committee Activities**

Search Committee, University of Oklahoma Mathematics, Member, 1983-1984

Undergraduate Mathematics Program Committee, University of Michigan, Member, 1986-1988

Honors Committee, University of Michigan Mathematics, Member, 1987-1988

Executive Committee, University of Michigan Mathematics, Member, 1988-1989

Undergraduate Counseling Committee, University of Michigan, Member, 1988-1990

MathNet Committee, University of Maryland Mathematics, Member, 1990-1999

Policy Committee, University of Maryland Mathematics, Member, 1991-1992

Minority Recruitment Committee, University of Maryland Mathematics, Member, 1991-1992

Math 220 Textbook Selection Committee, Member, 1992-1993

EEEEO, University of Maryland Mathematics, unknown, 1992-1994

Math 246 Computer Supplement, University of Maryland, University of Maryland, MD, 1993-1999

Instructional Improvement Grant, University of Maryland, Maryland, 1996-1997

Math 241 Teaching Theatre Experiment, University of Maryland, Maryland, 1997-1999

Honors Committee, University of Maryland Mathematics, Member, 1992-2000

Honors Committee, University of Maryland Mathematics, Chair, 1993-1997

Computing Technology, University of Maryland Mathematics, Director, 1994-1996

Joint Mathematics-Engineering Committee on Technology in Education, University of Maryland, Member, 1997

Junior Science and Humanities Symposium Selection Committee, University of Maryland, Member, 1997

Math-Stat Majors Committee, University of Maryland Mathematics, Member, 1998-1999

Peer Review Committee, University of Maryland Mathematics, Member, 1998-1999

Blue Ribbon Commission, MDACC, Member, 2002-2003

Faculty Oversight Committee for Database Development, MDACC, Member, 2003-2010

CRIS Advisory Committee, MDACC, Member, 2004-2005

Gulf Coast Consortium Oversight Committee, Member, 2004-2012

Academic Affairs Committee, Biostatistics Program, UT GSBS, Chair, 2004-2010

Graduate School of Biological Sciences, Member, 2004-2013

Clinical and Research Informatics Committee, Member, 2005-2011

**HONORS, AWARDS, RECOGNITION**

Phi Beta Kappa, Lehigh University, 1977

NSF Graduate Fellow, 1979-1981

NSF Postdoctoral Fellow, 1982-1984

Arts and Sciences Fellow, University of Oklahoma, Summer, 1984

NSF Summer Support, 1985-1990

CRLT-LSA Fellow, University of Michigan, 1987-1988

GRB Fellowship, University of Maryland, Summer, 1992

Best presentation - Conference on Critical Assessment of Microarray Data Analysis (CAMDA 01), Duke University, October, 2001

Best abstract, Annual Proteomics Data Mining Conference, Duke University, September, 2002

Best presentation - Conference on Critical Assessment of Microarray Data Analysis (CAMDA 02), Duke University, November, 2002

Best paper, BIOTECHNO 2011, Third International Conference on Bioinformatics, Biocomputational Systems, and Biotechnologies, Venice, May 2011.

## **PRESS COVERAGE**

60 Minutes, "Deception at Duke", 12 February 2012

The Economist, "An Array of Errors", 10 September 2011

New York Times, "How Bright Promise in Cancer Testing Fell Apart", 7 July 2011

Nature News, "Cancer trial errors revealed", 12 January 2011

NPR, "Scientists Question Cancer Gene Trials At Duke University", 20 July 2010

The Scientist, "Serum Proteomics Scrutinized", 1 May 2006

New York Times, "New Cancer Test Stirs Hope and Concern", 3 February 2004

## **RESEARCH**

### **Grants and Contracts**

#### **Funded**

Co-Investigator, 4%, Personalizing NSCLC Therapy: Exploiting KRAS Activated Pathways, 1 R01 CA155196 01A1, NIH/NCI (Subcontract from Yale University, PI - Roy Herbst, 11/18/2011-8/31/2016, \$2,358,228 (\$444,183/year)

Co-Investigator, 10%, Protein-coding and non-coding RNA biomarkers for early detection of CLL, 1R01CA182905-01, NIH/NCI, PI - George Calin and Lynne Abruzzo, 3/1/2014 - 2/28/2019, \$2,316,507 (\$453,491/year)

Bioinformatician, 10%, The Ohio State University and MD Anderson Cancer Center Thyroid Cancer SPORE, NIH/NCI, PI - Matthew Ringel. 7/1/2013-6/30/2018, \$11,300,000.

#### **Pending**

Co-Investigator, 5%, Short-term potentiation as the basis of aggression escalation: A new hypothesis, 1 R21 MH094893 01, NIH/NIMH (Subcontract from the University of Minnesota), PI - Michael Potegal, 4/1/2013-3/31/2015, \$25,172 (\$12,400/year)

Co Director, 5%, Developing New Rational, Personalized Medicine for Lung Cancer Based on Understanding of Lung Cancer Molecular and Cellular Biology, NIH/NCI (Subcontract from University of Texas Southwestern Medical Center, PI - John Minna, 7/1/2013-6/30/2018, \$770,090 (\$97,480/year)

Bioinformatician, 10%, Therapy of genomic high risk CLL, NIH/NCI, PI – John Byrd, 7/1/2014-6/30/2019, \$1,925,000.

Co-investigator, 5%, SBRT for early stage lung cancer: who may need additional therapy?, LUNGevity Foundation, 7/1/2014-6/30/2017, \$300,000.

### **Completed**

Core Director, 15%, Cancer Center Support Grant Bioinformatics Shared Resource (PP-SR22), 5 P30 CA016672 37, NIH/NCI, PI - Ronald DePinho, 7/1/2003-6/30/2013, \$548,220 (\$109,644/year)

Biostatistician, 10%, The University of Texas SPORE in Lung Cancer (PC-C), 5 P50 CA070907 15, NIH/NCI (Subcontract from the University of Texas Southwestern Medical Center), PI - John Minna, 5/1/2008-4/30/2013, \$415,104 (\$100,181/year)

Co-Director, 5%, University of Texas SPORE in Prostate Cancer (PC-B), 5 P50 CA140388 03, NIH/NCI, PI - Christopher Logothetis, 9/2/2009-8/31/2014, \$832,635 (\$166,501/year)

Investigator, 4%, Prediction of Pathologic Complete Response by Gene Expression Profiling in Esophageal Cancer, 5 R01 CA138671 03, NIH/NCI, PI - Jaffer Ajani, 2/1/2010-1/31/2015, \$1,014,750 (\$201,275/year)

Collaborator, 5%, Development and Validation of Prognostic Model for Gastric Cancer, 5 R01 CA150229 03, NIH/NCI, PI - Ju-Seog Lee, 9/1/2010-1/31/2014, \$728,325 (\$181,148/year)

Other Significant Contributor, Proteolytic processing of cyclin E in breast cancer, 2 R01 CA087548 10A1, NIH/NCI, PI - Khandan Keyomarsi, 12/1/2010-11/30/2015, \$1,250,000 (\$250,000/year)

Other Significant Contributor, Targeting the cell cycle in triple negative breast cancer, 1 R01 CA152228 01A1, NIH/NCI, PI - Khandan Keyomarsi, 4/1/2011-3/31/2016, \$2,001,526 (\$419,628/year)

Co-Investigator, 10%, Integrative methods for high-dimensional genomics data, 5 R01 CA160736 02, NIH/NCI, PI - Veera Baladandayuthapani, 8/23/2011-6/30/2015, \$830,000 (\$207,500/year)

Co-Investigator, 3%, Markers and therapeutic strategies for overcoming chemoradiotherapy resistance, 5 R01 CA168484-02, NIH/NCI, PI - John Heymach, 9/26/2011-7/31/2016, \$976,142 (\$183,360/year)

Co-Core Director, 10%, Therapy of AML (PC-C2), 5 P01 CA055164 19, NIH/NCI, PI - Michael Andreeff, 5/27/1997-8/31/2013, \$515,167 (\$101,259/year)

Co-Investigator, 5%, A Mutational Model for Childhood Cancer (PC-C), 5 P01 CA034936 23, NIH/NCI, PI - Louise C. Strong, 8/1/1997-4/30/2012, \$1,186,476 (\$245,101/year)

Co-Investigator, Extension of Radiotherapy Research (PC-B), 5 P01 CA006294 44, NIH/NCI, PI - Kie-Kian Ang, 3/6/1998-5/31/2009, \$554,683 (\$110,936/year)

Co-Investigator, Extension of Radiotherapy Research (PP-2) & (PC-B), 5 P01 CA006294 44, NIH/NCI, PI - Kie-Kian Ang, 3/6/1998-5/31/2009, \$541,852 (\$108,370/year)

Collaborator, 5%, VITAL (Vanguard Investigations of therapeutic approaches to lung cancer PC-B, W81XWH-04-1-0142 05, Department of Defense (DOD), PI - Waun Hong, 12/15/2003-1/14/2009, \$228,106 (\$75,305/year)

Collaborator, 5%, Molecular-based Therapy for Oral Cancer Prevention (PP-3), 5 P01 CA106451 05, NIH/NCI, PI - Scott Lippman, 8/1/2004-7/31/2010, \$694,880 (\$138,976/year)

Biostatistician, 5%, The P13K/PTEN/AKT Signal Transduction Cascade as a Predictor for Response to Therapy and Therapeutic Target in Breast Cancer., N/A, American Society of Clinical Oncology (ASCO), PI - Ana Maria Gonzalez-Angulo, 7/1/2005-6/30/2010, \$155,907 (\$52,045/year)

Co-Investigator, 5%, Validation of prognostic biomarker signatures in CLL, CLL Global Research Foundation, PI - Lynne V Abruzzo, 8/8/2005-4/30/2008, \$191,125 (\$95,563/year)

Investigator, 5%, UTMDACC SPORE in Breast Cancer (PC-B), 5 P50 CA116199 04, NIH/NCI, PI - Gabriel Hortobagyi, 9/23/2005-8/31/2008, \$659,063 (\$130,029/year)

Collaborator, 5%, The P13K/PTEN/AKT Signal Transduction Cascade in Breast Cancer, 5 K23 CA121994 05, NIH/NCI, PI - Ana Maria Gonzalez-Angulo, 7/1/2006-6/30/2012, \$630,000 (\$126,000/year)

Co-Investigator, 5%, A mouse model for glomerulosclerosis and early onset renal failure, 5 R01 DK069599 03, NIH/NIDDK, PI - Vicki D. Huff, 8/7/2006-5/31/2009, \$1,084,887 (\$213,892/year)

Biostatistician, 5%, Functional Proteomics and Response to Preoperative Therapy in Breast Cancer, 5 R21 CA120248 02, NIH/NCI, PI - Ana Maria Gonzalez-Angulo, 9/1/2006-8/31/2009, \$168,796 (\$84,398/year)

Co-Investigator, 5%, Validation of RNA and DNA Biomarkers of Prognosis in Chronic Lymphocytic Leukemia, 5 R01 CA123252 03, NIH/NCI, PI - Lynn Abruzzo, 9/27/2006-7/31/2011, \$522,206 (\$174,069/year)

Investigator, 15%, University of Texas SPORE in Prostate Cancer (PC-B), 5 P50 CA090270 05, NIH/NCI, PI - Christopher Logothetis, 5/1/2007-2/28/2008, \$705,228 (\$141,046/year)

Bioinformatician, 5%, PROSPECT (Profiling of Resistance Patterns & Oncogenic Signaling Pathways in Evaluation of Cancers of the Thorax and Therapeutic Target Identification) PC-B, W81XWH 07 1 0306 04, Department of Defense (DOD), PI - Waun K Hong, 6/1/2007-5/31/2012, \$390,434 (\$102,785/year)

Co-Investigator, 5%, Discovery and Clinical Validation of Cancer Biomarkers Using Printed Glycan Array, 7 U01 CA128526 02, NIH/NCI (Subcontract from New York University), PI - Margaret E. Huflejt, 9/7/2007-2/28/2009, \$531,260 (\$91,157/year)

Biostatistician, 5%, Determinants of signaling network regulation in combinatorial targeted therapies, 1 R01 CA125109 01 A2, NIH/NCI, PI - Prahlad Ram, 4/16/2008-3/31/2009, \$747,000 (\$249,000/year)

Co-Investigator, 5%, Adaptive Methodology for Functional Biomedical Data, 5 R01 CA107304 07, NIH/NCI, PI - Jeffrey Morris, 5/1/2008-2/28/2012, \$645,851 (\$160,001/year)

Statistician, 5%, Molecular Markers of Response to Chemoradiation in Localized Esophageal Cancer, 5 R21 CA127672 02, NIH/NCI, PI - Jaffer Ajani, 8/15/2008-7/31/2010, \$202,500 (\$101,250/year)

Investigator, 5%, M D Anderson Cancer Center Head and Neck SPORE (PC-B), 2 P50 CA097007 06A1, NIH/NCI, PI - Scott Lippman, 9/4/2008-7/31/2009, \$901,769 (\$170,171/year)

Co-Investigator, 5%, Bayesian Models for cancer prognosis by integrating diverse types of data, 5 R01 CA132897 02, NIH/NCI, PI - Yuan Ji, 9/15/2008-7/31/2011, \$645,000 (\$129,000/year)

Principal Investigator, 1%, Testing Genomic Predictors in Response to Chemotherapy, SR2011-00034428LG, NIH/NCI, 10/1/2011-12/31/2011, \$23,106 (\$23,106/year)

Bioinformatician, 5%, The microRNA epigenome in CLL, 121838-RSG-12-072-01-LIB 01, American Cancer Society (ACS), PI - Deepa Sampath, 1/1/2012-8/31/2012, \$560,000 (\$140,463/year)

#### **Grant Reviewer/Service on Study Sections**

Special Study Section on Genomics and Proteomics of Transplantation, NIH, Member, 2005

Special Study Section on SBIR Grants, NIH, Member, 2006

Special Study Section on "Asthma and Allergic Diseases Cooperative Research Centers", NIAID, Member, 2007

Study Section on Protection of Human Health by Immunology and Vaccines, NIH, Member, 2010

#### **PUBLICATIONS**

##### **Peer-Reviewed Original Research Articles**

1. **Coombes KR**. Relative algebraic K-theory. *Invent. Math* 70:13-25, 1982.
2. **Coombes KR**, Srinivas V. Relative K-theory and vector bundles on certain singular varieties. *Invent. Math* 70:1-12, 1982.
3. **Coombes KR**, Srinivas V. A remark on  $K_1$  of an algebraic surface. *Math. Ann* 265:335-342, 1983.
4. **Coombes KR**, Harbater D. Hurwitz families and arithmetic Galois groups. *Duke Math. J.* 52:821-839, 1985.
5. **Coombes KR**. On  $SK_1$  of curves and Kähler differentials. *Com. Alg* 13:697-716, 1985.
6. **Coombes KR**, Muder D. Zero cycles on del Pezzo surfaces over local fields. *J. Alg* 97:438-460, 1985.
7. **Coombes KR**, Fisher R. Inversion of abelian integrals on curves of small genus. *Math. Ann* 275:185-196, 1986.
8. **Coombes KR**. Motifs, L-functions, and the K-cohomology of rational surfaces over finite fields. *Math. Ann* 276:255-267, 1987.
9. **Coombes KR**. Every rational surface is separably split. *Comm. Math. Helv* 63:305-311, 1988.
10. **Coombes KR**. On the K-theory of curves on finite fields. *J. Pure Appl. Alg* 51:79-87, 1988.
11. **Coombes KR**, Grant D. On heterogeneous spaces. *J. Lon. Math. Soc* 40:385-397, 1989.
12. McCoy-Pardington D, Judd W, Knaf P, Abruzzo L, Coombes KR, Butch S, Oberman, H. Blood utilization during extracorporeal membrane oxygenation. *Transfusion* 30:303-309, 1990.
13. **Coombes KR**. The arithmetic of zero cycles on surfaces with geometric genus and irregularity zero. *Math. Ann* 291:429-452, 1991.

14. **Coombes KR**, Potegal M. Attack priming and aggressive arousal in female Syrian golden hamsters, *Mesocricetus auratus*: Observed attack latency and calculated attack probability as a function of the duration of contact with a conspecific. *Animal Behavior*, 1994.
15. **Coombes KR**. Elliptic curves and logarithmic derivatives. *J. Pure Appl. Alg* 138:21-38, 1999.
16. Zhang W, Labordé PM, **Coombes KR**, Berry DA, Hamilton SR. Cancer genomics: promises and complexities. *Clin Cancer Res* 7:2159-67, 2001.
17. Baggerly KA, **Coombes KR**, Hess KR, Stivers DN, Abruzzo LV, Zhang W. Identifying differentially expressed genes in cDNA microarray experiments. *J Comput Biol* 8:639-59, 2001.
18. Hess KR, Zhang W, Baggerly KA, Stivers DN, **Coombes KR**. Microarrays: handling the deluge of data and extracting reliable information. *Trends Biotechnol* 19:463-8, 2001.
19. Taylor E, Cogdell D, **Coombes K**, Hu L, Ramdas L, Tabor A, Hamilton S, Zhang W. Sequence verification as quality-control step for production of cDNA microarrays. *Biotechniques* 31:62-5, 2001.
20. Ramdas L, **Coombes KR**, Baggerly K, Abruzzo L, Highsmith WE, Krogmann T, Hamilton SR, Zhang W. Sources of nonlinearity in cDNA microarray expression measurements. *Genome Biol* 2(11):RESEARCH0047, 2001. PMID: PMC60308.
21. **Coombes KR**, Highsmith WE, Krogmann TA, Baggerly KA, Stivers DN, Abruzzo LV. Identifying and quantifying sources of variation in microarray data using high-density cDNA membrane arrays. *J Comput Biol* 9:655-69, 2002.
22. Hu L, Wang J, Baggerly K, Wang H, Fuller GN, Hamilton SR, **Coombes KR**, Zhang W. Obtaining reliable information from minute amounts of RNA using cDNA microarrays. *BMC Genomics* 3:16, 2002.
23. **Coombes KR**, Zhang L, Bueso-Ramos C, Brisbay S, Logothetis C, Roth J, Keating MJ, McDonnell TJ. TAD: a web interface and database for tissue microarrays. *Appl Bioinformatics* 1:155-8, 2002.
24. **Coombes KR**, Fritsche H, Jr, Clarke C, Chen J, Baggerly K, Morris J, Xiao L, Hung M, Kuerer H. Quality control and peak finding for proteomics data collected from nipple aspirate fluid by surface-enhanced laser desorption and ionization. *Clin Chem* 49:1615-23, 10/2003.
25. Baggerly K, Morris J, Wang J, Gold D, Xiao L, **Coombes KR**. A comprehensive approach to the analysis of matrix-assisted laser desorption/ionization-time of flight proteomics spectra from serum samples. *Proteomics* 3:1667-72, 2003.
26. Morris J, Baggerly K, **Coombes KR**. Bayesian shrinkage estimation of the relative abundance of mRNA transcripts using SAGE. *Biometrics* 59:476-86, 2003.
27. Goy A, Ramdas L, Remache Y, Gu J, Fayad L, Hayes K, **Coombes KR**, Barkoh B, Katz R, Ford R, Cabanillas F, Gilles F. Establishment and characterization by gene expression profiling of a new diffuse large B-cell lymphoma cell line, EJ-1, carrying t(14;18) and t(8;14) translocations. *Lab Invest* 83:913-6, 2003.

28. McCarthy H, Wierda W, Barron L, Cromwell C, Wang J, **Coombes KR**, Rangel R, Elenitoba-Johnson K, Keating M, Abruzzo L. High expression of activation-induced cytidine deaminase (AID) and splice variants is a distinctive feature of poor-prognosis chronic lymphocytic leukemia. *Blood* 101:4903-8, 2003.
29. Wang J, Hu L, Hamilton S, **Coombes KR**, Zhang W. RNA amplification strategies for cDNA microarray experiments. *Biotechniques* 34:394-400, 2003.
30. Udtha M, Lee S, Alam R, **Coombes KR**, Huff V. Upregulation of c-MYC in WT1-mutant tumors: assessment of WT1 putative transcriptional targets using cDNA microarray expression profiling of genetically defined Wilms' tumors. *Oncogene* 22:3821-6, 2003.
31. Baggerly KA, Morris JS, **Coombes KR**. Reproducibility of SELDI-TOF protein patterns in serum: comparing datasets from different experiments. *Bioinformatics* 20(5):777-85, 3/2004.
32. Gold D, **Coombes KR**, Medhane D, Ramaswamy A, Ju Z, Strong L, Koo J, Kapoor M. A comparative analysis of data generated using two different target preparation methods for hybridization to high-density oligonucleotide microarrays. *BMC Genomics* 5:2, 2004.
33. Spurgers K, **Coombes KR**, Meyn R, Gold D, Logothetis C, Johnson T, McDonnell T. A comprehensive assessment of p53-responsive genes following adenoviral-p53 gene transfer in Bcl-2-expressing prostate cancer cells. *Oncogene* 23:1712-23, 2004.
34. Kuerer H, **Coombes KR**, Chen J, Xiao L, Clarke C, Fritsche H, Krishnamurthy S, Marcy S, Hung M, Hunt K. Association between ductal fluid proteomic expression profiles and the presence of lymph node metastases in women with breast cancer. *Surgery* 136:1061-9, 2004.
35. Wang J, **Coombes KR**, Highsmith W, Keating M, Abruzzo LV. Differences in gene expression between B-cell chronic lymphocytic leukemia and normal B cells: a meta-analysis of three microarray studies. *Bioinformatics* 20:3166-78, 2004.
36. Baggerly K, Edmonson S, Morris J, **Coombes KR**. High-resolution serum proteomic patterns for ovarian cancer detection. *Endocr Relat Cancer* 11:583-4; author reply 585-7, 2004.
37. Pawlik TM, Fritsche H, **Coombes KR**, Xiao L, Krishnamurthy S, Hunt KK, Pusztai L, Chen JN, Clarke CH, Arun B, Hung MC, Kuerer HM. Significant differences in nipple aspirate fluid protein expression between healthy women and those with breast cancer demonstrated by time-of-flight mass spectrometry. *Breast Cancer Res Treat.* 2005 Jan;89(2):149-57. PMID: 15692757
38. Abruzzo L, Lee K, Fuller A, Silverman A, Keating M, Medeiros L, **Coombes KR**. Validation of oligonucleotide microarray data using microfluidic low-density arrays: a new statistical method to normalize real-time RT-PCR data. *Biotechniques* 38:785-92, 5/2005.
39. **Coombes KR**, Tsavachidis S, Morris JS, Baggerly KA, Hung MC, Kuerer HM. Improved peak detection and quantification of mass spectrometry data acquired from surface-enhanced laser desorption and ionization by denoising spectra with the undecimated discrete wavelet transform. *Proteomics* 5(16):4107-17, 11/2005.
40. Hu J, Kapoor M, Zhang W, Hamilton S, **Coombes KR**. Analysis of dose-response effects on gene expression data with comparison of two microarray platforms. *Bioinformatics* 21:3524-9, 2005.



41. Ramaswamy A, Lin E, Chen I, Mitra R, Morrisett J, **Coombes KR**, Ju Z, Kapoor M,. Application of protein lysate microarrays to molecular marker verification and quantification. *Proteome Science* 3:9, 2005.
42. Ji Y, Wu C, Liu P, Wang J, **Coombes KR**. Applications of beta-mixture models in bioinformatics. *Bioinformatics* 21:2118-22, 2005.
43. Baggerly KA, **Coombes KR**, Morris JS. Bias, randomization, and ovarian proteomic data: a reply to "producers and consumers". *Cancer Inform* 1:9-14, 2005.
44. Abruzzo L, Wang J, Kapoor M, Medeiros L, Keating M, Edward Highsmith W, Barron L, Cromwell C, **Coombes KR**. Biological validation of differentially expressed genes in chronic lymphocytic leukemia identified by applying multiple statistical methods to oligonucleotide microarrays. *J Mol Diagn* 7:337-45, 2005. PMID: PMC1867538.
45. Stec J, Wang J, **Coombes KR**, Ayers M, Hoersch S, Gold D, Ross J, Hess K, Tirrell S, Linette G, Hortobagyi G, Fraser Symmans W, Puztai L. Comparison of the predictive accuracy of DNA array-based multigene classifiers across cDNA arrays and Affymetrix GeneChips. *J Mol Diagn* 7:357-67, 2005.
46. Koomen J, Li D, Xiao L, Liu T, **Coombes KR**, Abbruzzese J, Kobayashi R. Direct tandem mass spectrometry reveals limitations in protein profiling experiments for plasma biomarker discovery. *J Proteome Res* 4:972-81, 2005.
47. Morris J, **Coombes KR**, Koomen J, Baggerly K, Kobayashi R. Feature extraction and quantification for mass spectrometry in biomedical applications using the mean spectrum. *Bioinformatics* 21:1764-75, 2005.
48. Gold D, Wang J, **Coombes KR**. Inter-gene correlation on oligonucleotide arrays: how much does normalization matter? *Am J Pharmacogenomics* 5:271-9, 2005.
49. Koomen J, Shih L, **Coombes KR**, Li D, Xiao L, Fidler I, Abbruzzese J, Kobayashi R. Plasma protein profiling for diagnosis of pancreatic cancer reveals the presence of host response proteins. *Clin Cancer Res* 11:1110-8, 2005.
50. Esteva F, Sahin A, Cristofanilli M, **Coombes KR**, Lee S, Baker J, Cronin M, Walker M, Watson D, Shak S, Hortobagyi G. Prognostic role of a multigene reverse transcriptase-PCR assay in patients with node-negative breast cancer not receiving adjuvant systemic therapy. *Clin Cancer Res* 11:3315-9, 2005.
51. Yokoi K, Shih L, Kobayashi R, Koomen J, Hawke D, Li D, Hamilton S, Abbruzzese J, **Coombes KR**, Fidler I. Serum amyloid A as a tumor marker in sera of nude mice with orthotopic human pancreatic cancer and in plasma of patients with pancreatic cancer. *Int J Oncol* 27:1361-9, 2005.
52. Baggerly K, Morris J, Edmonson S, **Coombes KR**. Signal in noise: evaluating reported reproducibility of serum proteomic tests for ovarian cancer. *J Natl Cancer Inst* 97:307-9, 2005.
53. Hu J, **Coombes KR**, Morris J, Baggerly K. The importance of experimental design in proteomic mass spectrometry experiments: some cautionary tales. *Brief Funct Genomic Proteomic* 3:322-31, 2005.

54. **Coombes KR**, Koomen J, Baggerly K, Morris J, Kobayashi R. Understanding the characteristics of mass spectrometry data through the use of simulation. *Cancer Informatics* 1:41-52, 2005. PMID: PMC19305631.
55. Xu H, Cheepala S, McCauley E, **Coombes K**, Xiao L, Fischer SM, Clifford JL. Chemoprevention of skin carcinogenesis by phenylretinamides: retinoid receptor-independent tumor suppression. *Clin Cancer Res* 12(3 Pt 1):969-79, 2/2006.
56. Giri U, Ashorn CL, Ramdas L, Stivers DN, **Coombes K**, El-Naggar AK, Ang KK, Story MD. Molecular signatures associated with clinical outcome in patients with high-risk head-and-neck squamous cell carcinoma treated by surgery and radiation. *Int J Radiat Oncol Biol Phys* 64(3):670-7, 3/2006.
57. Zhang J, Zhang L, **Coombes KR**. Gene sequence signatures revealed by mining the UniGene affiliation network. *Bioinformatics* 22:385-91, 2006.
58. Spurgers K, Gold D, **Coombes KR**, Bohnenstiehl N, Mullins B, Meyn R, Logothetis C, McDonnell T. Identification of cell cycle regulatory genes as principal targets of p53-mediated transcriptional repression. *J Biol Chem* 281:25134-42, 2006.
59. Wang J, Do KA, Wen S, Tsavachidis S, McDonnell TJ, Logothetis CJ, **Coombes KR**. Merging microarray data, robust feature selection, and predicting prognosis in prostate cancer. *Cancer Informatics* 2:99-109, 2006. PMID: PMC2675498.
60. Ji Y, **Coombes K**, Zhang J, Wen S, Mitchell J, Pusztai L, Symmans WF, Wang J. RefSeq refinements of UniGene-based gene matching improve the correlation of expression measurements between two microarray platforms. *Appl Bioinformatics* 5(2):89-98, 2006.
61. Vega F, **Coombes KR**, Thomazy V, Patel K, Lang W, Jones D. Tissue-specific function of lymph node fibroblastic reticulum cells. *Pathobiology* 73:71-81, 2006.
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  145. Bogenberger JM, Kornblau SM, Pierceall WE, Lena R, Chow D, Shi CX, Mantei J, Ahmann G, Gonzales IM, Choudhary A, Valdez R, Camoriano J, Fauble V, Tiedemann RE, Qiu YH, **Coombes KR**, Cardone M, Braggio E, Yin H, Azorsa DO, Mesa RA, Stewart AK, Tibes R. BCL-2

family proteins as 5-Azacytidine-sensitizing targets and determinants of response in myeloid malignancies. *Leukemia*. In Press.

146. Suraokar MB, Nunez MI, Diao L, Chow CW, Kim D, Behrens C, Lin H, Lee S, Raso G, Moran C, Rice D, Mehran R, Lee JJ, Pass HI, Wang J, Momin AA, James BP, Corvalan A, **Coombes K**, Tsao A, Wistuba II. Expression Profiling Stratifies Mesothelioma Tumors and Signifies Deregulation of Spindle Checkpoint Pathway and Microtubule Network with Therapeutic Implications. *Ann Oncol*. In Press.

#### Editorials

- 1 Lahad J, Mills G, **Coombes K**. Stem cell-ness: a "magic marker" for cancer. *J Clin Invest* 115:1463-7, 6/2005.
- 2 **Coombes KR**. Analysis of mass spectrometry profiles of the serum proteome. *Clinical Chemistry* 51:1-2, 2005.
- 3 **Coombes K**, Morris J, Hu J, Edmonson S, Baggerly K. Serum proteomics profiling--a young technology begins to mature. *Nat Biotechnol* 23:291-2, 2005.
- 4 Baggerly KA, **Coombes KR**. What Information Should Be Required to Support Clinical "Omics" Publications? *Clin Chem* 57:688-690, 3/2011.

#### Abstracts

- 1 Kornblau S.M., Qiu, Y., Chen, W.J., Liang, H., Ravandi, F., Coombes, K.R., Nagarajan, L. Expression of Prognostic impact of candidate suppressor sequence-specific single-stranded DNA binding protein (SSBP2) in AML using reverse phase proteins arrays (RPPA). *Blood* 110(11):707A-A, 2007.
- 2 Minna, J.D., Girard, L., Sato, M., Peyton, M., Lee, W., Shames, D., Honorio, S., Xie, Y., Xie, X.J., Lam, D., Lockwood, W., Lam, W., Wang, Y.Z., Lam, S., Kim, E., Pollack, J., Greer, R., Frink, R., Sullivan, J., Gao, B.N., Spinola, M., Wistuba, I., Coombes, K., Heymach, J., Nanjundan, M., Mao, L., Amos, C., Fang, B.L., Roth, J.A., Pertsemidlis, A., Nirodi, C., Story, M., Garner, H., White, M., De Brabander, J., Harran, P., Wang, X.D., Jeong, Y., Mangelsdorf, D., DiMaio, J.M., Schiller, J., Shay, J., Gazdar, A.F. Molecular pathogenesis of lung cancer with translation to the clinic. *Journal of Thoracic Oncology* 2(8):S178-S9, 2007.
- 3 Kornblau, S.M., Barnett, J., Qiu, Y., Chen, W., Faderl, S., Coombes, K.R., Andreeff, M. P53 protein, expression levels are prognostic in AML and predict for mutational status. *Blood* 110(11):708A-A, 2007.
- 4 Kornblau, S.M., Qiu, Y., Chen, W., Verstovsek, S., Coombes, K.R., Mills, G.B. Protein expression signatures determined by reverse phase proteins arrays (RPPA) accurately predict FLT3-ITD mutation status in AML. *Blood* 110(11):708A-A, 2007.
- 5 Averett L, Nanjundan M, Girard L, Coombes K R, Xie Y, Peyton M, Ma Y, Zachariah S, Nikolinakos P, Cigarroa R, Mills G B, Roth, J A, Minna J D, Heymach, J V. Reverse-phase protein array (RPPA) profiling of non-small cell lung cancer lines identifies tumor signatures for sensitivity and resistance to chemotherapy and targeted agents. *Molecular Cancer Therapeutics* 6(12):3490-S, 2007.

- 6 Singh, R., Prieto, V., Diwan, A., Coombes, K., Jeffery, G., Johnson, M. 38. Singh, R., Prieto, V., Diwan, A., Coombes, K., Jeffery, G., Johnson, M. Why do ulcerated melanomas have a worse prognosis? An analysis of their gene expression profiles as compared to non-ulcerated melanomas. *Journal of Cutaneous Pathology* 35(1):96, 2008.
- 7 Clarke CH, Fung ET, Yip C, Badgwell D, Joy C, Coombes K, Lu K, Bast RC. Proteomic markers increase CA125 sensitivity for early detection of epithelial ovarian cancer. *Gynecologic Oncology* 108(3):S36-S7, 2008.

### Book Chapters

- 1 Coombes KR. Local class field theory for curves. In *Applications of Algebraic K-theory to Algebraic Geometry and Number Theory*. In: *Contemporary Math. Part I*, 55, 117-134, 1986.
- 2 **Coombes KR**. The K-cohomology of Enriques surfaces. In *Proceedings of a Conference on K-theory, Commutative Algebra, and Algebraic Geometry*. In: *Contemporary Math.* 126, 47-57, 1992.
- 3 Coombes, KR, Baggerly, KA, Stivers, DN, Wang, J, Gold, D, Sung, HG, Lee, SJ. Biology-Driven Clustering of Microarray Data: Applications to the NCI60 Data Set. In: *Methods of Microarray Data Analysis II*. Kluwer Academic Publishers, 65-79, 2002.
- 4 Wang, J, **Coombes, KR**, Baggerly, KA, Hu, L, Hamilton, SR, Zhang, W. Statistical considerations in the assessment of cDNA microarray data obtained using amplification. In: *Computational and Statistical Approaches to Genomics*. Kluwer Academic Press, 23–39, 2002.
- 5 Baggerly, KA, Coombes, KR, Hess, KR, Stivers, DN, Abruzzo, LV, Zhang, W. Studentizing microarray data. In: *Computational and Statistical Approaches to Genomics*. Kluwer Academic Press, 53–64, 2002.
- 6 Coombes, KR, Wang, J, Abruzzo, LV. Monitoring the quality of microarray experiments. In: *Methods of Microarray Data Analysis III*. Kluwer Academic Publishers, 25-40, 2003.
- 7 Stivers, DN, Wang, J, Rosner, GL, Coombes, KR. Organ-specific differences in gene expression and UniGene annotations describing source material. In: *Methods of Microarray Data Analysis III*. Kluwer Academic Publishers, 59-72, 2003.
- 8 Zhang, L, Coombes, KR, Xiao, LC. Quantification of cross hybridization on oligonucleotide microarrays. In: *Methods of Microarray Data Analysis III*. Kluwer Academic Publishers, 175-184, 2003.
- 9 Baggerly DA, Coombes KR, Morris JS. An introduction to high-throughput bioinformatics data. In: *Bayesian Inference for Gene Expression and Proteomics*. Cambridge University Press, 1-39, 2006.
- 10 Morris JS, Brown PJ, Baggerly KA, Coombes KR. Analysis of mass spectrometry data using Bayesian Wavelet-Based Functional Mixed Models. In: *Bayesian Inference for Gene Expression and Proteomics*. Ed(s) Do, KA, Muller P, Vannucci M. Cambridge University Press, 269-292, 2006.
- 11 Morris JS, Baggerly KA, Coombes KR,. Shrinkage estimation for SAGE data using a Mixture Dirichlet Prior. In: *Bayesian Inference for Gene Expression and Proteomics*. Ed(s) Do KA, Muller P, Vannucci M. Cambridge University Press, 254-268, 2006.

- 12 Coombes KR, Baggerly KA, Morris JS. Pre-processing mass spectrometry data. In: Fundamentals of data mining in genomics and proteomics. Ed(s) Dubitsky W, Granzow M, Berrar DP. Springer, New York, 79-102, 2007.
- 13 Morris JS, Wu C, **Coombes KR**, Baggerly KA, Wang J, Zhang L. Alternative Probeset Definitions for Combining Microarray Data Across Studies Using Different Versions of Affymetrix Oligonucleotide Arrays. In: Meta-Analysis in Genetics. Ed(s) Rudy Guerra, David Allison. Chapman-Hall 157-174, 2011.
- 14 Baggerly KA; Coombes KR. Forensic Bioinformatics. In: Handbook of Statistics in Clinical Oncology, 605-17, 2012.
- 15 Broom BM, Do KA, Bondy M, Thompson P, **Coombes KR**. Methods for the Analysis of Copy Number Data in Cancer. In: Advances in Statistical Bioinformatics: Models and Integrative Inference for High-Throughput Data. Ed(s) Do KA, Qin ZS, Vannucci M. Cambridge University Press, 244-271, 2013.

#### **Books (edited and written)**

- 1 Coombes, KR, Hunt, B, Lipsman R, Osborn, J, Stuck, G. Differential Equations with Mathematica. John Wiley and Sons, 1995.
- 2 Coombes, KR, Hunt, B, Lipsman, R, Osborn, J, Stuck, G. Differential Equations with Maple. John Wiley and Sons, 1996.
- 3 Coombes, KR, Hunt, B, Lipsman, R, Osborn, J, Stuck, G. Differential Equations with Maple. John Wiley and Sons, 1997.
- 4 Coombes, KR, Hunt, B, Lipsman, R, Osborn, J, Stuck, GJ. Differential Equations with Mathematica. John Wiley and Sons, 1998.
- 5 Coombes, KR, Lipsman, R, Rosenberg, J. Multivariable Calculus and Mathematica, with Applications to Geometry and Physics. TELOS, an imprint of Springer-Verlag, 1998.
- 6 Coombes, KR, Hunt, B, Lipsman, R, Osborn, J, Stuck, G. The Mathematica Primer. Cambridge University Press, 1998.
- 7 Coombes, KR, Hunt, BR, Lipsman, RL, Osborn JE, Stuck, GJ. Differential Equations with MATLAB. John Wiley and Sons, 1999.

#### **Letters to the Editor**

- 1 Zhang L, Wu C, Carta R, Baggerly K, Coombes K. Response to Preprocessing of oligonucleotide array data. Nat Biotechnol 22:658, 2004.
- 2 Baggerly KA, Neeley ES, Coombes KR. Run Batch Effects Potentially Compromise the Usefulness of Genomic Signatures for Ovarian Cancer. J Clin Oncol 1(7):1186-7, 3/2008.

#### **EDITORIAL AND REVIEW ACTIVITIES**

##### **Editor/Service on Editorial Board(s)**

Associate Editor, Applied Bioinformatics, 2007

Associate Editor, BMC Bioinformatics, 2007

Associate Editor, BMC Proceeding, 2007

Associate Editor, Clinical Chemistry, 2007

Associate Editor, Molecular Carcinogenics, 2007

**Journal Reviewer**

Applied Bioinformatics

Bioinformatics

BMC Bioinformatics

Cancer Research

Clinical Cancer Research

Clinical Chemistry

Proteomics

**TEACHING**

**Formal Teaching**

**Courses Taught**

Co-Instructor with Keith Baggerly, Analysis of microarray data, UT GSBS, Course Number: GS01 0163

Fall Semester, 2004

Fall Semester, 2005

Fall Semester, 2006

Fall Semester, 2007

**Supervisory Teaching**

**Committees**

**Advisory Committees**

Rice University, Shannon Neeley, 2008

Texas A&M, David Gold

UT GSBS, Lagina Nosavanh, 2008

UT GSBS, Howard Rosoff, 2011

UT GSBS, Michelle Payton, 2011

UT GSBS, Chris Holsinger

UT GSBS, ChunLei Wu

UT GSBS, Jennifer Carter

UT GSBS, John Lahad

UT GSBS, Mahyar Sabripour

UT GSBS, Nick Koch

**Supervisory Committees**

UT GSBS, Hatice Duzkale, 2008-2010

UT GSBS, Hua Li, 2008-2010

UT GSBS, Haiying Pang, 2009-2011

UT GSBS, Chris Holsinger, 2010-2011

## **Direct Supervision**

### **Undergraduate and Allied Health Students**

Mentor, Bryn Mawr College, Rachel Newman, 5/2007

### **Graduate Students**

UT GSBS, Pan Tong, 8/2009-6/2013

UTSPH, Caimiao Wei, 12/2011-6/2013

University of Maryland, Kimberly King, Minimal Models of Genus One Curves, 5/1998

University of Maryland, Andreas Rosenschon, On the K-Cohomology of Algebraic Varieties, 5/1998

University of Maryland, James Nickerson, Homology of Noncommutative Polynomial Algebras over Valuation Domains, 5/1995

University of Maryland, Elena Black, Arithmetic Lifting of Galois Extensions, 5/1995

### **Postdoctoral Research Fellows**

Wenting Wang, 8/2010-2012

## **CONFERENCES AND SYMPOSIA**

### **Organization of Conferences/Symposia (Include chairing session)**

AMS Special Session on Galois Theory, Chattanooga, Organizer

### **Presentations at National or International Conferences**

Class field theory for curves over local fields, A.M.S. Annual Meeting, Cincinnati, 1/13/1982

Relative algebraic K-theory, A.M.S. Meeting, Bryn Mawr, 3/16/1982

Relative K-theory and applications, A.M.S. Meeting, Baton Rouge, 11/12/1982

Local class field theory for curves, A.M.S. Summer Research Conference, Boulder, 6/12/1983

Parshin's trick, Conference on Arithmetic Geometry, Storrs, 7/30/1984

On SK<sub>1</sub> of curves, A.M.S. Meeting, Chicago, 3/22/1985

Motifs, L-functions, and K-cohomology of rational surfaces, A.M.S. Meeting, Amherst, 10/26/1985

The Arithmetic of Algebraic Cycles, Series of four talks during Special Year on Algebraic Geometry, 2/1/1986

Speculations on genus two curves, Conference on the Arithmetic of Curves, Tucson, 1/7/1989

Zero cycles on Enriques surfaces, NSF-CNR Joint Seminar on K-theory, Commutative Algebra, and Algebraic Geometry, Genoa, 6/1/1989

Geometry recapitulates arithmetic, AMS Summer Research Conference on the Inverse Galois Problem, 8/1/1993

Interpolation of Galois branched covers, AMS Special Session on Galois Theory, Chattanooga, 10/1/1996

ACCG: The Anderson Cancer Center Genomics Database, Houston Forum on Cancer Genomics and Informatics, Houston, 2/1/1999

Clustering for quality control, BIOS 2001, SPIE, San Jose, 1/1/2001

Coombes, K, Baggerly, K, Abruzzo, L, Highsmith, W, Krogmann, T, Stivers, D. Identifying and quantifying sources of variation in high-density cDNA microarray data using 33P-labeled probe, Oncogenomics, Tucson, 1/26/2001

High throughput informatics: Dealing with a deluge of gene expression data, CALGB meeting, Ottawa, Canada, 6/1/2001

Rank coherence: Assessing the agreement between repeated experiments to detect differentially expressed genes, Houston Forum on Cancer Genomics and Informatics, Houston, 7/1/2001

High-throughput bioinformatics for gene expression data, 22nd Annual Conference of the International Society for Clinical Biostatisticians, Stockholm, Sweden, 8/1/2001

Biology-Driven Clustering of Microarray Data: Applications to the NCI60 Data Set, CAMDA, Durham , NC, 10/1/2001

cDNA Microarray Analysis of B-Cell Chronic Lymphocytic Leukemia, Meeting of the American Association of Clinical Chemists, 11/1/2001

Biology-Driven Clustering of Microarray Data, Oncogenomics Meeting, Dublin, 5/1/2002

Statistical analysis of proteomics spectra from serum samples, Keck Seminar, Houston, 9/1/2002

Statistical tools to identify proteomics patterns in neoplastic disease from serum samples, 11th Annual Beaumont Hospital Symposium on DNA Technology in the Clinical Laboratory, Troy , MI, 9/1/2002

Organ-Specific Differences in Gene Expression and UniGene Annotations Describing Source Material, CAMDA, Durham, NC, 10/2002

Statistical Analysis of proteomics data, Cancer Therapeutics Discovery Program Symposium, Houston, TX, 4/2003

Unusual findings from Project Normal, Conference of Texas Statisticians, College Station, 4/1/2003

Statistical analysis of proteomics patters from serum samples, National Lung SPORE meeting, 2/2004

Low-level processing of proteomics spectra, EDRN Meeting, Seattle, WA, 3/2004

Statistical Analysis of Proteomics patterns from serum samples, National Pancreatic SPORE Meeting, 4/2004

Statistical Analysis of proteomics patterns from serum samples, AACR Meeting, 10/2004

Preconference Seminar, CAMDA, Durham, NC, 11/2004

Protein Biomarkers, Association of Biomolecular Resource Facilities, Panel Discussion, Savanna, GA, 1/2005

Counting molecular signs of disease: A new method for developing Biomarker Panels from High-Throughput Data Sources, European Biomarkers Summit, Prague, 9/2006

Statistical Analysis of Reverse-Phase Protein Lysate Arrays, American Chemical Society Biochips Conference, Houston, TX, 10/2006

Statistical preprocessing of mass spectrometry data, 39th Symposium on the Interface: Computing Science and Statistics, Philadelphia, PA, 5/2007

Implementing Reproducible Research, The University of Texas MD Anderson Cancer Center, Houston, TX, 1/26/2011

'UMPIRE': Ultimate Microarray Prediction, Inference and Reality Engine, 2011 -The Third International Conference on Bioinformatics, Venice, Italy, 5/20/2011

Sources of Variation in False Discovery Rate Estimation Include Sample Size, Correlation, and Inherent Differences Between Groups, The 8<sup>th</sup> Annual Biotechnology and Bioinformatics Symposium (BIOT-2011), Houston, TX, 10/20/2011

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, Association for Molecular Pathology Annual Meeting, Dallas, TX, 11/18/2011

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, 58. Biometrisches-Kolloquium, Berlin, Germany, 4/16/2012

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, The 8<sup>th</sup> International R User Conference (user!), Nashville, TN, 6/13/2012

Methods to Improve Public Data Sharing: Perspective of a "Forensic" Statistician. International Life Sciences Institute Annual Meeting, Hamilton, Bermuda 1/20/2014

### **Seminar Invitations**

The Inverse Galois Problem, M.I.T., 1/1/1983

The Inverse Galois Problem, Harvard, 1/1/1983

Inversion of Abelian Integrals, University of Oklahoma, 1/1/1984

Inversion of Abelian Integrals, University of Chicago, 1/1/1984

The Inverse Galois Problem, Northeastern University, 1/1/1985

The Inverse Galois Problem, Washington University, 1/1/1985

The Inverse Galois Problem, University of Texas, 1/1/1985

Motifs, L-functions, and K-cohomology of rational surfaces, Lehigh University, 3/1/1985

Motifs, L-functions, and K-cohomology of rational surfaces, University of Pennsylvania, 3/1/1985

An Attempted Proof of Bloch's Conjecture, University of Michigan, 1/1/1986

An Attempted Proof of Bloch's Conjecture, University of Chicago, 1/1/1986

An Attempted Proof of Bloch's Conjecture, M. I. T., 1/1/1986

Motifs, L-functions, and K-cohomology of rational surfaces, Duke University, 5/1/1986

The Arithmetic of Cycles on Enriques Surfaces, University of Michigan, 1/1/1987

On Heterogeneous Spaces, University of Michigan, 1/1/1988

The Arithmetic of Surfaces, University of Florida, 1/1/1989

The Arithmetic of Surfaces, University of Maryland, 2/1/1989

The Arithmetic of Surfaces, Boston University, 2/1/1989

The Arithmetic of Surfaces, Tufts University, 2/1/1989

The Arithmetic of Surfaces, C. U. N. Y., 2/1/1989

The Arithmetic of Surfaces, Washington University, 3/1/1989

The Arithmetic of Surfaces, University of Colorado, 11/1/1990

The homology of regular algebras, University of Pennsylvania, 2/1/1991

The homology of regular algebras, Brown University, 9/1/1991

Interpolation of Galois branched covers, McGill University, 4/1/1994



Elliptic curves and logarithmic derivatives, Lehigh University, 12/1/1997

Analysis of microarray data, M. D. Anderson Cancer Center, 2/1/2001

Detecting subtle difference in gene expression using cDNA microarrays, University of Pennsylvania, 3/1/2001

The role of replication in the analysis of microarray data, Baylor College of Medicine, 5/1/2001

Statistical Analysis of Proteomics patters from serum samples, ARUP Laboratories, University of Utah, 3/2004

Statistical analysis of proteomics patterns from serum samples, Baylor College of Medicine, 4/2004

Statistical analysis of proteomics patters from serum samples, Keck Seminar, 4/2004

The tail-rank rest for finding biomarkers in microarray data, UT M.D. Anderson, Department of Biostatistics and Applied Mathematics Seminar, Houston, TX, 10/2004

Analysis and design of mass spectrometry proteomics profiling experiments, TGen, Phoenix, AZ, 11/2004

Biomarkers in cancer research, Mathematical Biosciences Institute, Ohio State Unversity, 4/2005

Statistical analysis of mass spectrometry data, Vanderbilt University, 4/2005

The tail-rank test: finding biomarkers in microarray data, UT M.D. Anderson Division of Pathology Grand Rounds, 5/2005

Statistical analysis of reverse-phase protein lysate arrays, Texas A&M University, 12/2006

Statistical analysis of reverse-phase protein lysate arrays, Georgetown Unversity, 2/2007

Sweave: First steps toward reproducible analyses, UT M.D. Anderson Department of Biostatics and Applied Mathematics Seminar, 2/2007

From Advertising to Science: Methods to Make Analysis of High-Throughput Data Reproducible and Auditable, Institutional Grand Rounds, University of Texas M. D. Anerson Cancer Center, Houston, TX, 1/11/2008

Microarrays, Cell Lines, Drugs and Disease: Predicting Response to Chemotherapy, Washington University, 3/14/2008

Microarrays, Cell Lines, Drugs and Disease: Predicting Response to Chemotherapy, Mayo Clinic, 3/18/2008

Who benefits from which drugs?, Mayo Clinic, 6/2008

Bimodality as a tool for exploring large gene expression datasets, University of Michigan, Ann Arbor, MI, 11/5/2008

Bioinformatics and Biostatistics in the CTSA, Mayo Clinic, Rochester, MN, 11/13/2008

Steps to Implement Reproducible Research, Vanderbilt University, Vanderbilt Ingram Cancer Center, Nashville, TN, 11/19/2010

Reproducible Research, NCI Translational Science Meeting, Washington, DC, 7/28/2011

Cell Lines, Chemotherapy Response, and the Need for, University of New Mexico, Albuquerque, NM, 8/28/2011

Binary Signals in Oncology, Vanderbilt University, Nashville, TN, 11/11/2011

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, Association of Molecular Pathology Annual Meeting, Dallas, TX, 11/14/2011

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, University of Arizona, Tucson, AZ, 11/30/2011

Binary Signals in Oncology, UT Southwestern, Biostatistics, Dallas, TX, 4/4/2012

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, University of Texas Medical Branch, Galveston, TX, 4/20/2012

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, Ohio State University, Columbus, OH, 6/6/2012

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, Vanderbilt University, Nashville, TN, 6/14/2012

Binary Signals in Oncology, Johns Hopkins University, Baltimore, MD, 6/18/2012

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, Yale University, New Haven, CT, 7/18/2012

The need for publically verifiable/reproducible data and analyses, Scientific Approaches to Strengthening Research Integrity in Nutrition and Energetics, New Paltz, NY, 8/8/2012

Binary Signal in Oncology, Ohio State University, Columbus, OH, 8/15/2012

Cell Lines, Chemotherapy Response, and the Need for Reproducible Research, Tulane University, New Orleans, LA, 1/18/2013

## **PROFESSIONAL MEMBERSHIPS/ACTIVITIES**

### **Professional Society Activities, with Offices Held**

#### **National and International**

SMP Bioinformatics, German Cancer Research Center (DKFZ), Houston, TX  
Scientific Advisory Board, 2004-2010

UCLA Lung SPORE, Los Angeles, CA  
External Advisory Board, 2004-present

Dana Farber Harvard Cancer Center, External Advisory Board, 2014

#### **Local/State**

Keck Executive Committee, Houston, TX  
Keck Executive Committee, 2003-2011