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Education:

2000	University of Washington	Ph.D., Biostatistics
1997	University of Washington	M.S., Biostatistics
1995	Rice University, <i>summa cum laude</i>	B.A., Mathematics/Statistics B.A., Economics/French Studies

Academic Positions:

2014-present	Associate Director, Bioinformatics Center for Biomedical Informatics and Personalized Medicine University of Colorado Anschutz Health Sciences Center, Aurora, CO
2014-present	Chair, Department of Biostatistics and Informatics Colorado School of Public Health, Aurora, CO
2014-present	Professor, Department of Biostatistics and Informatics Colorado School of Public Health, Aurora, CO
2011-2014	Investigator, The Methodology Center, Penn State University University Park, PA
2010-2014	Professor, Departments of Statistics and Public Health Sciences, Penn State University, University Park, PA
2008-2014	Affiliate Faculty, Penn State Cancer Institute Penn State College of Medicine, Hershey
2007-2010	Associate Professor, Department of Public Health Sciences, Penn State College of Medicine, Hershey
2007-2010	Associate Professor, Department of Statistics, Penn State University, University Park
2007-2014	Affiliate Faculty, Integrated Biosciences (IBIOS) Program Penn State University, University Park
2005-2007	Associate Professor, Department of Biostatistics, University of Michigan, Ann Arbor
2003-2007	Assistant Member, UM Comprehensive Cancer Center
2002-2007	Affiliate Faculty, Bioinformatics Program University of Michigan, Ann Arbor
2001-2005	Assistant Professor, Department of Biostatistics University of Michigan, Ann Arbor
2000	Postdoctoral Scholar, Institute for Pure and Applied Mathematics, University of California, Los Angeles

Awards and Honors:

2015	Myrto Lefkopolou Distinguished Lecture, Department of Biostatistics Harvard T.W. Chan School of Public Health
2015	University of Colorado Clinical and Translational Sciences Leadership in Innovative Team Science Program Participant
2014	University of Washington Department of Biostatistics Distinguished Alumni Speaker
2014 – present	Grohne Endowed Chair in Cancer Research University of Colorado Cancer Center
2013 – 2015	Chair, Biostatistical Methods and Research Design Study Section, National Institutes of Health
2013	Mortimer Spiegelman Award, American Public Health Association
2012	Fellow, American Statistical Association
2012	Featured Cover Article, <i>Genomics</i>
2011	Faculty Scholar, Methodology Center, Pennsylvania State University
2010–2012	College of CSR Reviewers, National Institutes of Health
2008	Featured <i>Biomed Central</i> Editorial Board Member
2008	<i>Biometrics</i> Best Paper Award
2006	UM CCMB Pilot Grant Award
2003	UM Bioinformatics Pilot Grant Award
2002	UM Bioinformatics Pilot Grant Award
2002	Pacific Symposium on Biocomputing Travel Award
2001	UM Prostate Cancer SPORE Seed Grant
2001	UM Cancer Center MUNN Idea Grant
1999	ENAR Student Travel Award
1999	Society of Clinical Trials Student Scholarship
1998–2000	NIH Predoctoral Cardiovascular Training Grant, Department of Biostatistics, University of Washington
1997	Donovan J. Thompson Outstanding Student Award for outstanding academic performance, Department of Biostatistics, University of Washington
1995–1997	National Science Foundation Graduate Research Fellowship
1995–1997	ARCS (Achievement Rewards for College Scientists) Fellowship Department of Biostatistics, University of Washington
1995	Phi Beta Kappa

Publications which have received peer review:

† denotes a master's student advised by Ghosh, * denotes a first-authored publication by Ph.D. student advised/co-advised by Ghosh.

1. Ghosh, D. and Godbole, A. (1997). Palindromes in random letter generation: Poisson approximations, rates of growth, and Erdős-Rényi laws. In *Proceedings of the Athens Conference on Applied Probability*, ed. C.C. Heyde *et al.*, Springer-Verlag Lecture Notes in Statistics, vol. 114, pp. 99–115.

2. Ghosh, D. and Lin, D.Y. (2000). Nonparametric analysis of recurrent events and death. *Biometrics* **56**, 554–562.

3. Ghosh, D. (2000). Methods for the analysis of multiple events and death. *Controlled Clinical Trials* **21**, 115–126.
4. Ghosh, D, Deisher, T.A. and Ellsworth, J.E. (2000). Methods for the analysis of repeated measures. *Journal of Pharmacological and Toxicological Methods* **42**, 157–162.
5. Ghosh, D. (2001). Efficiency considerations in the additive hazards model with current status data. *Statistica Neerlandica* **55**, 367 – 376.
6. Sreekumar, A., Nyati, M., Barrette, T. R., Ghosh, D., Lawrence, T. and Chinnaiyan, A. M. (2001). Profiling cancer cells using protein microarrays: discovery of novel radiation-regulated proteins. *Cancer Research* **61**, 7585 – 7593.
7. Dhanasekaran, S., Barrette, T., Ghosh, D., Shah, R., Kurachi, K., Pienta, K., Rubin, M. A. and Chinnaiyan, A. M. (2001). Molecular profiling of prostate cancer: delineation of candidate biomarkers and regulatory genes. *Nature* **412**, 422 – 426.
8. Ghosh, D. (2002). Singular value decomposition regression models for the classification of tumors from microarray experiments. In *Proceedings of the 2002 Pacific Symposium on Biocomputing*, Eds. Altman, R. B. et al. pp. 18 – 29.
9. Ghosh, D. and Chinnaiyan, A. M. (2002). Mixture modelling of gene expression data from microarray experiments. *Bioinformatics* **18**, 275–286.
10. Rubin, M. A., Zhou, M., Dhanasekaran, S. M., Varambally, S., Barrette, T. R., Sanda, M. G., Pienta, K. J., Ghosh, D. and Chinnaiyan, A. M. (2002). α -methylacyl coenzyme A racemase as a tissue biomarker for prostate cancer. *Journal of the American Medical Association* **287**, 1662–1670.
11. Goldstein, D., Ghosh, D. and Conlon, E. (2002). Statistical issues in the clustering of gene expression data. *Statistica Sinica* **12**, 219–241.
12. Ghosh, D. (2002). Resampling methods for variance estimation of singular value decomposition analyses from microarray experiments. *Functional and Integrative Genomics* **2**, 92 – 97.
13. Ghosh, D. and Lin, D. Y. (2002). Marginal regression models for recurrent and terminal events. *Statistica Sinica* **12**, 663 – 688.
14. Rhodes, D., Barrette, T. T., Rubin, M. A., Ghosh, D. and Chinnaiyan, A. M. (2002). Meta-analysis of microarrays: interstudy validation of gene expression profiles reveals pathway dysregulation in prostate cancer. *Cancer Research* **62**, 4427 – 4433.
15. Varambally, S., Dhanasekaran, S. M., Zhou, M., Barrette, T. R., Kumar-Sinha, C., Sanda, M. G., Ghosh, D., Pienta, K. J., Sewalt, R. G. A. B., Otte, A. P., Rubin, M. A. and Chinnaiyan, A. M. (2002). The polycomb group protein EZH2 is involved in progression of prostate cancer. *Nature* **419**, 624 – 629.
16. Wu, J., Haan, M., Liang, J., Ghosh, D., Gonzalez, H., Jagust, W. and Herman W. (2003). Im-

pact of antidiabetic medications on physical and cognitive functioning of older Mexican Americans with diabetes mellitus. *Annals of Epidemiology* **13**, 369 – 376.

17. Wu, J. H., Haan, M. N., Liang, J., Ghosh, D., Gonzalez, H. M. and Herman W. H. (2003). Diabetes as a predictor of change in functional status among older Mexican Americans: a population-based cohort study. *Diabetes Care* **26**, 314 – 319.

18. Wu, J. H., Haan, M. N., Liang, J., Ghosh, D., Gonzalez, H. M. and Herman W. H. (2003). Impact of diabetes on cognitive function among older Latinos: a population-based cohort study. *Journal of Clinical Epidemiology* **56**, 686 – 693.

19. Ghosh, D. (2003). Goodness of fit methods for the additive risk model in tumorigenicity experiments. *Biometrics* **59**, 721 – 726.

20. Ghosh, D., Barrette, T., Rhodes, D. and Chinnaiyan, A. M. (2003). Statistical issues and procedures for meta-analysis of microarray data: a case study in prostate cancer. *Functional and Integrative Genomics* **3**, 180 – 188.

21. †Smolkin, M. and Ghosh, D. (2003). Cluster stability scores for cancer subtypes in microarray experiments. *BMC Bioinformatics* **4**, 36 – 42.

22. Kleer, C. G., Cao, Q., Varambally, S., Shen, R., Ota, I., Tomlins, S. A., Ghosh, D., Sewalt, R. G., Otte, A. P., Hayes, D. F., Sabel, M. S., Livant, D., Weiss, S. J., Rubin, M. A. and Chinnaiyan, A. M. (2003). EZH2 is a marker of aggressive breast cancer and promotes neoplastic transformation of breast epithelial cells. *Proceedings of the National Academy of Sciences USA* **100**, 11606 – 11611.

23. Ghosh, D. and Lin, D. Y. (2003). Semiparametric analysis of recurrent events in the presence of dependent censoring. *Biometrics* **59**, 877 – 885.

24. Ghosh, D. (2003). Penalized discriminant methods for the classification of tumors from microarray experiments. *Biometrics* **59**, 992 – 1000.

25. Sreekumar, A., Laxman, B., Rhodes, D., Bhagavathula, S., Giacherio, D., Ghosh, D., Sanda, M. G., Rubin, M. and Chinnaiyan A. M. (2004). Humoral immune response to alpha-methylacyl-CoA racemase and prostate cancer. *Journal of the National Cancer Institute* **96**, 834 - 843.

26. Rhodes, D. R., Yu, J., Shanker, K., Deshpande, N., Varambally, R., Ghosh, D., Barrette, T., Pandey, A. and Chinnaiyan, A. M. (2004). ONCOMINE: a cancer microarray database and integrated data-mining platform. *Neoplasia* **6**, 1 – 6.

27. Yu, J., Mears, A. J., Yoshida, S., Farjo, R., Carter, T. A., Ghosh, D., Hero, A., Barlow, C., Swaroop, A. (2004). From disease genes to cellular pathways: A progress report. In “Retinal dystrophies: functional genomics to gene therapy.” Wiley, Chichester (Novartis Foundation Symposium 255), pp. 147-164.

28. Sen, S., Burmeister, M. and Ghosh, D. (2004). Meta-analysis of the association between a serotonin transporter promoter polymorphism (5-HTTLPR) and anxiety-related personality traits.

American Journal of Medical Genetics B Neuropsychiatric Genetics **127**, 85 – 89.

29. Zhang, L., Srinivasan, U., Marrs, C. F., Ghosh, D., Gilsdorf, J. R. and Foxman, B. (2004). Library on a slide for bacterial comparative genomics. *BMC Microbiology* **4**, 12.
30. Rhodes, D. R., Yu, J., Shanker, K., Deshpande, N., Varambally, R., Ghosh, D., Barrette, T., Pandey, A. and Chinnaiyan, A. M. (2004). Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. *Proceedings of the National Academy of Sciences USA* **101**, 9309 – 9314.
31. *Shen, R., Ghosh, D. and Chinnaiyan, A. M. (2004). Prognostic meta-signature of breast cancer developed by two-stage mixture modeling of microarray data. *BMC Genomics* **5**, 94. (**Note:** This paper earned Ronglai Shen an ENAR student travel award in 2003).
32. Ghosh, D. (2004). Mixture models for assessing differential expression in complex tissue using microarray data. *Bioinformatics* **20**, 1663 – 1669.
33. Ghosh, D. (2004). Accelerated rates regression models for recurrent failure time data. *Lifetime Data Analysis* **10**, 247 – 261.
34. Ghosh, D. (2004). Identification of shared components and sparse networks in gene expression data. *Journal of Virtual Learning Signal Integration and Signal Processing* **38**, 277 – 286.
35. Yu, J., He, S., Friedman, J. S., Ghosh, D., Mears, A. J., Hicks, D. and Swaroop, A. (2004). Altered expression of genes of the Bmp/Smad and Wnt/Calcium signaling pathways in the cone-only Nrl-knockout mouse retina, revealed by gene profiling using custom cDNA microarrays. *Journal of Biological Chemistry* **279**, 42211 - 42220.
36. Shah, R.B., Mehra, R., Chinnaiyan, A.M., Shen, R., Ghosh, D., Zhou, M., MacVicar, G.R., Varambally, S., Harwood, J., Bismar, T.A., Kim, R., Rubin, M.A. and Pienta, K.J. (2004). Androgen independent prostate cancer is a heterogeneous group of diseases: lessons from a rapid autopsy program. *Cancer Research* **64**, 9209 - 9216.
37. Ghosh, D. and Chinnaiyan, A. M. (2005). Covariate adjustment in the analysis of microarray data from clinical studies. *Functional and Integrative Genomics* **5**, 18 – 27.
38. Ghosh, D. (2005). Nonparametric methods for identifying multiple replications of origins in genomewide data. *Functional and Integrative Genomics* **5**, 28 – 31.
39. Shedden, K., Chen, W., Kuick, R., Ghosh, D., Macdonald, J., Cho, K., Giordano, T. J., Gruber, S. B., Fearon, E. R., Taylor, J. M. G.G. and Hanash, S. (2005). A comparison of seven methods for normalization with Affymetrix expression scores based on false discovery rates in disease profiling data. *BMC Bioinformatics* **6**, 26.
40. Mallick, B., Ghosh, D. and Ghosh, M. (2005). Bayesian kernel-based classification of microarray data. *Journal of the Royal Statistical Society Series B* **2**, 219 – 234. Republished in *Machine Learning in Bioinformatics*, ed. S. Mitra *et al.*. (2008). New York: Chapman and Hall.

41. Abecasis, G. R., Ghosh, D. and Nichols, T.E. (2005). Linkage disequilibrium: ancient history drives the new genetics. *Human Heredity* **59**, 118 – 124.
42. Rhodes, D. R., Kalyana-Sundaram, S., Mahavisno, V., Barrette, T. R., Ghosh, D. and Chinnaiyan, A. M. (2005). Mining for regulatory programs in the cancer transcriptome. *Nature Genetics* **37**, 579 – 583.
43. Witkiewicz, A., Varambally, S., Shen, R., Mehra, R., Sabel, M., Ghosh, D., Chinnaiyan, A. M., Rubin, M. A. and Kleer, C. G. (2005). Alpha-Methylacyl-CoA Racemase (AMACR) protein expression is associated with the degree of differentiation in breast cancer using quantitative image analysis. *Cancer Epidemiology, Biomarkers and Prevention* **14**, 1418 – 1423.
44. Rubin, M. A., Bismar, T. A., Andren, O., Mucci, L., Kim, R., Shen, R., Ghosh, D., Wei, J. T., Chinnaiyan, A. M., Adami, H. O., Kantoff, P. W., and Johansson, J. E. (2005). Decreased Alpha-Methylacyl CoA racemase expression in localized prostate cancer is associated with an increased rate of biochemical recurrence and cancer specific death. *Cancer Epidemiology, Biomarkers and Prevention* **14**, 1424 – 1432.
45. Levin, A. M., Ghosh, D., Cho, K. R. and Kardia, S. L. R. (2005). A model-based scan statistic for identifying extreme chromosomal regions of gene expression in human tumors. *Bioinformatics* **21**, 2867 – 2874.
46. Sen, S., Burmeister, M., and Ghosh, D. (2005). 5-HTTLPR and anxiety-related personality traits meta-analysis revisited: response to Munafo and colleagues. *Molecular Psychiatry* **10**, 893 – 895.
47. Ghosh, D. and Chinnaiyan, A. M. (2005). Classification and selection of biomarkers in genomic data using LASSO. *Journal of Biomedicine and Biotechnology* **2**, 147 – 154.
48. Rhodes, D. R., Tomlins, S. A., Varambally, S., Mahavisno, V., Barrette, T., Kalyana-Sundaram, S., Ghosh, D., Pandey, A. and Chinnaiyan, A. M. (2005). Probabilistic model of the human protein-protein interaction network. *Nature Biotechnology* **23**, 951 – 959.
49. Wang, X, Yu, J., Sreekumar, A., Varambally, S., Shen, R., Giacherio, D., Mehra, R., Montie, J., Pienta, K. J., Sanda, M. G., Kantoff, P. W., Rubin, M. A., Wei, J.T., Ghosh, D., and Chinnaiyan, A. M. (2005). Autoantibody signatures in prostate cancer. *New England Journal of Medicine* **353**, 1224 – 1235.
50. Mehra, R., Varambally, S., Shen, R., Hayes, D. F., Sabel, M. S., Ghosh, D., Chinnaiyan, A. M. and Kleer, C. G. (2005). Identification of GATA3 as a breast cancer prognostic marker by global gene expression meta-analysis. *Cancer Research* **65**, 11259 – 11264.
51. Varambally, S., Yu, J., Laxman, B., Rhodes, D. R., Mehra, R., Shah, R., Chandran, U., Monzon, F. A., Becich, M. J., Wei, J. T., Pienta, K. G., Ghosh, D., Rubin, M. A. and Chinnaiyan, A. M. (2005). Integrative molecular analysis of prostate cancer reveals signatures of metastatic progression. *Cancer Cell* **8**, 393 – 406.
52. McEwen, L. M., Kim, C., Haan, M., Ghosh, D., Lantz, P., Mangione, C., Safford, M., Marrero,

- D., Thompson, T. and Herman, W. (2006). Diabetes reporting as a cause of death: results from Translating Research Into Action for Diabetes (TRIAD). *Diabetes Care* **29**, 247 – 253.
53. Ghosh, D., Chen, W. and Raghunathan, T. E. (2006). The false discovery rate: a variable selection perspective. *Journal of Statistical Planning and Inference* **136**, 2668 – 2684.
54. Ghosh, D. (2006). Modelling tumor biology-progression relationships in screening trials. *Statistics in Medicine* **25**, 1872 – 1884.
55. Ghosh, D. (2006). Semiparametric inferences for the association parameter with semi-competing risks data. *Statistics in Medicine* **25**, 2059 – 2070.
56. Ghosh, D. (2006). Random projection-based clustering for finding cancer subtypes in cancer microarray data. *Neurocomputing* **69**, 2258 – 2267.
57. Elder, J. T., Ghosh, D. and Shah, R. B. (2006). Epidermal growth factor receptor (ErbB1) expression in prostate cancer progression: correlation with androgen independence. *Prostate* **66**, 1437 – 1444.
58. Tsai, H. J., Tsai, A. C., Nriagu, J., Ghosh, D., Gong, M. and Sandretto, A. (2006). Risk factors for respiratory symptoms and asthma in the residential environment of 5th grade schoolchildren in Taipei, Taiwan. *Journal of Asthma* **5**, 355 – 361.
59. *Shen, R., Ghosh, D., Chinnaiyan, A. M. and Meng, Z. (2006). Eigengene-based linear discriminant analysis for gene expression data. *Bioinformatics* **22**, 2635 – 2642.
60. Chang, S., Ghosh, D., Linderman, J. L. and Kirschner, D. E. (2006). Length-based prediction of peptide-MHC class II binding affinity. *Bioinformatics* **22**, 2761 – 2767.
61. Macdonald, J. W. and Ghosh, D. (2006). COPA - cancer outlier profile analysis. *Bioinformatics* **22**, 2950 – 2951.
62. Ghosh, D. (2006). Semiparametric global cross-ratio models for bivariate censored data. *Scandinavian Journal of Statistics* **33**, 609 – 619.
63. Banerjee, M., Biswas, P., and Ghosh, D. (2006). Semiparametric binary regression under monotonicity constraints. *Scandinavian Journal of Statistics* **33**, 673 – 697.
64. Ghosh, D. (2006). Shrunken p-values for assessing differential expression, with applications to genomic data analysis. *Biometrics* **62**, 1099 – 1106.
65. Xie, J., Juliao, P., Gilsdorf, J. R., Ghosh, D., Patel, M., McCrea, K. W. and Marrs, C. F. (2006). Identification of more prevalent virulence factors in nontypeable *Haemophilus influenzae* otitis media strains than in throat strains. *Journal of Clinical Microbiology* **44**, 4316 – 4325.
66. Srinivasan, U., Zhang, L., France, A. M., Ghosh, D., Shalaby, W., Xie, J., Marrs, C. F. and Foxman, B. (2007). Probe hybridization array typing (PHAT): a binary typing method for *E. coli*. *Journal of Clinical Microbiology* **45**, 206 – 214.

67. Ghosh, D. and Chinnaiyan, A. M. (2007). Empirical Bayes identification of tumor progressor genes from microarray data. *Biometrical Journal* **49**, 68 – 77.
68. Rhodes, D. R., Kalyana-Sundaram, S., Mahavisno, V., Varambally, R., Yu, J., Briggs, B. B., Barrette, T. R., Anstet, M. J., Kincead-Beal, C., Kulkarni, P., Varambally, S., Ghosh, D. and Chinnaiyan, A. M. (2007). Oncomine 3.0: genes, pathways, and networks in a collection of 18,000 cancer gene expression profiles. *Neoplasia* **9**, 166 – 180.
69. Slotnick, M. J., Meliker, J. R., Avruskin, G. A., Ghosh, D. and Nriagu, J. O. (2007). Toenails as a biomarker of inorganic arsenic intake from drinking water and foods. *Journal of Toxicology and Environmental Health* **70**, 148 – 158.
70. Ghosh, D. (2007). Incorporating monotonicity into the evaluation of a biomarker. *Biostatistics* **8**, 402 – 413.
71. Chen, G., Wang, X., Yu, J., Varambally, S., Yu, J., Thomas, D. G., Wang, Z., Fielhauer, J., Ghosh, D., Giordano, T. J., Giacherio, D., Chang, A. C., Orringer, M. B., Bigsbee, W., Beer, D. G. and Chinnaiyan, A. M. (2007). Diagnostic autoantibodies for lung adenocarcinoma includes ubiquilin 1. *Cancer Research* **67**, 3461 – 3467.
72. Mehra, R., Tomlins, S. A., Shen, R., Nadeem, O., Wang, L., Wei, J. T., Pienta, K. J., Ghosh, D., Rubin, M. A., Chinnaiyan, A. M. and Shah, R. B. (2007). Comprehensive assessment of TM-PRSS2 and ETS family gene aberrations in clinically localized prostate cancer. *Modern Pathology* **20**, 538 – 544.
73. *Poisson, L. M. and Ghosh, D. (2007). Statistical issues and analyses of *in vitro* and *in vivo* genomic data in order to identify clinically relevant profiles, *Cancer Informatics* **1**, 231 – 243.
74. Yu, J., Almal, A. A., Yu, J., Dhanasekaran, S. M., Ghosh, D., Worzel, W. P., and Chinnaiyan, A. M. (2007). Molecular classification of cancer and feature selection using genetic programming. *Neoplasia* **9**, 292 – 303.
75. Rhodes, D. R., Kalyana-Sundaram, S., Mahavisno, V., Varambally, R., Yu, J., Briggs, B. B., Barrette, T. R., Anstet, M. J., Kincead-Beal, C., Kulkarni, P., Ghosh, D., Varambally, S., and Chinnaiyan, A. M. (2007). The Oncomine concepts map links tumors, pathways, mechanisms and drugs. *Neoplasia* **9**, 443 – 454.
76. McEwen, L. N., Kim, C., Karter, A. J., Haan, M., Ghosh, D., Lantz, P. M., Mangione, C. M., Thompson, T. J. and Herman, W. H. (2007). Risk factors for mortality among patients with diabetes: the translating research into action for diabetes (TRIAD) study. *Diabetes Care* **30**, 1736 – 1741.
77. Davila, M., Jhala, D., Ghosh, D., Grizzle, W. E. and Chakrabarti, R. (2007). Expression of Lim kinase 1 is associated with reversible G1/S arrest, chromosomal instability and prostate cancer. *Molecular Cancer* **6**, 40.
78. Tsai, H. J., Tsai, A. C., Nriagu, J., Ghosh, D., Gong, M., and Sandretto, A. (2007). Associations of BMI, TV-watching time, and physical activity on respiratory symptoms and asthma in 5th grade

schoolchildren in Taipei, Taiwan. *Journal of Asthma* **44**, 397 – 401.

79. *Liu, D., Lin, X. and Ghosh, D. (2007). Semiparametric regression of multi-dimensional genetic pathway data: least squares kernel machines and linear mixed models. *Biometrics* **63**, 1079 – 1088. (**Note:** This paper earned Dawei Liu an ENAR student travel award in 2003 and the *Biometrics* best paper award in 2007).

80. Kim, J. H., Dhanasekaran, S. M., Mehra, R., Tomlins, S. A., Gu, W. J., Yu, J., Kumar-Sinha, C., Cao, X., Dash, A., Wang, L., Ghosh, D., Shedden, K., Montie, J. E., Rubin, M. A., Pienta, K. J., Shah, R. B., and Chinnaiyan, A. M. (2007). Integrative analysis of genomic aberrations associated with prostate cancer progression. *Cancer Research* **67**, 8229 – 39.

81. *Choi, H., *Shen, R., Chinnaiyan, A. M. and Ghosh, D. (2007). A latent variable approach for meta-analysis of gene expression data from multiple microarray experiments. *BMC Bioinformatics* **8**, 364.

82. Chakraborty, S., Mallick, B., Ghosh, D., Ghosh, M. and Dougherty, E. (2007). Gene expression-based glioma classification using hierarchical Bayesian vector machines. *Sankhya* **69**, 514 – 547.

83. Yu, J., Yu, J., Cao, Q., Mehra, R., Laxman, B., Creighton, C. J., Tomlins, S. Dhanasekaran, S. M., Zhou, W., Chen, G., Shah, R. B., Ghosh, D., Varambally, S. and Chinnaiyan, A. M. (2007). Integrative genomics analysis reveals silencing of β -adrenergic signaling by polycomb in cancer. *Cancer Cell* **12**, 419 – 431.

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85. Taylor, B. S., Pal, M., Yu, J., Laxman, B., Sundaram, S. K., Zhao, R., Menon, A., Wei, J. T., Nesvizhskii, A. I., Ghosh, D., Omenn, G. S., Lubman, D. M., Chinnaiyan, A. M. and Sreekumar, A. (2008). Humoral response profiling reveals pathways to prostate cancer progression. *Molecular and Cellular Proteomics* **7**, 600 – 611.

86. * Choi, H. W., Ghosh, D. and Nesvizhskii, A. (2008). Statistical validation of peptide identifications in large-scale proteomics using target-decoy database search strategy and flexible mixture modeling. *Journal of Proteome Research* **7**, 286 – 292.

87. Yu, J., Yu, J., Cordero, K. E., Johnson, M. D., Ghosh, D., Chinnaiyan, A. M., Rae, J. M., and Lippman, M. E.. (2008). A transcriptional fingerprint of estrogen in human breast cancer predicts patient survival. *Neoplasia* **10**, 79-88.

88. *Gu, W. J., Choi, H. W. and Ghosh, D. (2008). Global associations between copy number and transcript mRNA expression: an empirical study. *Cancer Informatics* **4**, 17 – 23.

89. Kwee, L. C., Liu, D., Lin, X., Ghosh, D. and Epstein, M. P. (2008). A powerful and flexible multilocus association test for quantitative traits. *American Journal of Human Genetics* **82**, 386 – 397.

90. Ghosh, D. (2008). Proportional hazards regression for cancer studies. *Biometrics* **64**, 141 – 148.
91. Ghosh, D. (2008). Semiparametric inference for surrogate endpoints with bivariate censored data. *Biometrics* **64**, 149 – 156.
92. *Shen, R., Ghosh, D. and Taylor, J. M. G.(2008). Analysis of tissue microarray data using measurement error models. *Statistics in Medicine* **27**, 1944 – 1959.
93. *Chen, W., Ghosh, D., Raghunathan, T. E. and Sargent, D. (2008). A loss function-based framework for simultaneous inference involving interactions. *Statistics in Medicine* **27**, 2004 – 2021.
94. *Yuan, Z. and Ghosh, D. (2008). Combining multiple biomarker models in logistic regression. *Biometrics* **64**, 431 – 439.
95. Ghosh, D. (2008). On the Plackett distribution with bivariate censored data. *The International Journal of Biostatistics* Vol. 4 : Issue 1, Article 7.
96. *Liu, D., Ghosh, D. and Lin, X. (2008). Assessing the effect of a genetic pathway on a disease outcome using logistic kernel machine regression via mixed models. *BMC Bioinformatics* **9**, 292.
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Submitted/Under Revision

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170. Phillips, D., Li, Q. and Ghosh, D. (2015). Maximum rank reproducibility: a nonparametric approach to assessing reproducibility in replicate high-throughput experiments, under revision.
171. Ghosh, D. and Sabel, M. S. (2015). Matching methods for biomarker evaluation: a mapping with causal inference, under revision.
172. Ghosh, D. and De, S. (2015). Detecting outliers from multi-platform data using ensemble learning approaches with application in cancer, submitted.
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176. Luo, W., Zhu, Y. and Ghosh, D. (2015). On estimating regression causal effects using sufficient dimension reduction, submitted.

In preparation

Zhang, W., and Ghosh, D. (2015). Links between the sequence kernel association and kernel-based adaptive cluster tests, in preparation.

Cho, Y. and Ghosh, D. (2015). Propensity score adjustments for recurrent events data with dependent censoring, in preparation.

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Publications which have not received peer review:

Daniels, M., Frangakis, C., Charu, V. and Ghosh, D. (2015). University of Pennsylvania seventh annual conference on statistical issues in clinical trials: Current issues regarding the use of biomarkers and surrogate endpoints in clinical trials (morning panel discussion). *Clinical Trials*, in press.

Ghosh, D. (2008). Progression-free survival as a surrogate for overall survival: a new paradigm for surrogacy?. Technical Report, Department of Statistics, Penn State University.

Ghosh, D. and Chinnaiyan, A. M. (2005). Statistical methods for identification of tumor progression genes in microarray data. Technical Report, Department of Biostatistics, University of Michigan.

Ghosh, D. (2005). Semiparametric methods for the binormal model with multiple biomarkers. Technical Report, Department of Biostatistics, University of Michigan.

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Ghosh, D. (2004). Model checking techniques for regression models in cancer screening. Technical Report, Department of Biostatistics, University of Michigan.

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Chapters of books

Ghosh, D. and Girirajan, S. (2014). Statistical considerations in the analysis of rare variant data. In *Statistical Analysis of Next-generation Sequencing Data*, ed: S. Datta and D. Nettleton. New York: Springer-Verlag, Chapter 20.

Poisson, L. M. and Ghosh, D. (2013). Functional enrichment methods: a review. In *Advances in Statistical Bioinformatics*, ed: Kim-Anh Do, Steve Qin, and Marina Vannucci. Cambridge University Press: Cambridge. Chapter 21.

Ghosh, D., Lee, S., and Park, T. (2010). Statistical models, inference and algorithms for large-scale biological data analysis. In *Statistical Bioinformatics*, ed: Jae K. Lee. New York: Wiley-Blackwell: 185 – 199.

Ghosh, D. (2009). Oncogenic outlier detection in high-throughput data. In *Statistical Methods for Microarray Data Analysis*, eds: A. Yakovlev, D. Gaile, and L. Klebanov. Humana Press, in press.

Ghosh, D., Rhodes, D. and Chinnaiyan, A. M. (2009). Combining genomic data in human studies. In *Meta-analysis and Combining Information in Genetics and Genomics*, eds: D. B. Allison and R. Guerra. Chapman and Hall/CRC Mathematical and Computational Biology, in press.

Ghosh, D. (2008). Multiple testing procedures under confounding. In *Beyond Parametrics in Interdisciplinary Research: Festschrift in honor of Prof. Pranab K. Sen*, eds: M. Silvapulle, E. Pena and N. Balakrishnan. IMS Monograph Series: 243 – 256.

Choi, H. and Ghosh, D. (2008). A comparison of meta-analysis methods for gene expression data. In *Statistical Advances in the Biomedical Sciences*, eds: A. Biswas, S. Datta, J. P. Fine and M. R. Segal. Wiley: 200 - 215.

Ghosh, D. (2000). Response conditional models for correlated binary data. In *Perspectives in Statistical Science*, ed. A.K. Basu *et al.* New Delhi: Oxford University Press, pp. 138–152.

Nonrefereed Publications:

Sreekumar A, Poisson LM, Rajendiran TM, Khan AP, Cao Q, Yu J, Laxman B, Mehra R, Lonigro

RJ, Li Y, Nyati MK, Ahsan A, Kalyana-Sundaram S, Han B, Cao X, Byun J, Omenn GS, Ghosh D, Pennathur S, Alexander DC, Berger A, Shuster JR, Wei JT, Varambally S, Beecher C, Chinnaiyan AM. (2010). Re: Florian Jentzmik, Carsten Stephan, Kurt Miller, et al. Sarcosine in Urine after Digital Rectal Examination Fails as a Marker in Prostate Cancer Detection and Identification of Aggressive Tumours. *Eur Urol*.

Ghosh, D. (2009). Review of *Modern Multivariate Statistical Techniques* by A. Izenman. *Biometrics* **65**, 990 – 991

Ghosh, D. (2009). Letter to the Editor on “Effect of preventive supplementation with ready-to-use therapeutic food on the nutritional status, mortality, and morbidity of children aged 6 to 60 months in Niger: a cluster randomized trial,” *Journal of the American Medical Association* **301**, 2208 – 2209.

Wang, X., Ghosh, D. and Chinnaiyan, A. M. (2005). Response to “Autoantibody signatures in prostate cancer.” *New England Journal of Medicine* **26**, 2816 – 2817.

Ghosh, D. (2002). Review of *Statistical Aspects of the Design and Analysis of Clinical Trials*, by B. S. Everitt and A. Pickles. *Controlled Clinical Trials* **23**, 299 – 300.

Ghosh, D. (2001). Review of *Post-genome informatics*, by M. Kanehisa. *Statistical Methods in Medical Research* **10**, 241–242.

Ghosh, D. (2001). Review of *Analysis of Multivariate Survival Data*, by P. Hougaard. *Statistical Methods in Medical Research* **10**, 306–307.

Current Grants

NSF ABI-1262538 (Ghosh, P.I.) 7/1/13 - 6/30/16
Multivariate Statistical Methods for Genomic Data Integration
Total \$177,027.00/year

This research focuses on multivariate methods of analysis with high-dimensional genomic data, with the goal of prioritizing the genome for further study. Two classes of problems will be studied during the course of the project. The first is Hidden Markov Models and the second is multiple testing procedures, whose use have become commonplace with genomic datasets. This project proposes novel multivariate extensions of both types of method with a goal of being characterized by sound theoretical statistical principles while simultaneously being computationally feasible on big datasets. The methodology will be evaluated using several real datasets as well as through simulation studies.

Role: Principal Investigator

NIH R01CA129102 (MPIs: J. M. G. Taylor, University of Michigan; D. Ghosh, Penn State University), 01/01/09 - present
Statistical Methods for Cancer Biomarkers
Total: \$160,000/year

This grant proposes new semiparametric and nonparametric modelling procedures with applications to cancer biomarkers. The aims are the following: (a) Development of semiparametric and

nonparametric multivariate isotonic regression modelling procedures for biomarkers; (b) Development of statistical methods for the analysis of surrogate endpoints in a single-trial and multiple-trial framework; (c) Development of hybrid model averaging methods and attendant projection-based framework for combining biomarkers to optimize predictive accuracy.

Role: Principal Investigator (PI of Penn State subcontract)

Completed Funding

NIH 1T32GM102057-01A1 (MPIs: R. Hardison, D. Ghosh, and C. Shashikant, Penn State University), 07/01/13 - 06/30/18

Total: \$80,713/Year 1

Computation, Bioinformatics, and Statistics (CBIOS) Training Program

Genomic data are transforming how scientists in medicine and basic science conduct research. The advancement of genome science requires a new generation of scientists with strong computational and statistical skills and the ability to effectively interact with experimentalists. The proposed Penn State Computation, Bioinformatics, and Statistics (CBIOS) Training Program will prepare a cadre of investigators to think innovatively and keep pace with the quickly evolving landscape of high throughput genomic technologies. The program faculty are interdisciplinary and highly collaborative, with expertise in computation, bioinformatics, statistics, functional, medical, and evolutionary genomics. Learning these discipline-crossing skills will make trainees competitive for future careers in emerging and rapidly advancing fields of comparative, systems, statistical and medical genomics.

Role: Co-Director/Principal Investigator

NIH UL1RR033184 (PI: L. Sinoway, Penn State University/Penn State College of Medicine), 09/01/11 - present

Penn State Clinical and Translational Institute

Total: \$5,468,625/year

This proposal describes the newly created Penn State Clinical and Translational Science Institute (CTSI). The overarching goal of our CTSI initiative is to revitalize the health science research and education enterprise at our University to better enable it to deliver on the promise of improved health.

Role: Biostatistician

NIH R01GM066411-05A2 Omiecinski (PI) 12/15/09 11/30/2013

Functional Analysis of Nuclear Receptor Variants

Total: \$314,000/year

In this grant, our studies will characterize the roles of a novel series of receptor proteins that interact with pharmaceuticals and environmental chemicals and function to regulate the liver's capacity to metabolize substances. These receptors are termed constitutive androstane receptors and are part of a battery of sensing proteins that exist with liver cells to assist in processing the nature of the cell's chemical environment so that it can better tune its ability to detoxify chemicals we are exposed to.

Role: Co-Investigator

NIH/NSF 1 R01 GM72007 (PI: D. Ghosh), 09/01/04 to 08/31/10
Statistical Methods for the Analysis of Functional Genomic Data
Total: \$150,000/year

The goal of this project is to develop statistical and bioinformatic procedures for the modeling of complex high dimensional biological data with an emphasis towards incorporating functional biological knowledge.

Role: Principal Investigator

Co-Investigators: A. Chinnaiyan (Univ. of Michigan, 2004-2007), F. Pugh (Penn State, 2007 - 2008)

NIH 5R01HG003618 (PI: M. Epstein, Emory University), 09/27/07 - 08/26/2009
Novel Statistical Methods for Human Gene Mapping

Total: \$200,000/year

This grant proposes a set of such statistical methods that either address novel problems or improve existing solutions to problems in human gene mapping studies. These proposed methods are applicable to a variety of genetic studies as they address topics in linkage, linkage disequilibrium, and high-dimensional genetic analyses of complex diseases and disease-related quantitative traits.

Role: Co-investigator

Collaborators: M. Epstein (Emory University)

NIH/NCRR M01 RR00042 (Omenn), 03/01/01 to 02/28/06

General Clinical Research Center

Total: \$145,749

The major goals of this project are to review protocols and consult on biostatistical and bioinformatic aspects of investigations that use the General Clinical Research Center.

American Cancer Society RSG-02-179-MGO (Chinnaiyan), 07/01/02 to 06/30/06

Molecular Classification of Prostate Cancer

Total: \$37,792.33

The major goal of this project is to advise researchers on the design, analysis and conduct of high-throughput studies in prostate cancer involving gene and protein expression microarrays.

NIH/NHLBI P30 CA46592 (Wicha), 06/01/99 to 05/31/04

Cancer Center Support Grant (Biostatistics Core)

Total: \$69,323

The major goal of this project is to provide statistical support to University of Michigan Cancer Center researchers in the areas of design, analysis and interpretation of data.

MUNN IDEA Grant (Ghosh)

7/1/02 to 6/30/03

Total: \$20,000

The goal was to develop Bayesian and penalized regression models for the classification of tumors.

Prostate SPORE Seed Grant (Ghosh)

7/1/02 to 6/30/03

Total: \$10,000

The goal was to develop Bayesian and penalized regression models for the classification of tumors.

NIH P60 DK20572 (Herman), 12/01/02 to 11/30/07

Michigan Diabetes Research and Training Center

Total: \$ 92,498.76

The major goal of this project is to advise diabetes researchers on statistical issues related to the use of microarrays.

NIH R03 A1054406A (Zhang), 04/01/03 to 03/31/05

Library on a Chip: Bacterial Strain Microarray

Total: \$5,636

The major goal of this project is to array the genomes of a library of bacterial strains on a single chip that can be probed for the presence or absence of specific genes and for the allelic variations of the genes.

NIH P50 CA069568 (Pienta), 04/01/03 to 05/31/08

SPORE in Prostate Cancer

Total: \$45,450

The major goal of this project is to provide statistical support to University of Michigan Cancer Center researchers in the areas of design, analysis and interpretation of data in prostate cancer studies.

Invited Talks

1. "Kernel machine methods: back to the future":

- Myrto Lefkopolou Distinguished Lecture, Department of Biostatistics, Harvard School of Public Health, Boston, MA , September 24, 2015.

2. "Stacking, support vector machines and censored data":

- Graybill/International Chinese Student Association Conference, Ft. Collins, Colorado, June 16, 2015.

3. "Funding for NIH grants: a reviewer's perspective":

- ENAR Junior Researchers Workshop, Miami, Florida, March 15, 2015.
- Graybill/International Chinese Student Association Conference, Ft. Collins, Colorado, June 16, 2015.

4. "Kernel machine methods for high-throughput data":

- Computational Biosciences Seminar Series, University of Colorado Health Sciences Center. Aurora, Colorado, February 2, 2015.
- Beyond Bioinformatics Workshop, Statistical and Applied Mathematical Sciences Institute, September 14, 2014.

5. "Measurement, inference and statistical science in the age of 'Big Data' ":

- American Public Health Association Annual Meeting, Boston, MA, November 5, 2013.

6. "Multivariate statistical methods for genomic data integration":

- Department of Statistics, University of Pennsylvania, Philadelphia, PA, March 27, 2014.
 - Department of Biostatistics and Medical Informatics, University of Wisconsin, January 7, 2014.
 - Department of Biostatistics and Informatics, University of Colorado, December 16, 2013.
 - Department of Biostatistics, University of Florida, November 14, 2013.
 - Joint seminar, Department of Biostatistics and Division of Oncology Biostatistics, Johns Hopkins University, August 28, 2013.
7. “Penalized regression methods for variable selection in causal inference”:
- Joint Statistical Meetings, Montreal, Canada, August 5, 2013.
8. “Data-adaptive modelling of propensity scores for causal inference”:
- Division of Biostatistics, Penn State College of Medicine, Hershey, PA, November 15, 2012.
9. “Kernel Machines: an overview and recent developments”:
- Department of Biostatistics, University of Michigan, Ann Arbor, MI, November 1, 2012.
 - Department of Biostatistics, M. D. Anderson Cancer Center, Houston, TX, February 19, 2013.
10. “Multivariate multiple testing procedures, with applications to finding gene fusions in TCGA data”:
- Joint Statistical Meetings, San Diego, CA, August 1, 2012.
11. “Introducing shrinkage into the Benjamini-Hochberg procedure”:
- International Chinese Statistical Association Applied Conference, Boston, MA, June 24, 2012.
12. “Multiple testing procedures in neuroimaging genomics”:
- ENAR Annual Spring Meeting, Washington, DC, April 4, 2012.
13. “Extending the Benjamini-Hochberg procedure using spacings”:
- Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA, January 19, 2012.
 - Department of Statistics, University of South Carolina, Columbia, SC, February 1, 2012.
 - Department of Biostatistics, University of North Carolina, Chapel Hill, NC, February 22, 2012.
 - Biostatistics Research Branch, National Institute of Allergy and Infectious Diseases, Bethesda, MD, March 13, 2012.
14. “Meta-analysis of genomic data and multiple testing”:
- Cancer Biostatistics Seminar, Department of Biostatistics, University of Michigan, Ann Arbor, MI, November 2, 2012.

- Starr Lectureship, Department of Biostatistics, Brown University, Providence, RI, November 14, 2011.
 - Division of Biostatistics, Vanderbilt University, Nashville, TN, November 16, 2011.
15. "A multivariate Benjamini-Hochberg procedure, with applications to genomics":
 - Indian International Statistical Association meeting, Raleigh, NC, March 24, 2011.
 16. "What can machine learning do for you? Algorithmic approaches to causal inference":
 - Methodology Center, Brownbag Seminar, Penn State University, February 21, 2011.
 17. "Risk prediction: model averaging, stability and calibration":
 - Division of Oncology Biostatistics, Johns Hopkins University, Baltimore, MD, February 17, 2011.
 18. "Multiple testing: a view using spacings":
 - Winter Workshop on high-dimensional data analysis, University of Florida, Gainesville, FL, January 14, 2011.
 19. "Identification of copy number-associated gene expression alterations in microarray experiments":
 - Joint Statistical Meetings, Washington, D. C., August 4, 2009.
 20. "Kernel machine-based methods in genomics":
 - Rao Prize Conference, Penn State University, University Park, PA, May 22, 2009.
 21. "Model-based meta-analysis for analysis of data from chromatin immunoprecipitation experiments":
 - Division of Biostatistics, University of Southern California, Los Angeles, CA, July 23, 2009.
 - IMS Asia/Pacific Rim Meeting, Seoul, South Korea, June 29, 2009.
 - Department of Biostatistics and Bioinformatics and Human Genetics, Emory University, Atlanta, GA, April 23, 2009.
 - Division of Statistical Sciences, Cornell University, Ithaca, NY, April 1, 2009.
 22. "Hierarchical Hidden Markov model-based meta-analysis of data from chromatin immunoprecipitation experiments":
 - Department of Human Genetics, UCLA, Los Angeles, CA, October 13, 2008.
 23. "Genomic outlier profile analysis with estimated null distributions":
 - Biostatistics and Medical Informatics, University of Wisconsin, Madison, WI, September 26, 2008.
 24. "Statistical issues in the design and analysis of '-omics' studies":

- Bioinformatics and Medical Informatics Retreat, Penn State College of Medicine, Hershey, PA, January 22, 2008.
25. "Multiple testing procedures in genomic studies":
- Silver Platinum Jubilee, Indian Statistical Institute, Calcutta, India, January 3, 2008.
26. "Kernel machines, mixed models and genomic studies":
- Division of Biostatistics, Yale University, New Haven, CT, September 25, 2007.
 - Center for Comparative Genomics and Bioinformatics, Penn State University, University Park, PA, September 19, 2007.
 - Department of Biological Statistics and Computational Biology, Cornell University, September 12, 2007.
27. "Statistical methods for the analysis of phage epitope array data":
- Statistics for Biomolecular Data Integration and Modeling Workshop, Ascona, Switzerland, June 11, 2007.
 - Interface meeting, Philadelphia, PA, May 25, 2007.
28. "Integrating copy number and gene expression microarray datasets":
- Department of Epidemiology and Biostatistics, Memorial Sloan Kettering, New York City, New York, May 9, 2007.
29. "Towards inference of chromosomal aberrations from genomic data":
- Department of Bioinformatics and Computational Biology, M. D. Anderson Cancer Center, Houston, Texas, October 2, 2006.
30. "Joint modelling of copy number and mRNA microarray data":
- 2007 ENAR annual meeting, Atlanta, Georgia, March 12, 2007.
31. "Statistical Methods for Integration of Copy Number and transcript mRNA data":
- Department of Statistics, Rice University, Houston, Texas, February 5, 2007.
 - Department of Biostatistics, Bioinformatics and Biomathematics, Georgetown University, Washington, D. C., September 1, 2006.
 - Joint Statistical Meetings, Seattle, Washington, August 8, 2006.
32. "Statistical Methods for Analysis of Genomic/Proteomic Data in Complex Tissue":
- Statistical Society of Canada, University of Western Ontario, London, Ontario, May 29, 2006.
33. "Meta-analysis of genomic data and multiple testing":
- Department of Statistics, Pennsylvania State University, State College, PA, March 14, 2006.
 - Department of Mathematics and Statistics, University of Windsor, Windsor, Ontario, March 9, 2006.

34. "Introduction to Statistical Methods for Genomic Data Analysis":
 - Association of Molecular Pathology Annual Meeting, Phoenix, Arizona, November 11, 2005.
35. "Multiple testing and shrinkage estimation":
 - Multiple Comparisons Procedures, Shanghai, China, August 18, 2005.
36. "Towards inference of chromosomal aberrations from genomic data":
 - Joint Statistical Meetings, Minneapolis, Minnesota, August 10, 2005.
37. "Combining Genomic Data in Human Cancer Studies":
 - Division of Oncology Biostatistics, Department of Oncology, Johns Hopkins University, Baltimore, Maryland, March 1, 2006.
 - Mathematical Biosciences Institute, Columbus, Ohio, April 22, 2005.
38. "Semiparametric Support Vector Machines for Gene Expression Data":
 - Joint Statistical Meetings, Toronto, Canada, August 8, 2004.
 - Institute for Pure and Applied Mathematics, UCLA, June 4, 2004.
39. "Association Models for Bivariate Censored Data":
 - Division of Biostatistics, Cleveland Clinic, April 23, 2004.
 - Division of Biostatistics, Columbia University, March 4, 2004.
40. "Statistical Methods for Chromosomal Localization using Gene Expression Data":
 - Department of Biostatistics, University of Pittsburgh, February 17, 2005.
 - Division of Biostatistics, University of Minnesota, March 22, 2004.
 - Division of Biostatistics, Columbia University, March 3, 2004.
 - Department of Statistics, University of Tennessee-Knoxville, January 23, 2004.
 - Statistical Methods in Bioinformatics Seminar Series, Brown University, November 10, 2003.
41. "Statistical Methods for Clustering Microarray Data in Cancer Studies":
 - First Canadian Workshop on Statistical Genomics, Toronto, Canada, September 3, 2003.
42. "Statistical Methods for the Analysis of Microarray Data":
 - East Tennessee State University, January 22, 2004.
43. "Global cross ratio models for bivariate censored data":
 - Fifth Triennial Symposium on Statistics, Calcutta University, Calcutta, India, December 29, 2003.
 - Department of Biostatistics, Johns Hopkins University, April 30, 2003.

44. "Meta-analysis of microarray data":
- Bioinformatics Seminar Series, Department of Statistics, Purdue University, February 1, 2005.
 - Biostatistics Seminar Series, Department of Statistics, University of Wisconsin-Madison, November 12, 2004.
 - International Indian Statistical Association Meeting, Dekalb, IL, June 14, 2002.
 - Joint Statistical Meetings, New York City, NY, August 8, 2002.
45. "Penalized Regression Models for the classification of tumors from microarray experiments":
- Center for Molecular Medicine and Genetics, Wayne State University, February 20, 2003.
 - Institute for Pure and Applied Mathematics, UCLA, June 21, 2002.
 - Department of Biostatistics, University of Minnesota, May 18, 2002.
 - Training Program in Bioinformatics, Texas A&M University, February 25, 2002.
 - Pacific Symposium on Biocomputing, Kauai, Hawaii, January 4, 2002.
46. "Mixture modelling of microarray data," Statistics Department, University of Washington, July 13, 2001.
47. "Semiparametric Analysis of Recurrent Failure Time Data Using Accelerated Rates Models":
- Department of Epidemiology and Biostatistics, Imperial Cancer Research Fund, London, England, June 9, 2002.
 - Statistics 2001 Canada Conference, Concordia University, Montreal, Canada, July 2, 2001.
48. "Semiparametric Analysis of Recurrent Failure Time Data and Dependent Censoring":
- Joint Statistical Meetings, Atlanta, Georgia, August 7, 2001.
 - Fourth Triennial Symposium on Statistics, Calcutta University, Calcutta, India, December 27, 2000.
49. "Marginal Regression Models for Recurrent and Terminal Events":
- Department of Biostatistics, M.D. Anderson Cancer Center, Houston, Texas, March 27, 2000.
 - Department of Biometry and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, March 24, 2000.
 - Department of Biostatistics, Harvard School of Public Health, Boston, Massachusetts, March 9, 2000.
 - Department of Biostatistics, University of North Carolina, Chapel Hill, North Carolina, March 6, 2000.
 - Division of Biostatistics, University of Minnesota, Minneapolis, Minnesota, March 3, 2000.
 - Department of Biostatistics, University of Michigan, Ann Arbor, Michigan, February 24, 2000.

- Department of Statistics, University of Florida, Gainesville, Florida, February 17, 2000.
50. "Nonparametric Analysis of Recurrent Events and Death," Society of Clinical Trials Annual Meeting, Anaheim, California, May 3, 1999.
 51. "Response Conditional Models for Correlated Binary Data," Third Triennial Symposium on Statistics, Calcutta University, Calcutta, India, December 27, 1997.

Papers Delivered at Professional Meetings

1. "Machine Learning Methods for Causal Inference," Contributed Paper, ENAR Spring Meeting, 2006, Tampa, Florida.
2. "Semiparametric Analysis of Recurrent Events and Dependent Censoring," Contributed Paper, ENAR Spring Meeting, 2001, Charlotte, North Carolina.
3. "Nonparametric Analysis of Recurrent Events and Death," Contributed Paper, ENAR Spring Meeting, 1999, Atlanta, Georgia.

Teaching:

University of Michigan:

Biostatistics 646 (Data Analysis in Molecular Biology): Winter 2007
 Biostatistics 699 (Design and Analysis of Biomedical Investigations): Winter 2007
 Biostatistics 503 (Applied Biostatistics): Fall 2001
 Biostatistics 560 (Statistical Methods in Epidemiology): Fall 2002, Fall 2003, Fall 2004, Fall 2005
 Biostatistics 602 (Biostatistical Inference): Winter 2002, Winter 2003, Winter 2005
 Biostatistics 830 (Machine Learning Methods in Biostatistics): Fall 2005
 Guest Lecturer in Bioinformatics 526: Fall 2002, Fall 2003
 Guest Lecturer in Biostatistics 646 (Data Analysis in Molecular Biology): Winter 2005
 University of Michigan Cancer Bioinformatics Short Course Instructor: Summer 2004
 Guest Lecturer in Human Genetics 632: Fall 2006
 Guest Lecturer in Epidemiology 631: Winter 2007

Penn State University:

Statistics 525 - Survival Analysis: Spring 2008, Spring 2009
 Statistics 505 - Applied Multivariate Statistical Analysis: Fall 2009, Fall 2010, Fall 2011
 Statistics 544 - Categorical Data Analysis: Fall 2010
 Instructor, Summer School for Astronomers: Summer 2009, Summer 2010, Summer 2011

Service

University of Michigan:

Faculty Search: 2000-2001, 2001-2002, 2005-2006
Candidacy: 2000-2001, 2001-2002, 2003 - 2004, 2005-2006 (chair), 2006 – 2007 (chair)
Statistical Genetics Search Committee: 2001-2002, 2002-2003
Web: 2002-2003
Associate Director, Cancer Biostatistics Training Grant: 2005 – 2006
Faculty-Student Affairs: 2003 - 2004
Microarray Working Group Organizer: 2001 - 2004
Bioinformatics Faculty Search Committee: 2001-2002
Aging/Bioinformatics Faculty Search Committee: 2003-2004
Bioinformatics Executive Advisory Committee: 2004 – 2005
Bioinformatics Graduate Affairs Committee: 2006 – 2007
Chair, Bioinformatics Pilot Grant Award Program: 2006
Genome Sciences Training Grant Faculty: 2001-2007
Genome Sciences Training Grant Review Panel: 2002, 2004, 2007

Penn State University:

Eberly Chair Search Committee: 2007
Cliff Clogg Memorial Lecture Committee: 2008
Ph.D. Qualifying Exam Committee: 2008, 2009
Promotion and Tenure Committee: 2010
Graduate Student Affairs Committee: 2009, 2010, 2011
Admissions Committee: 2010, 2011
Statistics Department Head Search Committee: 2009
Associate Dean Search Committee: 2011
CBIOS Training Grant Co-Director, 2013 – present

External:

Referee for the following journals:

Biometrics, Statistics in Medicine Journal of Multivariate Analysis, Biostatistics, Statistics and Probability Letters, Lifetime Data Analysis, Bioinformatics, Biometrika, Genome Biology, Journal of the American Statistical Association - Theory and Methods, Journal of Computational and Graphical Statistics, IMA Volume Series, Bayesian Statistics 7, Nature Medicine, Diabetes Care, Journal of Statistical Planning and Inference, Journal of Biological Chemistry, Journal of the American Statistical Association - Applications and Case Studies, Comptes rendus biologies, Neurocomputing, Journal of Multivariate Analysis, American Journal of Pharmacogenomics, Computational Statistics and Data Analysis, FEBS Letters, Annals of Statistics, Aging Cell, Comparative and Functional Genomics, Statistical Applications in Genetics and Molecular Biology, New England Journal of Medicine, IEEE Transactions in Computational Biology and Bioinformatics, Journal of Clinical Oncology, Journal of Very Large Databases, Journal of National Cancer Institute, BMC Bioinformatics, Applied Statistics, Lancet, Cancer Epidemiology, Biomarkers and Prevention, Journal of the Royal Statistical Society Series B, PLOS Genetics, Nucleic Acids Research, American Journal of Management Science, Journal of Computational and Applied Mathematics, Journal of Clinical Endocrinology and Metabolism, Statistical Advances in the Biomedical Sciences (book, 2 articles), Meta-Analysis in Genetics (book), Statistica Sinica, Journal of Molecular Diagnostics,

Proceedings of the National Academy of Sciences, BMC Developmental Biology, Journal of Proteome Research, Cancer Informatics, Canadian Journal of Statistics, Mammalian Genome, Pacific Symposium on Biocomputing, International Journal of Biostatistics, Gastroenterology, Statistical Papers, Genomics, BMC Cancer, Current Molecular Medicine, Statistical Analysis and Data Mining, Statistics and Computing, Neuroimage, Annals of Epidemiology, Journal of Biopharmaceutical Statistics, American Journal of Epidemiology, Nature, American Statistician, Journal of Proteomics and Bioinformatics, Nature Medicine, TEST, Journal of Psychiatric Research, JAMA, PLOS One, Journal of Biomedical Informatics, Clinical Cancer Research, Cancer Research, Computational and Mathematical Methods in Medicine, Genetic Epidemiology, Genome Medicine, Trends in Analytical Chemistry, BMC Medicine

Invited Session Organizer, 2002 IISA Conference.

IMS Invited Session Organizer, 2003 Spring ENAR meeting.

NSF Grant Reviewer, 2003, 2005.

Book Reviewer, 2003.

Regional Advisory Board Member, ENAR, 2004 - 2006.

European Union Young Research Investigator Award Reviewer, 2004.

Medical Research Council *ad hoc* Grant Reviewer, 2004.

National Institutes of Health *ad hoc* Grant Reviewer, 2004, 2006, 2007, 2008, 2009 (2 times), 2015

National Institutes of Health Challenge Grant Reviewer, 2009.

NSA *ad hoc* Grant Reviewer, 2006.

University of Cyprus Grant Reviewer, 2006.

Reviewer, Springer-Verlag proposal, 2006.

Utah State University New Faculty Research Grant Reviewer, 2007.

Pennsylvania Department of Health Grant Reviewer, 2007.

Singapore Ministry of Health Reviewer, 2007.

Qatar National Government Grant Reviewer, 2007.

Distinguished Student Paper Award Committee, ENAR, 2007 - 2009.

Panelist, Emerging Design and Analysis Issues in Genomic Studies in Population Sciences, Harvard

School of Public Health, 2008.

Reviewer, Neural Information Processing Systems (NIPS) Conference, 2009.

Reviewer, ASA Statistics in Epidemiology Student Paper Competition, 2009.

U.S.-Israel Binational Science Foundation reviewer, 2010.

Netherlands Organization for Health Research and Development reviewer, 2010.

Regular Member, Biostatistical Methods and Research Design (BMRD) Section, National Institutes of Health, 2010 – present

Member, Regional Committee (RECOM) board, ENAR, 2011 – present

Secretary/Treasurer, ASA Biometrics Section, 2011 – present

Reviewer, Feasibility Studies for Collaborative Interaction for Minority Institution/Cancer Center Partnership (P20), National Institutes of Health, 2011

Reviewer, The Netherlands Organisation for Health Research and Development, 2012

Reviewer, Utilizing the PLCO Biospecimens Resource to Bridge Gaps in Cancer Etiology and Early Detection Research (U01), 2013

External Reviewer, Biostatistics Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute, 2014

Section Chair, ASA Biometrics Section, 2015 – present.

Organizing Committee, Frontiers of Hierarchical Modeling in Observational Studies, Complex Sur-

veys and Big Data, 2014.
Reviewer, Israel Science Foundation, 2015.

Program Committee, Society of Mathematical Biology Annual Meeting, 2004.
Program Committee, NSF-DARPA workshop on Genomic Signal Processing, 2002, 2005, 2006.
Program Committee, Intelligent Systems for Molecular Biology, 2005.
Program Committee (Member At-Large), ENAR, 2007.
Program Chair, Biometrics Section, JSM, 2008.
Program Committee, International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2011, 2014.
Program Chair, ENAR, 2012.
Program Committee, International Biometric Conference, 2014.

Associate Editor, *Biometrics*, 2006 - 2010, 2011 – present
Associate Editor, *Statistica Sinica*, 2011 – present
Associate Editor, *Statistics in Biosciences*, 2009 - present
Associate Editor, *Molecular Cancer*, 2009 - present
Associate Editor, *BMC Bioinformatics*, 2009 - present
Associate Editor, *BMC Medical Genomics*, 2008 - present
Editorial Board, *BMC series*, 2005 - present
Editorial Board, *BMC Proceedings*, 2007 - present
Editorial Board, *Cancer Informatics*, 2005 - present
Associate Editor, *EURASIP Journal on Signal Processing and Bioinformatics*, 2005 - 2008
Associate Editor, *JASA - Theory and Methods*, 2008 – 2011
Section Head, Bioinformatics and Algorithms, Section, *BMC Medical Genomics*, 2010 – 2012
Associate Editor, *Statistical Applications in Genetics and Molecular Biology*, 2009 – 2012
Associate Editor, *International Journal of Biostatistics*, 2009 – 2012

Member, American Statistical Association (1997 to present)
Member, International Biometric Society (1998 to present)
Member, Institute of Mathematical Statistics (1999 to present)
Member, International Society for Computational Biology (2001 to present)
Member, International Indian Statistical Association, 2008 - present

Student Advising

Master's Students:

University of Michigan:

Erin Shellman, Biostatistics, 2007

Penn State University:

Qiong Yang, Statistics, 2014

Doctoral Students:

University of Michigan:

Dawei Liu, Biostatistics, 2002 – 2005 (co-chair with X. Lin), currently Assistant Professor of Biostatistics, University of Iowa

Wei Chen, Biostatistics, 2002 – 2006 (co-chair with T.E. Raghunathan), currently Assistant Professor of Oncology, Wayne State University

Zheng Yuan, Biostatistics, 2004 – 2006, currently Ph.D. Biostatistician, Clinical Oncology, Eli Lilly
Ronglai Shen, Biostatistics, 2002 – 2007 (co-chair with J. Taylor), currently investigator, Division of Epidemiology and Biostatistics, Memorial Sloan-Kettering Cancer Center

Hyungwon Choi, Biostatistics, 2006 – 2008 (co-chair with Z. S. Qin), currently assistant professor, Department of Biostatistics and Epidemiology, National University of Singapore Graduate Medical School

Laila Poisson, Biostatistics, 2003 – 2009 (co-chair with J. Taylor), current position, assistant professor, Department of Epidemiology and Biostatistics, Henry Ford Health System

Penn State University:

Muhammad Atiyat, Statistics, 2008 – 2011, currently Statistician, United Nations

Scott Roths, Statistics, 2009 – 2011 (joint with Prof. G. Jogesh Babu), currently Lecturer, Department of Statistics, Penn State University

Yeying Zhu, Statistics, 2010 – 2013 currently Assistant Professor, Department of Statistics and Actuarial Sciences, University of Waterloo

Yihan Li, Statistics, 2010 – 2014, currently Biostatistician, AbbVie Pharmaceuticals

Daisy Phillips, Statistics, 2011 – 2014

Wen-Yu Hua, Statistics, 2011 – 2014, currently postdoctoral fellow, NYU Medical Center

Youngjoo Cho, Statistics, 2011 – 2014

Xiang Zhan, Statistics, 2011 – 2014

Post-Doctoral Students:

Penn State University:

Yeonok Lee, Statistics, 2011 – 2014 (joint with Y. Zhang), currently statistical modeller, Development Office, St. Jude's Children Hospital.

Other Visitors:

Hande Konsuk, Hacettepe University, 2012

Dissertation Committees:

University of Michigan:

Mike Epstein, Biostatistics, 2001 – 2002.

Nichole Carlson, Biostatistics, 2001– 2003.

Jasmanda Wu, Epidemiology, 2001– 2002.

Shibao Feng, Biostatistics, 2001 – 2003.

Lei Liu, Biostatistics, 2001 – 2004.
Stephanie Borchardt, Epidemiology, 2003 – 2004.
Debbie Lown, Epidemiology, 2002 – 2005.
Al Levin, Epidemiology, 2003 – 2005.
Adi Andrei, Biostatistics, 2003 – 2005.
Laura McEwen-Mattei, Epidemiology, 2003 – 2005.
Shona Dallal, Epidemiology, 2003 – 2005.
Abdullah AISwuailem, Epidemiology, 2003 – 2005.
Chris Riolo, Epidemiology, 2000 – 2005.
Hsin-Jen Tsai, Nutritional Sciences, 2003 – 2006.
Patty Juliao, Epidemiology, 2002 – 2006.
Ying Kong, Epidemiology, 2004 – 2006.
Akarin Pharibul, Statistics, 2002 – 2006.
Dan Rhodes, Bioinformatics, 2004 – 2006.
Chad Creighton, Bioinformatics, 2004 – 2006.
Andrew Skol, Biostatistics, 2005 – 2006.
Rohit Kulkarni, Statistics, 2005 – 2006.
Aaron Sussell, Occupational and Environmental Health, 2002 – 2006.
Melissa Slotnick, Occupational and Environmental Health, 2004 – 2007.
Vivian Colon, Epidemiology, 2005 – 2007.
Kai Bullard, Epidemiology, 2005 – 2007.
Angela Liu, Biostatistics, 2006 – 2007.

Penn State University:

Natalia Tchetcherina, Statistics, 2007 – present
Sujana Ghosh, Biochemistry and Molecular Biology, 2008 – 2011
Ho Sung Rhee, Biochemistry and Molecular Biology, 2008 – 2011
Yan Zhuang, Agricultural Economics and Rural Sociology, 2009 – 2010
Jianping Sun, Statistics, 2009 – 2010
Chris Groendyke, Statistics, 2009 – 2010
Julia Jennings, Anthropology and Demography (Minor in Statistics), 2010
Song Li, Integrative Biosciences, 2010
Zhenhai Zhang, Bioinformatics, 2009 – 2011
Kiranmoy Das, Statistics, 2010 – 2011
Junyi Lin, Statistics, 2009 – 2011
Duy Vu, Statistics, 2010 – 2013
Qiuying Shen, Biology, 2011
Jian Li, Biochemistry and Molecular Biology, 2009 – 2012
Jialin Xu, Statistics, 2010 – 2012
Qianyi Ma, Nutritional Sciences, 2010 – 2012
Isaac Dialsingh, Statistics, 2010 – 2012
Celine Han, Integrative Biosciences, 2011 – present
Rene Koo Flasher, Accounting, 2011 – 2013
Denise Finney, Crop and Soil Sciences, 2011 – present
Yao Zheng, Human Development and Family Studies, 2012 – 2014
Neerja Katiyar, Integrative Biosciences, 2012 – 2013
Vishesh Karwa, Statistics, 2012 – 2014
Xizhen Cai, Statistics, 2012 – 2014

Lab Rotation Students:

University of Michigan:

Paul Nicholas, Biostatistics, Winter 2003
Kate Kirby, Biostatistics, Winter 2003
Viktoriya Strumba, Bioinformatics, Winter 2004
Omar Halawa, Bioinformatics, Winter 2006
Bin Zhu, Biostatistics, Fall 2006
Ali Shojaie, Statistics, Fall 2006, Winter 2007
Matt Zawitowski, Biostatistics, Winter 2007

Penn State University:

Yang Liu, Bioinformatics, Fall 2010
Scott Roths, Statistics, Summer 2010
Daisy Phillips, Statistics, Spring/Summer 2011
Yihan Li, Statistics, 2011
Yeying Zhu, Statistics, 2010–2011
Bahaedinne Toufak, Statistics, 2012 – 2014

Examination Committees:

University of Michigan:

Xing Li, Bioinformatics, 2003
Yili Chen, Bioinformatics, 2003
Jianjun Yu, Bioinformatics, 2003 (chair)
Carlos Santos, Bioinformatics, 2003
Yu Chen, Bioinformatics, 2003
Dan Rhodes, Bioinformatics, 2004 (chair)
Pete Ulintz, Bioinformatics, 2004 (chair)
Reagan Kelly, Bioinformatics, 2005
Abhik Shah, Bioinformatics, 2005
Barry Taylor, Bioinformatics, 2006 (chair)

Penn State University:

Akshay Katamansu, IBIOS, 2013
Juan Antonio Raygoza Garay, IBIOS, 2013
Yafei Lyu, IBIOS, 2014
Rahulsimham Vegesna, IBIOS, 2014