CURRICULUM VITAE of Giovanni Parmigiani [1]

CONTACT

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EDUCATION

Ph.D. in Statistics, Department of Statistics, Carnegie Mellon University, 1990.
   Thesis: "Optimal Scheduling of Inspections with an Application to Medical Screening Tests."
   Thesis advisor: J. B. Kadane.

M.S. in Statistics, Department of Statistics, Carnegie Mellon University, 1987.

B.S. (*cum laude*), in Economics and Social Sciences, Università L. Bocconi, Milano, 1984.
   Thesis: "Prediction Sufficiency in Statistical Decision Theory."
   Thesis advisor: D. M. Cifarelli.

POSITIONS

Harvard University:
   Associate Director for Population Sciences, Dana-Farber/Harvard Cancer Center 2010–present.
   Chair, Department of Biostatistics & Computational Biology, Dana Farber Cancer Institute 2009–2018.
   Professor, Department of Biostatistics, School of Public Health 2009–present.
   Program Leader, Dana-Farber/Harvard Cancer Center Program in Biostatistics
      and Computational Biology, 2010—2015.
   Visiting Assistant Professor, Department of Biostatistics, T.H. Chan School of Public Health
      and Department of Biostatistical Science, Dana-Farber Cancer Institute, Fall 1994.

Johns Hopkins University:
   Adjunct Professor, Department of Oncology, 2009—present.
   Professor, Department of Oncology, 2005—2009.
   Director, Bioinformatics Shared Resource, Kimmel Cancer Center 2004—2009.
   Associate Professor, Department of Oncology, 1999—2005.
      Joint appointments: Department of Biostatistics 2000—2009;
                          Department of Pathology, 2000—2009.

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Division of Health Sciences Informatics, 2006—2009.
Visiting Scholar, Department of Biostatistics, 1997—1998.

M.D Anderson Cancer Center: Edward Rotan Visiting Professorship, 2002

Duke University:
Adjunct Associate Professor, Institute of Statistics and Decision Sciences, 1999—2003
Associate Professor, Institute of Statistics and Decision Sciences, 1998—1999.
Joint appointments: Cancer Prevention, Detection and Control Program, 1996—1999.
Center for Clinical Health Policy Research, 1996—1999.
Assistant Professor, Institute of Statistics and Decision Sciences, 1991—1998.

Carnegie Mellon University: Research Scientist, Department of Statistics, 1990—1991.

Università L. Bocconi: Fellow, Institute of Quantitative Methods, Milano. 1984—1986.

HONORS AND FELLOWSHIPS

- Fellow of the American Association for the Advancement of Science, 2019
- Junior Faculty Mentoring Award, Harvard T.H. Chan School of Public Health, 2016
- DeGroot Prize for *Decision Theory*, by Giovanni Parmigiani and Lurdes Y T Inoue, with contributions by Hedibert Freitas Lopes, 2009
- Advising, Mentoring, and Teaching Recognition Award. Johns Hopkins School of Public Health Student Assembly, 2002
- Edward Rotan Visiting Professorship, M. D. Anderson Cancer Center, 2002
- Hecht Scholar, Johns Hopkins University, 2000
- Fellow of the American Statistical Association, 1999
- Myrto Lefkopoulou Distinguished Lecture, Harvard School of Public Health 1999.
- Biometrics ENAR Student Travel Award, 1991.
- L.J. Savage Ph.D. Thesis Award, International Society for Bayesian Analysis, 1990.
- Gavasakar Dissertation Prize, 1990.
- Graduate Student of the Year, 1990, Pittsburgh Chapter of the ASA.
- Thesis Publication Honor, 1984, Università L. Bocconi, Milano.

SOFTWARE

Ask2me [Website]

Decision support tool for precision prevention in individuals undergoing panel DNA testing for cancer susceptibility.

BayesMendel [Website]

comprehensive R environment for prediction of inherited cancer susceptibility using familial history

includes the BRCAPRO model for the breast/ovarian cancer syndrome, the MMRPRO model for the Lynch syndrome, the MELAPRO model for inherited cutaneous melanoma and the PANCPRO model for familial pancreatic cancer;

Bioconductor Packages

XDE Multi-level model for cross-study detection of differential gene expression.

 Authors: R.B. Scharpf, G. Parmigiani, A.B. Nobel, and H. Tjelmeland

 Maintainer: Robert Scharpf

MergeMaid Merging and visualization tools for cross-study validation of gene expression microarray analyses.

 Authors: Xiaogang Zhong Leslie Cope Elizabeth Garrett Giovanni Parmigiani

 Maintainer: Xiaogang Zhong

CANCER MUTATION ANALYSIS Tools for data analysis of cancer genome sequencing studies.

 Authors: Giovanni Parmigiani, Simina M. Boca

 Maintainer: Simina M. Boca

lungExpression Data from three large lung cancer studies provided as ExpressionSets.

 Authors: Robert Scharpf, Simens Zhong, Giovanni Parmigiani

 Maintainer: Robert Scharpf

PatientGeneSets Patient-oriented analysis of mutations from cancer genome studies.

 Authors: Simina M. Boca, Giovanni Parmigiani

 Maintainer: Simina M. Boca

curatedOvarianData Clinically Annotated Data for the Ovarian Cancer Transcriptome.

 Authors: Benjamin F. Ganzfried, Markus Riester, Steve Skates, Victoria Wang, Thomas Risch, Benjamin Haibe-Kains, Svitlana Tyekucheva, Jie Ding, Ina Jazic, Michael Birrer, Giovanni Parmigiani, Curtis Huttenhower, Levi Waldron

 Maintainer: Levi Waldron

PATENTS

1. Wiles TM, Turner DJ, O'Connell MA, Parmigiani G, and Clyde MA. *System and method for analyzing susceptibility of biological samples*, for Becton, Dickinson & Co. Patents EP1160564, US6849422, CA2349043, JP2002125697. [Patent Documents]

2. Vogelstein et al *Genomic Landscapes of Human Breast and Colorectal Cancers*, for The Johns Hopkins University. Patents US2009/0123,928, WO2009049166. [Patent Documents]

3. Vogelstein et al *Genetic Alterations in Isocitrate Dehydrogenase and other Genes in Malignant Gliomas*, for the Johns Hopkins University, Patent US2012/0202,207, EP2326735, EP2546365, CN102177251, AU2009288004, CA 2736125, MX2011002409, JP2012501652. [Patent Documents]

4. Vogelstein et al *Pathways Underlying Pancreatic Tumorigenesis* for the Johns Hopkins University, Patent US2012/0115,735, EP2326734, CA2736124, JP2012501651, AU2009288097. [Patent Documents]

5. Wood et al. *Genomic Landscapes of Human Breast and Colorectal Cancers*, for The Johns Hopkins University. Patent US2013/0196312.
6. Parmigiani G, Riester M. *Methods and Systems for the Treatment of Ovarian Cancer*, for the Dana-Farber Cancer Institute. Patent Application No PCT/US14/31295.
7. Vogelstein et al. *Genetic Alterations in Isocitrate Dehydrogenase and Other Genes in Malignant Glioma* for the Johns Hopkins University. Patent US2017/0081730 A1. [Patent Documents]

PUBLICATIONS

Link to Publications on Google Scholar

Books

[1] Parmigiani G. *Modeling in Medical Decision Making: A Bayesian Approach*. Chichester: Wiley 2002.

[2] Parmigiani G, Garrett ES, Irizarry R, Zeger SL, eds. *The analysis of gene expression data: an overview of methods and software*. New York: Springer 2003.

[3] Parmigiani G, Inoue LYT. *Decision Theory: Principles and Approaches*. Chichester: Wiley 2009.

Reports

[4] Marchionni L, Wilson RF, Marinopoulos SS, Wolff AC, Parmigiani G, Bass EB, Goodman SN. Impact of gene expression profiling tests on breast cancer outcomes. *Evid Rep Technol Assess Full Rep* 1–105 Dec 2007.

Articles

[5] Banks DL, Parmigiani G. Pre-analysis of super large industrial data sets. *Journal of Quality Technology* 24; 115–129 1992.

[6] Parmigiani G. Minimax, information and ultrapessimism. *Theory and Decision* 33; 241–252 1992.

[7] Parmigiani G. On optimal screening ages. *Journal of the American Statistical Association* 88; 622–628 1993.

[8] Muliere P, Parmigiani G, Polson NG. A note on the residual entropy function. *Probability in the Engineering and Informational Sciences* 7; 413–420 1993.

[9] Muliere P, Parmigiani G. On quasi-means. *Utilitas Mathematica* 43; 79–87 1993.

[10] Parmigiani G. Optimal inspection and replacement policies with age-dependent failures and fallible tests (stma V35 3349). *Journal of the Operational Research Society* 44; 1105–1114 1993.

[11] Muliere P, Parmigiani G. Utility and means in the 1930s. *Statistical Science* 8; 421–432 1993.

[12] Parmigiani G. Inspection times for stand-by units. *Journal of Applied Probability* 31; 1015–1025 1994.

[13] Müller P, Parmigiani G. Optimal design via curve fitting of Monte Carlo experiments. *Journal of the American Statistical Association* 90; 1322–1330 1995.

[14] Parmigiani G. Optimal scheduling of fallible inspections. *Operations Research* 44; 360–367 1996.

[15] Carota C, Parmigiani G, Polson NG. Diagnostic measures for model criticism. *Journal of the American Statistical Association* 91; 753–762 1996.

[16] Clyde MA, DeSimone H, Parmigiani G. Prediction via orthogonalized model mixing. *Journal of the American Statistical Association* 91; 1197–1208 1996.

[17] Berry DA, Parmigiani G, Sanchez J, Schildkraut J, Winer E. Probability of carrying a mutation of breast-ovarian cancer gene BRCA1 based on family history. *J Natl Cancer Inst* 89; 227–238 Feb 1997.

[18] Weinstein MP, Towns ML, Quartey SM, Mirrett S, Reimer LG, Parmigiani G, Reller LB. The clinical significance of positive blood cultures in the 1990s: a prospective comprehensive evaluation of the microbiology, epidemiology, and outcome of bacteremia and fungemia in adults. *Clin Infect Dis* 24; 584–602 Apr 1997.

[19] Parmigiani G, Samsa GP, Ancukiewicz M, Lipscomb J, Hasselblad V, Matchar DB. Assessing uncertainty in cost-effectiveness analyses: application to a complex decision model. *Med Decis Making* 17; 390–401 1997.

[20] Matchar DB, Samsa GP, Matthews JR, Ancukiewicz M, Parmigiani G, Hasselblad V, Wolf PA, D'Agostino RB, Lipscomb J. The stroke prevention policy model: linking evidence and clinical decisions. *Ann Intern Med* 127; 704–711 Oct 1997.

[21] Dominici F, Parmigiani G, Reckhow KH, Wolpert RL. Combining information from related regressions. *Journal of Agricultural Biological and Environmental Statistics* 2; 313–332 1997.

[22] Parmigiani G. Timing medical examinations via intensity functions. *Biometrika* 84; 803–816 1997.

[23] Parmigiani G, Berry D, Aguilar O. Determining carrier probabilities for breast cancer-susceptibility genes BRCA1 and BRCA2. *Am J Hum Genet* 62; 145–158 Jan 1998. PMC1376797.

[24] Lipscomb J, Parmigiani G, Hasselblad V. Combining expert judgment by hierarchical modeling: An application to physician staffing. *Management Science Journal of the Institute of Management Sciences* 44; 149–161 1998.

[25] Lipscomb J, Ancukiewicz M, Parmigiani G, Hasselblad V, Samsa G, Matchar DB. Predicting the cost of illness: a comparison of alternative models applied to stroke. *Med Decis Making* 18; S39–S56 1998.

[26] Berry DA, Parmigiani G. Assessing the benefits of testing for breast cancer susceptibility genes: a decision analysis. *Breast Dis* 10; 115–125 Apr 1998.

[27] Clyde MA, Parmigiani G. Protein construct storage: Bayesian variable selection and prediction with mixtures. *J Biopharm Stat* 8; 431–443 Jul 1998.

[28] Petersen GM, Parmigiani G, Thomas D. Missense mutations in disease genes: a bayesian approach to evaluate causality. *Am J Hum Genet* 62; 1516–1524 Jun 1998. PMC1377150.

[29] Carota C, Parmigiani G. A Dirichlet process elaboration diagnostic for binomial goodness of fit. *Test* 7; 133–145 1998.

[30] Clyde MA, Parmigiani G, Vidakovic B. Multiple shrinkage and subset selection in wavelets. *Biometrika* 85; 391–402 1998.

[31] Parmigiani G. Designing observation times for interval censored data. *Sankhya A* 60; 446–458 1998.

[32] Claus EB, Schildkraut J, Iversen ES, Berry D, Parmigiani G. Effect of BRCA1 and BRCA2 on the association between breast cancer risk and family history. *J Natl Cancer Inst* 90; 1824–1829 Dec 1998.

[33] Samsa GP, Reutter RA, Parmigiani G, Ancukiewicz M, Abrahamse P, Lipscomb J, Matchar DB. Performing cost-effectiveness analysis by integrating randomized trial data with a comprehensive decision model: application to treatment of acute ischemic stroke. *J Clin Epidemiol* 52; 259–271 Mar 1999.

[34] Dominici F, Parmigiani G, Wolpert RL, Hasselblad V. Meta-analysis of migraine headache treatments: Combining information from heterogeneous designs. *Journal of the American Statistical Association* 94; 16–28 1999.

[35] Parmigiani G, Berry DA, Winer EP, Tebaldi C, Iglehart JD, Prosnitz LR. Is axillary lymph node dissection indicated for early-stage breast cancer? a decision analysis. *J Clin Oncol* 17; 1465–1473 May 1999.

[36] Müller P, Parmigiani G, Schildkraut J, Tardella L. A bayesian hierarchical approach for combining case-control and prospective studies. *Biometrics* 55; 858–866 Sep 1999.

[37] Iversen Jr ES, Parmigiani G, Berry DA, Schildkraut J. Genetic susceptibility and survival: Application to breast cancer. *Journal of the American Statistical Association* 95; 28–42 2000.

[38] Dominici F, Parmigiani G, Clyde M. Conjugate analysis of multivariate normal data with incomplete observations. *The Canadian Journal of Statistics La Revue Canadienne de Statistique* 28; 533–550 2000.

[39] Dominici F, Parmigiani G. Bayesian semiparametric analysis of developmental toxicology data. *Biometrics* 57; 150–157 Mar 2001.

[40] Jones JB, Song JJ, Hempen PM, Parmigiani G, Hruban RH, Kern SE. Detection of mitochondrial DNA mutations in pancreatic cancer offers a "mass"-ive advantage over detection of nuclear DNA mutations. *Cancer Res* 61; 1299–1304 Feb 2001.

[41] Parmigiani G, Skates S. Estimating the age of onset of detectable asymptomatic cancer. *Mathematical and Computer Modeling* 33(1273); 1347–60 2001.

[42] Bova GS, Parmigiani G, Epstein JI, Wheeler T, Mucci NR, Rubin MA. Web-based tissue microarray image data analysis: initial validation testing through prostate cancer gleason grading. *Hum Pathol* 32; 417–427 Apr 2001.

[43] Ryu B, Jones J, Blades NJ, Parmigiani G, Hollingsworth MA, Hruban RH, Kern SE. Relationships and differentially expressed genes among pancreatic cancers examined by large-scale serial analysis of gene expression. *Cancer Res* 62; 819–826 Feb 2002.

[44] Wang TL, Rago C, Silliman N, Ptak J, Markowitz S, Willson JKV, Parmigiani G, Kinzler KW, Vogelstein B, Velculescu VE. Prevalence of somatic alterations in the colorectal cancer cell genome. *Proc Natl Acad Sci U S A* 99; 3076–3080 Mar 2002. PMC122475.

[45] Parmigiani G, Skates S, Zelen M. Modeling and optimization in early detection programs with a single exam. *Biometrics* 58; 30–36 Mar 2002.

[46] Berry DA, Iversen ES, Gudbjartsson DF, Hiller EH, Garber JE, Peshkin BN, Lerman C, Watson P, Lynch HT, Hilsenbeck SG, Rubinstein WS, Hughes KS, Parmigiani G. BRCAPRO validation, sensitivity of genetic testing of BRCA1/BRCA2, and prevalence of other breast cancer susceptibility genes. *J Clin Oncol* 20; 2701–2712 Jun 2002.

[47] Carota C, Parmigiani G. Semiparametric regression for count data. *Biometrika* 2; 265–281 2002.

[48] Kauff ND, Perez-Segura P, Robson ME, Scheuer L, Siegel B, Schluger A, Rapaport B, Frank TS, Nafa K, Ellis NA, Parmigiani G, Offit K. Incidence of non-founder BRCA1 and BRCA2 mutations in high risk Ashkenazi breast and ovarian cancer families. *J Med Genet* 39; 611–614 Aug 2002.

[49] Symer DE, Connelly C, Szak ST, Caputo EM, Cost GJ, Parmigiani G, Boeke JD. Human L1 retrotransposition is associated with genetic instability in vivo. *Cell* 110; 327–338 Aug 2002.

[50] Inoue LYT, Parmigiani G. Designing follow–up times. *jasa* 97; 847–858 2002.

[51] Parmigiani G, Garrett ES, Anbazhagan R, Gabrielson E. A statistical framework for expression-based molecular classification in cancers. *Journal of the Royal Statistical Society Series B* 64; 717–736 2002.

[52] Parmigiani G. Measuring uncertainty in complex decision analysis models. *Stat Methods Med Res* 11; 513–537 Dec 2002.

[53] Scharpf R, Garrett ES, Hu J, Parmigiani G. Statistical modeling and visualization of molecular profiles in cancer. *Biotechniques* Suppl; 22–29 Mar 2003.

[54] Bardelli A, Parsons DW, Silliman N, Ptak J, Szabo S, Saha S, Markowitz S, Willson JKV, Parmigiani G, Kinzler KW, Vogelstein B, Velculescu VE. Mutational analysis of the tyrosine kinome in colorectal cancers. *Science* 300(5674); 949 May 2003.

[55] Cappola TP, Cope L, Cernetich A, Barouch LA, Minhas K, Irizarry RA, Parmigiani G, Durrani S, Lavoie T, Hoffman EP, Ye SQ, Garcia JGN, Hare JM. Deficiency of different nitric oxide synthase isoforms activates divergent transcriptional programs in cardiac hypertrophy. *Physiol Genomics* 14; 25–34 Jun 2003.

[56] Chowers I, Liu D, Farkas RH, Gunatilaka TL, Hackam AS, Bernstein SL, Campochiaro PA, Parmigiani G, Zack DJ. Gene expression variation in the adult human retina. *Hum Mol Genet* 12; 2881–2893 Nov 2003.

[57] Parmigiani G, Ashih H, Samsa G, Duncan P, Lai S, Matchar D. Cross-calibration of stroke disability measures: Bayesian analysis of longitudinal ordinal categorical data using negative dependence. *Journal of the American Statistical Association* 98(462); 273–281 2003.

[58] Dang LH, Bettegowda C, Agrawal N, Cheong I, Huso D, Frost P, Loganzo F, Greenberger L, Barkoczy J, Pettit GR, Smith AB, Gurulingappa H, Khan S, Parmigiani G, Kinzler KW, Zhou S, Vogelstein B. Targeting vascular and avascular compartments of tumors with c. novyi-nt and anti-microtubule agents. *Cancer Biol Ther* 3; 326–337 Mar 2004.

[59] Wang TL, Diaz LA, Romans K, Bardelli A, Saha S, Galizia G, Choti M, Donehower R, Parmigiani G, Shih IM, Iacobuzio-Donahue C, Kinzler KW, Vogelstein B, Lengauer C, Velculescu VE. Digital karyotyping identifies thymidylate synthase amplification as a mechanism of resistance to 5-fluorouracil in metastatic colorectal cancer patients. *Proc Natl Acad Sci U S A* 101; 3089–3094 Mar 2004. PMC420348.

[60] Marroni F, Aretini P, D'Andrea E, Caligo MA, Cortesi L, Viel A, Ricevuto E, Montagna M, Cipollini G, Federico M, Santarosa M, Marchetti P, Bailey-Wilson JE, Bevilacqua G, Parmigiani G, Presciuttini S. Penetrances of breast and ovarian cancer in a large series of families tested for BRCA1/2 mutations. *Eur J Hum Genet* 12; 899–906 Nov 2004.

[61] Marroni F, Aretini P, D'Andrea E, Caligo MA, Cortesi L, Viel A, Ricevuto E, Montagna M, Cipollini G, Ferrari S, Santarosa M, Bisegna R, Bailey-Wilson JE, Bevilacqua G, Parmigiani G, Presciuttini S. Evaluation of widely used models for predicting BRCA1 and BRCA2 mutations. *J Med Genet* 41; 278–285 Apr 2004. PMC1735736.

[62] Mehrotra J, Ganpat MM, Kanaan Y, Fackler MJ, McVeigh M, Lahti-Domenici J, Polyak K, Argani P, Naab T, Garrett E, Parmigiani G, Broome C, Sukumar S. Estrogen receptor/progesterone receptor-negative breast cancers of young african-american women have a higher frequency of methylation of multiple genes than those of caucasian women. *Clin Cancer Res* 10; 2052–2057 Mar 2004.

[63] Parmigiani G, Garrett-Mayer ES, Anbazhagan R, Gabrielson E. A cross-study comparison of gene expression studies for the molecular classification of lung cancer. *Clin Cancer Res* 10; 2922–2927 May 2004.

[64] Wang Z, Shen D, Parsons DW, Bardelli A, Sager J, Szabo S, Ptak J, Silliman N, Peters BA, van der Heijden MS, Parmigiani G, Yan H, Wang TL, Riggins G, Powell SM, Willson JKV, Markowitz S, Kinzler KW, Vogelstein B, Velculescu VE. Mutational analysis of the tyrosine phosphatome in colorectal cancers. *Science* 304; 1164–1166 May 2004.

[65] Parmigiani G. Uncertainty and the value of diagnostic information, with application to axillary lymph node dissection in breast cancer. *Stat Med* 23; 843–855 Mar 2004.

[66] Hackam AS, Qian J, Liu D, Gunatilaka T, Farkas RH, Chowers I, Kageyama M, Parmigiani G, Zack DJ. Comparative gene expression analysis of murine retina and brain. *Mol Vis* 10; 637–649 Aug 2004.

[67] Chen S, Wang W, Broman KW, Katki HA, Parmigiani G. Bayesmendel: an r environment for mendelian risk prediction. *Stat Appl Genet Mol Biol* 3; Article 21 2004.

[68] Cope L, Zhong X, Garrett E, Parmigiani G. Mergemaid: R tools for merging and cross-study validation of gene expression data. *Stat Appl Genet Mol Biol* 3; Article 29 2004.

[69] Garrett ES, Parmigiani G. A nested unsupervised approach to identifying novel molecular subtypes. *Bernoulli* 10; 951–69 2004.

[70] Hackam AS, Strom R, Liu D, Qian J, Wang C, Otteson D, Gunatilaka T, Farkas RH, Chowers I, Kageyama M, Leveillard T, Sahel JA, Campochiaro PA, Parmigiani G, Zack DJ. Identification of gene expression changes associated with the progression of retinal degeneration in the rd1 mouse. *Invest Ophthalmol Vis Sci* 45; 2929–2942 Sep 2004.

[71] Kittleson MM, Ye SQ, Irizarry RA, Minhas KM, Edness G, Conte JV, Parmigiani G, Miller LW, Chen Y, Hall JL, Garcia JGN, Hare JM. Identification of a gene expression profile that differentiates between ischemic and nonischemic cardiomyopathy. *Circulation* 110; 3444–3451 Nov 2004.

[72] Iacobuzio-Donahue CA, Song J, Parmigiani G, Yeo CJ, Hruban RH, Kern SE. Missense mutations of MADH4: characterization of the mutational hot spot and functional consequences in human tumors. *Clin Cancer Res* 10; 1597–1604 Mar 2004.

[73] Zhou X, Iversen Jr ES, Parmigiani G. Classification of missense mutations of disease genes. *Journal of the American Statistical Association* 100; 51–60 2005. PMC2311507.

[74] Inoue L, Berry D, Parmigiani G. Correspondences between bayesian and frequentist sample size determination. *The American Statistician* 59; 79–87 2005.

[75] Müller P, Parmigiani G, Robert C, Rousseau J. Optimal sample size for multiple testing: the case of gene expression microarrays. *Journal of the American Statistical Association* 99; 990–1001 2005.

[76] Shen Y, Parmigiani G. A model-based comparison of breast cancer screening strategies: mammograms and clinical breast examinations. *Cancer Epidemiol Biomarkers Prev* 14; 529–532 Feb 2005.

[77] Molina H, Parmigiani G, Pandey A. Assessing reproducibility of a protein dynamics study using in vivo labeling and liquid chromatography tandem mass spectrometry. *Anal Chem* 77; 2739–2744 May 2005.

[78] Favorov AV, Andreewski TV, Sudomoina MA, Favorova OO, Parmigiani G, Ochs MF. A Markov Chain Monte Carlo technique for identification of combinations of allelic variants underlying complex diseases in humans. *Genetics* 171; 2113–2121 Dec 2005. PMC1456130.

[79] Dettling M, Gabrielson E, Parmigiani G. Searching for differentially expressed gene combinations. *Genome Biol* 6; R88 2005. PMC1257471.

[80] Sugg Skinner C, Rawl SM, Moser BK, Buchanan AH, Scott LL, Champion VL, Schildkraut JM, Parmigiani G, Clark S, Lobach DF, Bastian LA. Impact of the cancer risk intake system on patient-clinician discussions of tamoxifen, genetic counseling, and colonoscopy. *J Gen Intern Med* 20; 360–365 Apr 2005. PMC1490091.

[81] Chen S, Watson P, Parmigiani G. Accuracy of MSI testing in predicting germline mutations of MSH2 and MLH1: a case study in Bayesian meta-analysis of diagnostic tests without a gold standard. *Biostatistics* 6; 450–464 Jul 2005.

[82] Shih IM, Sheu JJC, Santillan A, Nakayama K, Yen MJ, Bristow RE, Vang R, Parmigiani G, Kurman RJ, Trope CG, Davidson B, Wang TL. Amplification of a chromatin remodeling gene, Rsf-1/HBXAP, in ovarian carcinoma. *Proc Natl Acad Sci U S A* 102; 14004–14009 Sep 2005. PMC1236547.

[83] Chen S, Iversen ES, Friebel T, Finkelstein D, Weber BL, Eisen A, Peterson LE, Schildkraut JM, Isaacs C, Peshkin BN, Corio C, Leondaridis L, Tomlinson G, Dutson D, Kerber R, Amos CI, Strong LC, Berry DA, Euhus DM, Parmigiani G. Characterization of BRCA1 and BRCA2 mutations in a large United States sample. *J Clin Oncol* 24; 863–871 Feb 2006. PMC232978.

[84] Dominici F, Zeger SL, Parmigiani G, Katz J, Christian P. Estimating percentile-specific treatment effects in counterfactual models: a case-study of micronutrient supplementation, birth weight and infant mortality. *Journal of the Royal Statistical Society Series C Applied Statistics* 55; 261–280 2006.

[85] Sjöblom T, Jones S, Wood LD, Parsons DW, Lin J, Barber TD, Mandelker D, Leary RJ, Ptak J, Silliman N, Szabo S, Buckhaults P, Farrell C, Meeh P, Markowitz SD, Willis J, Dawson D, Willson JKV, Gazdar AF, Hartigan J, Wu L, Liu C, Parmigiani G, Park BH, Bachman KE, Papadopoulos N, Vogelstein B, Kinzler KW, Velculescu VE. The consensus coding sequences of human breast and colorectal cancers. *Science* 314; 268–274 Oct 2006.

[86] Gandhi TKB, Zhong J, Mathivanan S, Karthick L, Chandrika KN, Mohan SS, Sharma S, Pinkert S, Nagaraju S, Periaswamy B, Mishra G, Nandakumar K, Shen B, Deshpande N, Nayak R, Sarker M, Boeke JD, Parmigiani G, Schultz J, Bader JS, Pandey A. Analysis of the human protein interactome and comparison with yeast, worm and fly interaction datasets. *Nat Genet* 38; 285–293 Mar 2006.

[87] Zilliox MJ, Parmigiani G, Griffin DE. Gene expression patterns in dendritic cells infected with measles virus compared with other pathogens. *Proc Natl Acad Sci U S A* 103; 3363–3368 Feb 2006. PMC1413941.

[88] Favorova OO, Favorov AV, Boiko AN, Andreewski TV, Sudomoina MA, Alekseenkov AD, Kulakova OG, Gusev EI, Parmigiani G, Ochs MF. Three allele combinations associated with multiple sclerosis. *BMC Med Genet* 7; 63 2006. PMC1557481.

[89] Chen S, Wang W, Lee S, Nafa K, Lee J, Romans K, Watson P, Gruber SB, Euhus D, Kinzler KW, Jass J, Gallinger S, Lindor NM, Casey G, Ellis N, Giardiello FM, Offit K, Parmigiani G, Colon Cancer Family Registry. Prediction of germline mutations and cancer risk in the Lynch syndrome. *JAMA* 296; 1479–1487 Sep 2006. PMC2538673.

[90] Bettegowda C, Huang X, Lin J, Cheong I, Kohli M, Szabo SA, Zhang X, Diaz LA, Velculescu VE, Parmigiani G, Kinzler KW, Vogelstein B, Zhou S. The genome and transcriptomes of the anti-tumor agent clostridium novyi-nt. *Nat Biotechnol* 24; 1573–1580 Dec 2006.

[91] Hayes DN, Monti S, Parmigiani G, Gilks CB, Naoki K, Bhattacharjee A, Socinski MA, Perou C, Meyerson M. Gene expression profiling reveals reproducible human lung adenocarcinoma subtypes in multiple independent patient cohorts. *J Clin Oncol* 24; 5079–5090 Nov 2006.

[92] Salvatori R, Serpa MG, Parmigiani G, Britto AVO, Oliveira JLM, Oliveira CRP, Prado CM, Farias CT, Almeida JC, Vicente TAR, Aguiar-Oliveira MH. GH response to hypoglycemia and clonidine in the GH-releasing hormone resistance syndrome. *J Endocrinol Invest* 29; 805–808 Oct 2006.

[93] Dominici F, Zeger SL, Parmigiani G, Katz J, Christian P. Does the effect of micronutrient supplementation on neonatal survival vary with respect to the percentiles of the birth weight distribution? *Bayesian Anal* 2; 1–30 03 2007.

[94] Emerick MC, Parmigiani G, Agnew WS. Multivariate analysis and visualization of splicing correlations in single-gene transcriptomes. *BMC Bioinformatics* 8; 16 2007. PMC1785386.

[95] Dahinden C, Parmigiani G, Emerick MC, Bühlmann P. Penalized likelihood for sparse contingency tables with an application to full-length cDNA libraries. *BMC Bioinformatics* 8; 476 2007. PMC2233645.

[96] Wood LD, Parsons DW, Jones S, Lin J, Sjöblom T, Leary RJ, Shen D, Boca SM, Barber T, Ptak J, Silliman N, Szabo S, Dezso Z, Ustyanksky V, Nikolskaya T, Nikolsky Y, Karchin R, Wilson PA, Kaminker JS, Zhang Z, Croshaw R, Willis J, Dawson D, Shipitsin M, Willson JKV, Sukumar S, Polyak K, Park BH, Pethiyagoda CL, Pant PVK, Ballinger DG, Sparks AB, Hartigan J, Smith DR, Suh E, Papadopoulos N, Buckhaults P, Markowitz SD, Parmigiani G, Kinzler KW, Velculescu VE, Vogelstein B. The genomic landscapes of human breast and colorectal cancers. *Science* 318; 1108–1113 Nov 2007.

[97] Wang W, Chen S, Brune KA, Hruban RH, Parmigiani G, Klein AP. PancPRO: risk assessment for individuals with a family history of pancreatic cancer. *J Clin Oncol* 25; 1417–1422 Apr 2007.

[98] Scharpf RB, Iacobuzio-Donahue CA, Sneddon JB, Parmigiani G. When should one subtract background fluorescence in 2-color microarrays? *Biostatistics* 8; 695–707 Oct 2007.

[99] Wu F, Dassopoulos T, Cope L, Maitra A, Brant SR, Harris ML, Bayless TM, Parmigiani G, Chakravarti S. Genome-wide gene expression differences in crohn's disease and ulcerative colitis from endoscopic pinch biopsies: Insights into distinctive pathogenesis. *Inflamm Bowel Dis* 13; 807–821 Jul 2007.

[100] Oliveira JLM, Aguiar-Oliveira MH, D'Oliveira A, Pereira RMC, Oliveira CRP, Farias CT, Barreto-Filho JA, Anjos-Andrade FD, Marques-Santos C, Nascimento-Junior AC, Alves EO, Oliveira FT, Campos VC, Ximenes R, Blackford A, Parmigiani G, Salvatori R. Congenital growth hormone (GH) deficiency and atherosclerosis: effects of GH replacement in GH-naive adults. *J Clin Endocrinol Metab* 92; 4664–4670 Dec 2007.

[101] Chen S, Parmigiani G. Meta-analysis of BRCA1 and BRCA2 penetrance. *J Clin Oncol* 25; 1329–1333 Apr 2007. PMC2267287.

[102] Chen S, Euhus DM, Parmigiani G. Quantitative models for predicting mutations in Lynch syndrome genes. *Current Colorectal Cancer Reports* 3(4); 206–211 2007.

[103] Zahurak M, Parmigiani G, Yu W, Scharpf RB, Berman D, Schaeffer E, Shabbeer S, Cope L. Pre-processing agilent microarray data. *BMC Bioinformatics* 8; 142 2007. PMC1876252.

[104] Ho YY, Cope L, Dettling M, Parmigiani G. Statistical methods for identifying differentially expressed gene combinations. *Methods Mol Biol* 408; 171–191 2007.

[105] Lin J, Gan CM, Zhang X, Jones S, Sjöblom T, Wood LD, Parsons DW, Papadopoulos N, Kinzler KW, Vogelstein B, Parmigiani G, Velculescu VE. A multidimensional analysis of genes mutated in breast and colorectal cancers. *Genome Res* 17; 1304–1318 Sep 2007. PMC1950899.

[106] Parmigiani G, Chen S, Iversen ES, Friebel TM, Finkelstein DM, Anton-Culver H, Ziogas A, Weber BL, Eisen A, Malone KE, Daling JR, Hsu L, Ostrander EA, Peterson LE, Schildkraut JM, Isaacs C, Corio C, Leondaridis L, Tomlinson G, Amos CI, Strong LC, Berry DA, Weitzel JN, Sand S, Dutson D, Kerber R, Peshkin BN, Euhus DM. Validity of models for predicting BRCA1 and BRCA2 mutations. *Ann Intern Med* 147; 441–450 Oct 2007. PMC2423214.

[107] Tai YC, Domchek S, Parmigiani G, Chen S. Breast cancer risk among male BRCA1 and BRCA2 mutation carriers. *J Natl Cancer Inst* 99; 1811–1814 Dec 2007. PMC2267289.

[108] Iversen ES, Katki HA, Chen S, Berry DA, Parmigiani G. Limited family structure and breast cancer risk. *JAMA* 298; 2007 Nov 2007.

[109] Scharpf RB, Parmigiani G, Pevsner J, Ruczinski I. Hidden Markov models for the assessment of chromosomal alterations using high-throughput SNP arrays. *Annals of Applied Statistics* 2; 687–713 2008. PMC2710854.

[110] Marchionni L, Wilson RF, Wolff AC, Marinopoulos S, Parmigiani G, Bass EB, Goodman SN. Systematic review: gene expression profiling assays in early-stage breast cancer. *Ann Intern Med* 148; 358–369 Mar 2008.

[111] Jones S, Chen WD, Parmigiani G, Diehl F, Beerenwinkel N, Antal T, Traulsen A, Nowak MA, Siegel C, Velculescu VE, Kinzler KW, Vogelstein B, Willis J, Markowitz SD. Comparative lesion sequencing provides insights into tumor evolution. *Proc Natl Acad Sci U S A* 105; 4283–4288 Mar 2008. PMC2393770.

[112] Jones S, Zhang X, Parsons DW, Lin JCH, Leary RJ, Angenendt P, Mankoo P, Carter H, Kamiyama H, Jimeno A, Hong SM, Fu B, Lin MT, Calhoun ES, Kamiyama M, Walter K, Nikolskaya T, Nikolsky Y, Hartigan J, Smith DR, Hidalgo M, Leach SD, Klein AP, Jaffee EM, Goggins M, Maitra A, Iacobuzio-Donahue C, Eshleman JR, Kern SE, Hruban RH, Karchin R, Papadopoulos N, Parmigiani G, Vogelstein B, Velculescu VE, Kinzler KW. Core signaling pathways in human pancreatic cancers revealed by global genomic analyses. *Science* 321; 1801–1806 Sep 2008. PMC2848990.

[113] Garrett-Mayer E, Parmigiani G, Zhong X, Cope L, Gabrielson E. Cross-study validation and combined analysis of gene expression microarray data. *Biostatistics* 9; 333–354 Apr 2008.

[114] Parsons DW, Jones S, Zhang X, Lin JCH, Leary RJ, Angenendt P, Mankoo P, Carter H, Siu IM, Gallia GL, Olivi A, McLendon R, Rasheed BA, Keir S, Nikolskaya T, Nikolsky Y, Busam DA, Tekleab H, Diaz LA, Hartigan J, Smith DR, Strausberg RL, Marie SKN, Shinjo SMO, Yan H, Riggins GJ, Bigner DD, Karchin R, Papadopoulos N, Parmigiani G, Vogelstein B, Velculescu VE, Kinzler KW. An integrated genomic analysis of human glioblastoma multiforme. *Science* 321; 1807–1812 Sep 2008. PMC2820389.

[115] Barber TD, McManus K, Yuen KWY, Reis M, Parmigiani G, Shen D, Barrett I, Nouhi Y, Spencer F, Markowitz S, Velculescu VE, Kinzler KW, Vogelstein B, Lengauer C, Hieter P. Chromatid cohesion defects may underlie chromosome instability in human colorectal cancers. *Proc Natl Acad Sci U S A* 105; 3443–3448 Mar 2008. PMC2265152.

[116] Schaeffer EM, Marchionni L, Huang Z, Simons B, Blackman A, Yu W, Parmigiani G, Berman DM. Androgen-induced programs for prostate epithelial growth and invasion arise in embryogenesis and are reactivated in cancer. *Oncogene* 27; 7180–7191 Dec 2008. PMC2676849.

[117] Dominici F, Wang C, Crainiceanu C, Parmigiani G. Model selection and health effect estimation in environmental epidemiology. *Epidemiology* 19; 558–560 Jul 2008.

[118] Venturini S, Dominici F, Parmigiani G. Gamma shape mixtures for heavy-tailed distributions. *Ann Appl Stat* 2; 756–776 2008.

[119] Parmigiani G, Chen S. Trab: testing whether mutation frequencies are above an unknown background. *Stat Appl Genet Mol Biol* 7; Article11 2008.

[120] Tai YC, Chen S, Parmigiani G, Klein AP. Incorporating tumor immunohistochemical markers in BRCA1 and BRCA2 carrier prediction. *Breast Cancer Res* 10; 401 2008. PMC2397515.

[121] Crainiceanu C, Dominici F, Parmigiani G. Adjustment uncertainty in effect estimation. *Biometrika* 95; 635–651 2008.

[122] Katki HA, Blackford A, Chen S, Parmigiani G. Multiple diseases in carrier probability estimation: accounting for surviving all cancers other than breast and ovary in BRCAPRO. *Stat Med* 27; 4532–4548 Sep 2008. PMC2562929.

[123] Pattaro C, Ruczinski I, Fallin DM, Parmigiani G. Haplotype block partitioning as a tool for dimensionality reduction in snp association studies. *BMC Genomics* 9; 405 2008. PMC2547855.

[124] Yang Z, Stratton C, Francis PJ, Kleinman ME, Tan PL, Gibbs D, Tong Z, Chen H, Constantine R, Yang X, Chen Y, Zeng J, Davey L, Ma X, Hau VS, Wang C, Harmon J, Buehler J, Pearson E, Patel S, Kaminoh Y, Watkins S, Luo L, Zabriskie NA, Bernstein PS, Cho W, Schwager A, Hinton DR, Klein ML, Hamon SC, Simmons E, Yu B, Campochiaro B, Sunness JS, Campochiaro P, Jorde L, Parmigiani G, Zack DJ, Katsanis N, Ambati J, Zhang K. Toll-like receptor 3 and geographic atrophy in age-related macular degeneration. *N Engl J Med* 359; 1456–1463 Oct 2008. PMC2573951.

[125] Leary RJ, Lin JC, Cummins J, Boca S, Wood LD, Parsons DW, Jones S, Sjöblom T, Park BH, Parsons R, Willis J, Dawson D, Willson JKV, Nikolskaya T, Nikolsky Y, Kopelovich L, Papadopoulos N, Pennacchio LA, Wang TL, Markowitz SD, Parmigiani G, Kinzler KW, Vogelstein B, Velculescu VE. Integrated analysis of homozygous deletions, focal amplifications, and sequence alterations in breast and colorectal cancers. *Proceedings of the National Academy of Science USA* 105; 16224–16229 Oct 2008. PMC2571022.

[126] Iversen Jr ES, Parmigiani G, Chen S. Multiple model evaluation absent the gold standard: BRCA1/2 mutation carrier probability models. *Journal of the American Statistical Association* 103(483); 897–909. 2008.

[127] Kortenhorst MSQ, Zahurak M, Shabbeer S, Kachhap S, Galloway N, Parmigiani G, Verheul HMW, Carducci MA. A multiple-loop, double-cube microarray design applied to prostate cancer cell lines with variable sensitivity to histone deacetylase inhibitors. *Clin Cancer Res* 14; 6886–6894 Nov 2008. PMC2603330.

[128] Braun R, Cope L, Parmigiani G. Identifying differential correlation in gene/pathway combinations. *BMC Bioinformatics* 9; 488 Nov 2008. PMC2613418.

[129] Parmigiani G, Boca S, Lin J, Kinzler KW, Velculescu V, Vogelstein B. Design and analysis issues in genome-wide somatic mutation studies of cancer. *Genomics* 93; 17–21 Jan 2009. PMC2820387.

[130] Jones S, Hruban RH, Kamiyama M, Borges M, Zhang X, Parsons DW, Lin JCH, Palmisano E, Brune K, Jaffee EM, Iacobuzio-Donahue CA, Maitra A, Parmigiani G, Kern SE, Velculescu VE, Kinzler KW, Vogelstein B, Eshleman JR, Goggins M, Klein AP. Exomic sequencing identifies palb2 as a pancreatic cancer susceptibility gene. *Science* 324(5924); 217 Mar 2009. PMC2684332.

[131] Blackford A, Parmigiani G, Kensler TW, Wolfgang C, Jones S, Zhang X, Parsons DW, Lin JCH, Leary RJ, Eshleman JR, Goggins M, Jaffee EM, Iacobuzio-Donahue CA, Maitra A, Klein A, Cameron JL, Olino K, Schulick R, Winter J, Vogelstein B, Velculescu VE, Kinzler KW, Hruban RH. Genetic mutations associated with cigarette smoking in pancreatic cancer. *Cancer Res* 69; 3681–3688 Apr 2009. PMC2669837.

[132] Chen S, Blackford AL, Parmigiani G. Tailoring BRCAPRO to Asian-Americans. *J Clin Oncol* 27; 642–3; author reply 643–4 Feb 2009.

[133] Lin X, Asfari B, Marchionni L, Cope L, Parmigiani G, Naiman D, Geman D. The ordering of expression among a few genes can provide simple cancer biomarkers and signal brca1 mutations. *BMC Bioinformatics* 10; 256 2009. PMC2745389.

[134] Zhou XK, Clyde MA, Garrett J, Lourdes V, O'Connell M, Parmigiani G, Turner DJ, Wiles T. Statistical methods for automated drug susceptibility testing: Bayesian minimum inhibitory concentration prediction from growth curves. *Annals of Applied Statistics* 2009,; Vol.3,No.2,710–730 Aug 2009.

[135] Favorova OO, Favorov AV, Boiko AN, Sudomoina MA, Andreevskii TV, Alekseenkov AD, Kulakova OG, Gusev EI, Parmigiani G, Ochs MF. Genetic predisposition to multiple sclerosis as a polygenic autoimmune disease. *Zh Nevrol Psikhiatr Im S S Korsakova* 109; 16–22 2009.

[136] Daniel VC, Marchionni L, Hierman JS, Rhodes JT, Devereux WL, Rudin CM, Yung R, Parmigiani G, Dorsch M, Peacock CD, Watkins DN. A primary xenograft model of small-cell lung cancer reveals irreversible changes in gene expression imposed by culture in vitro. *Cancer Res* 69; 3364–3373 Apr 2009.

[137] He X, Marchionni L, Hansel DE, Yu W, Sood A, Yang J, Parmigiani G, Matsui W, Berman DM. Differentiation of a highly tumorigenic basal cell compartment in urothelial carcinoma. *Stem Cells* 27; 1487–1495 Jul 2009.

[138] Blackford A, Serrano OK, Wolfgang CL, Parmigiani G, Jones S, Zhang X, Parsons DW, Lin JCH, Leary RJ, Eshleman JR, Goggins M, Jaffee EM, Iacobuzio-Donahue CA, Maitra A, Cameron JL, Olino K, Schulick R, Winter J, Herman JM, Laheru D, Klein AP, Vogelstein B, Kinzler KW, Velculescu VE, Hruban RH. SMAD4 gene mutations are associated with poor prognosis in pancreatic cancer. *Clin Cancer Res* 15; 4674–4679 Jul 2009. PMCID: PMC2819274.

[139] Caffo BS, Liu D, Scharpf RB, Parmigiani G. Likelihood estimation of conjugacy relationships in linear models with applications to high-throughput genomics. *Int J Biostat* 5; Article 18 2009. PMC2827886.

[140] Guda K, Moinova H, He J, Jamison O, Ravi L, Natale L, Lutterbaugh J, Lawrence E, Lewis S, Willson JKV, Lowe JB, Wiesner GL, Parmigiani G, Barnholtz-Sloan J, Dawson DW, Velculescu VE, Kinzler KW, Papadopoulos N, Vogelstein B, Willis J, Gerken TA, Markowitz SD. Inactivating germ-line and somatic mutations in polypeptide n-acetylgalactosaminyltransferase 12 in human colon cancers. *Proc Natl Acad Sci U S A* 106(31); 12921–25 Jul 2009. PMC2722285.

[141] Scharpf RB, Tjelmeland H, Parmigiani G, Nobel A. A Bayesian model for cross-study differential gene expression rejoinder. *jasa* 104 (488); 1318–1323 2009. PMCID: PMC2994029.

[142] Wang W, Niendorf KB, Patel D, Blackford A, Marroni F, Sober AJ, Parmigiani G, Tsao H. Estimating CDKN2A carrier probability and personalizing cancer risk assessments in hereditary melanoma using MelaPRO. *Cancer Res* 70; 552–559 Jan 2010. PMC2947347.

[143] Scharpf RB, Iacobuzio-Donahue CA, Cope L, Ruczinski I, Garrett-Mayer E, Lakkur S, Campagna D, Parmigiani G. Cross-platform comparison of two pancreatic cancer phenotypes. *Cancer Inform* 9; 257–264 2010. PMC2978933.

[144] Fertig EJ, Ding J, Favorov AV, Parmigiani G, Ochs MF. CoGAPS: an R/C++ package to identify patterns and biological process activity in transcriptomic data. *Bioinformatics* 26; 2792–2793 Nov 2010. PMC3025742.

[145] Boca SM, Kinzler KW, Velculescu VE, Vogelstein B, Parmigiani G. Patient-oriented gene set analysis for cancer mutation data. *Genome Biol* 11; R112 2010. PMC3156951.

[146] Parsons DW, Li M, Zhang X, Jones S, Leary RJ, Lin JCH, Boca SM, Carter H, Samayoa J, Bettegowda C, Gallia GL, Jallo GI, Binder ZA, Nikolsky Y, Hartigan J, Smith DR, Gerhard DS, Fults DW, VandenBerg S, Berger MS, Marie SKN, Shinjo SMO, Clara C, Phillips PC, Minturn JE, Biegel JA, Judkins AR, Resnick AC, Storm PB, Curran T, He Y, Rasheed BA, Friedman HS, Keir ST, McLendon R, Northcott PA, Taylor MD, Burger PC, Riggins GJ, Karchin R, Parmigiani G, Bigner DD, Yan H, Papadopoulos N, Vogelstein B, Kinzler KW, Velculescu VE. The genetic landscape of the childhood cancer medulloblastoma. *Science* 331; 435–439 Jan 2011. PMC3110744.

[147] Ho YY, Parmigiani G, Louis TA, Cope LM. Modeling liquid association. *Biometrics* 67; 133–141 Mar 2011.

[148] Trippa L, Parmigiani G. False discovery rates in somatic mutation studies of cancer. *The Annals of Applied Statistics* 5(2B); 1360–1378 2011.

[149] Favorov A, Lvovs D, Speier W, Parmigiani G, Ochs MF. Oniontree XML: A format to exchange gene-related probabilities. *Journal of Biomolecular Structure Dynamics* 29; 417–23 2011.

[150] Tyekucheva S, Marchionni L, Karchin R, Parmigiani G. Integrating diverse genomic data using gene sets. *Genome Biology* 12(10); R105 2011. PMC3333775.

[151] Joshu CE, Parmigiani G, Colditz GA, Platz EA. Opportunities for the primary prevention of colorectal cancer in the united states. *Cancer Prev Res Phila* 5; 138–145 Jan 2012. PMC3252472.

[152] Wang C, Parmigiani G, Dominici F. Bayesian effect estimation accounting for adjustment uncertainty. *Biometrics* 68; 661–71 Feb 2012.

[153] Biswas S, Tankhiwale N, Blackford A, Barrera AMG, Ready K, Lu K, Amos CI, Parmigiani G, Arun B. Assessing the added value of breast tumor markers in genetic risk prediction model brcapro. *Breast Cancer Res Treat* 133; 347–355 Jan 2012.

[154] Roberts N, Vogelstein J, Parmigiani G, Kinzler KW, Vogelstein B, Velculescu VE. The predictive capacity of personal genome sequencing. *Nature Translational Medicine* 4(133); 133ra58 2012. PMCID: PMC3741669.

[155] Waldron L, Simpson PT, Parmigiani G, Huttenhower C. Report on emerging technologies for translational bioinformatics: a symposium on gene expression profiling for archival tissues. *BMC Cancer* 12; 124 2012. PMC3342119.

[156] Trippa L, Lee EQ, Wen PY, Batchelor TT, Cloughesy T, Parmigiani G, Alexander BM. Bayesian adaptive randomized trial design for patients with recurrent glioblastoma. *J Clin Oncol* 30; 3258–63 May 2012. PMC3434985.

[157] Wang XV, Blades N, Ding J, Sultana R, Parmigiani. G. Estimation of sequencing error rates in short reads. *BMC Bioinformatics* 13(1); 185 Jul 2012 2012. PMC3495688.

[158] Waldron L, Ogino S, Hoshida Y, Shima K, Reed A, Simpson P, Baba Y, Nosho K, Segata N, Vargas AC, Cummings M, Lakhani S, Kirkner G, Giovannucci E, Quackenbush J, Golub T, Fuchs C, Parmigiani G, Huttenhower C. Expression profiling of archival tumors for long-term health studies. *Clin Cancer Res* 18; 6136–46 2012. PMC3500412.

[159] Coopey SB, Mazzola E, Buckley JM, Sharko J, Belli AK, Kim EMH, Polubriaginof F, Parmigiani G, Garber JE, Smith BL, Gadd MA, Specht MC, Guidi AJ, Roche CA, Hughes KS. The role of chemoprevention in modifying the risk of breast cancer in women with atypical breast lesions. *Breast Cancer Res Treat* 136; 627–33 Nov 2012.

[160] Sausen M, Leary RJ, Jones S, Wu J, Reynolds CP, Liu X, Blackford A, Parmigiani G, Luis A. Diaz J, Papadopoulos N, Vogelstein B, Kinzler KW, Velculescu VE, Hogarty MD. Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. *Nature Genetics* 45; 12–7 2012. PMCID: PMC3557959.

[161] Leary RJ, Sausen M, Kinde I, Papadopoulos N, Carpten JD, Craig D, O'Shaughnessy J, Kinzler KW, Parmigiani G, Vogelstein B, Diaz LA, Velculescu VE. Detection of chromosomal alterations in the circulation of cancer patients with whole-genome sequencing. *Sci Transl Med* 4; 162ra154 Nov 2012. PMC3641759.

[162] Telesca D, Muller P, Parmigiani G, Freedman RS. Modeling dependent gene expression. *The Annals of Applied Statistics* 6; 542–60 2012.

[163] Ding J, Trippa L, Zhong X, Parmigiani G. Hierarchical Bayesian analysis of somatic mutation data in cancer. *Annals of Applied Statistics* 7(2); 883–903 2013.

[164] Mazzola E, Cheng SC, Parmigiani G. The penetrance of ductal carcinoma in situ among BRCA1 and BRCA2 mutation carriers. *Breast Cancer Res Treat* 137; 315–318 Jan 2013. PMCID: PMC3836600.

[165] Thompson JR, Gögele M, Weichenberger CX, Modenese M, Attia J, Barrett JH, Boehnke M, Grandi AD, Domingues FS, Hicks AA, Marroni F, Pattaro C, Ruggeri F, Borsani G, Casari G, Parmigiani G, Pastore A, Pfeufer A, Schwienbacher C, Taliun D, Consortium C, Fox CS, Pramstaller PP, Minelli C. SNP prioritization using a bayesian probability of association. *Genet Epidemiol* 37; 214–221 Feb 2013. PMCID: PMC3725584.

[166] Minelli C, Grandi AD, Weichenberger CX, Gögele M, Modenese M, Attia J, Barrett JH, Boehnke M, Borsani G, Casari G, Fox CS, Freina T, Hicks AA, Marroni F, Parmigiani G, Pastore A, Pattaro C, Pfeufer A, Ruggeri F, Schwienbacher C, Taliun D, Pramstaller PP, Domingues FS, Thompson JR. Importance of different types of prior knowledge in selecting genome-wide findings for follow-up. *Genet Epidemiol* 37; 205–213 Feb 2013. PMCID: PMC3725558.

[167] Tomasetti C, Vogelstein B, Parmigiani G. Half or more of the somatic mutations in cancers of self-renewing tissues originate prior to tumor initiation. *Proc Natl Acad Sci U S A* 110(6); 1999–2004 Jan 2013. PMCID: PMC3568331.

[168] Ganzfried BF, Riester M, Haibe-Kains B, Risch T, Tyekucheva S, Jazic I, Wang XV, Ahmadifar M, Birrer MJ, Parmigiani G, Huttenhower C, Waldron L. curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. *Database Oxford* 2013; bat013 2013. PMCID: PMC3625954.

[169] Biswas S, Atienza P, Chipman J, Hughes K, Barrera AMG, Amos CI, Arun B, Parmigiani G. Simplifying clinical use of the genetic risk prediction model BRCAPRO. *Breast Cancer Res Treat* 139; 571–579 Jun 2013. PMCID: PMC3699331.

[170] Chipman J, Drohan B, Blackford A, Parmigiani G, Hughes K, Bosinoff P. Providing access to risk prediction tools via the HL7 XML-formatted risk web service. *Breast Cancer Res Treat* 140; 187–193 Jun 2013. PMCID: PMC3760685.

[171] Gorfine M, Hsu L, Zucker DM, Parmigiani G. Calibrated predictions for multivariate competing risks models. *Lifetime Data Anal* 20(2); 234–51 May 2013. PMCID: PMC3884047.

[172] Ahn J, Yuan Y, Parmigiani G, Suraokar MB, Diao L, Wistuba II, Wang W. DeMix: deconvolution for mixed cancer transcriptomes using raw measured data. *Bioinformatics* Jun 2013. PMCID: PMC3841439.

[173] Boca SM, Bravo HC, Caffo B, Leek JT, Parmigiani G. A decision-theory approach to interpretable set analysis for high-dimensional data. *Biometrics* 69(3); 614–623 Aug 2013. PMCID: PMC3927844.

[174] Gartner JJ, Parker SCJ, Prickett TD, Dutton-Regester K, Stitzel ML, Lin JC, Davis S, Simhadri VL, Jha S, Katagiri N, Gotea V, Teer JK, Wei X, Morken MA, Bhanot UK, Program NISCCS, Chen G, Elnitski LL, Davies MA, Gershenwald JE, Carter H, Karchin R, Robinson W, Robinson S, Rosenberg SA, Collins FS, Parmigiani G, Komar AA, Kimchi-Sarfaty C, Hayward NK, Margulies EH, Samuels Y. Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. *Proc Natl Acad Sci U S A* 110; 13481–13486 Aug 2013. PMCID: PMC3746936.

[175] Alexander BM, Wen PY, Trippa L, Reardon DA, Yung WKA, Parmigiani G, Berry DA. Biomarker-based adaptive trials for patients with glioblastoma–lessons from I-SPY 2. *Neuro Oncol* 15(8); 972–978 Aug 2013. PMCID: PMC3714161.

[176] Tomasetti C, Demetri GD, Parmigiani G. Why tyrosine kinase inhibitor resistance is common in advanced gastrointestinal stromal tumors. *F1000 Research* 2; 152 2013. PMCID: PMC3892920.

[177] Biswas S, Arun B, Parmigiani G. Reclassification of predictions for uncovering subgroup specific improvement. *Stat Med* 33(11); 1914–27 Dec 2014. PMCID: PMC4008681.

[178] Gorfine M, Hsu L, Parmigiani G. Frailty models for familial risk with application to breast cancer. *J Am Stat Assoc* 108; 1205–1215 Dec 2013. PMCID:PMC3963469.

[179] Cope L, Naiman DQ, Parmigiani G. Integrative correlation: properties and relation to canonical correlations. *Journal of Multivariate Analysis* 123; 270–280 2014.

[180] Bolli N, Avet-Loiseau H, Wedge DC, Loo PV, Alexandrov LB, Martincorena I, Dawson KJ, Iorio F, Nik-Zainal S, Bignell GR, Hinton JW, Li Y, Tubio JMC, McLaren S, Meara SO, Butler AP, Teague JW, Mudie L, Anderson E, Rashid N, Tai YT, Shammas MA, Sperling AS, Fulciniti M, Richardson PG, Parmigiani G, Magrangeas F, Minvielle S, Moreau P, Attal M, Facon T, Futreal PA, Anderson KC, Campbell PJ, Munshi NC. Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. *Nat Commun* 5; 2997 Jan 2014. PMCID: PMC3905727.

[181] Ho YY, Cope LM, Parmigiani G. Modular network construction using eQTL data: an analysis of computational costs and benefits. *Frontiers in Genetics Bioinformatics and Computational Biology* 5; 40 2014. PMCID: PMC3935177.

[182] Waldron L, Haibe-Kains B, Culhane AC, Riester M, Ding J, Wang XV, Ahmadifar M, Tyekucheva S, Bernau C, Risch T, Ganzfried BF, Huttenhower C, Birrer M, Parmigiani G. Comparative meta-analysis of prognostic gene signatures for late-stage ovarian cancer. *J Natl Cancer Inst* 106; dju049 Apr 2014.

[183] Riester M, Wei W, Waldron L, Culhane AC, Trippa L, Oliva E, Kim SH, Michor F, Huttenhower C, Parmigiani G, Birrer MJ. Risk prediction for late-stage ovarian cancer by meta-analysis of 1525 patient samples. *J Natl Cancer Inst* Apr 2014.

[184] Hammerling D, Cefalu M, Cisewski J, Dominici F, Parmigiani G, Paulson C, Smith RL. Completing the results of the 2013 Boston Marathon. *PLoS One* 9; e93800 2014. PMCID: PMC3984103.

[185] Bernau C, Riester M, Boulesteix AL, Parmigiani G, Huttenhower C, Waldron L, Trippa L. Cross-study validation for the assessment of prediction algorithms. *Bioinformatics* 30; i105–i112 Jun 2014. PMCID: PMC4058929.

[186] Mazzola E, Chipman J, Cheng SC, Parmigiani G. Recent BRCAPRO upgrades significantly improve calibration. *Cancer Epidemiol Biomarkers Prev* Jun 2014. PMCID:PMC4119541.

[187] Zhao SD, Parmigiani G, Huttenhower C, Waldron L. Más-o-menos: a simple sign averaging method for discrimination in genomic data analysis. *Bioinformatics* 30(21); 3062–9 Jul 2014. PMCID: PMC4201155.

[188] Braun D, Gorfine M, Parmigiani G. Misreported family histories and underestimation of risk. *J Clin Oncol* 32(32); 3682–3 Sep 2014.

[189] Ahern C, Shih YC, Dong W, Parmigiani G, Shen Y. Cost-effectiveness of alternative strategies for integrating mri into breast cancer screening for women at high risk. *British Journal of Cancer* 111(8); 1542–51 2014. PMCID: PMC4200098.

[190] Liu D, Parmigiani G, Caffo B. Screening for differentially expressed genes: Are multilevel models helpful? *Journal of Biometrics Biostatistics* 5(2); 192 2014.

[191] Rashid NU, Sperling AS, Bolli N, Wedge DC, Loo PV, Tai YT, Shammas MA, Fulciniti M, Samur MK, Richardson PG, Magrangeas F, Minvielle S, Futreal PA, Anderson KC, Avet-Loiseau H, Campbell PJ, Parmigiani G, Munshi NC. Differential and limited expression of mutant alleles in multiple myeloma. *Blood* 124(20); 3110–7 Sep 2014. PMCID: PMC4231420.

[192] Parmigiani G, Boca S, Ding J, Trippa L. Statistical tools and R software for cancer driver probabilities. *Methods in molecular biology* 1101; 113–134 2014.

[193] Biswas S, Arun B, Parmigiani G. Reclassification of predictions for uncovering subgroup specific improvement. *Statistics in medicine* 33; 1914–1927 2014.

[194] Trippa L, Wen PY, Parmigiani G, Berry DA, Alexander BM. Combining progression-free survival and overall survival as a novel composite endpoint for glioblastoma trials. *Neuro Oncology* 17; 1106–1113 Aug 2015.

[195] Tomasetti C, Marchionni L, Nowak MA, Parmigiani G, Vogelstein B. Only three driver gene mutations are required for the development of lung and colorectal cancers. *Proc Natl Acad Sci U S A* 112; 118–123 Jan 2015. PMCID: PMC4291633.

[196] Wang C, Dominici F, Parmigiani G, Zigler CM. Accounting for uncertainty in confounder and effect modifier selection when estimating average causal effects in generalized linear models. *Biometrics* 71; 654–665 Apr 2015.

[197] Hatchi E, Skourti-Stathaki K, Ventz S, Pinello L, Yen A, Kamieniarz-Gdula K, Dimitrov S, Pathania S, McKinney KM, Eaton ML, Kellis M, Hill SJ, Parmigiani G, Proudfoot NJ, Livingston DM. BRCA1 recruitment to transcriptional pause sites is required for R-loop-driven DNA damage repair. *Mol Cell* 57; 636–647 Feb 2015.

[198] Trippa L, Waldron L, Huttenhower C, Parmigiani. G. Bayesian nonparametric cross-study validation of prediction methods. *Ann Appl Stat* 9; 402–428 2015.

[199] Mazzola E, Blackford A, Parmigiani G, Biswas S. Recent enhancements to the genetic risk prediction model BRCAPRO. *Cancer Inform* 14; 147–157 2015. PMCID: PMC4428390.

[200] Tyekucheva S, Martin NE, Stack EC, Wei W, Vathipadiekal V, Waldron L, Fiorentino M, Lis RT, Stampfer MJ, Loda M, Parmigiani G, Mucci LA, Birrer M. Comparing platforms for messenger RNA expression profiling of archival formalin-fixed, paraffin-embedded tissues. *J Mol Diagn* 17; 374–381 Jul 2015.

[201] Venturini S, Dominici F, Parmigiani G. Generalized quantile treatment effect: A flexible bayesian approach using quantile ratio smoothing. *Bayesian Analysis* 10; 523–552 2015.

[202] Gerke TA, Martin NE, Ding Z, Nuttall EJ, Stack EC, Giovannucci E, Lis RT, Stampfer MJ, Kantoff PW, Parmigiani G, Loda M, Mucci LA. Evaluating a 4-marker signature of aggressive prostate cancer using time-dependent auc. *The Prostate* 75(16); 1926–33 2015. Doi: 10.1002/pros.23090.

[203] Zhang Y, Trippa L, Parmigiani G. Optimal bayesian adaptive trials when treatment efficacy depends on biomarkers. *Biometrics* 72; 414–421 Nov 2015.

[204] Biswas S, Atienza P, Chipman J, Blackford AL, Arun B, Hughes K, Parmigiani G. A two-stage approach to genetic risk assessment in primary care. *Breast Cancer Res Treat* 155; 375–383 Jan 2016.

[205] Mucci LA, Hjelmborg JB, Harris JR, Czene K, Havelick DJ, Scheike T, Graff RE, Holst K, Müller S, Unger RH, McIntosh C, Nuttall E, Brandt I, Penney KL, Hartman M, Kraft P, Parmigiani G, Christensen K, Koskenvuo M, Holm NV, Heikkil K, Pukkala E, Skytthe A, Adami HO, Kaprio J, of Cancer (NorTwinCan) Collaboration NTS. Familial risk and heritability of cancer among twins in nordic countries. *JAMA* 315; 68–76 Jan 2016.

[206] Marabelli M, Cheng SC, Parmigiani G. Penetrance of ATM gene mutations in breast cancer: A meta-analysis of different measures of risk. *Genet Epidemiol* Apr 2016.

[207] Waldron L, Riester M, Ramos M, Parmigiani G, Birrer M. The doppelgänger effect: Hidden duplicates in databases of transcriptome profiles. *J Natl Cancer Inst* 108 Nov 2016.

[208] Harrington D, Parmigiani G. I-SPY 2–a glimpse of the future of phase 2 drug development? *N Engl J Med* 375; 7–9 Jul 2016.

[209] Cefalu M, Dominici F, Arvold N, Parmigiani G. Model averaged double robust estimation. *Biometrics* 73; 410–421 2017.

[210] Ventz S, Barry WT, Parmigiani G, Trippa L. Bayesian response-adaptive designs for basket trials. *Biometrics* 73; 905–915 Sep 2017.

[211] Edefonti V, Parmigiani G. Combinatorial mixtures of multiparameter distributions: an application to bivariate data. *The International Journal of Biostatistics* 13 Feb 2017.

[212] Tanguturi SK, Trippa L, Ramkissoon SH, Pelton K, Knoff D, Sandak D, Lindeman NI, Ligon AH, Beroukhim R, Parmigiani G, Wen PY, Ligon KL, Alexander BM. Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. *Neuro Oncol* 19(7); 908–917 2017.

[213] Ventz S, Parmigiani G, Trippa L. Combining bayesian experimental designs and frequentist data analyses: motivations and examples. *Applied Stochastic Models in Business and Industry* 33; 302–313 Mar 2017.

[214] Braun D, Gorfine M, Parmigiani G, Arvold ND, Dominici F, Zigler C. Propensity scores with misclassified treatment assignment: a likelihood-based adjustment. *Biostatistics* 18; 695–710 Oct 2017.

[215] Ventz S, Alexander BM, Giovanni Parmigiani RDG, Trippa. L. Designing clinical trials that accept new arms: An example in metastatic breast cancer. *Journal of Clinical Oncology* 35; 3160–3168 Sep 2017.

[216] Mazzola E, Coopey SB, Griffin M, Polubriaginof F, Buckley JM, Parmigiani G, Garber JE, Smith BL, Gadd MA, Specht MC, Guidi A, Hughes KS. Reassessing risk models for atypical hyperplasia: age may not matter. *Breast Cancer Research and Treatment* 165(2); 285–291 2017.

[217] Ventz S, Cellamare M, Parmigiani G, Trippa L. Adding experimental arms to platform clinical trials: Randomization procedures and interim analyses. *Biostatistics* 19; 199–215 Apr 2018.

[218] Tyekucheva S, Bowden M, Bango C, Giunchi F, Huang Y, Zhou C, Bondi A, Lis R, Hemelrijck MV, Andren O, Andersson SO, Watson RW, Pennington S, Finn S, Martin N, Stampfer M, Parmigiani G, Penney K, Fiorentino M, Mucci L, Loda M. Stromal and epithelial transcriptional map of initiation progression and metastatic potential of human prostate cancer. *Nature Communications* 8(1); 420 2017.

[219] Tomasetti C, Durrett R, Kimmel M, Lambert A, Parmigiani G, Zauber A, Vogelstein B. Role of stem-cell divisions in cancer risk. *Nature* 548; E13–E14 Aug 2017.

[220] Cleynen A, Szalat R, Kemal Samur M, Robiou du Pont S, Buisson L, Boyle E, Chretien ML, Anderson K, Minvielle S, Moreau P, Attal M, Parmigiani G, Corre J, Munshi N, Avet-Loiseau H. Expressed fusion gene landscape and its impact in multiple myeloma. *Nature Communications* 8; 1893 Dec 2017. PMCID: PMC5711960.

[221] Braun D, Gorfine M, Katki HA, Ziogas A, Parmigiani G. Nonparametric adjustment for measurement error in time to event data: Application to risk prediction models. *Journal of the American Statistical Association* 113; 14–25 2018.

[222] Braun D, Yang J, Griffin M, Parmigiani G, Hughes KS. A Clinical Decision Support Tool to Predict Cancer Risk for Commonly Tested Cancer-Related Germline Mutations. *Journal of Genetic Counseling* 371; 1–13 Mar 2018.

[223] Patil P, Parmigiani G. Training replicable predictors in multiple studies. *Proceedings of the National Academy of Science USA* 115; 2578–2583 Mar 2018.

[224] Wang XV, Parmigiani G. Integrative factor analysis — An unsupervised method for quantifying cross-study consistency of gene expression data. *Genomics* 110; 80–88 Mar 2018.

[225] Vanderbeek AM, Rahman R, Fell G, Ventz S, Chen T, Redd R, Parmigiani G, Cloughesy TF, Wen PY, Trippa L, Alexander BM. The clinical trials landscape for glioblastoma: is it adequate to develop new treatments? *Neuro Oncology* noy027 2018.

[226] Samur MK, Minvielle S, Gulla A, Fulciniti M, Cleynen A, Samur AA, Szalat R, Shammas M, Magrangeas F, Tai YT, Auclair D, Keats J, Richardson P, Attal M, Moreau P, Anderson KC, Parmigiani G, Avet-Loiseau H, Munshi NC. Long intergenic non-coding RNAs have an independent impact on survival in multiple myeloma. *Leukemia* 15; 423 Mar 2018.

[227] Rebbeck TR, Burns-White K, Chan AT, Emmons K, Freedman M, Hunter DJ, Kraft P, Laden F, Mucci L, Parmigiani G, Schrag D, Syngal S, Tamimi RM, Viswanath K, Yurgelun MB, Garber JE. Precision Prevention and Early Detection of Cancer: Fundamental Principles. *Cancer Discovery* Jun 2018.

[228] Madsen T, Braun D, Peng G, Parmigiani G, Trippa L. Efficient computation of the joint probability of multiple inherited risk alleles from pedigree data. *Genetic Epidemiology* 371; 497 Jun 2018.

[229] Barber LE, Gerke T, Markt SC, Peisch SF, Wilson KM, Ahearn TU, Giovannucci EL, Parmigiani G, Mucci LA. Family history of breast or prostate cancer and prostate cancer risk. *Clinical Cancer Research* clincanres.0370.2018 Aug 2018.

[230] Chen GM, Kannan L, Geistlinger L, Kofia V, Safikhani Z, Gendoo DMA, Parmigiani G, Birrer MJ, Haibe-Kains B, Waldron L. Consensus on Molecular Subtypes of High-grade Serous Ovarian Carcinoma. *Clinical Cancer Research* clincanres.0784.2018 Jul 2018.

[231] Zhang Y, Bernau C, Parmigiani G, Waldron L. The impact of different sources of heterogeneity on loss of accuracy from genomic prediction models. *Biostatistics* kxy044 2018.

[232] Ma S, Ogino S, Parsana P, Nishihara R, Qian Z, Shen J, Mima K, Masugi Y, Cao Y, Nowak JA, Shima K, Hoshida Y, Giovannucci EL, Gala MK, Chan AT, Fuchs CS, Parmigiani G, Huttenhower C, Waldron L. Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. *Genome Biology* 19; 13 Sep 2018.

[233] Pernar CH, Ebot EM, Pettersson A, Graff RE, Giunchi F, Ahearn TU, Gonzalez-Feliciano AG, Markt SC, Wilson KM, Stopsack KH, Gazeeva E, Lis RT, Parmigiani G, Rimm EB, Finn SP, Giovannucci EL, Fiorentino M, Mucci LA. A Prospective Study of the Association between Physical Activity and Risk of Prostate Cancer Defined by Clinical Features and TMPRSS2:ERG. *European urology* Oct 2018.

[234] De Vito R, Bellio R, Trippa L, Parmigiani G. Multi-study Factor Analysis. *Biometrics* 75; 337–346 Oct 2018.

[235] Wang Z, Cao S, Morris JS, Ahn J, Liu R, Tyekucheva S, Gao F, Li B, Lu W, Tang X, Wistuba II, Bowden M, Mucci L, Loda M, Parmigiani G, Holmes CC, Wang W. Transcriptome deconvolution of heterogeneous tumor samples with immune infiltration. *iScience* 9; 451 – 460 2018.

[236] Antonelli J, Parmigiani G, Dominici F. High-dimensional confounding adjustment using continuous spike and slab priors. *Bayesian Anal* 2018. Advance publication.

[237] De Vito R, Lee YCA, Parpinel M, Serraino D, Olshan AF, Zevallos JP, Levi F, Zhang ZF, Morgenstern H, Garavello W, Kelsey K, McClean M, Schantz S, Yu GP, Boffetta P, Chuang SC, Hashibe M, La Vecchia C, Parmigiani G, Edefonti V. Shared and Study-specific Dietary Patterns and Head and Neck Cancer Risk in an International Consortium. *Epidemiology Cambridge Mass* 30; 93–102 Jan 2019.

[238] Aktas Samur A, Minvielle S, Shammas M, Fulciniti M, Magrangeas F, Richardson PG, Moreau P, Attal M, Anderson KC, Parmigiani G, Avet-Loiseau H, Munshi NC, Samur MK. Deciphering the chronology of copy number alterations in Multiple Myeloma. *Blood Cancer Journal* 9; 39 2019.

[239] Zhang Y, Trippa L, Parmigiani G. Frequentist operating characteristics of Bayesian optimal designs via simulation. *Statistics in Medicine* 3; 4026–4039 Jun 2019.

[240] Hashim D, Gonzalez-Feliciano AG, Ahearn TU, Pettersson A, Barber L, Pernar CH, Ebot EM, Isikbay M, Finn SP, Giovannucci EL, Lis RT, Loda M, Parmigiani G, Lotan T, Kantoff PW, Mucci LA, Graff RE. Family history of prostate cancer and the incidence of erg- and phosphatase and tensin homolog-defined prostate cancer. *International Journal of Cancer* 146; 2694–2702 2019.

[241] Kim J, Braun D, Ukaegbu C, Dhingra TG, Kastrinos F, Parmigiani G, Syngal S, Yurgelun MB. Clinical Factors Associated With Gastric Cancer in Individuals with Lynch Syndrome. *Clinical Gastroenterology and Hepatology* Jul 2019.

[242] Angus DC, Alexander BM, Berry S, Buxton M, Lewis R, Paoloni M, Webb SAR, Arnold S, Barker A, Berry DA, Bonten MJM, Brophy M, Butler C, Cloughesy TF, Derde LPG, Esserman LJ, Ferguson R, Fiore L, Gaffey SC, Gaziano JM, Giusti K, Goossens H, Heritier S, Hyman B, Krams M, Larholt K, LaVange LM, Lavori P, Lo AW, London AJ, Manax V, McArthur C, O'Neill G, Parmigiani G, Perlmutter J, Petzold EA, Ritchie C, Rowan KM, Seymour CW, Shapiro NI, Simeone DM, Smith B, Spellberg B, Stern AD, Trippa L, Trusheim M, Viele K, Wen PY, Woodcock J, Coalition TAPT. Adaptive platform trials: definition, design, conduct and reporting considerations. *Nature Reviews Drug Discovery* 2019.

[243] Deng Z, Yin K, Bao Y, Armengol VD, Wang C, Tiwari A, Barzilay R, Parmigiani G, Braun D, Hughes KS. Validation of a Semiautomated Natural Language Processing–Based Procedure for Meta-Analysis of Cancer Susceptibility Gene Penetrance. *JCO Clinical Cancer Informatics* 1–9 Aug 2019.

[244] Bao Y, Deng Z, Wang Y, Kim H, Armengol VD, Acevedo F, Ouardaoui N, Wang C, Parmigiani G, Barzilay R, Braun D, Hughes KS. Using machine learning and natural language processing to review and classify the medical literature on cancer susceptibility genes. *JCO Clinical Cancer Informatics* 1–9 2019. PMID: 31545655.

[245] McCarthy AM, Guan Z, Welch M, Griffin ME, Sippo DA, Deng Z, Coopey SB, Acar A, Semine A, Parmigiani G, Braun D, Hughes KS. Performance of breast cancer risk assessment models in a large mammography cohort. *Journal of the National Cancer Institute* Sep 2019.

[246] Schwede M, Waldron L, Mok SC, Wei W, Basunia A, Merritt MA, Mitsiades CS, Parmigiani G, Harrington DP, Quackenbush J, Birrer MJ, Culhane AC. The impact of stroma admixture on molecular subtypes and prognostic gene signatures in serous ovarian cancer. *Cancer Epidemiology and Prevention Biomarkers* 2019.

[247] Ramchandran M, Patil P, Parmigiani G. Tree-weighting for multi-study ensemble learners. *Pacific Symposium on Biocomputing* 451–462 2020.

[248] Spring LM, Fell G, Arfe A, Sharma C, Greenup RA, Reynolds KL, Smith BL, Alexander BM, Moy B, Isakoff SJ, Parmigiani G, Trippa L, Bardia A. Pathological complete response after neoadjuvant chemotherapy and impact on breast cancer recurrence and survival: a comprehensive meta-analysis. *Clinical Cancer Research* 2020.

[249] Thomas EG, Trippa L, Parmigiani G, Dominici F. Estimating the effects of fine particulate matter on 432 cardiovascular diseases using multi-outcome regression with tree-structured shrinkage. *Journal of the American Statistical Association* 0; 1–29 2020.

[250] Yin K, Liu Y, Lamichhane B, Sandbach JF, Patel G, Compagnoni G, Kanak RH, Rosen B, Ondrula DP, Smith L, Brown E, Gold L, Whitworth P, App C, Euhus D, Semine A, Dwight Lyons S, Lazarte MAC, Parmigiani G, Braun D, Hughes KS. Legacy Genetic Testing Results for Cancer

Susceptibility: How Common are Conflicting Classifications in a Large Variant Dataset from Multiple Practices? *Annals of Surgical Oncology* 2020.

[251] Parmigiani G. Receiver operating characteristic curves with an indeterminacy zone. *Pattern Recognition Letters* 2020.

[252] Wang C, Wang Y, Hughes KS, Parmigiani G, Braun D. Penetrance of Colorectal Cancer Among Mismatch Repair Gene Mutation Carriers: A Meta-Analysis. *JNCI Cancer Spectrum* 04 2020. Pkaa027.

[253] Huang T, Braun D, Lynch HT, Parmigiani G. Variation in cancer risk among families with genetic susceptibility. *Genetic Epidemiology* 1—13 2020.

[254] Chen J, Bae E, Zhang L, Hughes K, Parmigiani G, Braun D, Rebbeck TR. Penetrance of Breast and Ovarian Cancer in Women Who Carry a BRCA1/2 Mutation and Do Not Use Risk-Reducing Salpingo-Oophorectomy: An Updated Meta-Analysis. *JNCI Cancer Spectrum* 4 Apr 2020.

[255] Stopsack KH, Huang Y, Tyekucheva S, Gerke TA, Bango C, Elfandy H, Bowden M, Penney KL, Roberts TM, Parmigiani G, Kantoff PW, Mucci LA, Loda M. Multiplex immunofluorescence in formalin-fixed paraffin-embedded tumor tissue to identify single-cell–level pi3k pathway activation. *Clinical Cancer Research* 2020.

[256] Zhang Y, Parmigiani G, Johnson WE. ComBat-seq: batch effect adjustment for RNA-seq count data. *NAR Genomics and Bioinformatics* 2 Sep 2020.

[257] Hujoel MLA, Parmigiani G, Braun D. Statistical approaches for meta-analysis of genetic mutation prevalence. *Genetic Epidemiology* n/a 2020.

[258] Samur MK, Aktas Samur A, Fulciniti M, Szalat R, Han T, Shammas M, Richardson P, Magrangeas F, Minvielle S, Corre J, Moreau P, Thakurta A, Anderson KC, Parmigiani G, Avet-Loiseau H, Munshi N. Genome-Wide Somatic Alterations in Multiple Myeloma Reveal a Superior Outcome Group. *Journal of Clinical Oncology* 38; JCO2000461 2020.

[259] Yang Y, Hong C, Liang JW, Gruber S, Parmigiani G, Idos G, Braun D. A likelihood-based approach to assessing frequency of pathogenicity among variants of unknown significance in susceptibility genes. *Statistics in Medicine* 40; 593–606 2020.

[260] Geistlinger L, Oh S, Ramos M, Schiffer L, LaRue RS, Henzler CM, Munro SA, Daughters C, Nelson AC, Winterhoff BJ, Chang Z, Talukdar S, Shetty M, Mullany SA, Morgan M, Parmigiani G, Birrer MJ, Qin LX, Riester M, Starr TK, Waldron L. Multiomic analysis of subtype evolution and heterogeneity in high-grade serous ovarian carcinoma. *Cancer Research* 80; 4335–4345 2020.

[261] Zhang Y, Patil P, Johnson WE, Parmigiani G. Robustifying Genomic Classifiers To Batch Effects Via Ensemble Learning. *Bioinformatics* 11 2020. Btaa986.

Book Chapters

[262] Parmigiani G, Polson NG. Bayesian design for random walk barriers. In: Bernardo JM, Berger JO, Dawid AP, Smith AFM, eds., *Bayesian Statistics 4. Proceedings of the Fourth Valencia International Meeting*, 715–721. Oxford: Oxford University Press 1992.

[263] Parmigiani G. Scheduling inspections in reliability. In: Basu AP, ed., *Advances in Reliability*, 303–319. Amsterdam: Elsevier/North-Holland 1993.

[264] Parmigiani G, Kamlet M. Cost-utility analysis of alternative strategies in screening for breast cancer. In: Gatsonis C, Hodges J, Kass RE, Singpurwalla N, eds., *Case Studies in Bayesian Statistics*, 390–402. New York: Springer 1993.

[265] Parmigiani G, Berry DA. Applications of Lindley information measure to the design of clinical experiments. In: Freeman PR, Smith AFM, eds., *Aspects of Uncertainty. A Tribute to D. V. Lindley*, 351–362. Chichester: John Wiley & Sons 1994.

[266] Müller P, Parmigiani G. Simulation approach to one-stage and sequential optimal design problems. In: Kitsos C, Mueller W, eds., *MODA 4 – Advances in Model Oriented Data Analysis*, 37–48. Springer 1995.

[267] Clyde M, Müller P, Parmigiani G. Optimal design for heart defibrillators. In: *Case studies in Bayesian Statistics, Volume II (Lecture Notes in Statistics Vol. 105)*, 278–292. Springer-Verlag Inc 1995.

[268] Müller P, Parmigiani G. Numerical evaluation of information theoretic measures. In: Berry DA, Chaloner KM, Geweke JK, eds., *Bayesian Statistics and Econometrics: Essays in Honor of A. Zellner*, 397–406. New York: Wiley 1995.

[269] Parmigiani G, Ancukiewicz M, Matchar DB. Decision models in clinical recommendations development: the Stroke Prevention Policy Model. In: Berry DA, Stangl DK, eds., *Bayesian Biostatistics*, vol. 151 of *Statistics: Textbooks and Monographs*, 207–233. New York: Marcel Dekker 1996.

[270] Clyde MA, Müller P, Parmigiani G. Inference and design strategies for a hierarchical logistic regression model. In: Berry DA, Stangl DK, eds., *Bayesian Biostatistics*, vol. 151 of *Statistics: Textbooks and Monographs*, 297–320. New York: Marcel Dekker 1996.

[271] Carota C, Parmigiani G. On Bayes factors for nonparametric alternatives. In: Bernardo JM, Berger JO, Dawid AP, Smith AFM, eds., *Bayesian Statistics 5 – Proceedings of the Fifth Valencia International Meeting*, 507–511. Clarendon Press [Oxford University Press] 1996.

[272] Clyde MA, Parmigiani G. Orthogonalizations and priors for orthogonalized model mixing. In: Lee JC, Johnson WO, Zellner A, eds., *Modelling and Prediction: Honoring of Seymour Geisser*, 206–227. New York: Springer 1996.

[273] Parmigiani G. Utility in health studies. In: Rosner B, Glynn R, eds., *Encyclopedia of Biostatistics*. New York: Wiley 1998.

[274] Parmigiani G, Berry D, Iversen Jr ES, Müller P, Schildkraut J, Winer E. Modeling risk of breast cancer and decisions about genetic testing. In: Gatsonis C, et al., eds., *Case Studies In Bayesian Statistics*, vol. IV, 173–268. Springer 1998.

[275] Iversen Jr ES, Parmigiani G, Berry D. Validating Bayesian prediction models: a case study in genetic susceptibility to breast cancer. In: Gatsonis C, Kass RE, Carlin B, Carriquiry A, Gelman A, Verdinelli I, West M, eds., *Case Studies In Bayesian Statistics*, vol. IV, 321–338. NY: Springer 1998.

[276] Parmigiani G. Decision models in screening for breast cancer. In: Bernardo JM, Berger JO, Dawid AP, Smith AFM, eds., *Bayesian Statistics 6*, 525–546. Oxford: Oxford University Press 1999.

[277] Dominici F, Parmigiani G. Combining studies with continuous and dichotomous responses: a latent variables approach. In: Stangl DK, Berry DA, eds., *Meta–analysis in Medicine and Health Policy*, vol. 151, 105–126. New York, NY, USA: Marcel Dekker 2000.

[278] Parmigiani G. Decision theory: Bayesian. In: Smelser N, Baltes P, eds., *International Encyclopedia of Social and Behavioral Sciences*, 3327–3334. Oxford: Elsevier 2001.

[279] Parmigiani G, Garrett ES, Irizarry RA, Zeger SL. The analysis of gene expression data: an overview of methods and software. In: Parmigiani G, Garrett ES, Irizarry RA, Zeger SL, eds., *The analysis of gene expression data: methods and software*, 1–45. New York: Springer 2003.

[280] Garrett ES, Parmigiani G. POE: Statistical tools for molecular profiling. In: Parmigiani G, Garrett ES, Irizarry RA, Zeger SL, eds., *The analysis of gene expression data: methods and software*, 362–387. New York: Springer 2003.

[281] Garrett ES, Parmigiani G. Clustering and classification methods for gene expression data analysis. In: Nuber U, ed., *DNA Microarrays: Advanced Methods*, 241–256. New York: Taylor and Francis 2005.

[282] Shen Y, Parmigiani G. Optimization of breast cancer screening modalities. In: Nikoulina, Commenges, Huber, eds., *Probability, Statistics and Modeling in Public Health*, 405–420. New York: Springer 2006.

[283] Müller P, Parmigiani G, Rice K. FDR and Bayesian multiple comparisons rules. In: Bernardo JM, Bayarri S, Berger JO, Dawid A, Heckerman D, Smith AFM, West M, eds., *Bayesian Statistics 8*. Oxford University Press 2007.

[284] Blackford A, Parmigiani G. Familial cancer risk assessment using bayesMendel. In: Ochs M, Casagrande J, R D, eds., *Biomedical informatics in cancer research*, chap. 18, 301–314. Springer Verlag 2010.

[285] Zhong X, Marchionni L, Cope L, Iversen ES, Garrett-Mayer ES, Gabrielson E, Parmigiani G. Optimized cross-study analysis of microarray-based predictors. In: Do KA, Qin S, Vannucci M, eds., *Advances in Statistical Bioinformatics: Models and Integrative Inference for High-Throughput Data*, 398. Cambridge University Press 2013.

[286] Tyekucheva S, Parmigiani G. Bioinformatic analysis of epidemiological and pathological data. In: Loda M, Mucci L, Mittelstadt ML, Hemelrijck MV, Cotter MB, eds., *Pathology and Epidemiology of Cancer*, 91–105. Springer 2016.

[287] Kastrinos F, Idos G, Parmigiani G. Prediction Models for Lynch Syndrome. In: Valle L, Gruber SB, Capella G, eds., *Hereditary Colorectal Cancer: Genetic Basis and Clinical Implications*, 281–303. Cham: Springer International Publishing 2018.

Book Reviews Comments and Responses

[288] Parmigiani G. Review of "Scientific reasoning: The Bayesian approach". *Journal of the American Statistical Association* 86; 825–827 1991.

[289] Parmigiani G. Review of "Large deviation techniques in decision, simulation and estimation". *Technometrics* 34; 120–121 1992.

[290] Parmigiani G. Comment on "several Bayesians: A review". *Test* 2; 24–25 1993.

[291] Clyde M, DeSimone H, G. P. Comment on: Accounting for model uncertainty in survival analysis improves predictive performance, by Raftery et al. In: Bernardo JM, Berger JO, Dawid AP, Smith AFM, eds., *Bayesian Statistics 5 – Proceedings of the Fifth Valencia International Meeting*, 323–349. Clarendon Press [Oxford University Press] 1996.

[292] Berry DA, Parmigiani G. Response to: Re: probability of carrying a mutation of breast-ovarian cancer gene BRCA1 based on family history by Schaid, dj. *J Natl Cancer Inst* 89; 1634 1997.

[293] Berry D, Parmigiani G, Rubinstein W, Watson P. Response to Nonovarian Pelvic Cancers in BRCA1/2 Mutation Carriers and the BRCAPRO Statistical Model by Cremin et al. *J Clin Oncol* 20; 3936–3937 2002.

[294] Chen S, Iversen ESJ, Parmigiani G. In Reply to: BRCA1 and BRCA2 Cancer Risks by Antoniou et al. *J Clin Oncol* 24; 3313–3314 2006.

[295] Parmigiani G, Lin J, Boca S, Sjöblom T, Jones S, Wood LD, Parsons DW, Barber T, Buckhaults P, Markowitz SD, Park BH, Bachman KE, Papadopoulos N, Vogelstein B, Kinzler KW, Velculescu VE. Response to comments on 'The consensus coding sequences of breast and colorectal cancers'. *Science* 317 (5844); 1500d 2007.

[296] Parmigiani G, Chen S. In Reply to: One Risk Fits All? by De Bock et al. *J Clin Oncol* 25; 3384– 2007.

[297] Parmigiani G, Berry DA. In Reply to: Does the search for large genomic rearrangements impact BRCAPRO carrier prediction? by Capalbo et al. *J Clin Oncol* 25; 2634–2635 2007.

[298] Chng; WJ, Loeb LA, Bielas; JH, Strauss; BS, Sjoblom T, Jones S, Wood LD, Parsons DW, Lin J, Barber T, Mandelker D, Leary RJ, Ptak J, Silliman N, Szabo S, Buckhaults P, Farrell C, Meeh P, Markowitz SD, Willis J, Dawson D, Willson JKV, Gazdar AF, Hartigan J, Wu L, Liu C, Parmigiani G, Park BH, Bachman KE, Papadopoulos N, Vogelstein B, Kinzler KW, Velculescu VE. Limits to the Human Cancer Genome Project? *Science* 315; 762b–766 2007.

[299] Vogelstein B, Roberts NJ, Vogelstein JT, Parmigiani G, Kinzler KW, Velculescu VE. Response to comments on "the predictive capacity of personal genome sequencing". *Sci Transl Med* 4; 135lr3 May 2012.

[300] Trippa L, Lee EQ, Wen PY, Batchelor TT, Cloughesy T, Parmigiani G, Alexander BM. Reply to B. Freidlin et al. *J Clin Oncol* 31; 970–971 Mar 2013.

[301] Parmigiani G, Trippa L. Bayesian nonparametric inference why and how comment. *Bayesian Ana* 8(2); 346 2013.

Full Length Conference Proceedings Papers

[302] Carota C, Parmigiani G, Polson N. Bayesian model criticism. In: *ASA Proceedings of the Section on Bayesian Statistical Science*. American Statistical Association 1993.

[303] Lavine M, Parmigiani G. Introducing Bayesian statistics to undergraduates: A transitional approach. In: *ASA Proceedings of the Section on Bayesian Statistical Science*, 146–149. American Statistical Association (Alexandria, VA) 1993.

[304] Clyde MA, DeSimone H, Parmigiani G. A comparison of algorithms for sampling models. In: *ASA Proceedings of the Section on Bayesian Statistical Science*, 211–216. American Statistical Association (Alexandria, VA) 1994.

[305] Clyde M, Parmigiani G, Vidakovic B. Using Markov chain Monte Carlo to account for model uncertainty with applications to wavelets. In: Meyer M, Rosenberger JLE, eds., *Computing Science and Statistics: Proceedings of the Symposium on the Interface*, 209–218. Interface Foundation of North America 1996.

[306] Ashih HW, Berry DA, Parmigiani G. Modeling natural history of breast cancer tumor growth. In: *ASA Proceedings of the Biometrics Section*, 182–185. American Statistical Association (Alexandria, VA) 1998.

[307] Irizarry RA, Parmigiani G, Guo M, Dracheva T, Jen J. A statistical analysis of radiolabeled gene expression data. In: *Computing Science and Statistics: Proceedings of the Symposium on the Interface*, 26–49. Interface Foundation of North America 2001.

[308] Parmigiani G, Garret E, Anbazhagan B, Gabrielson E. Molecular classification of lung cancer - a cross-platform comparison of gene epxression data sets. In: Pass HI, Carbone DP, Johnson DH, Minna JD, Turrisi AT, eds., *46th Annual Thomas L Petty Aspen Lung Confrence*, 261–269. Philadelphia: Lippincott Williams and Wilkins 2003.

[309] Shih IM, Sheu JJC, Santillan A, Nakayama K, Yen MJ, Bristow RE, Vang R, Parmigiani G, Kurman RJ, Trope CG, Davidson B, Wang TL. Amplication of a chromatin remodeling gene, rsf-1/hbxap, in ovarian carincoma. In: *AACR/NCI.EORTC Internatioanl Conference on Molecular Targets and Cancer Therapeutics* 2005.

[310] Parsons D, Jones S, Leary R, Lin J, Zhang X, Wood L, Sjoblom T, Papadopoulos N, Parmigiani G, Kinzler K, Velculesco V, Vogelstein B. Large-scale mutational naalyses of human cancer: Lessons learned from sequencinf cancer genomes. In: *Proceedings of the 36th Meeting of the International Society of Oncology and Biomarkers* 2008.

[311] Blackford A, Parmigiani G, Kensler TW, Wolfgang C, Jones S, Zhang X, Parsons DW, Lin JCH, Leary RJ, Eshleman JR, Goggins M, Jaffee EM, Iacobuzio-Donahue CA, Maitra A, Klein A, Cameron JL, Olino K, Schulick R, Winter J, Vogelstein B, Velculescu VE, Kinzler KW, Hruban RH. Genetic mutations associated with cigarette smoking in pancreatic cancer. In: *98th Annual Meeting of the United States and Canadian Academy of Pathology* 2009.

[312] Coopey SB, Mazzola E, Buckley JM, Sharko J, Belli AK, Kim EMH, Polubriaginof F, Parmigiani G, Garber JE, Smith BL, Gadd MA, Specht MC, Guidi AJ, Roche CA, Hughes KS. Clarifying the risk of breast cancer in women with atypical breast lesions. In: *San Antonio Breast Cancer Symposium* 2011.

[313] National Academies of Sciences, Engineering, and Medicine. *Statistical Challenges in Assessing and Fostering the Reproducibility of Scientific Results: Summary of a Workshop*. Washington DC: The National Academies Press 2016.

[314] Huang T, Braun D, Gorfine M, Parmigiani. G. Using frailty models to improve familial cancer risk prediction. In: *Proceedings of the AACR Special Conference: Improving Cancer Risk Prediction for Prevention and Early Detection* 2017.

FUNDING

Training fellowship

1. Manca Fellowship for Research and Teaching at Università L. Bocconi, Milano, 1984–85 and 1985–86.

Funding at Duke

AS PRINCIPAL INVESTIGATOR OR PROJECT LEADER: [2]

2. NSF DMS-94 03818 (PI). "Bayesian Methods and Decisions for Observation Times." From 6-94 to 12-97.
3. NIH-NCI P20-CA66228-01 (PL). "Decision Models for Breast Cancer Screening." Pilot Project within "Planning a Program of Research in Early Breast Cancer" (PI: B. Rimer). From 6-94 to 6-95.
4. NSF DMS-95 0519 (PI). "Workshop on Model Uncertainty and Model Robustness" From 7-95 to 7-96.
5. NIH-NCI 95-018 (Co-PL). "Modeling Risk of Breast Cancer." Developmental Project within the Duke CPRU (P.I.: B. Rimer). From 6-96 to 6-98.
6. NIH-NCI R21-CA68438-01 (Co-PL). "Decision Models in Breast Cancer." Developmental project within the Duke SPORE in Breast Cancer (PI: D. Iglehart). From 7-96 to 7-97.
7. NIH-NCI (Co-PL). "Models for Assessing Risk of Familial Breast and Ovarian Cancer." Developmental project within the Duke SPORE in Breast Cancer (PI: D. Iglehart). From 7-97 to 7-98.
8. NSF DMS: (PI) "Workshop on stochastic model building and variable selection," From 7-97 to 7-98.
9. NIH-NCI (Co-PL in year 1, PL in year 2) "Modeling BRCA1&2 carrier probabilities." Project 4 within the Duke SPORE in Breast Cancer renewal application (PI: D. Iglehart). $180432 requested for Project 4. From 7-98 to 7-00.
10. NIH-NCI (Co-PL). "Tamoxifen for prevention of breast cancer in genetically susceptible women." Developmental project within the Duke SPORE in Breast Cancer (PI: D. Iglehart). From 7-98 to 7-99.
11. NIH-NCI 95-018 (PL). "External Validation of the CPRU Breast Cancer Risk Prediction Model." Developmental Project within the Duke CPRU (P.I.: I. Siegler). From 6-98 to 6-99.

AS INVESTIGATOR:

12. NSF DMS-93-05699. "Mathematical Sciences Computing Resource Environments." From 6-93 to 11-95.
13. NIH-NCI 1P50-CA68438-01. "Interventions in Breast Cancer: A Decision Model." Project 4 within the Duke SPORE in Breast Cancer (PI: D. Iglehart). From 7-95 to 7-96.
14. NIH-NCI Cancer Genetics Networks. (P.I. D. Iglehart)
15. DuPont Merck. "A randomized trial of anticoagulation services for stroke prevention". 11-98 to 11-99.

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[2]PI: Principal investigator; PL: Project leader; CL: Core leader

AS SPONSOR OF GRADUATE STUDENTS:

16. Duke University, Arts and Sciences Research Council seed grants.
    1992 (PI), 1993 (co-PI), 1994 (co-PI), 1995 (co-PI), 1996 (PI), 1998 (PI).
17. Becton Dickinson Research Center. Graduate student internship grant 1997/98 and 1998/99
18. Janssen Research Foundation. "A User-friendly Acute Stroke Treatment Model for Lubeluzole".
    (PI: D. Matchar) From 10-97 to 10-99.
19. Knoll Pharmaceuticals. From 9-99 to 8-00.

Funding at Johns Hopkins

AS PRINCIPAL INVESTIGATOR OR PROJECT/CORE LEADER: [3]

20. NIH-NCI "Biostatistics and Bioinformatics Core" (CL) within the "Johns Hopkins SPORE in Breast Cancer"(SPORE PI: Davidson). From 00 to 12.
21. NIH-NIDDK "Biostatistics Core" (CL) within the "The Hopkins DK Center for the Analysis of Gene Expression" (Center PI Germino). From 00 to 03.
22. NIH-NCI Cancer Genetics Networks. (PL) "Validation of BRCA1&2 Carrier Probability Models" (Center PI Griffin). From 01 to 02.
23. CRFA (PI) "Risk Prediction in Familial Colon Cancer". From 01 to 03.
24. NIH-NCI P50 (PI) "Susceptibility Prediction in Familial Colon Cancer". Project 3a of "Johns Hopkins SPORE in Gastrointestinal Cancer" (SPORE PI: Kern). From 02 to 07.
25. NSF (PI) "Multi-study genomic data analysis". From 04 to 09.
26. NIH-NCI R01 (PI) "Statistical Methods for Cancer Genes". From 04 to 08.
27. NIH-NCI "Sidney Kimmel Cancer Center Bioinformatics Shared Resource" (CL) within the "Regional Oncology Research Center" (PI: Abeloff). From 06 to 11.
28. NIH-NIGMS "Pre-doctoral biostatistical training in genetics/genomics" 1T32 GM074906-01A1/B7BSCW. From 06 to 10.
29. Komen Foundation "Improvement and Validation of BRCAPRO", from 08 to 11.

AS INVESTIGATOR:

30. NIH-NCI "Regional Oncology research center" (PI's: Abeloff, Baylin). From 99 to 11.
31. NIH-NCI "Johns Hopkins SPORE in Gastrointestinal Cancer" Biostatistics core (PI: Kern, CL: Goodman). From 99 to 11.
32. NIH-NCI "High throughput genetic analysis of bladder cancer" (PI Schoenberg). From 99 to 00.
33. NIH "Applied Genomics in Cardiopulmonary Disease" (PI: Garcia). From 00 to 02.
34. ACS "Molecular Genetic Alterations in Germ Cell Tumors" (PI Perlman) From 00 to 01
35. ACS "Genetic Analysis of Pediatric Germ Cell Tumors" (PI Perlman) From 01 to 01
36. NIH-NCI "Molecular epidemiology of progression to breast cancer" (PI: Helzlsour). Project 1 within the "Johns Hopkins SPORE in Breast Cancer". From 00 to 05.
37. NIH-NCI "Molecular classification of breast cancer" (PI: Gabrielson). Project 3 within the "Johns Hopkins SPORE in Breast Cancer". From 00 to 05.
38. NIH-NCI-EDRN "Evaluating Biomarkers of Carcinogenesis" (PI: Helzlsour). From 00 to 03.

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[3]PI: Principal investigator; PL: Project leader; CL: Core leader

39. Broad Foundation "Classification of Crohn's disease subtypes by gene expression profiles" (PI Chakravarti). From 03 to 04.
40. NIH-NIDDK R01 "Consequences of Lifetime Isolated GH Deficiency" (PI: Salvatori). From 04 to 08.
41. NIH-NCI "Phase II Imaging & Localizong Device the Barkhausen Effect" (PI: Dicello). From 06 to 08.
42. Lustgarden Foundation "Pancreatic Cancer Genome Sequencing" (PI: Vogelstein). From 07 to 09.
43. NIH-NCI "Institute for Clinical and Translational Research" (PI: Ford) 07 to 12.
44. NIH-NCI "Tools for Large-Scale Analysis of Driver Pathways" (PI: Karchin) 08 to 10.

AS CONSULTANT or MENTOR:

45. NIH "cDNA Microarrays in the Differential Diagnosis of Suspicious Thyroid Lesions" (PI: Zeiger). From 7/99 to 11/03.
46. NIH "Regulation of RHODOPSIN Gene Expression" (PI: Zack).
47. NLM "Johns Hopkins Health Sciences Informatics Training Program" (PI: Lehmann).
48. Fogarty International Center "International Collaborative Genetics Research Training Program" (PI: Jabs).
49. NIH-NIMH K01 "Bioinformatics for Gene Discovery in Psychiatric Disorders" (PI: Zandi)
50. NIH-NIAID K01 "Mutation profile analysis of HIV genetic heterogeneity" (PI: Kowalski)

Funding at Harvard

AS PRINCIPAL INVESTIGATOR OR PROJECT/CORE LEADER: [4]

51. NIH/NCI (PI), "Statistical Methods for Cancer Susceptibility Genes". From 04 to 10.
52. Susan G Komen Breast Cancer Foundation (PI), "Improvement and Validation of BRCAPRO". From 08 to 10.
53. NSF (PI) "Multi-study genomic data analysis". From 09 to 11.
54. NIH-NCI (PL) "CCSG Administrative Program Leaders". From 09 to 16.
55. NIH-NCI (PL) "CCSG Administrative Program Senior Leaders". From 10 to present.
56. NSF-NCI (PI) "ADT: Quantitative Methods for Estimating Sequencing Errors". From 12 to present.
57. NIH-NCI (PI) T32 CA009337 "Quantitative Sciences for Cancer Research". From 13 to present.
58. NIH-NCI (PI) "Bioinformatics Tools for Genomic Analysis of Tumor and Stromal Pathways in Cancer". From 13 to present.
59. NIH-NCI (PI) "Novel Tools for Familial Risk Prediction". From 13 to 16.

AS INVESTIGATOR:

60. American Cancer Society, "Refining Molecular Risk Assessment in the Familial Melanoma Population" (PI: Hensin Tsao). From 09 to 10.
61. NIH-NCI, "Genomic Stratification of Ovarian Cancer Patients" (PI: Michael Birrer). From 10 to 13.

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[4]PI: Principal investigator; PL: Project leader; CL: Core leader

62. Prostate Cancer Foundation, "Shedding Light on Stromal–Epithelial Interactions in Prostate Carcinogenesis and Mortality". (PI: Massimo Loda) From 12 to 16.
63. NIH, "SPORE in Multiple Myeloma". (PI: Kenneth Anderson). From 13 to present.
64. NIH-NCI "Integrative Oncogenomics of Multiple Myeloma" (PI: Nikhil Munshi) from 2011 to 2017.
65. NIH, "Statistical Analysis Methods for Validating Risk Prediction Models". (PI: Hajime Uno) From 14 to present.
66. NIH, "Host-Tumor Cell Interaction in Myeloma Therapeutic Applications". (PI: Kenneth Anderson). From 13 to present
67. Burroughs Wellcome Fund, "Development of a Biomarker Enriched Adaptive Trial for Patients with Glioblastoma" (PI: Brian Alexander) From 2014 to present.
68. NIH/NCI "Validation and Extension of the PREMM Model for Inherited Colorectal Cancer" (PI: Sapna Syngal).
69. CDC "Prevention Policy Modeling Lab" (PI: Joshua Solomon) From 16 to present.

AS CONSULTANT or MENTOR:

70. NCI, "An Open-Source Algorithm Isolating Signatures in Microarray Data" (PI: Michael Ochs). From 08 to 10.

LECTURES

Named Lectures

1. Harvard School of Public Health, Department of Biostatistics, Myrto Lefkopoulou Distinguished Lecture, September 1999: *Breast Cancer Genes: Modeling and Medical Care*.
2. Dana–Farber Cancer Center, October 2002: Dana Farber / Frontiers of Science Annual Lecture. *Statistical challenges in expression–based molecular classification of cancer*.
3. University of California at Irvine, February 2009: Distinguished Speaker, Genetic Epidemiology Research Institute. *Risk prediction in familial cancer syndromes.*
4. MRC Biostatistics Unit, Cambridge UK, November 2013: Armitage Lectureship. Cross Study Reproducibility of Prognostic Signatures From High Throughput Genomic Data.
5. Università di Perugia, Italy, July 2015: "Top Italian Scientist" Seminar.
6. The Blaffer Lecture, M. D. Anderson Cancer Center, October 2018 *Knowledge management and decision support for commonly tested susceptibility mutations*.

Grand Rounds

7. M. D. Anderson Cancer Center, Institutional Grand Rounds, October 2002: *Breast Cancer Genes: Modeling and Medical Care*.
8. Department of Pathology, Johns Hopkins University, Nov 2006: *Familial Risk Prediction: Examples from Colon, Pancreas and Breast Cancer*.
9. Massachusetts General Hospital, Breast Program, Feb 2008: *Risk assessment in familial breast and ovarian cancer*.
10. Welch Center, Johns Hopkins University, Apr 2007: *Comparing and combining multiple microarray datasets*.

11. Medical Grand Rounds at Juravinski Cancer Centre, Ontario, Nov 2016: *Assessing Risk in Families with Cancer*.

12. Brigham and Women's Hospital Pathology Grand Rounds, Dec 2016: *Precision Genetic Risk Assessment in Cancer*.

Invited Lectures at Conferences

13. 40-th Seminar on Bayesian Inference in Econometrics and Statistics, Washington, March 1990: *Inspecting For Failures While Learning About the Failure Rate*.

14. International Research Conference in Reliability, Columbia, MS, June 1991: *Optimal Scheduling of Inspections with Applications in Reliability and Bayesian Design*.

15. 10th National Symposium of Probability and Statistics (SINAPE), Rio de Janeiro, August 1992: *Statistical Issues in Screening for Chronic Disease*.

16. Joint Statistical Meetings, Boston, August 1992: *Optimal Screening Ages*.

17. 45-th Seminar on Bayesian Inference in Econometrics and Statistics, Durham, November 1992: *Sequential Design via Curve-Fitting of Monte-Carlo Experiments*.

18. Stroke PORT Annual Meeting, Durham, December 1992: *Modeling and Estimation Strategies for Transition Probabilities*.

19. Biometric Society ENAR Spring Meeting, Philadelphia, April 1993: *Bayesian Methods in the Design of Biomedical Experiments*.

20. International Society for Bayesian Analysis annual Meeting, San Francisco, August 1993: *Introducing Bayesian Statistics to Undergraduates*.

21. Southeastern Regional Conference of Statisticians in the Health Care Industry, RTP, March 1994: *Bayesian Variable Selection and Prediction via Mixtures*.

22. Royal Statistical Society of Spain, Madrid, June 1994: *Information and Model Criticism*.

23. International Society for Bayesian Analysis annual Meeting, Alicante, June 1994: *Information and Model Criticism*.

24. 26th Symposium on the interface: Computing Science and Statistics, RTP, June 1994. *Stochastic Optimization by Curve Fitting of Monte-Carlo Experiments*.

25. IMS Workshop: Directions in Sequential Analysis, Chapel Hill, June 1994: *Stochastic Optimization by Curve Fitting of Monte-Carlo Experiments*.

26. Joint Statistical Meetings, Toronto, August 1994: *Screening: is it all in the Timing?*

27. American Statistical Association, Winter Conference, Raleigh, January 1995: *Pre-analysis of super-large data set*.

28. Fourth Conference on Model-oriented Data Analysis, Spetzes, June 1995: *Design of repeated medical exams*.

29. III World Meeting of the International Society for Bayesian Analysis, Oaxaca, Mexico, September 1995. *Prediction via Model Mixing*.

30. Biometric Society ENAR Spring Meeting, Richmond, March 1996. "New strategies for model mixing in biostatistical analysis"

31. INFORMS meeting, Washington, May 1996. *Prediction via Model Mixing*.

32. Institute for Mathematics and its Applications, Summer Program, July 1997, Minneapolis, MN. *Timing Medical Examination via Intensity Functions*.

33. Annual NIH SPORE Investigators Meeting, Rockville, MD, July 1997 *Decision model for assessing the benefits of axillary lymph node dissection (ALND) in patients with breast cancer*.

34. Fourth Workshop on Bayesian Statistics in Science and Technology: Case Studies Carnegie Mellon University, Pittsburgh, September 1997. *Modeling Risk of Breast Cancer and Decisions about Genetic Testing.*

35. Doing and Understanding Meta-analysis. Rockville, MD, October 1997. *Combining Incomplete Information on Headache Treatments.*

36. International Conference on Health Policy Research: Methodologic Issues in Health Services and Outcomes Research, Washington, DC, December 1997. *Assessing Uncertainty in Cost-Effectiveness Analyses: Application to a Complex Decision Model*

37. Bayesian Statistics VI, Valencia, Spain, June 1998. *Decision Models in Screening for breast cancer.*

38. Carcinogenesis Modeling and Risk Assessment Conference, Park City UT, July 1998. "Semiparametric Bayesian models in risk analysis".

39. Joint Statistical Meetings, Dallas, August 1998: *Toward a Comprehensive Model of Breast Cancer Risk.*

40. Joint Working Group on Methodological Issues in Clinical Trials in Radiological Screening and Related Computer Modeling, Washington, DC, January 1999: *Uncertainty in decision models of screening illustrated with examples in breast cancer and stroke.*

41. Joint Statistical Meetings, Baltimore, August 1999: *Bayesian Approaches to Sample Size Determination: Concepts, Applications and Computing.*

42. Gertrude M Cox Statistics Conference Research Triangle Institute, RTP NC, September 1999. *Bayesian decision models and the genetics of breast cancer*

43. International Workshop on Foundational Issues and Statistical Practice, Bibbiena, Italy, October 1999. *Comprehensive medical decision models: toward a new foundational paradigm?*

44. Biometric Society ENAR Spring Meeting, Chicago, March 2000. *Genetic Susceptibility and Survival: A case study in the use of surveillance data in modeling*

45. Joint Statistical Meetings, Indianapolis, August 2000: *Bayesian methods in cancer prevention and early detection.*

46. Biometric Society ENAR Spring Meeting, Charlotte, March 2001. *Breast Cancer Genes: Modeling and Medical Care*

47. ISPOR, Washington, May 2001. *Making Models Better*

48. AIRC Workshop on Genetic Epidemiology of Inherited Breast Cancer, Pisa, July 2001: *Modeling inherited susceptibility to breast cancer.*

49. Joint Statistical Meetings, Atlanta, August 2001: *Molecular Classification of Cancer Using Gene Expression.*

50. American Society of Preventive Oncology, March 2002: *How can epidemiology inform interpretation of array experiments?*

51. Biometric Society ENAR Spring Meeting, Alexandria, March 2002. *A statistical framework for expression–based molecular classification of cancer.*

52. Royal Statistical Society meeting on *Statistical modelling and analysis of genetic data*, London, May 2002: *A statistical framework for expression–based molecular classification of cancer.*

53. Annual NIH SPORE Investigators Meeting, Chantilly, VA, July 2002 *A statistical framework for expression–based molecular classification of cancer.*

54. Joint Statistical Meetings, New York, August 2002: *Assessing uncertainty in complex decision models.*

55. Workshop On High-Dimensional Data. Leiden, NL, September 2002: *A statistical framework for expression–based molecular classification of cancer*

56. American Association for Cancer Research, Boston, October 2002: *Assessing and communicating the validity of individualized model of genetic risk*.

57. San Antonio Breast Cancer Symposium, San Antonio, December 2002: *Assessing and communicating the validity of individualized model of genetic risk*.

58. Bayesian Biostatistics: Introduction and Recent Advances, Houston, January 2003: *Can Nothing Teach Us Something? Bayesian Meta-analysis of Sparse Contingency Tables*.

59. Workshop on Statistical Analysis of Gene Expression Data. Wye, July 2003: *Molecular Classification of Lung Cancer: A Cross-Platform Comparison and Validation of Gene Expression Data Sets*.

60. Joint Statistical Meetings, San Francisco, August 2003: *Generating "Hit Lists" from High-throughput Genomic Assays: Are Hierarchical Models Helping?*

61. Seventh Workshop on Bayesian Statistics in Science and Technology: Case Studies, Carnegie Mellon University, Pittsburgh, September 2003. *Bayesian multilevel and mixture models in genomic analysis.*

62. University of Florida Sixth Annual Winter Workshop: "Data Mining, Statistical Learning, and Bioinformatics", Jan 2004: *Multilevel models and gene expression data analysis.*

63. Biometric Society ENAR Spring Meeting, Pittsburgh, March 2004: *Multi-study genomic data analysis.*

64. Cancer Risk Prediction Models: A Workshop on Development, Evaluation, and Application, Bethesda, May 2004: *Susceptibility Prediction in Familial Colon Cancer*.

65. Computational Biology, Systems Biology and Bioinformatics Symposium 2004, Johns Hopkins University, Baltimore, May 2004. *Multi-study genomic data analysis.*

66. Interface 2004: Computational Biology and Bioinformatics, Baltimore, May 2004. *Mixture models in gene expression data analysis.*

67. Annual NIH SPORE Investigators Meeting, Baltimore, MD, July 2004, *Integrating and Cross-Validating Microarray Studies: an Inter-SPORE Collaboration and Resource.*

68. Joint Statistical Meetings, Toronto, August 2004: *Multi-study genomic data analysis*.

69. American Public Health Association Meeting, Washington, DC, November 2004. *Microarray studies: Can they be reproduced? Can they be combined?*

70. US FDA, Microarrays in Transcriptional Profiling Course, Rockville, DC, November 2004. *Cross-study validation of molecular markers and profiles.*

71. Joint Statistical Meetings, Minneapolis, August 2005: *Decision Theory and Genomic Experiments*.

72. Joint Statistical Meetings, Salt Lake City, August 2007: *Application of Hierarchical Models to Study Genetic and Epidemiologic Risk Factors*.

73. Conference on Design and Analysis Issues in Genomic Studies in Population Sciences, Boston, October 2007: *Statistical Methods for Mutational Analysis of Cancer*.

74. Biometric Society ENAR Spring Meeting, Cristal City, March 2008: *What is New in Gene Set Enrichment Analysis?*.

75. Conferenza in Onore di D.M. Cifarelli, Milano, June 2008: *Coherent Bayesian Model Averaging*.

76. Joint Statistical Meetings, Denver, August 2008: *Bayesian and Frequentist Multiple Testing in Cancer Genome Sequencing*.

77. Workshop on Cancer Risk Prediction, Banff, March 2008: *Risk prediction in familial cancer syndromes.*

78. AACR Meeting, Denver, March 2009: *Meet the expert session: Development, Validation, Interpretation and Clinical Implementation of statistical models for familial risk prediction.*

79. Joint Statistical Meetings, Washington, August 2009: *Gene Set Analysis as a Tool for Cross-Platform Integration in Genomics.*.

80. Bayesian Biostatistics Meeting, Houston, January 2010: *Multi-study Analysis of Gene Expression: Data Exploration and Bayesian Modeling.*

81. ENAR Meeting, New Orleans, March 2010: *Using Statistics to Fight Cancer: Examples From Don Berry's Career*

82. Joint Statistical Meetings, Vancouver, August 2010: *Statistical Analysis of Somatic Changes in Cancer Genomics.*.

83. AACR Meeting, Orlando, April 2010: *Statistical Issues in Somatic Mutation Studies of Cancer*

84. High Dimensional Data Workshop, Nantucket, May 2011: *Integrating Diverse Genomic Data using Gene Sets.*

85. Joint Statistical Meetings, Miami, FL, August 2011: *In Honor of Jay Kadane's 70th Birthday: Decision Theory in All Walks of Life.*

86. Conference on Risk Assessment and Evaluation of Predictions, Silver Spring, MD, October 2011: *Assessing Risk in Families with Cancer.*

87. Innovative Methods Program for Advancing Clinical Trials (IMPACT) Symposium, Chapel Hill, NC, November 2011: *Adaptive randomized trial design for patients with recurrent glioblastoma.*

88. David Blackwell Memorial Conference, Howard University, April 2012: *Blackwell's Impact on Statistics: Bayesian.*

89. AAAS Annual Meeting, Boston, MA, February 2013: *How useful is it to know your genomes?.*

90. JSM Annual Meeting, Montreal, Canada, August 2013: *Bayesian effect estimation accounting for adjustment uncertainty.*

91. Symposium on Advances in Statistical Methods for Cancer Genetic Epidemiology, New York, NY, August 2013: *Statistical modeling of somatic mutation data .*

92. Paths of Precision Medicine Symposium, Harvard School of Public Health, Boston, MA, January 2014: *Cross-study reproducibility of ovarian cancer signatures.*

93. Statistics for the Century of Data, Rutgers University Statistics Symposium, Piscataway, NJ, May 2014: *Cross-study Reproducibility of Predictions, with Application to Genomics.*

94. IMS Meeting of New Researchers in Statistics and Probability, Harvard University, August 2014: *Cross-study Reproducibility of Predictions, with Application to Genomics.*

95. JSM Annual Meeting, Boston, MA, August 2014: *Cross-study Reproducibility of Predictions, with Application to Genomics.*

96. Johns Hopkins Young investigators' Genomics & Bioinformatics Symposium, Baltimore, MD, March 2016. Keynote presentation: *Cross-study Analysis of Prediction Algorithms in Genomics.*

97. Symposium on Statistical and Computational Methods for Pharmacogenetic Epidemiology of Cancer, Memorial Sloan Kettering Cancer Center, August 11-12, 2016: *Cross-study Analysis of Prediction Algorithms in Genomics.*

98. Biostatistics Training Initiative (BTI) Distinguished Lecture, at the Ontario Institute for Cancer Research (OICR), November 4 2016: *Cross-study Analysis of Prediction Algorithms in Genomics.*

99. Symposium on "Precision medicine, Tobacco and Air Pollution Control: New Evidence, Challenges and Future Directions", INSP Cuernavaca MX, January 2017: *Precision Medicine and Precision Public Health.*

100. Sackler Colloquia of the National Academy of Sciences, Reproducibility of Research: Issues and Proposed Remedies, March 10, 2017: *New statistical approaches to reproducibility.*

101. Big Data in Life Sciences Symposium, Dartmouth College, May 23, 2017: *Cross-study analysis of predictions.*

102. Pezcoller Symposium, Trento, Italy, June 22-23, 2017: *Novel Approaches to Clinical Trial Design in Cancer.*

103. AACR annual meeting; Major symposium on "Integrative Data Science for the Precision Medicine Era", April 17 2018: *Knowledge management and decision support for commonly tested susceptibility mutations.*

104. National Cancer Policy Forum's workshop on "Improving Cancer Diagnosis and Care: The Clinical Application of Computational Methods in Precision Oncology". Washington, DC, October 29 2018: *Validation and Replicability of Prediction Algorithms in Oncology.*

105. CSHL conference on "Biological Data Science", Cold Spring Harbor, NY, November 7-10 2018: *Training replicable predictors in multiple studies.*

106. Science for Peace 2018: Global Inequalities, Milan, Italy Nov 15-16. *Big Data and Global Inequalities.*

107. Florence Center for Data Science 2019 Workshop. *Replicability Challenges in Machine Learning and Prediction.*

Colloquia

108. Stanford University, Department of Statistics, August 1990:
Optimal Design of Screening Programs.

109. AT&T Bell Laboratories, Statistics Group, September 1990:
Problems in Optimal Scheduling of Inspections.

110. Università L. Bocconi, Milano, Institute of Quantitative Methods, September 1990:
Problems in Optimal Scheduling of Inspections.

111. University of Pittsburgh, Department of Biostatistics, November 1990:
Optimal Design of Screening Programs.

112. Duke University, Institute of Statistics and Decision Sciences, February 1991:
Optimal Design of Screening Programs.

113. Ohio State University, Department of Statistics, February 1991:
Optimal Design of Screening Programs.

114. Purdue University, Department of Statistics, February 1991:
Optimal Design of Screening Programs.

115. Northwestern University, Department of Statistics, February 1991:
Optimal Design of Screening Programs.

116. Massachusetts Institute of Technology, Sloan School of Management, March 1991:
Optimal Design of Screening Programs.

117. Università degli Studi di Roma *La Sapienza*, Istituto di Statistica Probabilità e Statistiche Applicate, June 1991:
Changes in Utility as Diagnostics.

118. CNR-IAMI, Milano, June 1991:
Changes in Utility as Diagnostics.

119. Duke University, Division of Biometry, March 1992:
Optimal Design of Screening Programs.

120. University of Chicago, Graduate School of Business, April 1992:
Optimal Design of Screening Programs.

121. University of North Carolina at Chapel Hill, Department of Biometry, October 1992:
    Optimal Screening Ages.
122. Duke University, Division of Biometry, April 1994:
    An Overview of Bayesian Tools for Decision Modeling in Medical Guideline Development.
123. University of Minnesota, Department of Statistics and Department of Economics, April 1994:
    Stochastic Optimization by Curve Fitting of Monte-Carlo Experiments.
124. University of Pavia, Dipartimento di Economia Politica, May 1994:
    Stochastic Optimization by Curve Fitting of Monte-Carlo Experiments.
125. Harvard School of Public Health, Department of Biostatistics, November 1994:
    Prediction via Orthogonalized Model Mixing.
126. University of Pavia, Dipartimento di Economia Politica, December 1994:
    Prediction via Orthogonalized Model Mixing.
127. University of North Carolina at Chapel Hill, Department of Statistics, January 1995:
    Prediction via Orthogonalized Model Mixing.
128. Purdue University, Department of Statistics, January 1996:
    Computing the probability of carrying a BRCA1 mutation based on family history.
129. North Carolina State University, Department of Operations Research, April 1996:
    Timing Medical Examination via Intensity Functions.
130. Politecnico di Milano, Dipartimento di Matematica e Statistica, June 1996:
    Timing Medical Examination via Intensity Functions.
131. Johns Hopkins University, Department of Biostatistics, October 1997:
    Determining Carrier Probabilities for Breast Cancer Susceptibility Genes BRCA1 and BRCA2.
132. University of Virginia, Department of Health Evaluation Sciences, March 1998:
    Determining Carrier Probabilities for Breast Cancer Susceptibility Genes BRCA1 and BRCA2.
133. Becton Dickinson Technologies, May 1998:
    Determining Carrier Probabilities for Breast Cancer Susceptibility Genes BRCA1 and BRCA2.
134. University of Utah, Huntsman Cancer Center, July 1998:
    Determining Carrier Probabilities for Breast Cancer Susceptibility Genes BRCA1 and BRCA2.
135. Iowa State University, Department of Statistics, October 1998:
    Modeling genetic susceptibility to breast cancer.
136. University of Pennsylvania, Department of Biostatistics and Epidemiology, October 1998:
    Modeling genetic susceptibility to breast cancer.
137. University of Pennsylvania, Department of Biostatistics and Epidemiology, February 1999:
    Decision Models in Screening for breast cancer.
138. University of Washington, Department of Biostatistics and Department of Statistics, February 1999:
    Modeling genetic susceptibility to breast cancer.
139. Iowa State University, Department of Statistics, February 1999:
    Bayesian Modeling of Genetic Susceptibility Data in Cancer.
140. University of Michigan, Department of Biostatistics, February 1999:
    Modeling genetic susceptibility to breast cancer.
141. National Cancer Institute, Division of Cancer Epidemiology and Genetics, March 1999:
    Modeling genetic susceptibility to breast cancer.
142. National Institute of Statistical Sciences, April 1999:
    Modeling genetic susceptibility to breast cancer.

143. Johns Hopkins University, Department of Oncology, April 1999:
Modeling inherited susceptibility to breast cancer.

144. Brown University, Center for Statistical Sciences, April 1999:
Decision Models in Screening for breast cancer.

145. Johns Hopkins University, Department of Biostatistics, October 1999:
Decision Models in Screening for breast cancer.

146. M. D. Anderson Cancer Center, Department of Biostatistics, June 2000:
Breast Cancer Genes: Modeling and Medical Care.

147. Columbia University, Department of Biostatistics, January 2001:
Breast Cancer Genes: Modeling and Medical Care.

148. Johns Hopkins University, Department of Mathematical Sciences, Mar 2001:
Modeling inherited susceptibility to breast cancer.

149. University of Wisconsin, Department of Biostatistics, April 2001:
Breast Cancer Genes: Modeling and Medical Care.

150. Fox Chase Cancer Center, Department of Biostatistics, May 2001:
Breast Cancer Genes: Modeling and Medical Care.

151. Memorial Sloan-Kettering Cancer Center, Department of Biostatistics, February 2002:
Breast Cancer Genes: Modeling and Medical Care.

152. M. D. Anderson Cancer Center, Department of Biostatistics, February 2002:
Assessing uncertainty in complex decision models.

153. Harvard School of Public Health, Department of Biostatistics, October 2002:
Hierarchical Mixture Models For Unsupervised Classification Using Microarrays.

154. Johns Hopkins University, Department of Biomedical Engineering, April 2002:
Molecular Classification of Lung Cancer: A Cross-Platform Comparison and Validation of Gene Expression Data Sets.

155. University of Delaware, Delaware Biotechnology Institute, May 2003:
Molecular Classification of Lung Cancer: A Cross-Platform Comparison and Validation of Gene Expression Data Sets.

156. Yale University, Department of Biostatistics, May 2003:
Statistical Modeling and Cancer Susceptibility Genes.

157. Food and Drug Administration, Center for Biologics Evaluation and Research, May 2003:
Molecular Classification of Lung Cancer: A Cross-Platform Comparison and Validation of Gene Expression Data Sets.

158. Fred Hutchinson Cancer Research Center, November 2003:
"Multilevel Models in Genomic Data Analysis".

159. Brown University, Center for Statistical Sciences, November 2003:
Molecular Classification of Lung Cancer: A Cross-Platform Comparison and Validation of Gene Expression Data Sets.

160. Food and Drug Administration, Center for Devices and Radiological Health, January 2004:
Interpreting gene expression microarray studies.

161. Università Vita-Salute San Raffaele, Dipartimento di Biostatistica, Milan, Italy, April 2004:
Statistical Methods for Analysis of gene expression data.

162. Consiglio Nazionale delle Ricerche, Pavia, Italy, April 2004.
Genomic Analysis and Statistical Modeling.

163. Harvard School of Public Health, Department of Biostatistics, April 2004:
    Microarray studies: are they reproducible? Can they be combined?.
164. University of Lancaster, Department of Mathematics and Statistics, June 2004:
    Multilevel models and gene expression data analysis.
    Microarray studies: are they reproducible? Can they be combined?
165. Johns Hopkins University, Department of Oncology, Translational Research Conference, February 2005:
    Microarray studies: are they reproducible? Can they be combined?
166. Columbia University, Department of Statistics, April 2005:
    Multilevel models and gene expression data analysis.
167. University of Rochester, Department of Biostatistics and Computational Biology, May 2005:
    Microarray studies: are they reproducible? Can they be combined?
168. Ohio State University, Department of Statistics, June 2005:
    Multilevel models and gene expression data analysis.
169. Rutgers University, Department of Statistics, April 2006:
    Apples Oranges and Pairs: Data analytic approaches for mining multiple microarray datasets.
170. University of Maryland, Greenebaum Cancer Center, April 2006:
    Multilevel models and gene expression data analysis.
171. University of Chicago, Department of Statistics, May 2006:
    Mining and modeling multiple microarray datasets.
172. Università Vita-Salute San Raffaele, Dipartimento di Biostatistica, Milan, Italy, September 2006:
    Risk prediction in familial cancer syndromes.
173. Johns Hopkins University, Cancer Prevention Seminar Series, October 2006:
    Mutation prediction in familial cancer syndromes.
174. Harvard University, Dana Farber Cancer Institute, Nov 2006:
    Risk prediction in familial cancer syndromes.
175. University of Michigan, Department of Biostatistics, Nov 2006:
    Comparing and combining multiple microarray datasets.
176. Carnegie Mellon University, Department of Statistics, Dec 2006:
    Bayesian models for mutation prediction in families at high risk for cancer.
177. Johns Hopkins University, Institute of Genetic Medicine, March 2007:
    Mutation prediction in familial cancer syndromes.
178. Towson University, Towson MD, March 2007. *Microarray studies: Can they be reproduced? Can they be combined?*
179. National Cancer Institute, Biostatistics Branch, Rockville MD, August 2007
    Risk prediction in familial cancer syndromes.
180. Yale University, Department of Biostatistics, April 2008:
    Statistical Methods for Mutational Analysis of Cancer.
181. Johns Hopkins University, Department of Biomedical Engineering, December 2008:
    Gene Set Analysis as a Tool for Cross-Platform Integration in Genomics.
182. Harvard School of Public Health, Department of Biostatistics, September 2008:
    Thinking quantitatively about cancer genes.
183. University of Wisconsin, Department of Biostatistics, September 2008:
    Thinking quantitatively about cancer genes.

184. Harvard School of Public Health, Department of Biostatistics, September 2009: *Integrating diverse genomic data with gene sets.*

185. Dana-Farber Cancer Institute, Department of Biostatistics & Computational Biology, October 2009: *Modeling risk in families with cancer.*

186. Harvard School of Public Health Program in Quantitative Genomics, November 2009: *Cross-study Differential Gene Expression.*

187. Harvard School of Public Health, Department of Biostatistics, January 2010: *Assessing Risk in Families with Cancer.*

188. Harvard Center for Biomedical Informatics, Countway Library, July 2010: *Modeling Risk in Families with Cancer.*

189. Massachusetts General Hospital, Biostatistics Center, September 2010: *Statistical Issues in Cancer Genome Sequencing Studies.*

190. University of Massachusetts Amherst, Department of Mathematics and Statistics, November 2010: *Statistical Issues in Cancer Genome Sequencing Studies.*

191. National Human Genome Research Institute, Division of Intramural Research February 2011: *Statistical Issues in Somatic Mutation Studies of Cancer.*

192. Memorial Sloan Kettering Cancer Center, Department of Epidemiology and Biostatistics, March 2011: *Statistical Issues in Cancer Genome Sequencing Studies.*

193. Brown University, Center for Statistical Sciences, April 2011: *Statistical Issues in Cancer Genome Sequencing Studies.*

194. University of Connecticut Seminar Series, November 2011: *Bayesian Effect Estimation Accounting for Adjustment Uncertainty*

195. The University of Texas MD Anderson Cancer Center, Department of Bioinformatics and Computational Biology, January 2012: *Gene set analysis as a tool for cross-platform integration in genomics.*

196. Massachusetts General Hospital Multidisciplinary Breast Rounds, February 2012: *Breast Cancer Risk Models and Web Services.*

197. Fred Hutchinson Cancer Research Center, Division of Public Health Sciences, February 2012: *Gene Set Analysis as a Tool for Cross-Platform Integration in Genomics.*

198. University of Washington, Department of Biostatistics, March 2012: *Bayesian Effect Estimation Accounting for Adjustment Uncertainty.*

199. Harvard School of Public Health Department of Epidemiology, March 2012: *Analyzing genome-wide data by gene set: history, caveats, and recent trends.*

200. Department of Statistics, Wharton School at University of Pennsylvania, April 2012: *Bayesian Effect Estimation Accounting for Adjustment Uncertainty.*

201. Tufts Medical Center, Biostatistics Research Center, January 2013: *Statistical Issues in Cancer Genome Sequencing Studies.*

202. Center for Biomedical Informatics Seminar Series, Harvard Medical School, April, 2013: *Validation of molecular signatures in cancer.*

203. Program in Molecular and Genetic Epidemiology Seminar Series, Harvard School of Public Health, April 2013: *Evaluating the predictiveness of genomic signatures by systematic reviews and cross-study reproducibility.*

204. Clinical Investigators Seminar Series, Dana-Farber Cancer Institute, April 2013: *Validation and Clinical Utility of Genomic Signatures.*

205. Department of Biostatistics, Boston University, September 2013: *Statistical modeling of somatic mutation data*.

206. Center for Translational and Public Health Genomics, The University of Texas M. D. Anderson Cancer Center, January 2014: *Cross-study Reproducibility of Predictions, with Application to Genomics*.

207. Big Data Seminar Series, Department of Biostatistics, Harvard School of Public Health, February 2014: *Cross-study Replicability of Predictions, with Application to Genomics*.

208. Neyman Seminar Series, Department of Biostatistics, University of California at Berkeley, December 2014: *Cross-study Reproducibility of Predictions, with Application to Genomics*.

209. Computational and Systems Biology Seminar Series, UT Southwestern, December 2015: *Cross-study Analysis of Prediction Algorithms in Genomics*.

210. The MBI Colloquium, The Ohio State University, April 2016: *Cross-study Performance of Predictions, with Application to Genomics*.

211. Stanford University, Center for Population Health Sciences, September 2018 *Knowledge management and decision support for commonly tested susceptibility mutations*.

212. Università L. Bocconi, BIDSA, Dondena and IGIER Research Centers Joint Seminar, November 2018: *Training replicable predictors in multiple studies*.

213. University of Pisa, Department of Clinical and Experimental Medicine, June 2018: *Knowledge management and decision support for commonly tested susceptibility mutations*.

214. Norwegian University of Science and Technology, Department of Statistics, June 2019: *Training replicable predictors in multiple studies*.

215. Moffit Cancer Center, Department of Integrated Mathematical Oncology, September 2019: *Training replicable predictors in multiple studies*.

Interviews

1. NPR story on Axillary Lymph Nodes in Early Breast Cancer, by Diane Toomey, WUNC Radio, UNC-Chapel Hill. Broadcast on May 6, 1999. [Transcript]

2. *Nodes Under Fire*. Short television story on Axillary Lymph Nodes in Early Breast Cancer, by Ivanhoe Broadcasting, 1999.

3. Live webcast interview on *Familial risk prediction in breast cancer*, April 30, 2001. [Transcript].

4. Radio 3 Scienza interview about the Human Protein Interactome, 2006. [Podcast].

5. Cancer Therapy Advisor interview about Adaptive Randomization and the I-SPY 2 Trial Platform, 2016. [Article]

TEACHING

Program Leadership

Co-chair of Steering Committee developing the Bioinformatics MHS, School of Public Health, 2002–2004.

Courses [5]

COURSES AT CARNEGIE MELLON:

Probability and Applied Statistics for Physical Scientists and Engineers, Summer 1987.

Statistical Concepts with Computer Applications, Summer 1988.

Engineering Statistics and Quality Control, Fall 1990 and Spring 1991.

COURSES AT DUKE:

Statistics and Data Analysis for Economics (STA110-B) Fall 1998.

* Probability and Statistics in Engineering (STA113) Fall 1991–1993, Spring 1992–1994.
    Developed *Using Probability to Learn from Data* (with M. Lavine).
    Supplement on Bayesian statistics for the Underate Engineering curriculum.

Statistical Inference (STA215) Spring 1994, Spring 1995.

* Statistical Decision Theory (STA226) Spring 1992, 1993, 1998, and 1999; Fall 1995 and 1996.
    Developed notes for *Decision Theory: Principles and Approaches* (with L. Inoue).

Experimental Design (STA246) Spring 1995 (co-taught).

Topics in Statistics (STA 294) Spring 1995 (co-taught).

COURSES AT JOHNS HOPKINS:

Oncology Fellows Journal Club 1999–present (statistical discussant)

* Decision Theory for Biomedical Applications, 4th term 1999/00. [Course Website]
    Taught from the book: *Modeling in Medical Decision Making*.

* Statistics for Gene Expression, 4th term 2000/01, 2001/02 and 2002/03.
    [2001 Course Website] [2002 Course Website] [2003 Course Website]

* Statistical Topics in Genetics and Genomics, 2th term 2002/03.
    Co-taught with K. Broman

* Analysis of Biological Sequences, 2nd term 2004/04 and 2004/05.
    Co-taught with S. Chen

* Foundation of Statistics I: Decision Theory, 3rd term 2003/04, 2004/05, 2005/06 and 2006/07; 1st term 2008/09.

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[5] Starred courses involved substantial course development

COURSES AT HARVARD:

- Methods for Comparative Effectiveness Research, Spring 2012

- Statistical Inference II, Spring 2015

- Freshman Seminar: My Genes and Cancer, Spring 2016, Fall 2016, Spring 2018.

- Data Analysis in Modern Biostatistics, Spring 2017, Spring 2018.

SHORT COURSES:

* *Utility and Decision Making*, Università di Pavia, May 1993.

  Bayesian Biostatistics: Applications to Clinical and Pharmaceutical Research. Houston, TX, January 2001;

* *Gene Expression Data Analysis*; Graduate Summer Institute of Epidemiology and Biostatistics, JHU, 2002. [Course Website]

  Gene Expression Data Analysis; Food and Drug Administration, Rockville, MD January 2004.

  Genomics Data Analysis and Clinical Trials; Food and Drug Administration, Rockville, MD July 2009.

  Statistical Genomics, Summer School on Modern Methods in Biostatistics and Epidemiology, Cison di Valmarino-Treviso, Italy, June 2010

  Bioinformatics, Istituto di Genetica Molecolare, CNR Pavia Italy, Co-taught with L. Marchionni, July 2014

  Multi-Study Biomarker Analysis, University of Florence, Department of Statistics.

Advising

UNDERGRADUATE STUDENT ADVISING AT HARVARD:

Honor Theses
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Student	Year	Title
Ina Jazic	2013	*Cross-Talk Analysis in Breast Cancer Tissues*
Benjamin Mu-En Hsu	2017	*Understanding the Mutation Process in Normal Cells through Simulations and Cancer Sequencing Data* (co-advised with Cristian Tomasetti
Benjamin Glass	2018	*Accounting for Differing Feature Sets when Training Predictors in Multiple Studies*
Tessa Han	2020	*Applying Mediation Analysis to Predict Feed Forward Loops as Gene Regulatory Mechanisms in Multiple Myeloma – A Novel Statistical Approach*
Tejal Patwardan	2020	*A Method to Systematically Identify Casual Genes for Common Diseases*

PhD Thesis committee member of Gabriel Huerta, Lurdes Inoue and Chengchang Li.

Master Thesis supervisor of Richard Realbuto, Zhong Shen, Ying Su.

Master and PhD Thesis external member of Kerem Harmanci, Department of Electrical and Computer Engineering.

GRADUATE STUDENT ADVISING AT DUKE:

PhD Theses

Student	Year	Title
Heather DeSimone	1996	*Prediction Using Orthogonalized Model Mixing*
Fusheng Su	1996	*Limit Theorems on Deviation Probabilities with Applications in Two-Armed Clinical Trials*
Heidi Ashih	2000	*Joint Estimation of Mammographic Sensitivity and Tumor Growth*
Daniel Gudbjartsson	2000	*Multipoint Linkage Analysis based on Allele Sharing Models*
Xi "Kathy" Zhou	2002	*Classification of Missense Mutations of Disease Genes*

PhD Thesis committee member of Gabriel Huerta, Lurdes Inoue and Chengchang Li.

Master Thesis supervisor of Richard Realbuto, Zhong Shen, Ying Su.

Master and PhD Thesis external member of Kerem Harmanci, Department of Electrical and Computer Engineering.

GRADUATE STUDENT ADVISING AT JOHNS HOPKINS:

PhD Theses

Student	Year	Title
Natalie Blades	2002	*Statistical Methods for Serial Analysis of Gene Expression*
Dongmei Liu	2005	*Inference on functional classes using gene expression data*
Cristian Pattaro	2005	*Haplotype block partitioning as a tool for dimensionality reduction in complex disease modeling*
Valeria Edefonti	2006	*Integrating Supervised and Unsupervised Learning in Genomics Applications*
Hormuzd Katki	2006	*Extending Mendelian Models That Predict if One has a Disease-Causing Mutation Based on Family History of Disease*
Ainong Zhou	2006	*Bayes factors comparing two multi-normal covariance matrices and their application to microarray data analysis*
Robert Scharpf	2007	*Combining high-throughput genomic data: methods and utility*
Wenyi Wang	2007	*Statistical Methods for Cancer Risk Assessment and Copy Number Estimation*
YenYi Ho	2009	*Gene Association Networks and Higher Order Interactions: Algorithms and Statistical Models*
Simina Boca	2011	*Analysis of Cancer Genome Data*

MHS Thesis supervised or co-supervised, *and areas*
  Jian Wang   *Comparison of classification approaches for microarray data*

MPH Thesis supervised or co-supervised, *and areas*
  Rosemary Braun   *Searching for differentially expressed gene-pathway combinations*

PhD Thesis committee member for Majnu John, Mary Lin, Xiaogang Zhong (Applied Mathematics and Statistics) Michelle Shardell, Rongheng Lin (Biostatistics) Sonja Berndt, Elizabeth Brown, Preeta Rajamaran, Reiko Sato (Epidemiology) Erica Breslau, Helen Meissner, Claire Snyder (Health Care Policy and Management), Micheal Zilliox (Molecular Microbiology and Immunology), Genevieve Weber (Neurosurgery), Xiao Liu, Matthew Pletcher and Nidhi Saran (Physiology).

PhD Oral exam committee member for Majnu John, Xiaolin Wu (Applied Mathematics and Statistics) Hormuzd Katki (Biostatistics) Janine Genking, Elizabeth Brown, Preeta Rajamaran (Epidemiology) Helen Meissner (Health Care Policy and Management) Xiao Liu, Matthew Pletcher (Physiology), Jerry Cai (Genetic Medicine) and Michael Zilliox (Molecular Microbiology and Immunology).

SKCCC Cancer in the Under-Privileged Indigent or Disadvantaged summer fellowship: Ije Abejoma.

GRADUATE STUDENT ADVISING AT HARVARD:

PhD Theses

Student	Year	Title
Danielle Braun	2014	*Statistical Methods to Adjust for Measurement Error in Risk Prediction Models and Observational Studies*
Yifan Zhang	2014	*Bayesian Adaptive Clinical Trials*
Christina McIntosh	2017	*An Analysis of Using Pedigrees in Family Based Studies and an Exploration of Cancer Risk and Cancer Resistance Using Twin Studies*
Theodore Huang	2019	*Statistical and Machine Learning Approaches for Family History Data*
Yuqing Zhang	2020	*Statistical and Computational Methods for Understanding and Addressing Heterogeneity in Genomic Data Analysis for Personalized Medicine*
Zoe Guan	2020	*Statistical and Machine Learning Methods for Clinical Risk Prediction*
Margaux Hujoel	2020	*Statistical inferences about the genetic architecture of disease (co advised with Alkes Price)*
Maya Ramchandran		*In Progress*
Gabriel Loewinger		*In Progress*
Cathy Wang		*In Progress*
Jane Liang		*In Progress*

PhD Thesis committee member of Matthew Cefalu, David Zhou, Alejandro Quiroz Zarate, Yuqing Zhang, Sarah Anoke, Claire Pernar, Ericka Ebot, Emma Schwager, Georgia Papadogeorgou, Boyu Ren, Emma Thomas, Tom Madsen, Sam Tracy, Kelly Mossesso, Matt Ploenzke, Yuxi Liu, Sarah Kalia, Eric Dunipace, Deborah Plana.

MS Thesis supervised or co-supervised, *and areas*
  Linying Zhang   *Interactio*
  Caleb Bae   *Variant-l*
  Xutao Wang *Investigation of ensemble learning methods and weighting strategies in multiple studies*
  Yunqi Yang
  Tianqi Chen
  Yujie Wu

GRADUATE STUDENT AWARDS:

Natalie Blades:

2003: Merrell Award for outstanding research by a PhD student. Johns Hopkins School of Public Health, Department of Biostatistics.

Wenyi Wang:

2005 The June B. Culley Award for outstanding achievement in the second-year oral exam, Johns Hopkins School of Public Health Biostatistics.

2006 Travel Award for the International Genetic Epidemiology Society 15th Annual Meeting.

2006 Student Conference Fund Award at Johns Hopkins Bloomberg School of Health, The 15th Genetic Analysis Workshop.

2007: Travel Award for the 11th International Conference on Research in Computational Molecular Biology.

2008: Elected member of Phi Beta Kappa Society, Johns Hopkins University.

2008: Elected member of Delta Omega Honor Society, Alpha Chapter Johns Hopkins Bloomberg School of Public Health.

2008: The Jane and Steve Dykacz Award for outstanding student paper in medical statistics Johns Hopkins School of Public Health Department of Biostatistics.

Hormuzd Katki:

2006: Merrell Award for outstanding research by a PhD student. Johns Hopkins School of Public Health, Department of Biostatistics.

Dongmei Liu:

ENAR travel award.

Simina Boca: 2007: Glaxo SmithKline Award, for outstanding achievement on the Department of Biostatistics first-year exam.

Rob Scharpf:

2007: Merrell Award for outstanding research by a PhD student. Johns Hopkins School of Public Health, Department of Biostatistics.

Chi Wang:

Distinguished Student Paper Awards. Biometric Society, ENAR.

Valeria Edefonti:

2008: Best Doctoral thesis in Statistics. Italian Statistical Society, 2008

POSTDOCTORAL FELLOWS MENTORING AT JOHNS HOPKINS:

Fellow	Years	Area
Sining Chen	2003-05	*Risk prediction in familial cancer*
Qiushan Tao	2004-05	*Networks in genomics*
Jianweng Zhang	2004-05	*Genomics of resistance to chemotherapy*
Marcel Dettling	2004-06	*Multivariate Differential Expression*
Luigi Marchionni	2005-07	*Multi-study genomic data analysis*
YuChuan Tai	2005-07	*Spatial modeling of cancer-causing mutations*
Suraj Peri	2005-07	*miRNA analysis*
Betty Doan	2005-09	*Colonoscopy screening modeling*
Sierra Min Li	2006-07	*Bayesian Variable Selection*
Loris Mularoni	2008-11	*Sequence Analysis*
Jeff Leek	2008-09	*Microarray-based classification*
Corrie Joshu	2008-10	*Colorectal Cancer Risk*

POSTDOCTORAL FELLOWS MENTORING AT HARVARD:

Fellow	Years	Area
Svitlana Tyekucheva	2008–11	*Next Generation Sequencing*
Lorenzo Trippa	2009–11	*Bayesian Modeling*
Victoria Wang	2010–11	*Cross-Platform Genomic Integration*
Emanuele Mazzola	2010–12	*Models for in situ breast carcinomas*
Jie Ding	2008–13	*Modeling Signaling Pathways*
Cristian Tomasetti	2011–13	*Mathematical modeling of cancer evolution, drug resistance, stem cell dynamics*
Levi Waldron	2011–13	*Improving the reproducibility and robustness of conclusions drawn from high-dimensional genomic data, focusing on translational relevance*
Steffen Ventz	2012–15	*Adaptive clinical trials, next generation sequencing methodology*
Reuma Admanit	2012–15	*Ovarian cancer prognosis, AIDS research*
Naim Rashid	2013–14	*High dimensional data analysis, genomics, statistical genetics, next generation sequencing data analysis, classification, variable selection in non-independent data*
Mehmet Samur	2013–15	*Bioinformatics, Genomics and Computational Biology, Next generation sequencing and integrative data analysis, gene networks*
Danielle Braun	2014–16	*Cancer risk prediction, comparative effectiveness research, measurement error*
Alice Cleynen	2014–15	*Statistical genetics; Decision theory, survival analysis, model selection*
David Mosen Ansorena	2015–16	*Statistical analysis of high-throughput genomics; Genomic copy number analysis in cancer; Algorithmics and optimization problems*
Nathanael Fillmore	2016–17	*Machine learning, medical informatics, multiple myeloma*
Anil Aktasamur	2016–	*Alternative splicing, multiple myeloma genomics*
Prasad Patil	2016–19	*Personalized medicine, genomic biomarker development, prediction, study reproducibility/replicability, data visualization*
Boyu Ren	2017–	*Bayesian nonparametrics*
Marco Roncador	2018–19	*Mutational signatures, multiple myeloma genomics*
Andrea Arfé	2019–	*Bayesian adaptive trials*

SERVICE

EDITORIAL WORK

Associate Editor, *Journal of the American Statistical Association — Theory and Methods*, 1999–2002.

Associate Editor, *Journal of the American Statistical Association — Applications and Case Studies*, 2003–2007.

Associate Editor, *Biometrics*, 2000–2002.

Editorial Board Member of *Medical Decision Making*, 1999–2005.

Editorial Board Member of *Source Code for Biology and Medicine*, 2005–present.

Book Series Editor, *UseR!*, Springer, 2004–present.

Statistical Board of Reviewing Editors (SBoRE) Member, *Science Magazine*, 2014–present.

Referee for: *American Journal of Epidemiology*, *American Journal of Human Genetics*, *Annals of Applied Statistics*, *Annals of Internal Medicine*, *Bioinformatics*, *Biometrics*, *Biometrika*, *Cancer Research*, *Clinical Chemistry*, *Computational Statistics and Data Analysis*, *Journal of Biomedical Informatics*, *Journal of the American Statistical Association*, *Journal of Econometrics*, *Journal of Statistical Computations and Graphics*, *Journal of Statistical Planning and Inference*, *Journal of the Royal Statistical Society B*, *Medical Decision Making*, *New England Journal of Medicine*, *Statistics in Medicine*.

Book reviewer for MIT Press, McMillan, Marcel Dekker, Springer, Wiley.

GRANT REVIEWS

Grant proposal reviewer for:

Alberta Heritage Foundation for Medical Research;

Department of Higher Education and Scientific Research, Italy;

National Coordinating Center for Health Technology Assessment;

CIHR, Canada Research Chairs

Swiss National Science Foundation

NIH Study Sessions:

CA-99-013 "Cancer Surveillance Modeling Network (CISNET)", 1999

NIH "Genome" Study Section, *Ad hoc* member, 2003.

NIH "Genomics, Computational Biology and Technology" Study Section, *Ad hoc* member, 2004.

NIH Special Emphasis Panel/Scientific Review Group 2007/01 ZCA1 RTRB-2. *Ad hoc* member, 2006.

NIH Special Emphasis Panel/Scientific Review Group 2008/05 ZRG1 HOP-Z (29) "Diversity Predoctoral Fellowship" *Ad hoc* member, 2008.

NIH "Epidemiology of Cancer" Study Section, *Ad hoc* member, 2007. Charter member 2008–2012.

NIH Site Visits:

P01 "Statistical Methods for Medical Studies", Fred Hutchinson Cancer Research Center, 2000.

National Science Foundation Panels

Mathematical Biology 2019

PANELS, COMMITTEES AND ADVISORY BOARDS

Member, American Cancer Society's *Breast Cancer Risk Communication* workshop and consensus statement. October 1999.

Member, NIH-NIDDK mPSA Biomarkers Consortium External Advisory Panel. 2002–2005.

Member (Chair since 2018), External Advisory Committee, The University of North Carolina-Chapel Hill Innovative Methods Program for Advancing Clinical Trials (IMPACT), 2010-present.

Member, The University of Texas M.D. Anderson Cancer Center CCSG External Advisory Board. 2010–present.

Member, Case Western University SPORE in Gastrointestinal Cancer External Advisory Board. 2009–present.

Member, External Advisory Board, R01 "Personalizing NSCLC Therapy: Exploiting KRAS Activated Pathways". 2011-2014.

Member, Scientific Advisory Board, The Akbaraly Foundation, 4AWoman Project to Fight against Gynecological and Breast Cancer, 2012-present.

Member, Steering Committee, National Brain Tumor Society Endpoints. 2012-present.

Member, Committee on Applied and Theoretical Statistics (CATS), National Academies of Science. 2012-2015.

Member, Intelligence Science and Technology Experts Group (ISTEG), The National Academies of Sciences, Engineering, and Medicine, 2015-present.

Member, External Advisory Board, Pancreatic Cancer SPORE at UNC-Chapel Hill, 2016-present.

Member, External Advisory Board, Dana Farber Physical Science / Oncology Center. 2016-present.

Member, The Fred Hutchinson Cancer Research Center CCSG External Advisory Board. 2018–present.

Member, National Academies study committee on Assessment of Options for Managing Cancer Risks Associated with Radiation Exposure following Crewed Space Missions.

PROFESSIONAL SOCIETIES

Member of Sigma Xi, IMS, ISI, ASA, SMDM, AACR and Biometric Society.

International Biometric Society / ENAR.

    Member of the ENAR Regional Advisory Board, 2000-2003.

    Member of the ENAR Education Advisory Committee 2004.

American Statistical Association: Section on Risk Analysis.

    Charter Member, 1995.

    Publication Officer, 1998-1999.

    Chair, 2002.

International Society for Bayesian Analysis

    Member of the presidential nominating committee. 1995.

CONFERENCES

Ideator and organizer (with D. Draper and M. West) of the Workshop on Model Uncertainty and Model Robustness, Bath, England, June 30 and July 1, 1995.

Program Committee member of the III-rd World Meeting of the International Society for Bayesian Analysis, Oaxaca, Mexico, 29-30 September 1995.

Chair of the program committee and organizing committee of the Workshop on Stochastic Model Building and Variable Selection, Duke University, October 9 and 10, 1997.

Member of the scientific committee of the International Workshop on Foundational Issues and Statistical Practice, October 14–16, 1999 Bibbiena, Italy.

Co-organizer of the IMA Workshop on Statistical Methods for Gene Expression: Microarrays and Proteomics. Minneapolis, September 2003.

Member of the scientific committee of the Genomic Signal Processing and Statistics (GENSIPS) workshop on "Computational Techniques for Genomic Regulatory Networks", Baltimore, May 26-28, 2004.

Member of the scientific committee of the Third Annual AACR International Conference on Frontiers in Cancer Prevention Research, Seattle, October 16-20, 2004.

Member of the scientific committee of the Second International IMS/ISBA Joint Meeting, Bormio, Italy, January 12-14, 2005.

Scientific Committee. AACR Annual Meeting 2018.

Session organizer.

    1996 ENAR meetings. Richmond, VA. Invited session.

    1996 Joint Statistical Meetings. Chicago, IL. Special contributed session.

    1998 Joint Statistical Meetings. Dallas TX. Invited session.

    1999 Joint Statistical Meetings. Baltimore MD. Invited session.

AWARD COMMITTEES

ASA, Risk Analysis Section. Best Contributed Paper Award, 1999—2003.

ASA, Risk Analysis Section. Student Travel Award, 2001—2003.

Myrto Lefkopoulou Lecture, 2000

Savage Award Committee, 2004—2007.

SERVICE AT DUKE

Committee for the revision of the ISDS PhD curriculum. 1991/92 and 1998/99.

Committee for Ph.D. Exam, 1991/92 1992/93 and 1996/97.

Organizer of the ISDS Departmental Seminar. 1992/93 through 1994/95.

Organizer of the ISDS Student/Faculty Workshop. 1992/93 through 1994/95.

Committee for the Review of the ISDS PhD program. 1997-1998.

SERVICE AT JOHNS HOPKINS

Administration

Director, Bioinformatics Shared Resource, Kimmel Cancer Center. 2004–2009.

Committees

Organizer, Gene Expression Methodology Seminar Series, Department of Oncology, 1999–2001.

Organizer, Grand Rounds, Department of Biostatistics, 2000–2002.

Organizer, Genomics Working Group, Departments of Oncology and Biostatistics, 2001–2003.

Chair, Search Committee for Oncology Biostatistics faculty position, Department of Oncology, 2001.

Member, Search Committee for Genetic Epidemiology faculty position, Department of Epidemiology, 2001.

Member, Advisory Board for the JHMI Microarray Core Facility, School of Medicine. 2002—2009.

Chair, Steering Committee for Genomics in Public Health, School of Public Health, 2002–present.

Member, *Ad hoc* committee to evaluate the cancer prevention and control program, School of Medicine, 2002–2003.

Ad hoc member, Appointment/Promotion Committee, School of Public Health, 3 associate professor cases.

Member, Committee on information technology in research, Department of Oncology 2003–2004.

Member, Shared Resources Committee, Department of Oncology, 2003–present.

Member, Search Committee for Director of the Cancer Prevention and Control Program in the Cancer Center. 2003–2004.

Member, Search Committee for Director of Information Technology in the Cancer Center. 2004–2005.

Chair, Joint Search Committee for Bioinformatics Faculty in Oncology, Biostatistics and MMI. 2004–2005 and 2005–2006.

Member, Search Committee for Biostatistics Faculty in Oncology. 2007–2008.

SERVICE AT HARVARD

Chair, Task Force on Research Computing, DFCI Strategic Plan 2012.

Chair, Senior Faculty Search Committee, Cancer Epidemiology and Cancer Prevention, HSPH, 2014.

co-Chair, Task force on Prevention and Early Detection; DFCI Strategic Plan 2018.

Member, Executive Committe on Research, DFCI, 2009-2018.

Member, Executive Committee, DF/HCC, 2009–present.

Member, Committee of Comparative Effectiveness, HMS, 2010–2011.

Member, Subcommittee on the Degree of Doctor of Philosophy in Biostatistics, HSPH 2010–2011, 2012-2014, 2014-2015.

Member, Committee on Professional Conduct, HSPH, 2010-present.

Member, External Advisory Board, Cancer Genetics Program, DFCI, 2010.

Member, Milton Fund Committee, HU 2010-present.

Member, Scientific Council, DF/HCC 2010-present.

Member, Office for Faculty Development Advisory Committee, DFCI, 2011-present.

Member, OnCore Faculty Advisory Committee, DFCI, 2012-2013.

Member, Faculty Database Steering Committee, DFCI 2012-2018.

Member, Research Computing Working Group, DFCI, 2012-2014.

Member, Internal Advisory Board for the Harvard Cancer Prevention Education and Career Development Program, 2013-present.

Member, Claudia Adams Barr Funds Review Committee, DFCI, 2014-present.

Member, Junior Faculty Search Committee (Genetics), DFCI, 2014.

Member, Junior Faculty Search Committee (Center for Cancer Precision Medicine), DFCI, 2013-2014.

Member, Junior Faculty Search Committee (Biostatistics), CHB, 2010, 2014

Member, Junior Facuty Search Committee (Medical Oncology), DFCI, 2013-2014.

Member, Junior Faculty Search Committee (Biostatistics), HSPH, 2009-2010. 2010-2011, 2013-2014.

Member, Senior Vice President of Research Administration Search Committee, DFCI, 2013-2014

Member, Research Backfill Task Force, Dana-Farber Cancer Institute, 2013-2014.

Member, Faculty Advisory Committee of the Harvard Office for Scholarly Communication, HU 2015-present.

member, Dana-Farber Cancer Institute Award Nomination Committee, 2014—present.

Member, Casty Award Selection Committee 2013—present.

Member, Medical Oncology Chair Search Committee, DFCI, 2017.

Member, Junior Faculty Search Committee (Biomedical Informatics), DFCI and HMS, 2017.

Member, Dana-Farber Cancer Institute Office of Faculty Affairs faculty Advisory Board, 2015—present

Member, Dana-Farber Cancer Institute Committee for Women Faculty, 2018—present

Member, Dana-Farber Cancer Institute Strategic Planning Committee (Cancer Prevention), 2018—present.

Member, Steering Committee, The Zhu Family Center for Global Cancer Prevention, Chan School of Public Health, 2018—present.

Member, Dana-Farber Cancer Institute Promotion Committee, 2019—present.

Member, Early Career Faculty Development Fund: Review Committee. 2019—present.

EXTERNAL ACTIVITIES

Consultant, Italian Association of Machine-tool Producers (UCIMU), Milan, Italy, 1985—1986.

Consultant, Lombardy's Institute of Regional Research (IRER), Milan, Italy, 1985—1986.

Consultant, Institute for Social Research, Milan, Italy, 1985—1986.

Consultant, PPG Industries, Pittsburgh, PA 1989—1991.

Consultant, Becton Dickinson Technologies, RTP, 1997—1999.

Consultant, Requisite Consulting, Chapel Hill, 1999–2000.

Consultant, RTI, Research Triangle Park, 2009.

Member, Scientific Advisory Board, Counsyl, 2007–2018

Member, Scientific Advisory Board, CRA Health 2010–present.

Book Series Editor, UseR, Springer, 2010-present.

Consultant, Dainippon Sumitomo Pharma Co Ltd, 2014.

Consultant, Metamark, Boston, 2014.

Member, Scientific Advisory Board, Konica-Minolta Precision Medicine, 2018–present.

Co-founder and Chair of Scientific Advisory Board, Phaeno Biotechnology, 2018–present.

Member, Data Safety Monitoring Board, Geisinger, 2018—present.

Consultant, Biogen, 2019—present.

Expert witness, Turner Boyd. 2019—2020.

Expert witness, Gibson, Dunn & Crutcher LLP 2019.