CHIARA SABATTI

May 10, 2019

PERSONAL DATA

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ACADEMIC HISTORY

Degrees

B.S. and M.S. summa cum laude in Economics and Statistics, Bocconi University, Milan, Italy (1993).
Professor Eugenio Regazzini, advisor.

Ph.D. in Statistics, Stanford University, Stanford, CA (1998).
Professor Jun Liu, advisor.

Postdoctoral Training

Genetics Department, Stanford Medical School, Stanford, CA (1998-2000).
Professor Neil Risch, advisor.

EMPLOYMENT

Current Professor of Biomedical Data Science and Statistics, Stanford University. Member of BioX and of the Biomedical Informatics Training Program. Associate Chair of the Department of Biomedical Data Science (since September 2018).

November 2015–July 2016 Associate Professor of Biomedical Data Science, Stanford University.

January 2015–July 2016 Associate Professor of Statistics, Stanford University.

September 2009–October 2015 Associate Professor of Health Research and Policy, division of Biostatistics, Stanford University.

July 2009–August 2011 Professor of Human Genetics and Statistics, University of California, Los Angeles. (On leave for part of the period.)

July 2006–June 2009 Associate Professor of Human Genetics and Statistics, University of California, Los Angeles. Associate of UCLA-NASA Institute for Cell Mimetic Space Exploration (2003–2008). Associate of the UCLA Center for Society and Genetics (2004–2009).

July 2000–June 2006 Assistant Professor of Human Genetics and Statistics, University of California, Los Angeles.

HONORS AND MEMBERSHIPS IN PROFESSIONAL SOCIETIES

- "Vasa cube" award for continuous commitment to *Fiat lux* seminars (2008).
- NSF Division of Mathematical Sciences CAREER award (2003).

- UCLA Career award (2002-3)
- Statistics Department Teaching Assistant Award, Stanford University (1998)
- Doctoral Research Fellowship of the Italian Ministry of University and Scientific Research, declined (1993)
- Fellowship "Amici della Bocconi" (1993-1994)
- Fellowship "Credito Bergamasco" (1993 and 1991)

Member of the American Society of Human Genetics, the American Statistical Association, the Institute of Mathematical Statistics, and the International Society for Computational Biology.

PUBLIC AND PROFESSIONAL SERVICE

Editorial Board Memebership

- Genetics (2012–present)
- Journal of the American Statistical Association (2011–2015)
- The Annals of Applied Statistics (2010–present)
- BMC Bioinformatics (2010–present)
- IEEE/ACM Transactions on Computational Biology and Bioinformatics (2004-2010)
- Biology Direct (Genomics, Bioinformatics, and Systems Biology section)
- Member of Faculty of 1000.

Journal Reviewer

Statistical Methodology The Annals of Applied Statistics, Bayesian Analysis, Biometrics, Biostatistics, IEEE Transactions on Image Processing, IEEE Transactions on Neural Networks, the Journal of the American Statistical Association, the Journal of Computational and Graphical Statistics, the Journal of the Royal Statistical Society B, the Journal of Statistical Planning and Inference, Statistica Sinica, Statistics and Computing, Statistics and Probability Letters.

Genetics and computational biology The American Journal of Epidemiology, the American Journal of Human Genetics, the Annals of Human Genetics, Bioinformatics, Biological Psychiatry, BMC Bioinformatics, BMC System Biology, the FASEB Journal, Genetic Epidemiology, Genetics, Human Heredity, the Journal of Cellular Biochemistry, Mathematical Biosciences, Nature Genetics, Nature Biotechnology, PLOS Genetics, PLOS Computational Biology, Statistical Applications in Genetics and Molecular Biology.

Science at large Proceedings of the National Academy of Science, Science.

Membership in grant review panels

- NIH, ad hoc review panel (October 2017).
- NIH, review panel for T32 (Biomedical Big Data) (October 2016).
- National Science Foundation (NSF) review panel for Statistics (January 2016).
- NIH Special Emphasis Panel on Genes, Genomes and Genetics (June 2015).
- NIH Special Emphasis Panel of the Therapeutic Approaches to Genetic Diseases (July 2014).

- NIH Special Emphasis Panel on Genetics of Health and Disease (November 2013).
- NIH Special Emphasis Panel on Computational Genetics and Genomics (March 2011).
- Genomics, Computational Biology and Technology study section [GCAT] (guest member February 2008, October 2008, October 2010).
- NIH Biostatistical Methods and Research Design study section (guest member, October 2007).
- Review Panel for the Statistics and Probability Program at the National Science Foundation (2003).

Ad hoc grant reviews

Reviewer of grant proposals to the National Science Foundation (DMS 2005, 2003; and MCB 2009, 2004), the Welcome Trust (2005, 2006), the UCLA AIDS institute, and the Netherlands Organization for Scientific Research, the United States–Israel Binational Science Foundation.
Reviewer of proposals for the Spectrum Pilot grants "Population Health Sciences and Community Engagement" (2012), the Seed grant opportunity in Big Data for Human Health (Winter 2014), the Stanford Data Science Initiative (Fall 2014).

Organization of Scientific Conferences

- IMS sponsored section at the Joint Statistical Meetings 2011: "Bioinformatics and Genomics," Miami, July 31st, 2011.
- Workshop "Computational Genetics," February 9, 2007, IPAM, Los Angeles.
- Session on "Statistical Genomics" for Interface 2006 "Massive Datasets and Streams," Pasadena, May 24-27, 2006.
- Workshop: "Sequence analysis towards system biology," IPAM January 9-13, 2006. (Co-organizer with Jun Liu.)
- Invited session titled "Genome-wide Association Analysis: Finding the Needles in the Haystack," at the ASHG Annual Meeting, Salt Lake City, October 25-29, 2005. (Co-organizer with M. Ritchie.)
- Member of the International Program Committee of the 27th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, September 1-5, 2005, Shanghai, China.
- Chair of the session on "Computational Genomics and Proteomics," 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, September 1-5, 2004, San Francisco.

Committee Service

Stanford

- Faculty search committee for HRP Biostat, Biomedical Data Science, and Statistics (fall 2015, winter 2016) (fall 2017, winter 2018); psychiatry (sleep; 2018).
- Faculty search committee for Associate Director of Population Science (Stanford Cancer Center, 2018)
- Member of the Data Science Design Team (Fall 2018)
- Member of the natural sciences pathways committee (2018)
- Co-chair of the committee for Planning for Undergraduate education in the Physical Sciences (winter 2017);
- Steering committee for Biomedical Data Science (summer and fall 2014; summer 2015);

- Executive committee for the France-Stanford Center for Interdisciplinary Studies (2012–present);
- Executive committee for the Center for Computational, Evolutionary, and Human Genomics (2012–present);
- Big Data in medicine initiative (2013–2014);
- Judicial Panels (2011– 2013);
- Strategic planning group for the Children's Health Research Institute at Stanford (2012);
- Search committee for an Associate Director for Population Sciences in the Stanford Cancer Center (2011-12);
- Population Sciences Focus Group (2011).

UCLA

- Provost's committee on faculty work/life issues (2008–2009)
- Executive committee for the Interdepartmental Program in Bioinformatics (2007–2009).
- Executive Committee on Information Technology for the Life Sciences in the UC-Industry Cooperative Research Program (2005–2009).
- UCLA Early Care and Education advisory board (2003–2009).
- Childcare Subcommittee of the Academic senate faculty welfare committee (2006–2007).

RESEARCH GRANTS

Research projects for which C.S. is the principal investigator are indicated with bold fonts.

Discovery Science Innovation Fund (PI: Sabatti)
Stanford School of Medicine 10/1/17– 9/30/19
Reproducible identification of cance cell types via scRNAseq

DMS 1712800 (PI: Sabatti)
NSF 09/01/17-08/31/20
Discovering what matters: informative and reproducible variable selection with applications to genomics

R01MH113078 (PI: Freimer; Stanford PI: Sabatti)
NIH /NIMH primary, subcontract from UCLA 4/1/2017–3/31/2022
Genetics of Severe Mental Illness

01MH110437 (PI: Zandi; Stanford PI: Sabatti)
NIH primary, subcontract from John Hopkins University 08/01/16–05/31/19
The Bipolar Sequencing Consortium for Combined Analysis and Follow-Up

U01MH105578 (PI: Freimer; Stanford PI: Sabatti)
NIH /NIMH primary, subcontract from UCLA 9/1/14 –8/31/18
Genomic Strategies to Identify High-impact Psychiatric Risk Variants

R01 MH101782 (PI: Sabatti)
NIH/NIMH 8/1/13–7/31/18
Genetic Regulation of Gene Expression and its Impact on Phenotypes

4UL1 TR001085 (PI: Greenberg)
NIH 9/26/13 ? 4/30/18
Stanford Center for Clinical and Translational Education and Research

Discovery Science Innovation Fund (PI: Olshen, Sabatti, Tian)
Stanford School of Medicine 9/1/14– 8/31/15
How do genes influence the interactions between multiple traits?

Discovery Science Innovation Fund (PI: Olshen, Sabatti, Tian)
Stanford School of Medicine 9/1/13– 8/31/14
New Approaches to Quantifying the Phenotype-Genotype Relationship

R01 HL118612 (PI: Nadeau and Miller)
NIH 9/1/13–8/31/17
Secondhand Smoke and Asthma: Mechanistic Outcomes of DNA Methylation in T Cells

U01 HG007419 (PI: Matise; Stanford PI: Bustamante)
NIH /NHGRI, subcontract from Rutgers 6/1/13 –5/31/17
NHGRI PAGE Coordinating Center

R01 HG006695 (PI: Sabatti)
NIH/NHGRI 4/1/13–3/31/17
New Statistical Methods for High Resolution Mapping of Multiple Phenotypes

R21 CA185804 (PI: Wang)
NIH 12/2/14–11/30/16
Analysis of CTC's for Early Prediction of Response to Treatment in RCC

R21 CA169964 (PI: Felsher)
NIH/NCI 8/1/12–7/31/14
Nanoscale proteomic profiles of hypoxia pathways to develop biomarkers of renal cell carcinoma

T32 GM096982 (PI: Tibshirani, Olshen, Sabatti)
NIH/NIGMS 7/1/12–6/30/17
Interdisciplinary Training Program in Biostatistics

R01 HL113315 (PI: Freimer, Palotie; Stanford PI: Sabatti)
NIH/NHLBI, subcontract from UCLA 6/15/12–3/31/17
Genomic and Metabolomic Profiling of Finnish Familial Dyslipidemia Families

R01 ES02092601 (PI: Nadeau)
NIH 6/1/12–2/28/17
Phenotyping/Epigenetic studies of PAH-associated Treg impairment in asthma

R01 MH095454 (PI: Freimer; Stanford PI: Sabatti)
NIH/NIMH, subcontract from UCLA 6/1/12–05/31/15
Genome Sequencing in Extended Bipolar Pedigrees

RC2 AG036607 (PI: Schaefer, Risch; Stanford PI: Tang)
NIH (ARRA), subcontract from Kaiser 9/30/09–8/31/12
A resource for genetic epidemiology research in adult health and aging

R01 GM053275-14 (PI: Lange)
NIH/NIGMS 4/01/08–3/31/13
Statistical Methods for Gene Mapping

P30 1MH083268 (PI: Bilder)
NIH 9/01/07–8/31/12
Interdisciplinary Research Consortia – Whole Genome Association Analysis Strategies for Multiple Phenotypes

R01 MH075007 (PI: Freimer)
NIH/NIMH 12/1/06–5/30/11
Bipolar Endophenotypes in Population Isolates

R01 HL087679-01 (PI: Peltonen)
NIH 10/10/06–9/30/09
Genetics of Cardiovascular Risk Factors in a Large Birth Cohor from a Founder Population

R01 MG078075-01 (PI: Ophoff)
NIH/NIMH 7/1/06–6/30/10
Genome-wide Association Study of Schizophrenia

R01 NS37484 (PI: Freimer)
NIH 4/1/04–3/31/09
Population Genetic Mapping of Tourette Syndrome

R01 GM53275 (PI: Lange)
NIH/NIGMS 4/1/04–3/31/08
Statistical Methods for Gene Mapping

CCF-0326606 (PI: Liao)
NSF 12/3/03-12/2/07
ITR:"Regulography"- Quantitative Reconstruction of Transcriptional Regulatory Networks

DMS0239427 (PI: Sabatti)
NSF 6/1/03–5/31/08
CAREER: Statistical and Computational Tools for the Analysis of High Dimensional Genetic Data

NCC2-1364 (PI: Ho)
NASA/AMES research center 9/1/02–8/30/07
Institute for Cell Mimetic Space Exploration (CIMSE)

TEACHING

Stanford Courses

Stats 48N: Riding the data wave, Fall 2012, Fall 2013, Fall 2014, Fall 2015, Fall 2016. I designed this introductory seminar to provide students with the awareness and some of the tools necessary to be citizens in our data rich world. `http://statweb.stanford.edu/~sabatti/Stat48/`

Stats 101: Data Science 101, Spring 2017, Spring 2018. I was a member of the "Data Science Working group" that designed this new class and will teach its second edition this spring.

Stats 200: Introduction to Statistical Inference, Winter 2018.
`http://statweb.stanford.edu/~sabatti/Stat200/`

Stats 367: Statistical Models in Genetics, Fall 2011, Winter 2015
`http://statweb.stanford.edu/~sabatti/Stat367/`

Stats 319: Satististic Literature: Inference and Selection, Winter 2014.

Stats 370: A course in Bayesian Statistics, Winter 2013, Winter and Spring 2016.
`http://statweb.stanford.edu/~sabatti/Stat370/`

Stats 390: Consulting Workshop, Fall 2011.

HRP 260: Workshop in Biostatistics (2010-2015).

Gene 271: Human Molecular Genetics, Fall 2010. Lectures on population genetics, linkage disequilibrium and association mapping.

Stats 190: Introduction to statistical methods for social scientists, Summer 1997.

UCLA Courses

Stat 202c: Monte Carlo Methods in Statistics. (2007-09)

Hum Gen 236: Advanced human genetics (2001-09) Responsible for lectures on population genetics and linkage disequilibrium.

Stat 180–236: Introduction to Bayesian statistics (2001-08).

HG 19–sem 2: Genetics enhancements and the quest for perfection. A fiat lux seminar, Winter 2008, Spring 2009.

Stat 19–sem 2: The science and morality of Genetics. A fiat lux seminar, Fall 2006.

Stat 254: Statistical methods for computational biology. (2002-2005) A core course for the interdepartmental PhD program in Bioinformatics.

Stat 189: Honors section for Stat 180, Winter 2005: "Early progress in statistics and links to the eugenics movement."

Stat 19–sem 5: Eugenics and statistics. A fiat lux seminar, Fall 2005.

Stat 19–sem 4: Decoding bioinformation. A fiat lux seminar, Fall 2003.

Hum Gen 210: Medical genetics. UCLA, Fall 2000. Responsible for a lecture on linkage and linkage disequilibrium methods.

Short Courses

- "XII CIMAT School in a Probability and Statistics," CIMAT in Guanajuato, Mexico, March 2014.
- "8th Annual Statistical Genetics Short Course for Obesity & Nutrition Researchers," San Diego, April 2008.
- "Statistical Genetics Short Course, featuring Mendel," UCLA, August 2006, August 2004, August 2001
- "Statistical genetics with Mendel," University of Pavia, July 2005.
- "Linkage and association analyses using mendel and SimWalk software," IGES meeting, November 2003.
- "DNA microarray workshop," UCLA September 14-15, 2002.
- "Bayesian genomics," Università degli Studi di Pavia, June 2002.
- "DNA Microarrays: The New Frontier in Gene Discovery and Gene Expression," Neuroscience 31st annual meeting in San Diego, November 10, 2001.
- "DNA microarray: principles and biotechnological applications," UCLA September 10-13, 2001.

Student Advising – Stanford

Undergraduate pre-major advisor for a total of 13 Freshmen (2010-12).

Undergraduate advisor for the inter-departmental major in Mathematical and Computational Science (2012–present; 35 current advisees)

Master students Provided research opportunities for Alden Timme (MS in Statistics, 2012) and Hadi Zarkoob (MS in MS&E, 2012).

Doctoral dissertation committee Henry Li (Structural Biology); Jingshu Wang (Statistics, Ph. D. 2016); Olivia Liao (Statistics, Ph.D. 2013); Arwen Meister (ICME, PhD 2013); Gourab Mukherjee (Statistics, Ph.D. 2013); Bokyung Choi (Applied Physics, Ph.D.2012); Nicholas Johnson (Statistics, Ph.D. 2011); Zhengqing Ouyang (Biology, Ph.D. 2010).

Doctoral Advisor for Eugene Katsevich (2016–present) and Junjie Zhu (2016–present).

Postdoctoral advisor for Christine Peterson (2014–2016, now at M.D. Anderson Cancer center) and for Zhongyang Zhang (2012, currently at Mount Sinai).

Training grants Co-director of the Training Program in Biostatistics for Personalized Medicine (2012-17); mentor for the training grant in Biomedical Informatics.

Student Advising – UCLA

Doctoral Advisor for the Statistics Ph.D. students Zhongyang Zhang (2008–2012, currently assistant professor at Mount Sinai); Jae Brodski (2006–2010; currently at Affymetrix); Hui Wang (2003–2006; currently at the Palo Alto VA); and Steve Erickson (2002–2006; recipient of the Chancellor fellowship and of the TAG training grant; currently at RTI international).

Master Advisor for Statistics students Chia-Ho Lin (M.S. 2005) and Kaiding Zhu (M.S. 2004).

Post-doctoral Advisor for Iouri Chepelev (September 2004–2007), currently at the Cincinnati Children's Hospital Medical Center.

Doctoral dissertation committee Alejandra Young (MBI, Ph.D. 2010); Michael Mason (Statistics, Ph.D. 2010); Samuel Strom (Human Genetics, Ph.D. 2010); Linh Tran (Chemical engineering, Ph.D. 2010); Sara Tajyar (MIMG, Ph.D. 2008); Allen Day (Human Genetics, Ph.D. 2008); Yuhan Lee (Genetics, Ph.D. 2008); Sara Tajyar (MIMG, Ph.D. 2008); Kristin Ayers (Biomathematics, Ph.D. 2008); Mark Brynilnsen (Chemical Engineering, Ph.D. 2008); Wei Sun (Statistics, Ph.D. 2007); Robert Riley (Human Genetics, Ph.D. 2007); Rebecca Krupp (MIMG, Ph.D. 2006); Ching-Ti Liu (Statistics, Ph.D. 2006); Angela Presson (Statistics, Ph.D. 2006); Ben Redelings (Biomathematics, Ph.D. 2006); Katherine Comanor (Electrical Engineering, Ph.D. 2005); Joseph Dougherty (Neuroscience, Ph.D. 2005); Yumao Lu (Electrical Engineering, Ph.D. 2005); Tianwei Yu (Statistics, Ph.D. 2005); Robert Granat (Electrical Engineering, Ph.D. 2004); Lars Rohlin (Chemical Engineering, Ph.D. 2004); Riccardo Boscolo (Electrical Engineering, Ph.D. 2003).

INVITED LECTURES

Conferences

- April 29–May 1, 2019, BFF6, Duke University: "Selecting Important Features in Presence of Correlation– a Story from Genetics."

- December 17–20, 2018, Joint Statistical Event, Jerusalem: "Controlling FDR while highlighting selected discoveries."
- October 29–November 2, 2018, Robust and High-Dimensional Statistics, Simons Institute, Berkeley: "Controlling FDR while highlighting selected discoveries."
- October 1–5, Bertinoro Computational Biology 2018, Bertinoro, Italy: "Controlling FDR while highlighting selected discoveries."
- July 24–24, 2018, Workshop on Principles of Adaptive Data Analysis, Simons Institute, Berkeley: "Controlling FDR while sorting through discoveries."
- January 10–12, 2018, Algorithmic Challenges in Protecting Privacy for Biomedical Data, IPAM, Los Angeles: "Knockoff genotypes: value in counterfeit."
- JSM 2017, July 29–August 3, 2017, Baltimore: "Selective inference in Genomics."
- Mathematical Methods of Modern Statistics, July 10-14, 2017, Marseille: "False discovery rate control in genetics."
- 2nd Probabilistic Modeling in Genomics Conference, September 12-14, 2016, Oxford, England: "Selective inference for gene mapping."
- Advances in Statistics, Probability and Mathematical Physics, June 10-11, 2016, Pavia, Italy: "Selective inference in genetics."
- Joint Statistical Meetings, August 9, 2015, Seattle: "Identifying genetic variants that regulate gene expression: how to insure reproducibility," (scheduled, but cancelled due to illness).
- Bertinoro Computational Biology—Statistical and Computational Genetics, Bertinoro, Italy, September 27-October 2, 2014: "Global error control in multiple phenotype mapping."
- Italian Society of Statistics Meeting, Cagliari, Italy, June 11-13, 2014: "In the mist of the data deluge, how to let the interesting findings surface? Tales from genetics." (Plenary speaker)
- 7th Annual Bayesian Biostatistics and Bioinformatics Conference, Houston, TX, February 12-14, 2014: "Multiple testing, family and selection in gene mapping."
- BigData in Biomedicine, Stanford, May 23, 2013: "Big data and reproducibility."
- ComBio2012, Adelaide, Australia, September 23–27, 2012: "Limiting false discoveries in mapping multiple phenotypes."
- Joint Statistical Meetings, San Diego, July 28–August 2, 2012: "Bayesian Models for rare genetic variants."
- BIRS workshop on Challenges and Advances in High Dimensional and High Complexity Monte Carlo Computation and Theory, Banff, March 18–23, 2012: "Rare variants in genomic studies and the potential of Bayesian models."
- IPAM workshop in Co-ancestry, Association, and Population Genomics, November 29–December 2, 2011: "Reconstructing CNV in a central american population."
- Joint Statistical Meetings, Miami July 30–August 4, 2011: "Reconstructing DNA copy number by penalized estimation and imputation"
- JSM 2009, Washington DC, August 1-6, 2009: "Modeling population structure in genomewide association studies."
- DIMACS Workshop on Computational Issues in Genetic Epidemiology, Rutgers University, August 21-22, 2008: "The genetics of quantitative traits: what's new since the days of R.A. Fisher?"

- International Chinese Statistical Association Applied Statistics Symposium, Piscataway, New Jersey, June 4-7, 2008: "Reconstructing Copy Number Variations with Illumina Platform."
- Bioinformatics, Genetics and Stochastic Computation: Bridging the Gap, Banff Centre, Alberta, Canada, July 1-6, 2007: "Volume measures for linkage disequilibrium."
- EMBO Practical Course on SNP Genotyping and Haploblock Analysis, Helsinki, August 21-27, 2005: "High density SNPs: genotype calling and other statistical issues."
- Joint Statistical Meetings, Minneapolis, August 11, 2005: "Transcription regulation networks."
- Joint Statistical Meetings, Minneapolis, August 8, 2005: "Bayes and empirical Bayes approaches for large-scale simultaneous hypothesis testing." (Discussion)
- Workshop on Genomewide Association Studies, Los Angeles, April 14, 2005: "Interpreting long stretches of homozygous markers in high density SNP genotyping."
- Plant and Animal Genome XIV Conference, San Diego, January 16, 2005: "Gaussian models for high density SNP genotyping."
- 26th Conference of Engineering in Medicine and Biology Society, San Francisco, September 1-5, 2004: "Bayesian network component analysis."
- 2nd Markov Chain Monte Carlo Workshop, Boston, August 27-28, 2004: "MCMC in statistical genomics."
- at IPAM Functional Genomics Reunion Conference, Los Angeles, June 1-4, 2004: "Regulatory networks in E. Coli."
- ENAR, Pittsburgh, March 28-31, 2004: "FDR applications in genetics."
- MSRI Workshop on the Genetics of Complex Human Diseases, Berkeley, February, 2004: "Dictionary models and gene expression regulation."
- 25th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Cancun, 17-21 September, 2003: "A Vocabulon analysis of E. Coli."
- SNP and Haplotypes Workshop, DIMACS, Rutgers University, November 22-23, 2002: "Parsing the genome in haplotype blocks."
- First Cape Cod MCMC Workshop, September 13-14, 2002: "Multiresolution MCMC and microarrays."
- Southern California Statistical Genetics Meeting, USC, June 6, 2002: "Ancestral haplotype reconstruction."
- IEEE EMBS Symposyum on Biomedical Informatics, Istanbul, June 1, 2002: "A dictionary model for genome sequences."
- ENAR/IMS meeting, Charlotte, March 25-28, 2001: "Microarrays and statistics in high dimensions."
- SIAM Annual Meeting, Atlanta, May 12-15, 1999: "A generalization of the Gibbs sampler."
- Multiple Comparison Procedures 2002, Bethesda, August 5-7, 2002: "Association genome screens and FDR." (Contributed presentation)

Seminars

- Department of Medicine, Quantitative Science Unit, Stanford, October 3, 2017: "Testing hypotheses on a tree: new error rates and controlling strategies."

- Neyman Seminar Series, UC Berkeley, March 15, 2017: "Selective Inference in Genomics."
- Human Genetics Speaker Series, UCLA, March 6, 2017: "Controlling the rate of GWAS false discoveries."
- Biostatistics Workshop, Stanford University, October 15, 2015: "Controlling the false discovery rate in genome wide association studies: two stories."
- Department of Statistical Sciences, Cornell University, October 7, 2015: "Controlling the false discovery rate in genome wide association studies: two stories."
- Department of Statistical Sciences, Università di Padova, July 1, 2015: "TreeQTL: Selective Inference for genetic regulation of gene expression."
- UCSF Institute for Human Genetics 'hot topics' series, San Francisco, January 9, 2015: "Controlling the false discovery rate in genetic association studies with multiple phenotypes."
- Department of Statistics and Operation Research, Tel Aviv University, June 30, 2014: "Penalized estimation for model selection."
- Department of Statistical Sciences, Università di Padova, July 4, 2013: "P-values in the Big Data age."
- Departments of Biostatistics and Statistics, UC Berkeley, April 4, 2013: "Statistical Challenges in the Analysis of Resequencing Data."
- Departments of Biostatistics, Columbia University, February 7, 2013: "Statistical Challenges in the Analysis of Resequencing Data."
- Results for RC2 Project: A Resource for Genetic Epidemiology Research in Adult Health and Aging: Opportunities for Research in the GERA Cohort, Symposium at NIH, June 4, 2012: "Detecting CNV in a cohort of 100,000."
- Department of Statistics, Università di Padova, July 19, 2011: "Reconstructing DNA Copy Number by Penalized Estimation and Imputation."
- Claremont Colleges Mathematics Colloquia, April 20, 2011: "Reconstructing DNA Copy Number by Penalized Estimation and Imputation."
- International Speaker Series, CIHR STAGE, Toronto, April 1, 2011: "Genetics in a Finnish Birth Cohort."
- Statistics Department, University of Toronto, March 31, 2011: "Reconstructing DNA Copy Number by Penalized Estimation and Imputation."
- UC Berkeley Statistics and Genomics Seminar, September 16, 2011: "Reconstructing DNA Copy Number by Penalized Estimation and Imputation."
- Department of Statistics, Università di Padova, July 5, 2010: "Model selection problems in genetic association studies: a review of current practices and open problems."
- Mathematics Department, Politecnico di Milano, June 23, 2008: "The genetics of quantitative traits: what's new since the days of R.A. Fisher?"
- Biostatistics Department, Stanford, November 2, 2007: "Reconstructing Copy Number Variations with Illumina Platform."
- Computer Science Department, UCLA, April 30, 2007: "Hierarchical Bayes models for SNP probes intensities."

- Biostatistics Department, University of Wisconsin, April 13, 2007: "Hierarchical Bayes models for SNP probes intensities."
- Biomathematics Department, UCLA, December 7th, 2006: "Volume measures for linkage disequilibrium."
- Statistics Department, Stanford, December 5th, 2006: "Transcription regulation in E.Coli."
- Statistics Department, UC Berkeley, October 17th, 2006: "Volume measures for linkage disequilibrium."
- School of life sciences, EPFL, Lausanne, January 31st, 2006: "High density genotyping: challenges and opportunities."
- Institute for Human Genetics, UCSF, November 4, 2005: "Interpreting long homozygous segments in high density genotyping data."
- Department of Biostatistics, UCLA, November 2, 2005: "High density genotyping: challenges and opportunities."
- Mathematics Section, EPFL, Lausanne, June 30, 2005: "Regulatory networks in E. Coli."
- Department of Human Genetics, UCLA, June 6, 2005: "Novel genotyping technologies: challenges and opportunities for statistical analysis."
- Department of Ecology and Environmental Biology, UCLA, June 1, 2005: "Regulatory networks: a view from genome and transcriptome."
- Department of Statistics, UCLA, May 17, 2005: "Genetics of quantitative traits: looking forward standing on the shoulders of giants."
- Department of Biostatistics, The University of Pittsburgh, November 17, 2004: "Regulatory networks."
- Computer science department, Université Libre de Bruxelles, July 9, 2004: "A bioinformatics approach to transcription regulation in E. Coli."
- Seminar für Statistik, ETH, Zürich, July 15, 2004: "A bioinformatics approach to transcription regulation in E. Coli."
- UCLA-DOE Institute for genomics and proteomics, UCLA, April 24, 2004: "Multiple testing in microarrays?"
- Section on Statistical Genetics, Department of Biostatistics, University of Alabama at Birmingham, April 2, 2004: "Regulatory networks in E. Coli."
- Department of Biostatistics, UCLA, March 3, 2004: "Regulatory networks in E. Coli."
- Department of Statistics, UCLA, February 24, 2004: "Dictionary models for regulatory regions in DNA and gene expression arrays."
- UCLA-DOE Institute for genomics and proteomics, UCLA, March 2003: "Data analysis in E. Coli using a dictionary model."
- Department of Mathematics, University of California at San Diego, November 14, 2002: "Dictionary models for DNA sequences and gene expression."
- Department of Statistics, University of Paris XI, July 12, 2002: "A dictionary model for genomes."
- Department of Mathematics, Pavia University and CNR, June 25, 2002: "Minimum description length and dictionary size selection."

- Division of Biostatistics, USC, May 2002: "False discovery rate: a paradigm for genomewise comparisons?"
- UCLA-DOE Institute for genomics and proteomics, UCLA, April 2002: "Dictionary models for DNA sequences."
- Department of Statistics, University of Chicago, April 2002: "Genomewide motif identification using the dictionary model."
- Department of Human Genetics, UCLA November 2000: "Homozygosity and linkage disequilibrium."
- Department of Information and Operations Management, USC, October 2000: "Measures of dependence and volume tests."
- Biostatistics Workshop, Stanford University Medical School, April 22, 1999: "Comparison of some measures of linkage disequilibrium."

CHIARA SABATTI'S PUBLICATIONS

In the .pdf document, the symbol ◁ is linked to the electronic edition of the paper, whenever this is available.

Research Papers - Peer reviewed (Journals)

1. Liu, J. and **C. Sabatti** (2000) "Generalized Gibbs sampler and multigrid Monte Carlo for Bayesian computation," *Biometrika* **87**: 353–369. ◁

2. Bressman, S., **C. Sabatti**, D. Raymond, D. de Leon, C. Klein, P. L. Kramer, M. F. Brin, S. Fahn, X. Breakefield, L. J. Ozelius and N. J. Risch (2000) "The DYT1 phenotype and guidelines for diagnostic testing," *Neurology* **54**: 1746–1752. ◁

3. Liu, J., **C. Sabatti**, J. Teng, B. Keats and N. Risch (2001) "Bayesian analysis of haplotypes for linkage disequilibrium mapping," *Genome Research* **11**: 1716–24. ◁

4. Pastinen, T., I. Jaakko, M. Perola, **C. Sabatti**, P. Tainola, M.Levander, A. Syvänen and L. Peltonen (2001) "Dissecting a population genome for targeted screening of disease mutations," *Human Molecular Genetics* **10**: 2961–2972. ◁

5. **Sabatti, C.**, S. Karsten and D. Geschwind (2002) "Thresholding rules for recovering a sparse signal from microarray experiments," *Mathematical Biosciences* **176**: 17–34. ◁

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