Stanford

Chiara Sabatti

Professor of Biomedical Data Science and of Statistics

Department of Biomedical Data Science

NIH Biosketch available Online Curriculum Vitae available Online

CONTACT INFORMATION

- **Alternate Contact**

  Natalie La Mariana - Administrative Associate

  Email nlamaria@stanford.edu

  Tel (650) 773-7744

Bio

ACADEMIC APPOINTMENTS

- Professor, Department of Biomedical Data Science
- Professor, Statistics
- Member, Bio-X
- Member, Stanford Cancer Institute
- Associate Director, Stanford Data Science
- Member, Women in Data Science

ADMINISTRATIVE APPOINTMENTS

- Associate Director, HAI, (2026- present)
- Associate Director, Data Science BS (working with the MCS major since 2012), (2022- present)
- Associate Chair for Education and Training, Biomedical Data Science, (2020- present)
- Associate Director, Stanford Data Science , (2018-2025)
- Vice chair, Biomedical Data Science, (2018-2019)

HONORS AND AWARDS

- Fellow, Institute of Mathematical Statistics (2022)
- CAREER, NSF (2003-08)

PROFESSIONAL EDUCATION

- PostDoctoral, Stanford , Genetics (2000)
- Ph D, Stanford , Statistics (1998)
- BS & MS, Bocconi University , Statistics and Economics (1993)

LINKS

- Lab web site: https://chiarasabatti.su.domains

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Statistical models and reasoning are key to our understanding of the genetic basis of human traits. Modern high-throughput technology presents us with new opportunities and challenges. We develop statistical approaches for high dimensional data in the attempt of improving our understanding of the molecular basis of health related traits.

CLINICAL TRIALS

- Perfusion CT Monitoring to Predict Treatment Efficacy in Renal Cell Carcinoma, Not Recruiting

Teaching

COURSES

2025-26

- Biomedical Data Science Student Seminar: BMDS 201A, BMDS 201B, BMDS 201C (Spr)
- Data Narratives: DATASCI 120 (Spr)
- Data Studio: Consulting Workshop on Biomedical Data Science: BMDS 291A (Aut)
- Data Studio: Consulting Workshop on Biomedical Data Science: BMDS 291B (Win)
- Data Studio: Consulting Workshop on Biomedical Data Science: BMDS 291C (Spr)
- The Data Science Experience: DATASCI 190 (Spr)

2024-25

- Consulting Workshop on Biomedical Data Science: BIODS 232 (Aut, Win, Spr)
- Data Narratives: DATASCI 120, MCS 120 (Spr)
- Data Science Mentoring: BIODS 360, BIOMEDIN 360 (Win)
- The Data Science Experience: DATASCI 190 (Spr)

2023-24

- Consulting Workshop on Biomedical Data Science: BIODS 232 (Aut, Win, Spr)
- Critical Exploration of Topics in Biomedical Data Science: Generative AI: BIODS 290 (Aut)
- Data Narratives: DATASCI 120, MCS 120 (Spr)
- Inclusive Mentorship in Data Science: BIODS 360, BIOMEDIN 360 (Win)
- The Data Science Experience: DATASCI 190 (Spr)

2022-23

- Consulting Workshop on Biomedical Data Science: BIODS 232 (Aut, Win, Spr)
- Data Narratives: DATASCI 120, MCS 120 (Spr)
- Inclusive Mentorship in Data Science: BIODS 360, BIOMEDIN 360 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Ginnie Ma, Yash Nair, Sarah Zhao

Postdoctoral Faculty Sponsor

Yusuph Mavura

Master's Program Advisor

Misha Baitemirova

Doctoral (Program)

Max Schuessler

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Phd Program)
- Biomedical Data Science (Masters Program)

Publications

PUBLICATIONS

- **Searching for Local Associations while Controlling the False Discovery Rate** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Gablenz, P., Sesia, M., Sun, T., Sabatti, C.
  2026
- **Near-Peer Mentoring in Data Science: A Plot for Mutual Growth** *AMERICAN STATISTICIAN*
  Sabatti, C., Zhao, Q.
  2025
- **It's a wrap: deriving distinct discoveries with FDR control after a GWAS pipeline.** *bioRxiv : the preprint server for biology*
  Chu, B. B., He, Z., Sabatti, C.
  2025
- **Uncovering Heterogeneous Effects via Localized Feature Selection.** *bioRxiv : the preprint server for biology*
  Liu, X., Gu, J., Chen, Z., Chu, B., Liu, L., Morrison, T., Butler, R. R., Edelson, J., Li, J., Longo, F. M., Tang, H., Ionita-Laza, I., Sabatti, et al
  2025
- **Curriculum Design in an Evolving Field: Perspectives on Biomedical Data Science from Stanford.** *Annual review of biomedical data science*
  Yeh, C. Y., Wall, D. P., Matthys, K., Sabatti, C., Palacios, J.
  2025
- **Catch me if you can: signal localization with knockoff e-values.** *Journal of the Royal Statistical Society. Series B, Statistical methodology*
  Gablenz, P., Sabatti, C.
  2025; 87 (1): 56-73
- **Predicting Diagnostic Conversion From Major Depressive Disorder to Bipolar Disorder: An EHR Based Study From Colombia.** *Bipolar disorders*
  Service, S. K., De La Hoz, J. F., Diaz-Zuluaga, A. M., Arias, A., Pimplaskar, A., Luu, C., Mena, L., Valencia-Echeverry, J., Ramírez, M. C., Bearden, C. E., Sabatti, C., Reus, V. I., López-Jaramillo, et al
  2024
- **A blended genome and exome sequencing method captures genetic variation in an unbiased, high-quality, and cost-effective manner**
  Boltz, T., Chu, B., Sealock, J., Liao, C., Zhan, L., Fu, J., Ye, R., Majara, L., Chapman, S., DeFelice, M., Grimsby, J., Rubinacci, S., Akena, et al
  SPRINGERNATURE.2024: 1790
- **A blended genome and exome sequencing method captures genetic variation in an unbiased, high-quality, and cost-effective manner**
  Boltz, T., Chu, B., Sealock, J., Liao, C., Zhan, L., Fu, J., Ye, R., Majara, L., Chapman, S., DeFelice, M., Grimsby, J., Rubinacci, S., Akena, et al
  SPRINGERNATURE.2024: 1790
- **Second-order group knockoffs with applications to GWAS.** *Bioinformatics (Oxford, England)*
  Chu, B. B., Gu, J., Chen, Z., Morrison, T., Candès, E., He, Z., Sabatti, C.
  2024
- **A blended genome and exome sequencing method captures genetic variation in an unbiased, high-quality, and cost-effective manner.** *bioRxiv : the preprint server for biology*

Boltz, T. A., Chu, B. B., Liao, C., Sealock, J. M., Ye, R., Majara, L., Fu, J. M., Service, S., Zhan, L., Medland, S. E., Chapman, S. B., Rubinacci, S., DeFelice, et al
2024

- **Catch me if you can: signal localization with knockoff e-values** *JOURNAL OF THE ROYAL STATISTICAL SOCIETY SERIES B-STATISTICAL METHODOLOGY*
  Gablenz, P., Sabatti, C.
  2024
- **In silico identification of putative causal genetic variants.** *bioRxiv : the preprint server for biology*
  He, Z., Chu, B., Yang, J., Gu, J., Chen, Z., Liu, L., Morrison, T., Belloy, M. E., Qi, X., Hejazi, N., Mathur, M., Le Guen, Y., Tang, et al
  2024
- **Geospatial investigations in Colombia reveal variations in the distribution of mood and psychotic disorders.** *Communications medicine*
  Song, J., Ramirez, M. C., Okano, J. T., Service, S. K., de la Hoz, J., Diaz-Zuluaga, A. M., Upegui, C. V., Gallago, C., Arias, A., Sanchez, A. V., Teshiba, T., Sabatti, C., Gur, et al
  2024; 4 (1): 26
- **Controlled Variable Selection from Summary Statistics Only? A Solution via GhostKnockoffs and Penalized Regression.** *ArXiv*
  Chen, Z., He, Z., Chu, B. B., Gu, J., Morrison, T., Sabatti, C., Candes, E.
  2024
- **Filtering the rejection set while preserving false discovery rate control.** *Journal of the American Statistical Association*
  Katsevich, E., Sabatti, C., Bogomolov, M.
  2023; 118 (541): 165-176
- **GhostKnockoff inference empowers identification of putative causal variants in genome-wide association studies.** *Nature communications*
  He, Z., Liu, L., Belloy, M. E., Le Guen, Y., Sossin, A., Liu, X., Qi, X., Ma, S., Gyawali, P. K., Wyss-Coray, T., Tang, H., Sabatti, C., Candes, et al
  2022; 13 (1): 7209
- **Transfer Learning in Genome-Wide Association Studies with Knockoffs** *SANKHYA-SERIES B-APPLIED AND INTERDISCIPLINARY STATISTICS*
  Li, S., Ren, Z., Sabatti, C., Sesia, M.
  2022
- **Transfer Learning in Genome-Wide Association Studies with Knockoffs.** *Sankhya. Series B (2008)*
  Li, S., Ren, Z., Sabatti, C., Sesia, M.
  2022
- **GENETICS OF SEVERE MENTAL ILLNESS IN SOUTH AMERICA**
  Loohuis, L., Diaz-Zuluaga, A., Service, S., De la Hoz, J., Belangero, S., Valencia, J., Teshiba, T., Santoro, M., Escobar, J., Ophoff, R., Reus, V., Sabatti, C., Gadelha, et al
  ELSEVIER.2022: E25
- **Searching for robust associations with a multi-environment knockoff filter.** *Biometrika*
  Li, S., Sesia, M., Romano, Y., Candès, E., Sabatti, C.
  2022; 109 (3): 611-629
- **Searching for robust associations with a multi-environment knockoff filter** *BIOMETRIKA*
  Li, S., Sesia, M., Romano, Y., Candes, E., Sabatti, C.
  2022; 109 (3): 611-629
- **DETECTING MULTIPLE REPLICATING SIGNALS USING ADAPTIVE FILTERING PROCEDURES** *ANNALS OF STATISTICS*
  Wang, J., Gui, L., Su, W. J., Sabatti, C., Owen, A. B.
  2022; 50 (4): 1890-1909
- **DETECTING MULTIPLE REPLICATING SIGNALS USING ADAPTIVE FILTERING PROCEDURES.** *Annals of statistics*
  Wang, J., Gui, L., Su, W. J., Sabatti, C., Owen, A. B.
  2022; 50 (4): 1890-1909
- **Data Science in a Time of Crisis: Lessons from the Pandemic** *STATISTICAL SCIENCE*

Sabatti, C., Chambers, J. M.
2022; 37 (2): 160-161

- **Hypotheses on a tree: new error rates and testing strategies** *CLINICAL INFECTIOUS DISEASES*
  Bogomolov, M., Peterson, C. B., Benjamini, Y., Sabatti, C.
  2021; 73 (11): 575-590

- **False discovery rate control in genome-wide association studies with population structure** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Sesia, M., Bates, S., Candes, E., Marchini, J., Sabatti, C.
  2021; 118 (40)

- **Increased activation product of complement 4 protein in plasma of individuals with schizophrenia.** *Translational psychiatry*
  Kalinowski, A., Liliental, J., Anker, L. A., Linkovski, O., Culbertson, C., Hall, J. N., Pattni, R., Sabatti, C., Noordsy, D., Hallmayer, J. F., Mellins, E. D., Ballon, J. S., O'Hara, et al
  2021; 11 (1): 486

- **Hypotheses on a tree: new error rates and testing strategies.** *Biometrika*
  Bogomolov, M., Peterson, C. B., Benjamini, Y., Sabatti, C.
  2021; 108 (3): 575-590

- **Revealing enzyme functional architecture via high-throughput microfluidic enzyme kinetics.** *Science (New York, N.Y.)*
  Markin, C. J., Mokhtari, D. A., Sunden, F., Appel, M. J., Akiva, E., Longwell, S. A., Sabatti, C., Herschlag, D., Fordyce, P. M.
  2021; 373 (6553)

- **Revealing enzyme functional architecture via high-throughput microfluidic enzyme kinetics** *SCIENCE*
  Markin, C. J., Mokhtari, D. A., Sunden, F., Appel, M. J., Akiva, E., Longwell, S. A., Sabatti, C., Herschlag, D., Fordyce, P. M.
  2021; 373 (6553): 411-+

- **Filtering the Rejection Set While Preserving False Discovery Rate Control** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Katsevich, E., Sabatti, C., Bogomolov, M.
  2021

- **Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease.** *Cell*
  de Goede, O. M., Nachun, D. C., Ferraro, N. M., Gloudemans, M. J., Rao, A. S., Smail, C., Eulalio, T. Y., Aguet, F., Ng, B., Xu, J., Barbeira, A. N., Castel, S. E., Kim-Hellmuth, et al
  2021

- **False discovery rate control in genome-wide association studies with population structure.** *Proceedings of the National Academy of Sciences of the United States of America*
  Sesia, M., Bates, S., Candès, E., Marchini, J., Sabatti, C.
  2021; 118 (40)

- **Discussion of the Paper "Prediction, Estimation, and Attribution" by B. Efron** *INTERNATIONAL STATISTICAL REVIEW*
  Candes, E., Sabatti, C.
  2020; 88: S60–S63

- **Progenitor identification and SARS-CoV-2 infection in human distal lung organoids.** *Nature*
  Salahudeen, A. A., Choi, S. S., Rustagi, A., Zhu, J., van Unen, V., de la O, S. M., Flynn, R. A., Margalef-Catala, M., Santos, A. J., Ju, J., Batish, A., Usui, T., Zheng, et al
  2020

- **The GTEx Consortium atlas of genetic regulatory effects across human tissues** *SCIENCE*
  Aguet, F., Barbeira, A. N., Bonazzola, R., Brown, A., Castel, S. E., Jo, B., Kasela, S., Kim-Hellmuth, S., Liang, Y., Parsana, P., Flynn, E., Fresard, L., Gamazon, et al
  2020; 369 (6509): 1318-+

- **Genome-wide mapping of brain phenotypes in extended pedigrees with strong genetic loading for bipolar disorder.** *Molecular psychiatry*
  Fears, S. C., Service, S. K., Kremeyer, B., Araya, C., Araya, X., Bejarano, J., Ramirez, M., Castrillon, G., Gomez-Franco, J., Lopez, M. C., Montoya, G., Montoya, P., Aldana, et al
  2020

- **Distinct and shared contributions of diagnosis and symptom domains to cognitive performance in severe mental illness in the Paisa population: a case-control study** *LANCET PSYCHIATRY*
  Service, S. K., Vargas Upegui, C., Castano Ramirez, M., Port, A. M., Moore, T. M., Umanes, M., Agudelo Arango, L., Diaz-Zuluaga, A. M., Melo Espejo, J., Cecilia Lopez, M., David Palacio, J., Ruiz Sanchez, S., Valencia, et al
  2020; 7 (5): 411–19

- **Discussion of the Paper "Prediction, Estimation, and Attribution" by B. Efron** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Candes, E., Sabatti, C.
  2020; 115 (530): 656–58

- **Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates.** *Translational psychiatry*
  Sul, J. H., Service, S. K., Huang, A. Y., Ramensky, V., Hwang, S., Teshiba, T. M., Park, Y., Ori, A. P., Zhang, Z., Mullins, N., Olde Loohuis, L. M., Fears, S. C., Araya, et al
  2020; 10 (1): 74

- **Multi-resolution localization of causal variants across the genome.** *Nature communications*
  Sesia, M. n., Katsevich, E. n., Bates, S. n., Candès, E. n., Sabatti, C. n.
  2020; 11 (1): 1093

- **Publisher Correction: Multi-resolution localization of causal variants across the genome.** *Nature communications*
  Sesia, M. n., Katsevich, E. n., Bates, S. n., Candès, E. n., Sabatti, C. n.
  2020; 11 (1): 1799

- **A Quantitative Proteome Map of the Human Body.** *Cell*
  Jiang, L. n., Wang, M. n., Lin, S. n., Jian, R. n., Li, X. n., Chan, J. n., Dong, G. n., Fang, H. n., Robinson, A. E., Snyder, M. P.
  2020

- **Causal inference in genetic trio studies.** *Proceedings of the National Academy of Sciences of the United States of America*
  Bates, S. n., Sesia, M. n., Sabatti, C. n., Candès, E. n.
  2020

- **Genetic analysis of activity, brain and behavioral associations in extended families with heavy genetic loading for bipolar disorder.** *Psychological medicine*
  Vreeker, A., Fears, S. C., Service, S. K., Pagani, L., Takahashi, J. S., Araya, C., Araya, X., Bejarano, J., Lopez, M. C., Montoya, G., Montoya, C. P., Teshiba, T. M., Escobar, et al
  2019: 1–9

- **Genetic regulation of gene expression and splicing during a 10-year period of human aging.** *Genome biology*
  Balliu, B., Durrant, M., Goede, O. d., Abell, N., Li, X., Liu, B., Gloudemans, M. J., Cook, N. L., Smith, K. S., Knowles, D. A., Pala, M., Cucca, F., Schlessinger, et al
  2019; 20 (1): 230

- **LEVERAGING ELECTRONIC HOSPITAL RECORDS FOR PSYCHIATRIC PHENOTYPING**
  Loohuis, L., Gomez, J., Song, J., Castano, M., Castro Navarro, J., Gallago, C., Vargas, C., David Palacio, J., Service, S., Escobar, J., Sabatti, C., Reus, V., Bearden, et al
  ELSEVIER.2019: S40–S41

- **NLP STRATEGIES FOR ANALYZING FREE-TEXT PSYCHIATRIC ELECTRONIC HOSPITAL RECORDS**
  De la Hoz, J., Loohuis, L., Castano, M., Song, J., Service, S., Teshiba, T., Gallego, C., Sabatti, C., Escobar, J., Reus, V., Bui, A., Bearden, C. E., Lopez-Jaramillo, et al
  ELSEVIER.2019: S127

- **GENETICS OF SEVERE MENTAL ILLNESS: THE "PAISA PROJECT"**
  Lopez-Jaramillo, C., Loohuis, L., Service, S., Vargas, C., Castano, M., Lopez Tobon, M., Guillermo Agudelo, L., Melo, J., Gur, R., Gur, R., Sabatti, C., Escobar, J., Reus, et al
  ELSEVIER.2019: S38–S39

- **THE RELATIONSHIP BETWEEN GENOME-WIDE SIGNIFICANT GWAS LOCI AND PSYCHIATRIC PHENOTYPES IN A COLOMBIAN POPULATION ISOLATE**

Service, S., Loohuis, L., Jensen, S., Teshiba, T., Umanes, M., Vargas, C., Escobar, J., Reus, V., Sabatti, C., Bearden, C., Lopez-Jaramillo, C., Freimer, N.

ELSEVIER.2019: S39–S40

- **NLP STRATEGIES FOR ANALYZING FREE-TEXT PSYCHIATRIC ELECTRONIC HOSPITAL RECORDS**

  De la Hoz, J., Loohuis, L., Castano, M., Song, J., Service, S., Teshiba, T., Gallego, C., Sabatti, C., Escobar, J., Reus, V., Bui, A., Bearden, C. E., Lopez-Jaramillo, et al

  ELSEVIER.2019: S127

- **GENETICS OF SEVERE MENTAL ILLNESS: THE "PAISA PROJECT"**

  Lopez-Jaramillo, C., Loohuis, L., Service, S., Vargas, C., Castano, M., Lopez Tobon, M., Guillermo Agudelo, L., Melo, J., Gur, R., Gur, R., Sabatti, C., Escobar, J., Reus, et al

  ELSEVIER.2019: S38–S39

- **Exome sequencing of Finnish isolates enhances rare-variant association power.** *Nature*

  Locke, A. E., Steinberg, K. M., Chiang, C. W., Service, S. K., Havulinna, A. S., Stell, L., Pirinen, M., Abel, H. J., Chiang, C. C., Fulton, R. S., Jackson, A. U., Kang, C. J., Kanchi, et al

  2019

- **Selection-adjusted inference: an application to confidence intervals for cis-eQTL effect sizes.** *Biostatistics (Oxford, England)*

  Panigrahi, S., Zhu, J., Sabatti, C.

  2019

- **Genetic analyses of diverse populations improves discovery for complex traits.** *Nature*

  Wojcik, G. L., Graff, M., Nishimura, K. K., Tao, R., Haessler, J., Gignoux, C. R., Highland, H. M., Patel, Y. M., Sorokin, E. P., Avery, C. L., Belbin, G. M., Bien, S. A., Cheng, et al

  2019

- **Exploratory Gene Ontology Analysis with Interactive Visualization.** *Scientific reports*

  Zhu, J., Zhao, Q., Katsevich, E., Sabatti, C.

  2019; 9 (1): 7793

- **Gene hunting with hidden Markov model knockoffs** *BIOMETRIKA*

  Sesia, M., Sabatti, C., Candes, E. J.

  2019; 106 (1): 1–18

- **MULTILAYER KNOCKOFF FILTER: CONTROLLED VARIABLE SELECTION AT MULTIPLE RESOLUTIONS.** *The annals of applied statistics*

  Katsevich, E., Sabatti, C.

  2019; 13 (1): 1-33

- **MULTILAYER KNOCKOFF FILTER: CONTROLLED VARIABLE SELECTION AT MULTIPLE RESOLUTIONS** *ANNALS OF APPLIED STATISTICS*

  Katsevich, E., Sabatti, C.

  2019; 13 (1): 1–33

- **Gene hunting with hidden Markov model knockoffs.** *Biometrika*

  Sesia, M., Sabatti, C., Candes, E. J.

  2019; 106 (1): 1–18

- **Rejoinder: "Gene hunting with hidden Markov model knockoffs'** *BIOMETRIKA*

  Sesia, M., Sabatti, C., Candes, E. J.

  2019; 106 (1): 35–45

- **Author Correction: Exome sequencing of Finnish isolates enhances rare-variant association power.** *Nature*

  Locke, A. E., Steinberg, K. M., Chiang, C. W., Service, S. K., Havulinna, A. S., Stell, L. n., Pirinen, M. n., Abel, H. J., Chiang, C. C., Fulton, R. S., Jackson, A. U., Kang, C. J., Kanchi, et al

  2019

- **Organoid Modeling of the Tumor Immune Microenvironment.** *Cell*

  Neal, J. T., Li, X., Zhu, J., Giangarra, V., Grzeskowiak, C. L., Ju, J., Liu, I. H., Chiou, S., Salahudeen, A. A., Smith, A. R., Deutsch, B. C., Liao, L., Zemek, et al

  2018; 175 (7): 1972

- **Multiregion Quantification of Extracellular Signal-regulated Kinase Activity in Renal Cell Carcinoma.** *European urology oncology*
  Hoerner, C. R., Massoudi, R., Metzner, T. J., Stell, L., O'Rourke, J. J., Kong, C. S., Liliental, J. E., Brooks, J. D., Sabatti, C., Leppert, J. T., Fan, A. C.
  2018
- **Understanding the Hidden Complexity of Latin American Population Isolates.** *American journal of human genetics*
  Mooney, J. A., Huber, C. D., Service, S., Sul, J. H., Marsden, C. D., Zhang, Z., Sabatti, C., Ruiz-Linares, A., Bedoya, G., Costa Rica/Colombia Consortium for Genetic Investigation of Bipolar Endophenotypes, Freimer, N., Lohmueller, K. E., Fears, S. C., et al
  2018; 103 (5): 707–26
- **Facile generation of single-cell transcriptome and immune repertoire freshly isolated from clinical tumor specimens**
  Zhu, J., Salahudeen, A. A., Giangarra, V., Montesclaros, L., Sapida, J., Sharifi, O., Lee, J., Zheng, G. X., Wagh, D., Coller, J., Sabatti, C., Kuo, C. J.
  AMER ASSOC CANCER RESEARCH.2018
- **Whole genome sequencing in psychiatric disorders: the WGSPD consortium (vol 20, pg 1661, 2017)** *NATURE NEUROSCIENCE*
  Sanders, S. J., Neale, B. M., Huang, H., Werling, D. M., An, J., Dong, S., Abecasis, G., Arguello, P., Blangero, J., Boehnke, M., Daly, M. J., Eggan, K., Geschwind, et al
  2018; 21 (7): 1017
- **Organoid-based characterization of patient tumors and microenvironments at single cell resolution**
  Salahudeen, A. A., Zhu, J., Ju, J., Batish, A., Sutha, K., Neal, J. T., Giangarra, V., Montesclaros, L., Sapida, J., Sharifi, O., Lee, J., Zheng, G. X., Wagh, et al
  AMER ASSOC CANCER RESEARCH.2018
- **Exposure to NO2, CO, and PM2.5 is linked to regional DNA methylation differences in asthma** *CLINICAL EPIGENETICS*
  Prunicki, M., Stell, L., Dinakarpandian, D., de Planell-Saguer, M., Lucas, R. W., Hammond, S., Balmes, J. R., Zhou, X., Paglino, T., Sabatti, C., Miller, R. L., Nadeau, K. C.
  2018; 10: 2
- **Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate** *NATURE GENETICS*
  Jasinska, A. J., Zelaya, I., Service, S. K., Peterson, C. B., Cantor, R. M., Choi, O., DeYoung, J., Eskin, E., Fairbanks, L. A., Fears, S., Furterer, A. E., Huang, Y. S., Ramensky, et al
  2017; 49 (12): 1714-+
- **Whole genome sequencing in psychiatric disorders: the WGSPD consortium** *NATURE NEUROSCIENCE*
  Sanders, S. J., Neale, B. M., Huang, H., Werling, D. M., An, J., Dong, S., Abecasis, G., Arguello, P., Blangero, J., Boehnke, M., Daly, M. J., Eggan, K., Geschwind, et al
  2017; 20 (12): 1661–68
- **Controlling the Rate of GWAS False Discoveries** *GENETICS*
  Brzyski, D., Peterson, C. B., Sobczyk, P., Candes, E. J., Bogdan, M., Sabatti, C.
  2017; 205 (1): 61-75
- **Controlling the Rate of GWAS False Discoveries.** *Genetics*
  Brzyski, D., Peterson, C. B., Sobczyk, P., Candès, E. J., Bogdan, M., Sabatti, C.
  2017; 205 (1): 61-75
- **Genetic effects on gene expression across human tissues.** *Nature*
  Battle, A. n., Brown, C. D., Engelhardt, B. E., Montgomery, S. B.
  2017; 550 (7675): 204–13
- **TreeQTL: hierarchical error control for eQTL findings** *BIOINFORMATICS*
  Peterson, C. B., Bogomolov, M., Benjamini, Y., Sabatti, C.
  2016; 32 (16): 2556-2558
- **Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder** *PLOS GENETICS*
  Peterson, C. B., Service, S. K., Jasinska, A. J., Gao, F., Zelaya, I., Teshiba, T. M., Bearden, C. E., Cantor, R. M., Reus, V. I., Macaya, G., Lopez-Jaramillo, C., Bogomolov, M., Benjamini, et al
  2016; 12 (5)

- **Genetic contributions to circadian activity rhythm and sleep pattern phenotypes in pedigrees segregating for severe bipolar disorder** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Pagani, L., Clair, P. A., Teshiba, T. M., Service, S. K., Fears, S. C., Araya, C., Araya, X., Bejarano, J., Ramirez, M., Castrillon, G., Gomez-Makhinson, J., Lopez, M. C., Montoya, et al
  2016; 113 (6): E754-E761

- **Genetic Variant Selection: Learning Across Traits and Sites** *GENETICS*
  Stell, L., Sabatti, C.
  2016; 202 (2): 439-?

- **Many Phenotypes Without Many False Discoveries: Error Controlling Strategies for Multitrait Association Studies** *GENETIC EPIDEMIOLOGY*
  Peterson, C. B., Bogomolov, M., Benjamini, Y., Sabatti, C.
  2016; 40 (1): 45-56

- **Many Phenotypes Without Many False Discoveries: Error Controlling Strategies for Multitrait Association Studies.** *Genetic epidemiology*
  Peterson, C. B., Bogomolov, M., Benjamini, Y., Sabatti, C.
  2016; 40 (1): 45-56

- **SLOPE-ADAPTIVE VARIABLE SELECTION VIA CONVEX OPTIMIZATION.** *The annals of applied statistics*
  Bogdan, M., van den Berg, E., Sabatti, C., Su, W., Candès, E. J.
  2015; 9 (3): 1103-1140

- **SLOPE-ADAPTIVE VARIABLE SELECTION VIA CONVEX OPTIMIZATION** *ANNALS OF APPLIED STATISTICS*
  Bogdan, M., Van Den Berg, E., Sabatti, C., Su, W., Candes, E. J.
  2015; 9 (3): 1103-1140

- **Characterizing Race/Ethnicity and Genetic Ancestry for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort.** *Genetics*
  Banda, Y., Kvale, M. N., Hoffmann, T. J., Hesselson, S. E., Ranatunga, D., Tang, H., Sabatti, C., Croen, L. A., Dispensa, B. P., Henderson, M., Iribarren, C., Jorgenson, E., Kushi, et al
  2015; 200 (4): 1285-1295

- **Brain structure-function associations in multi-generational families genetically enriched for bipolar disorder** *BRAIN*
  Fears, S. C., Schur, R., Sjouwerman, R., Service, S. K., Araya, C., Araya, X., Bejarano, J., Knowles, E., Gomez-Makhinson, J., Lopez, M. C., Aldana, I., Teshiba, T. M., Abaryan, et al
  2015; 138: 2087-2102

- **Brain structure-function associations in multi-generational families genetically enriched for bipolar disorder.** *Brain : a journal of neurology*
  Fears, S. C., Schür, R., Sjouwerman, R., Service, S. K., Araya, C., Araya, X., Bejarano, J., Knowles, E., Gomez-Makhinson, J., Lopez, M. C., Aldana, I., Teshiba, T. M., Abaryan, et al
  2015; 138 (Pt 7): 2087-102

- **Cross-Disorder Genome-Wide Analyses Suggest a Complex Genetic Relationship Between Tourette's Syndrome and OCD** *AMERICAN JOURNAL OF PSYCHIATRY*
  Yu, D., Mathews, C. A., Scharf, J. M., Neale, B. M., Davis, L. K., Gamazon, E. R., Derks, E. M., Evans, P., Edlund, C. K., Crane, J., Osiecki, L., Gallagher, P., Gerber, et al
  2015; 172 (1): 82-93

- **Multisystem component phenotypes of bipolar disorder for genetic investigations of extended pedigrees.** *JAMA psychiatry*
  Fears, S. C., Service, S. K., Kremeyer, B., Araya, C., Araya, X., Bejarano, J., Ramirez, M., Castrillón, G., Gomez-Franco, J., Lopez, M. C., Montoya, G., Montoya, P., Aldana, et al
  2014; 71 (4): 375-387

- **Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci** *PLOS GENETICS*
  Service, S. K., Teslovich, T. M., Fuchsberger, C., Ramensky, V., Yajnik, P., Koboldt, D. C., Larson, D. E., Zhang, Q., Lin, L., Welch, R., Ding, L., McLellan, M. D., O'Laughlin, et al
  2014; 10 (1)

- **Genome-wide association study of Tourette's syndrome.** *Molecular psychiatry*

Scharf, J. M., Yu, D., Mathews, C. A., Neale, B. M., Stewart, S. E., Fagerness, J. A., Evans, P., Gamazon, E., Edlund, C. K., Service, S. K., Tikhomirov, A., Osiecki, L., Illmann, et al
2013; 18 (6): 721-728

- **Increased paternal age and the influence on burden of genomic copy number variation in the general population** *HUMAN GENETICS*
  Buizer-Voskamp, J. E., Blauw, H. M., Boks, M. P., van Eijk, K. R., Veldink, J. H., Hennekam, E. A., Vorstman, J. A., Mulder, F., Tiemeier, H., Uitterlinden, A. G., Kiemeney, L. A., Van den Berg, L. H., Kahn, et al
  2013; 132 (4): 443-450

- **Reconstructing DNA copy number by joint segmentation of multiple sequences** *BMC BIOINFORMATICS*
  Zhang, Z., Lange, K., Sabatti, C.
  2012; 13

- **A genome-wide meta-analysis of association studies of Cloninger's Temperament Scales** *TRANSLATIONAL PSYCHIATRY*
  Service, S. K., Verweij, K. J., Lahti, J., Congdon, E., Ekelund, J., Hintsanen, M., RAIKKONEN, K., Lehtimaki, T., Kahonen, M., Widen, E., Taanila, A., Veijola, J., Heath, et al
  2012; 2

- **Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals.** *PLoS genetics*
  Dastani, Z., Hivert, M., Timpson, N., Perry, J. R., Yuan, X., Scott, R. A., Henneman, P., Heid, I. M., Kizer, J. R., Lyytikäinen, L., Fuchsberger, C., Tanaka, T., Morris, et al
  2012; 8 (3)

- **Genome-Wide Analysis Shows Increased Frequency of Copy Number Variation Deletions in Dutch Schizophrenia Patients** *BIOLOGICAL PSYCHIATRY*
  Buizer-Voskamp, J. E., Muntjewerff, J., Strengman, E., Sabatti, C., Stefansson, H., Vorstman, J. A., Ophoff, R. A.
  2011; 70 (7): 655-662

- **A Molecular Screening Approach to Identify and Characterize Inhibitors of Glioblastoma Stem Cells** *MOLECULAR CANCER THERAPEUTICS*
  Visnyei, K., Onodera, H., Damoiseaux, R., Saigusa, K., Petrosyan, S., De Vries, D., Ferrari, D., Saxe, J., Panosyan, E. H., Masterman-Smith, M., Mottahedeh, J., Bradley, K. A., Huang, et al
  2011; 10 (10): 1818-1828

- **Phenotype mining in CNV carriers from a population cohort** *HUMAN MOLECULAR GENETICS*
  Pietilainen, O. P., Rehnstrom, K., Jakkula, E., Service, S. K., Congdon, E., Tilgmann, C., Hartikainen, A., Taanila, A., Heikura, U., Paunio, T., Ripatti, S., Jarvelin, M., Isohanni, et al
  2011; 20 (13): 2686-2695

- **RECONSTRUCTING DNA COPY NUMBER BY PENALIZED ESTIMATION AND IMPUTATION** *ANNALS OF APPLIED STATISTICS*
  Zhang, Z., Lange, K., Ophoff, R., Sabatti, C.
  2010; 4 (4): 1749-1773

- **Biological, clinical and population relevance of 95 loci for blood lipids** *NATURE*
  Teslovich, T. M., Musunuru, K., Smith, A. V., Edmondson, A. C., Stylianou, I. M., Koseki, M., Pirruccello, J. P., Ripatti, S., Chasman, D. I., Willer, C. J., Johansen, C. T., Fouchier, S. W., Isaacs, et al
  2010; 466 (7307): 707-713

- **SPARSE REGULATORY NETWORKS** *ANNALS OF APPLIED STATISTICS*
  James, G. M., Sabatti, C., Zhou, N., Zhu, J.
  2010; 4 (2): 663-686

- **Sparse Regulatory Networks.** *The annals of applied statistics*
  James, G. M., Sabatti, C., Zhou, N., Zhu, J.
  2010; 4 (2): 663-686

- **Variance component model to account for sample structure in genome-wide association studies** *NATURE GENETICS*
  Kang, H. M., Sul, J. H., Service, S. K., Zaitlen, N. A., Kong, S., Freimer, N. B., Sabatti, C., Eskin, E.
  2010; 42 (4): 348-U110

- **The dysbindin-containing complex (BLOC-1) in brain: developmental regulation, interaction with SNARE proteins and role in neurite outgrowth.** *Molecular psychiatry*
  Ghiani, C. A., Starcevic, M., Rodriguez-Fernandez, I. A., Nazarian, R., Cheli, V. T., Chan, L. N., Malvar, J. S., De Vellis, J., Sabatti, C., Dell'Angelica, E. C.
  2010; 15 (2): 115-?

- **The dysbindin-containing complex (BLOC-1) in brain: developmental regulation, interaction with SNARE proteins and role in neurite outgrowth** *MOLECULAR PSYCHIATRY*
  Ghiani, C. A., Starcevic, M., Rodriguez-Fernandez, I. A., Nazarian, R., Cheli, V. T., Chan, L. N., Malvar, J. S., De Vellis, J., Sabatti, C., Dell'Angelica, E. C.
  2010; 15 (2): 204-215

- **A Narrow and Highly Significant Linkage Signal for Severe Bipolar Disorder In the Chromosome 5q33 Region in Latin American Pedigrees** *AMERICAN JOURNAL OF MEDICAL GENETICS PART B-NEUROPSYCHIATRIC GENETICS*
  Jasinska, A. J., Service, S., Jawaheer, D., DeYoung, J., Levinson, M., Zhang, Z., Kremeyer, B., Muller, H., Aldana, I., Garcia, J., Restrepo, G., Lopez, C., Palacio, et al
  2009; 150B (7): 998-1006

- **Robust discrimination between self and non-self neurites requires thousands of Dscam1 isoforms** *NATURE*
  Hattori, D., Chen, Y., Matthews, B. J., Salwinski, L., Sabatti, C., Grueber, W. B., Zipursky, S. L.
  2009; 461 (7264): 644-U87

- **Disruption of the neurexin 1 gene is associated with schizophrenia** *HUMAN MOLECULAR GENETICS*
  Rujescu, D., Ingason, A., Cichon, S., Pietilainen, O. P., Barnes, M. R., Toulopoulou, T., Picchioni, M., Vassos, E., Ettinger, U., Bramon, E., Murray, R., Ruggeri, M., Tosato, et al
  2009; 18 (5): 988-996

- **Genome-wide association analysis of metabolic traits in a birth cohort from a founder population** *NATURE GENETICS*
  Sabatti, C., Service, S. K., Hartikainen, A., Pouta, A., Ripatti, S., Brodsky, J., Jones, C. G., Zaitlen, N. A., Varilo, T., Kaakinen, M., Sovio, U., Ruokonen, A., Laitinen, et al
  2009; 41 (1): 35-46

- **Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts** *NATURE GENETICS*
  Aulchenko, Y. S., Ripatti, S., Lindqvist, I., Boomsma, D., Heid, I. M., Pramstaller, P. P., Penninx, B. W., Janssens, A. C., Wilson, J. F., Spector, T., Martin, N. G., Pedersen, N. L., Kyvik, et al
  2009; 41 (1): 47-55

- **Markov Models for Inferring Copy Number Variations from Genotype Data on Illumina Platforms** *HUMAN HEREDITY*
  Wang, H., Veldink, J. H., Blauw, H., Van den Berg, L. H., Ophoff, R. A., Sabatti, C.
  2009; 68 (1): 1-22

- **Recurrent CNVs Disrupt Three Candidate Genes in Schizophrenia Patients** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Vrijenhoek, T., Buizer-Voskamp, J. E., van der Stelt, I., Strengman, E., Sabatti, C., van Kessel, A. G., Brunner, H. G., Ophoff, R. A., Veltman, J. A.
  2008; 83 (4): 504-510

- **Large recurrent microdeletions associated with schizophrenia** *NATURE*
  Stefansson, H., Rujescu, D., Cichon, S., Pietilainen, O. P., Ingason, A., Steinberg, S., Fossdal, R., Sigurdsson, E., Sigmundsson, T., Buizer-Voskamp, J. E., Hansen, T., Jakobsen, K. D., Muglia, et al
  2008; 455 (7210): 232-U61

- **Clinical features and associated syndromes of mal de debarquement** *JOURNAL OF NEUROLOGY*
  Cha, Y., Brodsky, J., Ishiyama, G., Sabatti, C., Baloh, R. W.
  2008; 255 (7): 1038-1044

- **Bayesian Gaussian mixture models for high-density genotyping arrays** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Sabatti, C., Lange, K.
  2008; 103 (481): 89-100

- **A dictionary model for haplotyping, genotype calling, and association testing** *GENETIC EPIDEMIOLOGY*
  Ayers, K. L., Sabatti, C., Lange, K.
  2007; 31 (7): 672-683

- **Tag SNPs chosen from HapMap perform well in several population isolates** *GENETIC EPIDEMIOLOGY*
  Service, S., Sabatti, C., Freimer, N.
  2007; 31 (3): 189-194

- **Human genetics - Variants in common diseases** *NATURE*
  Freimer, N. B., Sabatti, C.
  2007; 445 (7130): 828-830

- **Genome scan for Tourette disorder in affected-sibling-pair and multigenerational families** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Cath, D., Heutink, P., Grados, M., Singer, H. S., Walkup, J. T., Illmann, C., Scharf, J. M., Santangelo, S., Stewart, S. E., Platko, J., Pauls, D. L., Cox, N. J., Robertson, et al
  2007; 80 (2): 265-272

- **The relevance of migraine in patients with Meniere's disease** *ACTA OTO-LARYNGOLOGICA*
  Cha, Y. H., Brodsky, J., Ishiyama, G., Sabatti, C., Baloh, R. W.
  2007; 127 (12): 1241-1245

- **Avoiding false discoveries in association studies.** *Methods in molecular biology (Clifton, N.J.)*
  Sabatti, C.
  2007; 376: 195-211

- **Volume measures for linkage disequilibrium** *BMC GENETICS*
  Chen, Y., Lin, C., Sabatti, C.
  2006; 7

- **Overrepresentation of rare variants in a specific ethnic group may confuse interpretation of association analyses** *HUMAN MOLECULAR GENETICS*
  Keen-Kim, D., Mathews, C. A., Reus, V. I., Lowe, T. L., Diego Herrera, L., Budman, C. L., Gross-Tsur, V., Pulver, A. E., Bruun, R. D., Erenberg, G., Naarden, A., Sabatti, C., Freimer, et al
  2006; 15 (22): 3324-3328

- **Convergent linkage evidence from two Latin-American population isolates supports the presence of a susceptibility locus for bipolar disorder in 5q31-34** *HUMAN MOLECULAR GENETICS*
  Herzberg, I., Jasinska, A., Garcia, J., Jawaheer, D., Service, S., Kremeyer, B., Duque, C., Parra, M. V., Vega, J., Ortiz, D., Carvajal, L., Polanco, G., Restrepo, et al
  2006; 15 (21): 3146-3153

- **Results of a SNP genome screen in a large Costa Rican pedigree segregating for severe bipolar disorder** *AMERICAN JOURNAL OF MEDICAL GENETICS PART B-NEUROPSYCHIATRIC GENETICS*
  Service, S., Molina, J., DeYoung, J., Jawaheer, D., Aldana, I., Vu, T., Bejarano, J., Fournier, E., Ramirez, M., Mathews, C. A., Davanzo, P., Macaya, G., Sandkuijl, et al
  2006; 141B (4): 367-373

- **Magnitude and distribution of linkage disequilibrium in population isolates and implications for genome-wide association studies** *NATURE GENETICS*
  Service, S., DeYoung, J., Karayiorgou, M., Roos, J. L., Pretorious, H., Bedoya, G., Ospina, J., Ruiz-Linares, A., Macedo, A., PALHA, J. A., Heutink, P., Aulchenko, Y., Oostra, et al
  2006; 38 (5): 556-560

- **Reconstructing ancestral haplotypes with a dictionary model** *JOURNAL OF COMPUTATIONAL BIOLOGY*
  Ayers, K. L., Sabatti, C., Lange, K.
  2006; 13 (3): 767-785

- **Bayesian sparse hidden components analysis for transcription regulation networks** *BIOINFORMATICS*
  Sabatti, C., James, G. M.
  2006; 22 (6): 739-746

- **A genome-wide linkage scan of familial benign recurrent vertigo: linkage to 22q12 with evidence of heterogeneity** *HUMAN MOLECULAR GENETICS*
  LEE, H., Jen, J. C., Wang, H., Chen, Z. G., Mamsa, H., Sabatti, C., Baloh, R. W., Nelson, S. F.
  2006; 15 (2): 251-258

- **Linkage disequilibrium and haplotype homozygosity in population samples genotyped at a high marker density** *HUMAN HEREDITY*
  Wang, H., Lin, C., Service, S., Chen, Y., Freimer, N., Sabatti, C.
  2006; 62 (4): 175-189
- **Distribution and dynamics of Lamp1-containing endocytic organelles in fibroblasts deficient in BLOC-3** *JOURNAL OF CELL SCIENCE*
  Falcon-Perez, J. M., Nazarian, R., Sabatti, C., Dell'Angelica, E. C.
  2005; 118 (22): 5243-5255
- **A generalized framework for Network Component Analysis** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*
  Boscolo, R., Sabatti, C., Liao, J. C., Roychowdhury, V. P.
  2005; 2 (4): 289-301
- **Guidelines for association studies in human molecular genetics** *HUMAN MOLECULAR GENETICS*
  Freimer, N. B., Sabatti, C.
  2005; 14 (17): 2481-2483
- **Vocabulon: a dictionary model approach for reconstruction and localization of transcription factor binding sites** *BIOINFORMATICS*
  Sabatti, C., Rohlin, L., Lange, K., Liao, J. C.
  2005; 21 (7): 922-931
- **Empirical Bayes estimation of a sparse vector of gene expression changes** *STATISTICAL APPLICATIONS IN GENETICS AND MOLECULAR BIOLOGY*
  Erickson, S., Sabatti, C.
  2005; 4
- **Inferring protein domain interactions from databases of interacting proteins** *GENOME BIOLOGY*
  Riley, R., Lee, C., Sabatti, C., Eisenberg, D.
  2005; 6 (10)
- **Suggestive linkage to chromosome 6q in families with bilateral vestibulopathy** *NEUROLOGY*
  Jen, J. C., Wang, H., LEE, H., Sabatti, C., Trent, R., Hannigan, I., Brantberg, K., Halmagyi, G. M., Nelson, S. F., Baloh, R. W.
  2004; 63 (12): 2376-2379
- **A novel mutation in KCNA1 causes episodic ataxia without myokymia.** *Human mutation*
  Lee, H., Wang, H., Jen, J. C., Sabatti, C., Baloh, R. W., Nelson, S. F.
  2004; 24 (6): 536-?
- **The use of pedigree, sib-pair and association studies of common diseases for genetic mapping and epidemiology** *NATURE GENETICS*
  Freimer, N., Sabatti, C.
  2004; 36 (10): 1045-1051
- **Transcriptome-based determination of multiple transcription regulator activities in Escherichia coli by using network component analysis** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Kao, K. C., Yang, Y. L., Boscolo, R., Sabatti, C., Roychowdhury, V., Liao, J. C.
  2004; 101 (2): 641-646
- **A Bayesian approach to expression network component analysis.** *Conference proceedings : ... Annual International Conference of the IEEE Engineering in Medicine and Biology Society. IEEE Engineering in Medicine and Biology Society. Conference*
  Sabatti, C., Rohlin, L.
  2004; 4: 2933-2936
- **A Bayesian approach to expression network component analysis** *26th Annual International Conference of the IEEE-Engineering-in-Medicine-and-Biology-Society*
  Sabatti, C., Rohlin, L.
  IEEE.2004: 2933–2936
- **Network component analysis: Reconstruction of regulatory signals in biological systems** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Liao, J. C., Boscolo, R., Yang, Y. L., Tran, L. M., Sabatti, C., Roychowdhury, V. P.

2003; 100 (26): 15522-15527

- **Global analysis of gene expression in neural progenitors reveals specific cell-cycle, signaling, and metabolic networks** *DEVELOPMENTAL BIOLOGY*
  Karsten, S. L., Kudo, L. C., Jackson, R., Sabatti, C., Kornblum, H. I., Geschwind, D. H.
  2003; 261 (1): 165-182
- **False discovery rate in linkage and association genome screens for complex disorders** *GENETICS*
  Sabatti, C., Service, S., Freimer, N.
  2003; 164 (2): 829-833
- **The Human Phenome Project** *NATURE GENETICS*
  Freimer, N., Sabatti, C.
  2003; 34 (1): 15-21
- **Dictionary model for the analysis of E-Coli promoter regions** *25th Annual International Conference of the IEEE-Engineering-in-Medicine-and-Biology-Society*
  Sabatti, C., Rohlin, L., Liao, J.
  IEEE.2003: 3711–3714
- **Genomewide motif identification using a dictionary model** *PROCEEDINGS OF THE IEEE*
  Sabatti, C., Lange, K.
  2002; 90 (11): 1803-1810
- **Microanalysis of DNA microarrays** *ASM NEWS*
  Liao, J. C., Sabatti, C.
  2002; 68 (9): 432-437
- **Familial horizontal gaze palsy with progressive scoliosis maps to chromosome 11q23-25** *NEUROLOGY*
  Jen, J., Coulin, C. J., Bosley, T. M., Salih, M. A., Sabatti, C., Nelson, S. F., Baloh, R. W.
  2002; 59 (3): 432-435
- **Co-expression pattern from DNA microarray experiments as a tool for operon prediction** *NUCLEIC ACIDS RESEARCH*
  Sabatti, C., Rohlin, L., Oh, M. K., Liao, J. C.
  2002; 30 (13): 2886-2893
- **Homozygosity and linkage disequilibrium** *GENETICS*
  Sabatti, C., Risch, N.
  2002; 160 (4): 1707-1719
- **Thresholding rules for recovering a sparse signal from microarray experiments** *MATHEMATICAL BIOSCIENCES*
  Sabatti, C., Karsten, S. L., Geschwind, D. H.
  2002; 176 (1): 17-34
- **An evaluation of tyramide signal amplification and archived fixed and frozen tissue in microarray gene expression analysis** *NUCLEIC ACIDS RESEARCH*
  Karsten, S. L., Van Deerlin, V. M., Sabatti, C., Gill, L. H., Geschwind, D. H.
  2002; 30 (2)
- **Dissecting a population genome for targeted screening of disease mutations** *HUMAN MOLECULAR GENETICS*
  Pastinen, T., Perola, M., Ignatius, J., Sabatti, C., Tainola, P., Levander, M., Syvanen, A. C., Peltonen, L.
  2001; 10 (26): 2961-2972
- **Bayesian analysis of haplotypes for linkage disequilibrium mapping** *GENOME RESEARCH*
  Liu, J. S., Sabatti, C., Teng, J., Keats, B. J., Risch, N.
  2001; 11 (10): 1716-1724
- **Generalised Gibbs sampler and multigrid Monte Carlo for Bayesian computation** *BIOMETRIKA*
  Liu, J. S., Sabatti, C.
  2000; 87 (2): 353-369

- **The DYT1 phenotype and guidelines for diagnostic testing** *NEUROLOGY*
  Bressman, S. B., Sabatti, C., Raymond, D., de Leon, D., Klein, C., Kramer, P. L., Brin, M. F., Fahn, S., Breakefield, X., Ozelius, L. J., Risch, N. J.
  2000; 54 (9): 1746-1752
- **A genetic region on chromosome 16 may predispose to the development of Crohn's disease at an early age in Ashkenazi Jews.**
  Gulwani-Akolkar, B., Akolkar, P. N., Daly, M., Sabatti, C., Lin, X. Y., Danzi, S. E., Pergolizzi, R., Storch, I., Risch, N., Katz, S., Levine, J., Silver, J.
  CELL PRESS.1999: A99–A99
- **Simulated sintering: Markov chain Monte Carlo with spaces of varying dimensions** *6th Valencia International Meeting on Bayesian Statistics*
  Liu, J. S., Sabatti, C.
  OXFORD UNIV PRESS.1999: 389–413