Stanford



Chiara Sabatti

Professor of Biomedical Data Science and of Statistics, and Senior Fellow at the Stanford Institute for Human-Centered Artificial Intelligence (HAI)

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
- Senior Fellow, Institute for Human-Centered Artificial Intelligence (HAI)
- 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

2026-27

- Critical Exploration of Topics in Biomedical Data Science: BMDS 290 (Spr)
- Data Science Mentoring: BMDS 360 (Win)
- 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)

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)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Ginnie Ma, Yash Nair, Sarah Zhao

Postdoctoral Faculty Sponsor

Yusuph Mavura

Master's Program Advisor

Ryan Hsu

Doctoral (Program)

Max Schuessler

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **Uncovering heterogeneous effects via localized feature selection.** *Proceedings of the National Academy of Sciences of the United States of America*
  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
  2026; 123 (38): e2527033123
- **It's a wrap: deriving distinct discoveries with FDR control after a GWAS analysis.** *Bioinformatics advances*
  Chu, B. B., He, Z., Sabatti, C.
  2026; 6 (1): vbag260
- **Contextualizing Opioid Consumption After Ambulatory Surgery in Adolescents.** *Paediatric anaesthesia*
  Groenewald, C. B., Rabbitts, J. A., Borucki, A. N., Agarwal, R., Sabatti, C., Palermo, T. M., Rogers, A. H.
  2026
- **CIT-Lasso: a scalable approach beyond guilty by association for identifying causal variants from genome-wide summary statistics.** *Genome 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
  2026; 27 (1)
- **Anti-CAR Immunity Drives Acquired Therapeutic Resistance to GD2-CAR T Cell Therapy in Diffuse Midline Glioma.** *medRxiv : the preprint server for health sciences*
  Chen, Y., Reynolds, K., Koch, M. R., Petrakian, C. F., Good, Z., Yamada-Hunter, S., Sotillo, E., Song, K. W., Mahdi, J., Majzner, R., Desai, M. H., Huang, Y. W., Daghagh, et al
  2026
- **A blended genome and exome sequencing method captures genetic variation in an unbiased and cost-effective manner.** *Nature genetics*
  Boltz, T. A., Chu, B. B., DeFelice, M., Liao, C., Sealock, J. M., Ye, R., Goldstein, J. I., Majara, L., Fu, J. M., Service, S. K., Zhan, L., Medland, S. E., Chapman, et al
  2026
- **Fine-tuning and structured prompting strategies for question answering over full-text biomedical research articles.** *PloS one*
  Tao, K., Satija, R., Zhou, J., Osman, Z. A., Ahluwalia, V., Sabatti, C., Shafer, R. W.
  2026; 21 (6): e0351631
- **Effect of ancestry and shared genetic architecture of serious mental illness on symptoms and cognition in an admixed Latin American population.** *Research square*

Lopera-Maya, E., Service, S. K., Díaz-Zuluaga, A. M., Ramírez, M. C., Mejia, J. C., Valencia, J., Teshiba, T., Ramirez, A. M., De la Hoz, J. F., Valdez, J., Umanes, M. M., Moore, T. M., Chapman, et al
2026

- **Effect of ancestry and shared genetic architecture of serious mental illness on symptoms and cognition in an admixed Latin American population.** *medRxiv : the preprint server for health sciences*
  Lopera-Maya, E., Service, S. K., Díaz-Zuluaga, A. M., Ramírez, M. C., Mejia, J. C., Valencia, J., Teshiba, T., Ramirez, A. M., De la Hoz, J. F., Valdez, J., Umanes, M. M., Moore, T. M., Chapman, et al
  2026
- **Association Between High-Risk Preexisting Substance Use and Increased Postoperative Opioid Dose Use Among Adolescents Undergoing Ambulatory Orthopedic Surgery.** *Paediatric anaesthesia*
  Groenewald, C. B., Rabbitts, J. A., Borucki, A. N., Agarwal, R., Sabatti, C., Palermo, T. M., Rogers, A. H.
  2026
- **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

- **Genetic dysregulation of gene expression and splicing during a ten-year period of human aging**
  Balliu, B., Durrant, M., de Goede, O., Abell, N., Li, X., Liu, B., Gloudemans, M., Cook, N., Smith, K., Pala, M., Cucca, F., Schlessinger, D., Jaiswal, et al
  NATURE PUBLISHING GROUP.2019: 1688

- **GENETICS OF SEVERE MENTAL ILLNESS IN A COLOMBIAN POPULATION ISOLATE**
  Freimer, N., Loohuis, L., Service, S., Vargas, C., Gomez, J., Castano, M., Gur, R., Gur, R. E., Neale, B., Teshiba, T., Sabatti, C., Escobar, J., Reus, et al
  ELSEVIER.2019: S24–S25

- **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**
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