Stanford

Chiara Sabatti

Professor of Biomedical Data Science and of Statistics

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, 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, 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- present)
- 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

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)

2021-22

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

2020-21

- Consulting Workshop on Biomedical Data Science: BIODS 232 (Aut, Win, Spr)
- Inclusive Mentorship in Data Science: BIODS 360 (Spr)
- Introduction to Statistical Inference: STATS 200 (Win)
- Race, Data Algorithms, and Health: BIODS 240, BIOMEDIN 240 (Aut)
- Riding the Data Wave: BIODS 48N, STATS 48N (Aut)
- Workshop in Biostatistics: BIODS 260A, STATS 260A (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Zhaomeng Chen, Julie Zhang

Postdoctoral Faculty Sponsor

Benjamin Chu

Doctoral Dissertation Advisor (AC)

Paula Gablenz

Master's Program Advisor

Misha Baitemirova

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Biomedical Informatics (Masters Program)

Publications

PUBLICATIONS

- **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
- **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
- **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., 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
- **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**
  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

- **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
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