Tian Ge

Contact Information

Psychiatric & Neurodevelopmental Genetics Unit
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Research Interests

Statistical genetics; Computational imaging genetics; Neuroimaging statistics

Current Appointment

Assistant Professor, Harvard Medical School — Nov 2019 — present
Assistant Investigator, MGH Center for Genomic Medicine — Nov 2019 — present
Director of Data Science, MGH Center for Precision Psychiatry — Jan 2021 — present

Appointment History

Instructor in Psychiatry, Harvard Medical School — May 2017 — Oct 2019
Instructor in Investigation, Massachusetts General Hospital — May 2017 — Oct 2019

Education & Training

Research Fellow, Massachusetts General Hospital, Harvard Medical School — 2014 — 2017
Mentors: Mert R. Sabuncu & Jordan W. Smoller

Ph.D. in Applied Mathematics, Fudan University, China — 2009 — 2014
Advisor: Jianfeng Feng

Ph.D. in Computer Science, The University of Warwick, United Kingdom — 2010 — 2013
Advisors: Jianfeng Feng & Thomas E. Nichols

B.S. in Mathematics and Applied Mathematics, Fudan University, China — 2005 — 2009

Honors & Awards

NIH Pathway to Independence Award — 2017
MGH ECOR Tosteson Postdoctoral Fellowship Award — 2015
Merit Abstract Award for the OHBM Annual Meeting — 2015
Trainee Abstract Travel Award for the OHBM Annual Meeting — 2012 & 2013

Current Grants

R00 AG054573 (Ge) — 12/15/2019 — 11/30/2022
NIH/NIA — $435,840
Exploring the genetic basis of AD progression
Role: Principal Investigator

U01 HG008685 (Karlson) — 07/01/2020 — 04/30/2025
NIH/NHGRI
eMERGE phase IV Clinical Center at Partners Healthcare
Role: Co-Investigator

The Tommy Fuss Fund (Smoller) — 01/01/2021 — 12/31/2021
Linking genomics, brain structure and the development of psychiatric disorders
Role: Co-Investigator

The Harvard Program in Precision Psychiatry (Smoller) — 07/01/2019 — 06/30/2021
President and Fellows of Harvard College
Role: Co-Investigator

Completed Grants

K99 AG054573 (Ge) — 08/15/2017 — 11/30/2019
NIH/NIA — $254,000
Exploring the genetic basis of AD progression
Role: Principal Investigator

MGH ECOR Tosteson Postdoctoral Fellowship Award (Ge) — 09/01/2015 — 08/31/2016
MGH Executive Committee On Research — $54,800
Novel computational tools to bridge genomic, neuroimaging, and behavioral traits
Role: Principal Investigator

Teaching Experience

Director and Instructor, A Practical Introduction to Statistical Genetics 10 90-min lecture series; sponsored by MGH Division of Clinical Research	Fall 2019, 2020

Advising & Mentoring

Zhaowen Liu (Research Fellow, MGH)	Jan 2019 — present
Yunfeng Ruan (Postdoctoral Researcher, Broad Institute)	Mar 2019 — present
Kai Yuan (Research Fellow, MGH)	Jan 2020 — present
Qidi Feng (Research Fellow, MGH)	Oct 2020 — present
Ryan Longchamps (Postdoctoral Researcher, Broad Institute)	Sept 2019 — Apr 2021
Yen-Chen Anne Feng (Research Fellow, MGH)	Sept 2017 — Nov 2020
Qunxi Zhu (Visiting graduate student, Fudan University)	Jan 2019 — Dec 2019

Professional Services

Reviewer for Wellcome Trust grant applications

Ad hoc Reviewer for *Biological Psychiatry*; *Bioinformatics*; *Biostatistics*; *BMC Psychiatry*; *Brain Sciences*; *Cerebral Cortex*; *Communications Biology*; *eLife*; *European Journal of Neurology*; *Frontiers in Computational Neuroscience*; *Frontiers in Neuroinformatics*; *Neuropsychopharmacology*; *Genetic Epidemiology*; *Genome Medicine*; *Human Brain Mapping*; *Human Reproduction*; *Journal of Computational and Graphical Statistics*; *Journal of Neuroscience*; *IEEE Journal of Biomedical and Health Informatics*; *IEEE Transactions on Medical Imaging*; *International Journal of Bifurcation and Chaos*; *Medical Image Analysis*; *MICCAI*; *Molecular Ecology Resources*; *Molecular Psychiatry*; *Nature Communications*; *Nature Genetics*; *Nature Methods*; *Nature Neuroscience*; *Network Neuroscience*; *Neurobiology of Aging*; *NeuroImage*; *NeuroImage: Clinical*; *Neuroinformatics*; *PLoS Computational Biology*; *PLoS ONE*; *Schizophrenia Bulletin*; *Scientific Reports*; *Statistics in Medicine*; *Statistical Methods in Medical Research*; *Statistics and Computing*

Book Chapters

1. Ge T, Smoller JW, Sabuncu MR. Kernel machine regression in neuroimaging genetics. In: *Machine Learning and Medical Imaging*, Wu G, Shen D, Sabuncu MR (Eds.). Academic Press, Cambridge, MA, 2016; 31-68.

Preprints

*co-senior author

1. Tian R, Ge T, Liu JZ, Lam M, Biogen Biobank Team, Levey DF, Gelernter J, Stein MB, Tsai EA, Huang H, Lencz T, Runz H, Chen CY. Whole-exome sequencing in the UK Biobank reveals risk gene *SLC2A1* and biological insights for major depressive disorder. *medRxiv preprint*, 2021; `https://doi.org/10.1101/2021.05.04.21256398`.
2. Chen CY, Chen TT, Feng YCA, Longchamps RJ, Lin SC, Wang SH, Hsu YH, Yang HI, Kuo PH, Daly MJ, Chen WJ, Huang H*, Ge T*, Lin YF*. Analysis across Taiwan Biobank, Biobank Japan and UK Biobank identifies hundreds of novel loci for 36 quantitative traits. *medRxiv preprint*, 2021; `https://doi.org/10.1101/2021.04.12.21255236`.
3. Setton R, Mwilambwe-Tshilobo L, Girn M, Lockrow AW, Baracchini G, Lowe AJ, Cassidy BN, Li J, Luh WM, Bzdok D, Leahy RM, Ge T, Margulies DS, Misic B, Bernhardt BC, Stevens WD, De Brigard F, Kundu P, Turner GR, Spreng RN. Functional architecture of the aging brain. *bioRxiv preprint*, 2021; `https://doi.org/10.1101/2021.03.31.437922`.
4. Ruan Y, Feng YA, Chen CY, Lam M, Stanley Global Asia Initiatives, Sawa A, Martin AR, Qin S*, Huang H*, Ge T*. Improving polygenic prediction in ancestrally diverse populations. *medRxiv preprint*, 2021; `https://doi.org/10.1101/2020.12.27.20248738`.
5. Feng YA, Ge T, Cordioli M, FinnGen, Ganna A, Smoller JW, Neale BM. Findings and insights from the genetic investigation of age of first reported occurrence for complex disorders in the UK Biobank and FinnGen. *medRxiv preprint*, 2020; `https://doi.org/10.1101/2020.11.20.20234302`.
6. Schizophrenia Working Group of the Psychiatric Genomics Consortium. Mapping genomic loci prioritises genes and implicates synaptic biology in schizophrenia. *medRxiv preprint*, 2020; `https://doi.org/10.1101/2020.09.12.20192922`.
7. Lam M, Thompson M, Li B, Edwards AC, Chen CY, Ge T, Cai N, Bigdeli T, Lencz T, Kendler K, Huang H. Elucidating the joint genetic architecture of mood disorder and schizophrenia. *medRxiv preprint*, 2020; `https://doi.org/10.1101/2020.09.14.20193870`.

Peer-reviewed Journal Publications

1. Ni G, Zeng J, Revez JR, Wang Y, Ge T, Restaudi R, Kiewa J, Nyholt DR, Coleman JRI, Smoller JW, Schizophrenia Working Group of the Psychiatric Genomics Consortium, Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium, Yang J, Visscher PM, Wray NR. A comprehensive evaluation of polygenic score methods across cohorts in psychiatric disorders. *Biological Psychiatry*, 2021; in press.
2. Lam M, Chen CY, Ge T, Xia Y, Hill DW, ⋯, Liu C, Malhotra AK, Lencz T. Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. *Neuropsychopharmacology*, 2021; in press.
3. Kong R, Yang Q, Gordon E, Xue A, Yan X, Orban C, Zuo XN, Spreng N, Ge T, Holmes AJ, Eickhoff S, Yeo BTT. Individual-specific areal-level parcellations improve functional connectivity prediction of behavior. *Cerebral Cortex*, 2021; in press.
4. Sønderby IE, Ching CRK, Thomopoulos SI, van der Meer D, Sun D, ⋯, Ge T, ⋯, Thompson PM, Bearden CE, Andreassen OA. Effects of copy number variations on brain structure and risk for psychiatric illness: Large-scale studies from the ENIGMA Working Groups on CNVs. *Human Brain Mapping*, 2021; in press.
5. Dennis JK, Sealock JM, Straub P, Lee YH, Hucks D, Actkins K, Faucon A, Feng YA, Ge T, Goleva SB, Niarchou M, Singh K, Morley T, Smoller JW, Ruderfer DM, Mosley JD, Chen G, Davis LK. Clinical laboratory test-wide association scan of polygenic scores identifies biomarkers of complex disease. *Genome Medicine*, 2021; 13:6.
6. Sønderby IE, van der Meer D, Moreau C, Kaufmann T, Walters B, ⋯, Ge T, ⋯, Jacquemont S, Thompson PM, Andreassen OA. 1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. *Translational Psychiatry*, 2021; 11:182.
7. Anderson KM, Ge T, Kong R, Patrick LM, Spreng RN, Sabuncu MR, Yeo BTT, Holmes AJ. Heritability of individualized cortical network topography. *Proceedings of the National Academy of Sciences USA*, 2021; 118(9).
8. Jiang X, Ge T, Chen CY. The causal role of circulating vitamin D concentrations in human complex traits and diseases: a large-scale Mendelian randomization study. *Scientific Reports*, 2021; 11:184.
9. Spreng RN, Dimas E, Mwilambwe-Tshilobo L, Dagher A, Koellinger P, Nave G, Ong A, Kernbach JM, Wiecki TV, Ge T, Li Y, Holmes AJ, Yeo BTT, Turner GR, Dunbar RIM, Bzdok D. The default network of the human brain is associated with perceived social isolation. *Nature Communications*, 2020; 11:6393.
10. Choi KW, Stein MB, Nishimi KM, Ge T, Coleman JRI, Chen CY, Ratanatharathorn A, Zheutlin AB, Dunn EC, 23andMe Research Team, Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium, Breen G, Koenen KC, Smoller JW. An exposure-wide and Mendelian Randomization approach to identifying modifiable factors for the prevention of depression. *The American Journal of Psychiatry*, 2020; 177(10):944-954.
11. Mealer RG, Jenkins BG, Chen CY, Daly MJ, Ge T, Lehoux S, Marquardt T, Palmer CD, Park JH, Parsons PJ, Sackstein R, Williams SE, Cummings RD, Scolnick EM, Smoller JW. The schizophrenia risk locus in *SLC39A8* alters brain metal transport and plasma glycosylation. *Scientific Reports*, 2020; 10:13162.
12. Anderson KM, Collins MA, Chin R, Ge T, Rosenberg MD, Holmes AJ. Transcriptional and imaging-genetic association of cortical interneurons, brain function, and schizophrenia risk. *Nature Communications*, 2020; 11:2889.
13. Grasby KL, Jahanshad N, Painter JN, Colodro-Conde L, Bralten J, ⋯, Ge T, ⋯, Stein JL, Thompson PM, Medland SE. The genetic architecture of the human cerebral cortex. *Science*, 2020; 367(6484):eaay6690.
14. Lee PH, Anttila V, Won H, Feng YCA, Rosenthal J, ⋯, Ge T, ⋯, Neale BM, Kendler KS, Smoller JW. Genomic relationships, novel loci, and pleiotropic mechanisms across eight psychiatric disorders. *Cell*, 2019; 179(7):1469-1482.
15. Zheutlin AB, Dennis J, Karlsson Linner R, Moscati A, Restrepo N, Straub P, Ruderfer D, Castro VM, Chen CY, Ge T, Huckins LM, Charney A, Kirchner HL, Stahl EA, Chabris CF, Davis LK, Smoller JM. Penetrance and pleiotropy of polygenic risk scores for schizophrenia in 106,160 patients across four healthcare systems. *The American Journal of Psychiatry*, 2019; 176(10):846-855.

16. Liegeois R, Li J, Kong R, Van De Ville D, Ge T, Sabuncu MR, Yeo BTT. Resting brain dynamics at different timescales capture distinct aspects of human behavior. *Nature Communications*, 2019; 10:2317.

17. Chen X, Formisano E, Blokland GAM, Strike LT, McMahon KL, de Zubicaray GI, Thompson PM, Wright MJ, Winkler AM, Ge T, Nichols TE. Accelerated estimation and permutation inference for ACE modeling. *Human Brain Mapping*, 2019; 40:3488-3507.

18. Ge T, Chen CY, Ni Y, Feng YA, Smoller JW. Polygenic prediction via Bayesian regression and continuous shrinkage priors. *Nature Communications*, 2019; 10:1776.

19. Li J, Kong R, Ligeois R, Orban C, Tan Y, Sun N, Holmes AJ, Sabuncu MR, Ge T, Yeo BTT. Global signal regression strengthens association between resting-state functional connectivity and behavior. *NeuroImage*, 2019; 196:126-141.

20. Mwilambwe-Tshilobo L, Ge T, Chong M, Ferguson MA, Misic B, Burrow AL, Leahy R, Spreng RN. Loneliness and meaning in life are reflected in the intrinsic network architecture of the brain. *Social Cognitive and Affective Neuroscience*, 2019; 14(4):423-433.

21. Ge T, Chen CY, Doyle AE, Vettermann R, Tuominen LJ, Holt DJ, Sabuncu MR, Smoller JW. The shared genetic basis of educational attainment and cerebral cortical morphology. *Cerebral Cortex*, 2018; 29(8):3471-3481.

22. Elliott ML, Belsky DW, Anderson K, Corcoran DL, Ge T, Knodt A, Prinz JA, Sugden K, Williams B, Ireland D, Poulton R, Caspi A, Holmes A, Moffitt T, Hariri AR. A polygenic score for higher educational attainment is associated with larger brains. *Cerebral Cortex*, 2018; 29(8):3496-3504.

23. Ge T, Sabuncu MR, Smoller JW, Sperling RA, Mormino EC. Dissociable influences of APOE $\varepsilon 4$ and polygenic risk of AD dementia on amyloid and cognition. *Neurology*, 2018; 90(18):e1605-e1612.

24. Tong T, Aganj I, Ge T, Polimeni JR, Fischl B. Functional density and edge maps: Characterizing functional architecture in individuals and improving cross-subject registration. *NeuroImage*, 2017; 158:346-355.

25. Ge T, Holmes AJ, Buckner RL, Smoller JW, Sabuncu MR. Heritability analysis with repeat measurements and its application to resting-state functional connectivity. *Proceedings of the National Academy of Sciences USA*, 2017; 114(21):5521-5526.

26. Ge T, Chen CY, Neale BM, Sabuncu MR, Smoller JW. Phenome-wide heritability analysis of the UK Biobank. *PLoS Genetics*, 2017; 13(4):e1006711.

27. Wang C, Sun J, Guillaume B, Ge T, Hibar DP, Greenwood CMT, Qiu A. A set-based mixed effect model for gene-environment interaction and its application to neuroimaging phenotypes. *Frontiers in Neuroscience*, 2017; 11:191.

28. Adams HH, Hibar DP, Chouraki V, Stein JL, Nyquist PA, $\cdots$, Ge T, $\cdots$, Medland SE, Ikram MA, Thompson PM. Novel genetic loci underlying human intracranial volume identified through genome-wide association. *Nature Neuroscience*, 2016; 19(12):1569-1582.

29. Lee PH, Baker JT, Holmes AJ, Jahanshad N, Ge T, Jung JY, Cruz Y, Manoach DS, Hibar DP, Faskowitz J, McMahon KL, de Zubicaray GI, Martin NG, Wright MJ, Öngür D, Buckner R, Roffman J, Thompson PM, Smoller JW. Partitioning heritability analysis reveals a shared genetic basis of brain anatomy and schizophrenia. *Molecular Psychiatry*, 2016; 21(12):1680-1689.

30. Ge T, Reuter M, Winkler AM, Holmes AJ, Lee PH, Tirrell LS, Roffman JL, Buckner RL, Smoller JW, Sabuncu MR. Multidimensional heritability analysis of neuroanatomical shape. *Nature Communications*, 2016; 7:13291.

31. Sabuncu MR, Ge T, Holmes AJ, Smoller JW, Buckner RL, Fischl B. Morphometricity as a measure of the neuroanatomical signature of a trait. *Proceedings of the National Academy of Sciences USA*, 2016; 113(39):E5749-5756.

32. Krienen FM, Yeo BT, Ge T, Buckner RL, Sherwood CC. Transcriptional profiles of supragranular-enriched genes associate with corticocortical network architecture in the human brain. *Proceedings of the National Academy of Sciences USA*, 2016; 113(4):E469-E478.

33. Ge T, Nichols TE, Ghosh D, Mormino EC, Smoller JW, Sabuncu MR. A kernel machine method for detecting effects of interaction between multidimensional variable sets: An imaging genetics application. *NeuroImage*, 2015; 109:505-514.

34. Liu J, Mo Y, Ge T, Wang Y, Luo XJ, Feng J, Li M, Su B. Allelic variation at 5-HTTLPR is associated with brain morphology in a Chinese population. *Psychiatry Research*, 2015; 226(1):399-402.
35. Ge T, Nichols TE, Lee PH, Holmes AJ, Roffman JL, Buckner RL, Sabuncu MR, Smoller JW. Massively expedited genome-wide heritability analysis (MEGHA). *Proceedings of the National Academy of Sciences USA*, 2015; 112(8):2479-2484.
36. Ge T, Tian X, Kurths J, Feng J, Lin W. Achieving modulated oscillations by feedback control. *Physical Review E*, 2014; 90(2):022909.
37. Ge T, Müller-Lenke N, Bendfeldt K, Nichols TE, Johnson TD. Analysis of multiple sclerosis lesions via spatially varying coefficients. *The Annals of Applied Statistics*, 2014; 8(2):1095-1118.
38. Ge T, Schumann G, Feng J. Imaging genetics — Towards discovery neuroscience. *Quantitative Biology*, 2013; 1(4):227-245.
39. Luo Q, Ge T, Grabenhorst F, Feng J, Rolls ET. Attention-dependent modulation of cortical taste circuits revealed by Granger causality with signal-dependent noise. *PLoS Computational Biology*, 2013; 9(10):e1003265.
40. Thompson PM, Ge T, Glahn DC, Jahanshad N, Nichols TE. Genetics of the connectome. *NeuroImage*, 2013; 80:475-88.
41. Tao H, Guo S, Ge T, Kendrick KM, Xue Z, Liu Z, Feng J. Depression uncouples brain hate circuit. *Molecular Psychiatry*, 2013; 18(1):101-111.
42. Ge T, Feng J, Hibar DP, Thompson PM, Nichols TE. Increasing power for voxel-wise genome-wide association studies: The random field theory, least square kernel machines and fast permutation procedures. *NeuroImage*, 2012; 63(2):858-873.
43. Ge T, Cui Y, Kurths J, Lin W, Liu C. Characterizing time series: When Granger causality triggers complex networks. *New Journal of Physics*, 2012; 14:083028.
44. Ge T, Lin W, Feng J. Invariance principles allowing of non-Lyapunov functions for estimating attractor boundaries of discrete dynamical systems. *IEEE Transactions on Automatic Control*, 2012; 57(2):500-505.
45. Ge T, Feng J, Grabenhorst F, Rolls ET. Componential Granger causality, and its application to identifying the source and mechanisms of the top-down biased activation that controls attention to affective vs sensory processing. *NeuroImage*, 2012; 59(2):1846-1858.
46. Luo Q, Ge T, Feng J. Granger causality with signal-dependent noise. *NeuroImage*, 2011; 57(4):1422-1429.
47. Ge T, Kendrick KM, Feng J. A novel extended Granger Causal Model approach demonstrates brain hemispheric differences during face recognition learning. *PLoS Computational Biology*, 2009; 5(11):e1000570.

Peer-reviewed Conference Publications

1. Taschler B, Ge T, Bendfeldt K, Müller-Lenke N, Johnson TD, Nichols TE. Spatial modeling of multiple sclerosis for disease subtype prediction. In: *Medical Image Computing and Computer Assisted Intervention – MICCAI. Lecture Notes in Computer Science*, 2014; 8674:797-804.

Miscellaneous Publications

1. Ge T, Holmes AJ, Buckner RL, Smoller JW, Sabuncu MR. Reply to Risk and Zhu: Mixed-effects modeling as a principled approach to heritability analysis with repeat measurements. *Proceedings of the National Academy of Sciences USA*, 2018; 115(2):E123.
2. Ge T, Yeo BTT, Winkler AM. A brief overview of permutation testing with examples. *OHBM Official Blog*, 2018; `https://goo.gl/nA34LR`.
3. Li M, Ge T, Feng J, Su B. SLC6A15 rs1545843 and depression: implications from brain imaging data. *The American Journal of Psychiatry*, 2013; 170(7):805.

Invited Talks

PRS-CSx: improving cross-population polygenic prediction using coupled continuous shrinkage priors PGC Cross-Population Special Interest Group	Apr, 2021 Virtual
PRS-CSx: improving cross-population polygenic prediction using coupled continuous shrinkage priors eMERGE PRS Validation & Evaluation Workgroup	Dec, 2020 Virtual
Within- and cross-population polygenic prediction using continuous shrinkage priors Channing Division of Network Medicine, Brigham and Women's Hospital	Nov, 2020 Virtual
PRS-CSx: cross-population polygenic prediction using coupled continuous shrinkage priors World Congress of Psychiatric Genetics	Oct, 2020 Virtual
Within- and cross-population polygenic prediction using continuous shrinkage priors DIAMANTE Consortium	July, 2020 Virtual
Machine learning for risk prediction in electronic health records World Congress of Psychiatric Genetics	Oct, 2019 Anaheim, CA
Polygenic prediction: theory, methods and clinical applications Bio-X Institutes, Shanghai Jiao Tong University	Aug, 2019 Shanghai, China
A unified framework of moment-matching methods for high-dimensional heritability and genetic correlation analysis ENAR International Biometric Society Spring Meeting	Mar, 2018 Atlanta, GA
Moment-matching methods for heritability and co-heritability analysis Broad Institute Online Genetics Presentation	Mar, 2018 Boston, MA
Heritability analysis: from neuroimaging genetics to large-scale health informatics Trauma Genomics Group Meeting	Dec, 2016 Boston, MA
Heritability-based prioritization of structural neuroimaging phenotypes ENAR International Biometric Society Spring Meeting	Mar, 2016 Austin, TX
Large-scale prioritization of neuroimaging phenotypes 12th International Imaging Genetics Conference	Jan, 2016 Irvine, CA
Probing the genetic underpinnings of structural neuroimaging phenotypes SAMSI Beyond Bioinformatics Transition Workshop	May 2015 Durham, NC
Kernel machines for imaging genetics SAMSI Imaging Genetics Working Group Seminar	Nov 2014 Boston, MA
Imaging genetics: from univariate to multivariate analyses University of Leeds	Aug 2013 Leeds, UK
Analysis of multiple sclerosis lesions via spatially varying coefficients 19th Annual Meeting of the Organization for Human Brain Mapping	June 2013 Seattle, WA
A Spatial GLMM and the estimation of spatially varying coefficients with application to multiple sclerosis MRI data Athinoula A. Martinos Center for Biomedical Imaging	June 2013 Charlestown, MA
Modulating the oscillations produced by discrete biological models International Symposium on Nonlinear Theory and its Applications	Oct 2012 Palma de Mallorca, Spain
Increasing power for voxel-wise genome-wide association studies 18th Annual Meeting of the Organization for Human Brain Mapping	June 2012 Beijing, China

Last update: May, 2021