

Tian Ge

GENERAL INFORMATION	Instructor , Harvard Medical School Research Staff , Massachusetts General Hospital Psychiatric & Neurodevelopmental Genetics Unit Center for Genomic Medicine Simches Research Building, 185 Cambridge Street Boston, Massachusetts 02114, USA	May 2017 — present Email: tge1@mgh.harvard.edu Homepage: http://scholar.harvard.edu/tge
RESEARCH INTERESTS	Computational imaging genetics; Statistical genetics; Neuroimaging statistics	
EDUCATION & TRAINING	Research Fellow , Massachusetts General Hospital, Harvard Medical School Mentors: Mert R. Sabuncu & Jordan W. Smoller	2014 — 2017
	Ph.D. in Applied Mathematics, Fudan University, China Advisor: Jianfeng Feng	2009 — 2014
	Ph.D. in Computer Science, The University of Warwick, United Kingdom Advisors: Jianfeng Feng & Thomas E. Nichols	2010 — 2013
	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
GRANTS	K99AG054573 NIH/NIA Exploring the genetic basis of AD progression Role: Principal Investigator	08/15/2017 — 11/30/2019 \$254,000
	MGH ECOR Tosteson Postdoctoral Fellowship Award MGH Executive Committee On Research (ECOR) Novel computational tools to bridge genomic, neuroimaging, and behavioral traits Role: Principal Investigator	09/01/2015 — 08/31/2016 \$54,800
PROFESSIONAL SERVICES	Ad hoc reviewer for <i>Biological Psychiatry</i> ; <i>Bioinformatics</i> ; <i>BMC Psychiatry</i> ; <i>Brain Sciences</i> ; <i>Cerebral Cortex</i> ; <i>Communications Biology</i> ; <i>Frontiers in Computational Neuroscience</i> ; <i>Frontiers in Neuroinformatics</i> ; <i>Neuropsychopharmacology</i> ; <i>Genetic Epidemiology</i> ; <i>Human Brain Mapping</i> ; <i>Human Reproduction</i> ; <i>Journal of Computational and Graphical Statistics</i> ; <i>Journal of Neuroscience</i> ; <i>IEEE Journal of Biomedical and Health Informatics</i> ; <i>IEEE Transactions on Medical Imaging</i> ; <i>International Journal of Bifurcation and Chaos</i> ; <i>MICCAI</i> ; <i>Molecular Ecology Resources</i> ; <i>Molecular Psychiatry</i> ; <i>Nature Communications</i> ; <i>Nature Genetics</i> ; <i>Nature Neuroscience</i> ; <i>Neurobiology of Aging</i> ; <i>NeuroImage</i> ; <i>NeuroImage: Clinical</i> ; <i>Neuroinformatics</i> ; <i>PLoS ONE</i> ; <i>Schizophrenia Bulletin</i> ; <i>Scientific Reports</i> ; <i>Statistical Methods in Medical Research</i> ; <i>Statistics and Computing</i>	
ADVISING & MENTORING	Zhaowen Liu (Research Fellow, MGH)	Jan 2019 — present
	Qunxi Zhu (Visiting graduate student, Fudan University)	Jan 2019 — present
	Yunfeng Ruan (Postdoctoral Researcher, Broad Institute)	Mar 2019 — present
BOOK CHAPTERS	1. Ge T, Smoller JW, Sabuncu MR. Kernel machine regression in neuroimaging genetics. In: <i>Machine Learning and Medical Imaging</i> , Wu G, Shen D, Sabuncu MR (Eds.). Academic Press, Cambridge, MA, 2016; 31-68.	

1. Anderson KM, Collins MA, Chin R, Ge T, Rosenberg MD, Holmes AJ. The transcriptional landscape of cortical interneurons underlies in-vivo brain function and schizophrenia risk. *bioRxiv preprint*, 2018; <https://doi.org/10.1101/481036>.
2. 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. *bioRxiv preprint*, 2018; <https://doi.org/10.1101/399402>.
3. 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. *bioRxiv preprint*, 2019; <https://doi.org/10.1101/421164>.

1. 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(1):2317.
2. 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; <https://doi.org/10.1002/hbm.24611>.
3. Ge T, Chen CY, Ni Y, Feng YA, Smoller JW. Polygenic prediction via Bayesian regression and continuous shrinkage priors. *Nature Communications*, 2019; 10(1):1776.
4. Li J, Kong R, Liegeois 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.
5. Mwilambwe-Tshilobo L, Ge T, Chong M, Ferguson MA, Mistic 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; <https://doi.org/10.1093/scan/nsz021>.
6. 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; <https://doi.org/10.1093/cercor/bhy216>.
7. 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; <https://doi.org/10.1093/cercor/bhy219>.
8. Ge T, Sabuncu MR, Smoller JW, Sperling RA, Mormino EC. Dissociable influences of APOE ϵ 4 and polygenic risk of AD dementia on amyloid and cognition. *Neurology*, 2018; 90(18):e1605-e1612.
9. 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.
10. 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.
11. Ge T, Chen CY, Neale BM, Sabuncu MR, Smoller JW. Phenome-wide heritability analysis of the UK Biobank. *PLoS Genetics*, 2017; 13(4):e1006711.
12. 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.
13. Adams HH, Hibar DP, Chouraki V, Stein JL, Nyquist PA, Rentería ME, ..., Ge T, ..., 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.
14. 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, ngr 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.

15. 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.
16. 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.
17. 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.
18. 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.
19. 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.
20. 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.
21. Ge T, Tian X, Kurths J, Feng J, Lin W. Achieving modulated oscillations by feedback control. *Physical Review E*, 2014; 90(2):022909.
22. 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.
23. Ge T, Schumann G, Feng J. Imaging genetics — Towards discovery neuroscience. *Quantitative Biology*, 2013; 1(4):227-245.
24. 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.
25. Thompson PM, Ge T, Glahn DC, Jahanshad N, Nichols TE. Genetics of the connectome. *NeuroImage*, 2013; 80:475-88.
26. 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.
27. 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.
28. 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.
29. 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.
30. 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.
31. Luo Q, Ge T, Feng J. Granger causality with signal-dependent noise. *NeuroImage*, 2011; 57(4):1422-1429.
32. 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

- 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, 2019