CURRICULUM VITAE
Phil Hyoun Lee

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RESEARCH INTERESTS

Computational Genomics and Neuropsychiatry

- Disease gene discovery for psychiatric and neurodevelopmental disorders
- Systems biology approaches for integrating high-throughput biology data
- Application and development of statistical methods for genome data analysis

EDUCATION and TRAINING

2009-2012 Center for Human Genetic Research, Massachusetts General Hospital
Post-doctoral fellow training in *Psychiatric Statistical Genetics*

Advisor: *Jordan Smoller, M.D., Sc.D., Shaun Purcell, Ph.D.*

2004-2009 Queen's University, Canada
Ph.D. in *Computational Biology and Machine Learning*

Dissertation: Prioritizing SNPs for disease-gene association studies: algorithms and systems
Advisor: *Hagit Shatkay, Ph.D.*

2003-2004 KAIST (Korea Advanced Institute of Science and Technology), Korea
M.S. in *Bioinformatics*

Dissertation: Inferring large-scale genetic interactions using Bayesian networks
Advisor: *Doheon Lee, Ph.D.*

1993-1998 Seoul National University, Korea
B.S. in *Computer Science and Statistics*

Dissertation: Application-focused review of clustering algorithms
Advisor: *Sanghyung Lee, Ph.D.*

PROFESSIONAL ACTIVITIES

2012- Instructor in Psychiatry
Harvard Medical School

2012- Assistant in Research
Department of Psychiatry
Massachusetts General Hospital

2009- Affiliated Research Fellow
Stanley Center for Psychiatric Research
Broad Institute of MIT and Harvard

HONORS and AWARDS

2015 Career Development Travel Award, Center for Faculty Development, Massachusetts General Hospital

2012 Semi-finalist, Charles J. Epstein Trainee Award for Excellence in Human Genetics Research, American Society of Human Genetics (ASHG'12)

2012 Early Career Investigator Award, International Society of Psychiatric Genetics (WCPG'12)

2011 Best Poster Presentation Award, International Society of Psychiatric Genetics (WCPG'11)

2009 Finalist, Ray and Stephanie Lane Fellowship, Carnegie Mellon University

2009 Best Student Oral Presentation Award, International Society for Computational Biology (ISMB'09)

2008 Student Council Travel Award, International Society for Computational Biology (ISMB'08)

2007-2008 Carmichael Fellowship, Queen's University, ON, Canada

2006-2007 Ontario Graduate Scholarship, Ministry of Training Colleges and Universities, Canada

2004-2008 Queen's Graduate Scholarship, Queen's University, ON, Canada

2004-2008 Tuition Bursary Award for Foreign Students, Queen's University, ON, Canada

2004-2008 Korea Information and Telecommunication National Scholarship, The Ministry of Information and Communication, Korea

2004 Young Scientist Award for Korea-UK Collaboration, Korea Science Foundation

2003 Best Student Presentation Award, International Meeting of The Microarray Gene Expression Data Society (MGED'03)

GRANTS

2014-2019 NIMH/NIH - K99/R00 Pathway to Independence Award
Title: *Neuroimaging Genetics to Study Social Cognitive Deficits in Autism Spectrum Disorders and Schizophrenia*
Funding: $987,165

PUBLICATIONS (PEER REVIEWED)

1. The Network and Pathway Analysis Subgroup of the Psychiatric Genomics Consortium; O'Dushlaine C*, Rossin L*, Lee PH* (**co-first author;** *I co-led statistical analysis and manuscript writing*), et al. Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nat Neurosci* 2015; 18(2):199-209.
2. SanGiovanni JP, Chen J, Gupta AS, Chew EY, Smith LE, Sapieha P, Lee PH. Netrin-1 activated systems and age-related macular degeneration. *PLoS One* 2015; 10(5):e0125548.
3. Ge Tian, Nichols T, Lee PH, Holmes A, Roffman J, et al. Massively expedited genome-wide heritability analysis (MEGHA). *Proc Natl Acad Sci USA* 2015; 112(8):2479-84.
4. Hibar DP, Stein JL, Renteria ME, Arias-Vasquez A, Desrivieres S, et al. Common genetic variants influence human subcortical brain structures. *Nature* 2015; 520(7546):224-9.
5. Choi JH, Balasubramanian R, Lee PH, Shaw ND, Hall JE, et al. Expanding the Spectrum of Founder Mutations Causing Isolated Gonadotropin-Releasing Hormone Deficiency. *J Clin Endocrinol Metab* 2015; 100(10):E1378-85.
6. Lee SH, Byrne EM, Hultman CM, Kähler A, Vinkhuyzen AA, et al. New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. *Int J Epidemiol* 2015; Epub ahead of print.
7. Pearson-Fuhrhop K, Dunn EC, Mortero S, Devan WJ, Falcone GJ, Lee PH, Holmes AJ, et al. Dopamine genetic risk score predicts depressive symptoms in healthy adults and adults with depression. *PLoS ONE* 2014; 9(5): e93772.
8. Thompson PM, Stein JL, Medland SE, Hibar DP, Vasquez AA, Renteria ME, Toro R, et al. The ENIGMA consortium: large-scale collaborative analyses of neuroimaging and genetic data. *Brain Imaging Behav* 2014; 8(2):153-182.
9. Schizophrenia Working Group of the Psychiatric Genomics Consortium; Ripke S, Neale BM, Corvin A, Walters JT, Farh KH, Holmans PA, Lee PH, et al. Biological insights from 108 schizophrenia-associated genetic loci. *Nature* 2014; 511(7510):421-427.
10. Bergen SE, O'Dushlaine CT, Lee PH, Fanous AH, Ruderfer DM, et al. Genetic modifiers and subtypes in schizophrenia: investigations of age at onset, severity, sex and family history. *Schizophr Res* 2014; 154(1-3):48-53.
11. Duncan LE, Holmans PA, Lee PH, O'Dushlaine CT, Kirby AW, Smoller JW, Ongur D, Cohen BM. Pathway analyses implicate glial cells in schizophrenia. *PLoS One* 2014; 9(2):e89441.
12. Walton E, Geisler D, Lee PH, Hass J, Turner JA, Liu J, Sponheim SR, White T, Wassink TH, Roessner V, Gollub RL, Calhoun VD, Ehrlich S. Prefrontal inefficiency is associated with polygenic risk for schizophrenia. *Schizophr Bull* 2014; 40(6):1263-1271.
13. Cross-Disorder Group of the Psychiatric Genomics Consortium; Smoller JW, Ripke S, Lee PH* (*I was a lead analyst, performed cross disorder modeling analysis, pathway analysis, and brain eQTL data analysis*), et al. Genome-wide analysis identifies loci with shared effects on five major psychiatric disorders. *Lancet* 2013; 381(9875):1371-1379.
14. Cross-Disorder Group of the Psychiatric Genomics Consortium, Lee SH, Ripke S, Neale BM, et al. Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nat Genet* 2013; 45(9):984-994.

15. Solovieff N, Cotsapas C, Lee PH, Purcell SM, Smoller JW. Pleiotropy in complex traits: challenges and strategies. *Nat Rev Genet* 2013; 14(7):483-495.

16. SanGiovanni JP, Lee PH. AMD-associated genes encoding MAPK pathway constituents are identified by interval-based enrichment analysis. *PLoS ONE* 2013; 8(8):e71239.

17. McGrath LM, Cornelis MC, Lee PH, Robinson EB, Duncan LE, et al. Genetic predictors of risk and resilience in psychiatric disorders: A cross-disorder genome-wide association study of functional impairment in major depressive disorder, bipolar disorder, and schizophrenia. *Am J Med Genet B Neuropsychiatr Genet* 2013; 162B(8):779-788.

18. Bergen SE, O'Dushlaine CT, Ripke S, Lee PH, Ruderfer DM, et al. Genome-wide association study in a Swedish population yields support for greater CNV and MHC involvement in schizophrenia compared to bipolar disorder. *Mol Psychiatry* 2012; 17(9):880-889.

19. Holmes A, Lee PH (***co-first author;** *I led whole genome genetic data analysis*), Hollinshead M, Bakst L, Roffman JL, Smoller JW, Buckner RL. Individual differences in amygdala-medial prefrontal anatomy link negative affect, impaired social functioning, and polygenic depression risk. *J Neurosci* 2012; 32(50): 18087-18100.

20. Stein JL, Medland SE, Vasquez AA, Hibar DP, Senstad RE, et al. Identification of common variants associated with human hippocampal and intracranial volumes. *Nat Genet* 2012; 44(5):552-561.

21. Lee PH, Perlis RH, Jung JY, Byrne EM, Rueckert E, et al. Multi-locus genome-wide association analysis supports the role of glutamatergic synaptic transmission in the etiology of major depressive disorder. *Transl Psychiatry* 2012; 2:e184.

22. Sabuncu M, Buckner R, Smoller JW, Lee PH, Fischl B, Sperling R; Alzheimer's Disease Neuroimaging Initiative. The association between a polygenic Alzheimer score and cortical thickness in cognitively normal subjects. *Cereb Cortex* 2012; 22(11):2653-2661.

23. Lee PH, O'Dushlaine C, Thomas B, Purcell SM. INRICH: Interval-based enrichment analysis for genome wide association studies. *Bioinformatics* 2012; 28(13):1797-1799.

24. Willour VL, Seifuddin F, Mahon PB, Jancic D, Pirooznia M, et al. A genome-wide association study of attempted suicide. *Mol Psychiatry* 2012; 17(4): 433-444.

25. Hall MH, Smoller JW, Cook NR, Schulze K, Lee PH, Taylor G, Bramon E, Coleman MJ, Murray RM, Salisbury DF, Levy DL. Patterns of deficits in brain function in bipolar disorder and schizophrenia: a cluster analytic study. *Psychiatry Res* 2012; 200(2-3):272-280.

26. Lee PH, Bergen SE, Perlis RH, Sullivan PF, Sklar P, Smoller JW, Purcell SM. Modifiers and subtype-specific analyses in whole-genome association studies: a likelihood framework. *Hum Hered* 2011; 72(1):10-20.

27. Yu Y, Bhangale T, Fagerness J, Ripke S, Thorleifsson G, et al. Common variants near FRK/COL10A1 and VEGFA are associated with advanced age-related macular degeneration. *Hum Mol Genet* 2011; 20(18):3699-3709.

28. Psychiatric GWAS Consortium Bipolar Disorder Working Group; Sklar P, Ripke S, Scott LJ, et al. Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. *Nat Genet* 2011; 43(10):977-983.

29. Middeldorp CM, de Moor MH, McGrath LM, Gordon SD, Blackwood DH, Costa PT, Terracciano A, et al. The genetic association between personality traits and major depression or bipolar disorder. A polygenic score analysis using genome-wide association

data. *Trans Psychiatry* 2011; 1:e50.

30. Belmonte Mahon P, Pirooznia M, Goes FS, Seifuddin F, Steele J, Lee PH, Huang J, et al. Genome-wide association analysis of age at onset and psychotic symptoms in bipolar disorder. *Am J Med Genet B Neuropsychiatr Genet B* 2011; 156B(3): 370-378.
31. Huang J, Perlis R, Lee PH, Rush AJ, Fava M, Sachs GS, Lieberman J, Hamilton SP, et al. Cross-disorder genome-wide analysis of schizophrenia, bipolar disorder and depression. *Am J Psychiatry* 2010; 167(10):1254-1263.
32. Lee PH, Jung J-Y, and Shatkay H. Functionally informative tag SNP Selection using a pareto-optimal approach: playing the game of life. *Adv Exp Med Biol* 2010; 680:173-180.
33. Lee PH, Shatkay H. An integrative scoring system for ranking SNPs by their potential deleterious effects. *Bioinformatics* 2009; 25(8):1048-1055.
34. Lee PH, Shatkay H. Ranking single nucleotide polymorphisms by potential deleterious effects. *AMIA Annu Symp Proc* 2008; 6:667-671.
35. Lee PH, Shatkay H. F-SNP: Computationally predicted functional SNPs for disease association studies. *Nucleic Acids Res* 2008; 36(Database-Issue): d820-824.
36. Lee PH, Shatkay H. Ranking single nucleotide polymorphisms by their potential deleterious effects. *In the Proc. of the American Medical Informatics Association Annual Symposium (AMIA'08)*, Nov. 2008; pp. 667-671.
37. Shen JJ, Lee PH, Holden JJ, Shatkay H. Using cluster ensemble and validation to identify subtypes of pervasive developmental disorders. *In the Proc. of the American Medical Informatics Association Annual Symposium (AMIA'07)*, Nov. 2007; pp. 666-670.
38. Lee PH, Shatkay H. Two birds one stone: selecting functionally informative tag SNPs for disease association studies. *Springer Lecture Notes in Computer Science*. 2007; 4645:61-72.
39. Lee PH, Shatkay H. BNTagger: improved tagging SNP selection using Bayesian networks. *Bioinformatics* 2006; 22(14):e211-e219.
40. Jung JY, Lee PH. A neural network model for maximizing prediction accuracy in haplotype tagging SNP selection. *In the Proc. of the Int. Joint Conf. on Neural Networks (IJCNN'06)*, July, 2006. Vancouver, BC, Canada; pp. 2303-2307.
41. Lee PH, Lee D. Modularized learning of genetic interaction networks from biological annotations and mRNA expression data. *Bioinformatics* 2005; 21(11):2739-2747.
42. Lee PH, Nam H, Lee D, Lee K-H. In-silico inferences for expression data using IGAM: applied to fuzzy-clustering & regulatory network modeling. *In the Proc. of the Korean Fuzzy Logic and Intelligent Systems Conference (KFIS'04)*, April 2004; pp. 129-138.
43. Lee PH, Lee D, Lee KH. An integrated Bayesian network framework for reconstructing representative genetic regulatory networks. *In the Proc. of the Korea Bioinformatics Conference (KSBI'03)*, Oct. 2003; pp.12-21.
44. Lee S, Lee PH, Na D, Lee D, Lee K-H, Bae M. Requirement analysis for bio-information integration systems. In the Proc. of the 4th International Symposium on Advanced Intelligent Systems (ISIS'03), Sep. 2003; pp. 230-242.
45. Na D, Lee PH, Lee S, Lee D, Lee K-H, Bae M. EBIS: bio-data integration middle-ware system. *In the Proc. of the Korea Information Science Conference (KISS'03)* May 2003; pp. 198-213.

PUBLICATIONS (SUBMITTED)

1. Lee PH, Baker J, Holmes A, Jahanshad N, Ge T, et al. Partitioning heritability analysis reveals a shared genetic basis of brain anatomy and schizophrenia.
2. The Autism Spectrum Disorder Working Group of the Psychiatric Genomics Consortium. High-resolution meta analysis of genome-wide association studies of autism spectrum disorder.
3. Adams H, Hibar D, Chouraki V, Stein J, Nyquist P, et al. Common genetic variation underlying human intracranial volume highlights developmental influences and continued relevance during late life.
4. Hibar D, Adams Hieab, Jahanshad N, Chauhan G, Stein J, et al. Novel genetic loci associated with hippocampal volume are relevant to aging and dementia.
5. Germaine L, Robinson EB, Smoller J, Calkins M, Moore T, et al. Polygenic risk for schizophrenia is associated with differences in social cognition across development.
6. Gormley P, Anttila V, Winsvold BS, Palta P, Esko T, et al. Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine.
7. Franke B, Stein J, Ripke S, Anttila V, Hibar D, et al. Evaluating the overlap between common genetic influences on schizophrenia and subcortical brain volumes.
8. Kim Y, Giusti-Rodriguez P, Crowley JJ, Nonneman RJ, Ryan AK, et al. Evidence for the involvement of schizophrenia risk genes in antipsychotic effects.
9. Ge T, Reuter M, Winkler AM, Holmes A, Lee PH, et al. The heritability of neuroanatomical shape.
10. Thompson PM, Andreassen OA, Arias-Vasquez AA, Bearden CE, Boedhoe PS, et al. ENIGMA and the individual: predicting factors that affect the brain in 35 countries worldwide.

PUBLICATIONS (BOOK CHAPTERS)

1. Lee PH, Jung JY, Shatkay H. Ch. 11. Functionally informative tag SNP prioritization using a pareto-optimal approach. Advances in Experimental Medicine and Biology, Springer Vol. 680. H.R. Arabia (ed) 2010.
2. Lee PH, Shatkay H. Ch. 18. Machine learning for computational haplotype analysis. Machine Learning in Bioinformatics, John Wiley & Sons, Y-Q Zhang, J.C. Rajapakse (Ed) 2008.

CONFERENCE PRESENTATIONS

1. Lee PH. Elucidating the shared genetic architecture of eight psychiatric disorders. *Oral Presentation*. The Cross Disorder Group of the Psychiatric Genomics Consortium meeting The 23rd World Congress on Psychiatric Genetics (WCPG'15), Oct. 2015.
2. Ge T, Nichols TE, Lee PH, Holmes AJ, Roffman JL, Buckner RL, Sabuncu MR, Smoller JW. Massively Expedited genome-wide heritability analysis (MEGHA). The 21st Annual Meeting of the Organization for Human Brain Mapping (OHBM'15), June 2015.
3. Lee PH, on behalf of the Network and Pathway Analysis Subgroup of the Psychiatric

Genomics Consortium. Pathway analyses of PGC GWAS data implicate a role of altered histone methylation in bipolar disorder. *Oral Presentation*. The 2nd Annual Molecular Psychiatry Meeting (MPA'14), Nov. 2014.

4. Anttila V, Ripke S, Malik R, Pers T, Farh K-H, Laramie Duncan L, Biffi A, Lee PH, Kendler K, Scharf J, Smoller J, Palotie A, Daly M, Rosand J, Neale B. The Brainstorm project; a cross-phenotype analysis of 14 brain disorders by heritability-, constraint- and pathway-based methods, using genome-wide association data from 500,000 samples. The 64th Annual Meeting of American Society of Human Genetics (ASHG'14), Oct. 2014.
5. Lee PH, Holmes A, Gallagher P, Germine L, Hollinshead M, Roffman J, Buckner R, Smoller JW. Genetic variation underlying amygdala-volume is highly enriched with schizophrenia susceptibility variants in healthy young individuals. The 21st World Congress on Psychiatric Genetics (WCPG'13), Oct. 2013.
6. Lee PH, Goldstein J, Howrigan D, Green T, Stevens C, Neale B, Goldberg AP, Buxbaum JD, Daly MJ. Exome array analyses of autism spectrum disorder reveal an etiologic role of low frequency protein coding variants. *Oral Presentation*. The 63th Annual Meeting of American Society of Human Genetics (ASHG'13), Oct. 2013.
7. Anttila V, Rosand J, Scharf J, Lee PH, Palotie A, Smoller JW, Daly MJ, Neale B. The Brainstorm project; a cross-disorder approach to the genetics of common neurological and psychiatric diseases. The 21st World Congress on Psychiatric Genetics (WCPG'13).
8. Lim ET, Lee PH, Goldstein JI, Stevens C, Raychaudhuri S, Buxbaum J, Daly MJ. Screening for rare recessives in autism spectrum disorders. The 63th Annual Meeting of American Society of Human Genetics (ASHG'13), Oct. 2013.
9. Lee PH. Exploring normal to pathological variation in the human brain: the Harvard brain genomics Superstruct project. *Oral Presentation*. The 68th Annual Meeting of Society of Biological Psychiatry (SBOP'13), May 2013.
10. Hibar DP, The ENIGMA Consortium ENIGMA2: Genome-wide scans of subcortical brain volumes in 16,125 subjects from 28 cohorts worldwide. The 19th Annual Meeting of the Organization for Human Brain Mapping (OHBM'13), June 2013.
11. Walton E, Geisler D, Lee PH, Hass J, Turner JA, Liu J, Sponheim SR, Wassink TH, et al. Prefrontal cortex activity is associated with cumulative polygenetic risk in schizophrenia patients. The 19th Annual Meeting of the Organization for Human Brain Mapping (OHBM'13), June 2013.
12. McGrath LM, Gerber G, Cornelis M, Lee PH, et al. Risk and resilience in psychiatric disorders: a cross-disorder genome-wide association study of functional impairment in major depressive disorder, bipolar disorder, and schizophrenia. The 36th Annual Scientific Advisory Committee Meeting (SAC'12), April 2012.
13. McGrath LM, Pollastri A, Lee PH, Block S, et al. Williams-Beuren syndrome as a neurodevelopmental model for childhood anxiety disorders. The 31th Annual Conference of Anxiety Disorders Association of America (ADAA'12), April 2012.
14. Roffman J, Silverstein N, Holmes A, Lee PH, Hollingshead M, Smoller J, Buckner R. Genetic variation across the folate metabolic pathway influences frontal cortical thickness: implications for altered neurodevelopment in schizophrenia. The 51st Annual Meeting of American College of Neuropsycho Pharmacology (ACNP'12), Dec. 2012.
15. Lee PH. Network and pathway analysis for deciphering the pathogenic role of microRNAs in psychiatric disorders. *Oral Presentation*. The 20th World Congress on Psychiatric

Genetics (WCPG'12), Oct. 2012.

16. Bergen SE, O'Dushlaine C, Lee PH, Fanous AH, Ruderfer D, et al. Genetic contributions to heterogeneity in schizophrenia. Poster Presentation. The 20th World Congress on Psychiatric Genetics (WCPG'12), Oct. 2012.
17. Holmes AJ, Lee PH, Hollinshead M, Roffman JL, et al. Polygenic depression risk in young adults predicts decreased medial prefrontal thickness. The 42nd Annual Meeting of Society for Neuroscience (SFN'12), Oct. 2012.
18. Bergen SE, O'Dushlaine CT, Ripke S, Lee PH, Ruderfer DM, et al. Genetic associations with schizophrenia and bipolar disorder in a large Swedish sample. The 36th Annual Scientific Advisory Committee Meeting (SAC'12), April 2012.
19. McGrath LM, , Pollastri A, Lee PH, Block S, et al. Williams-Beuren syndrome as a neurodevelopmental model for childhood anxiety disorders. The 31th Annual Conference of Anxiety Disorders Association of America (ADAA'12), April 2012.
20. McGrath LM, Gerber G, Cornelis M, Lee PH, et al. Risk and resilience in psychiatric disorders: a cross-disorder genome-wide association study of functional impairment in major depressive disorder, bipolar disorder, and schizophrenia. The 36th Annual Scientific Advisory Committee Meeting (SAC'12), Apr 2012.
21. Lee PH, Holmes AJ, Fagerness J, Roffman JL, Purcell SM, Buckner RL, Smoller JW. Genome-wide analyses of neuro-cognitive/brain-imaging phenotypes reveal enriched association of neuronal and psychiatric candidate genes. The 19th World Congress on Psychiatric Genetics (WCPG'11), Oct. 2011 (*Best Poster Presentation Award*).
22. McGrath LM, Lee PH, Block S, Haddad S, et al. Genetic syndromes as neurodevelopmental models for anxiety disorders. The 19th World Congress on Psychiatric Genetics (WCPG'11), Oct. 2011.
23. Stein J, Medland S, et al. Genome-wide association meta-analysis of hippocampal volume via the ENIGMA consortium. The 17th Annual Meeting of the Organization on Human Brain Mapping (OHBM'11), June 2011.
24. Wiste A, McGrath LM, Lee PH, Smoller JW. Genome-wide association study of smoking behavior in the context of schizophrenia: preliminary results. The 66th Annual Meeting of Society of Biological Psychiatry (SOBP'11), May 2011.
25. Hall MH, Salisbury DF, Lee PH, Taylor G, et al. Patterns of deficits in brain function in bipolar disorder and schizophrenia: a cluster analytic study. The 13th International Congress on Schizophrenia Research (ICSR'11), April 2011.
26. Lee PH, Purcell S. INRICH: improved enrichment testing method that integrates an unbiased GWAS strategy with prior biological knowledge: application to type 2 diabetes. The 19th Int. Conf. on Intelligent Systems for Molecular Biology (ISMB'11), July 2011.
27. Medland SE, et al. ENIGMA: enhancing neuro imaging genetics through meta-analysis. The 10th Australasian Human Gene Mapping Meeting. 2011.
28. Chen DT, Akula N, Steele CJM, Smoller JW, Lee PH, the Bipolar Disorder Genetics (BiGs) Consortium, and F. J. McMahon. Genome-wide association study suggests a risk locus for pediatric-onset bipolar disorder on chromosome 5q. The 60th Annual Meeting of American Society of Human Genetics (ASHG'10), Nov. 2010.
29. Lee PH, Mayerfeld CE, O'Dushlaine C, Haddad S, Siburian R, et al. Integrative pathway analysis approaches to mining psychiatric genome wide association studies: application to

major depressive disorder. *Oral Presentation*. The 18th World Congress on Psychiatric Genetics (WCPG'10), Oct. 2010.

30. Lee PH, Sklar P, Purcell S, Smoller JW. Rare variants: a common cause of common variant association in genome-wide association studies? The 18th World Congress on Psychiatric Genetics (WCPG'10), Oct. 2010.
31. Wilkins JM, Bergen SE, Ferreira MAR, et al. Large-scale sequencing of DISC1 in schizophrenia and bipolar disease yields novel variants. The 18th World Congress on Psychiatric Genetics (WCPG'10), Oct. 2010.
32. Mahon PB, Pirooznia M, Goes FS, Seifuddin F, Steele J, Lee PH, et al. Genome-wide association analysis of age at onset and psychotic symptoms in Bipolar disorder. The 18th World Congress on Psychiatric Genetics (WCPG'10), Oct. 2010.
33. McGrath LM, Lee PH, Perlis R, et al. A cross-disorder genome-Wide association study of functional impairment in bipolar disorder, depression, and schizophrenia. The 18th World Congress on Psychiatric Genetics (WCPG'10), Oct. 2010.
34. Lee PH, Jung JY, Shatkay H. Functionally informative tag SNP Selection using a pareto-optimal approach: playing the game of life. *Oral Presentation.* Student Council. The 17th Int. Conf. on Intelligent Systems for Molecular Biology (ISMB'09), June 2009.
35. Lee PH, Shatkay H. Ranking single nucleotide polymorphisms by their potential deleterious effects. *Oral Presentation.* Student Council. The 16th Int. Conf. on Intelligent Systems for Molecular Biology (ISMB'08), July 2008.
36. Lee PH, Shatkay H. Two birds one stone: selecting functionally informative tag SNPs for disease association studies. Poster, The 15th In the Proc. of the Int. Conf. on Intelligent Systems for Molecular Biology (ISMB'07), July 2007.
37. Lee PH, Doheon Lee. GeneRuby: genetic-network reconstruction using Bayesian networks. The 6th International Meeting of Microarray Gene Expression Data (MGED) Society, Sep. 2003 (*Best Poster Presentation Award*).

INVITED TALKS

2015	Deciphering the genetic etiology of major psychiatric disorders. Imaging Genetics Center Lecture, University of Southern California
2015	Etiologic role of histone methylation genes in psychiatric disorders. Schizophrenia and Bipolar Disorder Program Seminar – Öngür Lab, McLean Hospital
2015	Set-based association tests for genomics data analysis. Invited lecturer for CISC-844 Computational Biomedicine, Department of Computer Science and Information Sciences, University of Delaware
2015	Histone H3-K4 methylation in schizophrenia and bipolar disorder. Sawa Lab - Schizophrenia Research Center, Department of Psychiatric and Behavioral Sciences, John's Hopkins University
2014	Cross disorder pathway analysis of major mental disorders. Genetics Interdisciplinary Meeting, Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard

2013 Imaging genetic analysis and the Genomic Superstruct Project. Genetics Interdisciplinary Meeting, Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard

2012 Pathway analysis for genome-wide genetic variation data: motivation, methods, and major challenges. Behavioral Genetics Seminar, Department of Psychiatry, Brown University

2012 Integrative pathway analysis for mining psychiatric genome wide association studies. CHGR Seminar Series, Center for Human Genetic Research, Massachusetts General Hospital

2011 Gene-set-based GWAS analysis supports the role of glutamatergic synaptic genes in major depression. CHGR Seminar Series, Center for Human Genetic Research, Massachusetts General Hospital

2011 Pathway analysis for genome-wide association studies. Human Behavioral Genetics Lecture, Department of Psychology, Brandeis University

2010 Genetic architecture shared by schizophrenia, bipolar disorder and major depression. Psychiatric Genetics and Translational Research Seminar, Department of Psychiatry, Massachusetts General Hospital

2008 F-SNP: annotating single nucleotide polymorphisms with potential functional significance to human health. The Eleventh Annual Scientific Meeting for Health Sciences Research Trainees, Queen's University, ON, Canada

2008 State-of-the-art computational resources for SNP analysis. Population and Public Health's Research Day, Queen's University, ON, Canada

TEACHING

2011 Guest Lecturer
PSYC-118 Human Behavioral Genetics
Brandeis University, MA, USA

2005-2009 Guest Lecturer
CISC-490 Algorithms and Machine Learning Methods in Computational Biology
Queen's University, ON, Canada

2007- Teaching Assistant
CISC-471 Biomedical Computing
Queen's University, ON, Canada

2005 Teaching Assistant
CISC-490 Algorithms and Machine Learning Methods in Computational Biology
Queen's University, ON, Canada

2005 Teaching Assistant
CISC-365 Algorithm I
Queen's University, ON, Canada

2004 Teaching Assistant
CISC-352 Artificial Intelligence
Queen's University, ON, Canada

MENTORING and ADVISING

2015- Yanela Cruz, B.S.
Supervising neuroimaging genetics research projects.
Harvard University

2014- Chia-yen Chen, Ph.D.
Offering statistical mentoring. Currently preparing two manuscripts.
Massachusetts General Hospital

2014- Tian Ge, Ph.D.
Mentoring in whole genome data analysis. One manuscript accepted, and another one under review.
Massachusetts General Hospital

2014- Gabriella Blokland, Ph.D.
Offering statistical mentoring
Massachusetts General Hospital

2013- Laura Germine, Ph.D.
Offering statistical mentoring, and one manuscript under review.
Massachusetts General Hospital

ACADEMIC SERVICES

2012- Research Committee, Department of Psychiatry, Massachusetts General Hospital

2012- Editorial Board Member, Frontiers in Statistical Genetics

2010-2011 Journal Club Organizer, Psychiatric and Neurodevelopmental Genetics Unit, Massachusetts General Hospital

2009-2010 Research Fellow Seminar Organizer, Psychiatric and Neurodevelopmental Genetics Unit, Massachusetts General Hospital

2007-2009 Program Organizing Committee, Student Council Symposium (SC), International Conference on Intelligent Systems for Molecular Biology (ISMB)

2007-2009 Scientific Review Committee, International Joint Conference on Neural Networks (IJCNN)

2007 Scientific Review Committee, International Symposium on Bioinformatics Research and Applications (ISBRA)

2007 Review Committee, The Second Annual Canadian Student Conference on Biomedical Computing (CSCBC'07)

2006 Scientific Program Committee Chair, The First Canadian Students Conference on Biomedical Conference (CSCBC'06)

2004-2006 Organizer, BioMedical Computing Seminar, School of Computing, Queen's University

AD HOC REVIEWER

2015 Nature Neuroscience, JAMA Psychiatry, Molecular Autism, Molecular Psychiatry, Nature Scientific Report, Neuropsychiatric Genetics, BMC Bioinformatics, PLoS Computational Biology, PLoS ONE

2014 Translational Psychiatry, Molecular Human Genetics, PLoS ONE

2013	Bio Imaging and Behavior, General Archive of Psychiatry
2012	Bio Imaging and Behavior, Frontier in Statistical Genetics, Pacific Symposium on Biocomputing
2011	SNP Special Interest Group - International Conference on Intelligent Systems for Molecular Biology (ISMB), Bioinformatics
2007-2009	Bioinformatics, BMC Bioinformatics

DATABASE and SOFTWARE

INRICH	http://atgu.mgh.harvard.edu/inrich Multi-locus pathway analysis method for genome-wide data analysis (PubMed citation = 85).
F-SNP	http://compbio.cs.queensu.ca/F-SNP/ Database for predicting the functional impact of genetic variants (PubMed citation = 233).
BNTagger	Tagging SNP selection algorithm implemented in C++ (PubMed citation = 51)
GeneRUBY	Patent Registration: Korea 10-0610240 / 2005-0064754 Method for reverse-engineering genetic circuits based on Bayesian network learning (PubMed citation = 60).