

CURRICULUM VITAE

MOLLY HALL, PHD

E-mail Address: mah546@psu.edu

Education

PhD 2015	Pennsylvania State University (Biochemistry & Molecular Biology)
MS 2011	Columbia University (Neuroscience & Education)
BS 2005	Cornell University (Human Development)

Professional Employment

2017-present	Assistant Professor (Tenure-track) Department of Veterinary and Biomedical Sciences Huck Institutes of the Life Sciences Pennsylvania State University
2015-2017	Postdoctoral Researcher – Dr. Jason Moore Institute for Biomedical Informatics Perelman School of Medicine University of Pennsylvania
2011-2015	Graduate Research Assistant – Dr. Marylyn Ritchie Department of Biochemistry & Molecular Biology Pennsylvania State University

Teaching Positions & Courses Taught

2022-present	VBSC 590 – Pathobiology Graduate Student Colloquium (1 credit)
2021-present	BMB/VBSC 485 – Human Genomics and Biomedical Informatics (3 credits) Instructor Pennsylvania State University
2020	CAMB 698 – Cell & Molecular Biology Graduate Group Guest Lecturer University of Pennsylvania
2018-present	MCIBS 503 – Critical Elements of Molecular and Cellular Biology (1 credit) Instructor and Course Organizer Pennsylvania State University
2011-2013	Teaching Assistant – Microbiology Laboratory Department of Biochemistry & Molecular Biology Pennsylvania State University
2007-2009	Middle School Science Teacher Williamsburg Collegiate Charter School, Uncommon Schools, Inc. Brooklyn, NY

Curriculum Vitae: Molly Hall

2005-2007 Middle School Science Teacher
Teach For America (TFA)
Bronx, NY

Fellowships/Professorships

2019 Dr. Frances Keesler Graham Early Career Professorship for Neural Development Research
2015 Ruth L. Kirschstein National Research Service Award (NRSA) Individual Predoctoral Fellowship (Parent F31)
2011 Braddock-Roberts Fellowship (Penn State University, Department of Biochemistry and Molecular Biology)

Awards

2021 Environmental Influences on Child Health Outcomes (ECHO) Opportunities and Infrastructure Fund (OIF) (funded by NICHD) Early-Career Award
2021 NIH Loan Repayment Program Recipient (Renewal, funded by NHGRI)
2020 Joan Luerssen Faculty Enhancement Fund Award (College of Agricultural Sciences, Penn State University)
2019 NIH Loan Repayment Program Recipient (funded by NHGRI)
2019 Roy C. Buck Faculty Award for Outstanding Publication, College of Agricultural Sciences, Penn State University
2016 Wedler Outstanding Doctoral Dissertation Thesis Award
2014 Pacific Symposium on Biocomputing Travel Award, funded through the National Library of Medicine/National Institutes of Health
2013 Paul M. Althouse Outstanding Teaching Assistant Award
2012 Cold Spring Harbor Laboratory Programming for Biology Course Scholarship
2012 Genetic Analysis of Complex Human Disease Travel Scholarship, funded through the National Institutes of Health

Service

2022-present Member, Pharmacology/Toxicology Faculty Search Committee
2021-Present Review Editor, Editorial Board of Applied Genetic Epidemiology, *Frontiers in Genetics*
2021-Present Member, Biobehavior Health Department Faculty Search Committee
Precision Population Health Faculty Search
2020-2021 Session organizer, “What about the environment? Leveraging multi-omic datasets to characterize the environment’s role in human health”, 2021 Pacific Symposium on Biocomputing (PSB), Hawaii, HI
2020 Reviewer, NIH, U01 NIDDK Special Emphasis Panel (ZDK1 GRB-G(03))
2019 Session Moderator, “What about the phenotype? Integrating electronic health records to drive discovery in precision health”, American Society of Human Genetics (ASHG), Houston, TX
2018-present Member, Center for Computational Biology and Bioinformatics (CCBB) Committee, Penn State

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- 2019-present Member, Molecular, Cellular, and Integrated Biosciences (MCIBS) Candidacy Committee, Huck Institutes, Penn State
- 2019-present Member, Pathobiology Graduate Program Selection Committee, Department of Veterinary & Biomedical Sciences, Penn State
- 2019-present Member, Bioinformatics and Genomics Program Committee, Huck Institutes, Penn State
- 2019-2020 Member, College of Agricultural Sciences Nominations and Elections Committee
- 2018-2019 Member, Penn State High Performance Computing Working Group
- 2017-Present Member, Department of Veterinary & Biomedical Sciences Undergraduate and Graduate Scholarship Committee
- 2017-2020 Founder, Penn State College of Agriculture Sciences Women Faculty Group
- 2017-2018 Member, Penn State Data Life Course Working Group
- 2015-Present Reviewer, *Cell*, *PLoS One*, *BioData Mining*, *Scientific Reports*, *Bioinformatics*, *American Journal of Human Genetics*
- 2014 Conference session co-organizer for *Pacific Symposium of Biocomputing* session, Characterizing the Importance of Environmental Exposures, Interactions between the Environment and Genetic Architecture and Genetic Interactions
- 2014-2015 Biochemistry & Molecular Biology Department Climate and Diversity Committee – Graduate Student Liaison
- 2012-2015 Biochemistry & Molecular Biology Graduate Student Association – Vice President
- 2012-2015 Biochemistry & Molecular Biology Graduate Student Association – Mentor to incoming first-year students
- 2011-Present Cornell University – Alumni Mentor to undergraduate students
- 2007-2015 Teach For America – Recruitment support, Columbia University
- 2005-2007 Teach For America – Corps Member

Major Research Interests

The Exposome
Human Genetics
Multi-Omic Data Integration
Metabolomics
The Role of Adverse Childhood Experiences in Childhood on Health
Gene-Environment Interactions
Environment-Wide Association Studies
Gene-Gene Interactions
Polygenic Risk Scores
Predictive Modeling
Personalized Medicine
Complex Disease
Psychosocial outcomes
Neurodevelopmental disorders
Genetic Epidemiology
Phenome-Wide Association Studies

Publications (Hall Lab current and former trainees and staff are underlined)

González Zarzar T, Palmiero N, Kim D, Shen L, **Hall MA**. Sex-specific associations between phenotypes and environmental exposures (under review, *Biology of Sex Differences*). Pre-print available at *Research Square* (2023): <https://doi.org/10.21203/rs.3.rs-3246585/v1>.

Passero K, Noll JG, Selin C, **Hall MA**. Longitudinal method comparison: Modeling polygenic risk for posttraumatic stress disorder over time in individuals of African and European ancestry (revise and resubmission, *Frontiers in Genetics: Statistical Methodology special issue*).

Zhou J, Palmiero N, Passero K, McGuigan JR, Zarzar TG, Prabhu KS, and **Hall MA**. Environment-Wide Association Studies of Anemia in the National Health and Nutrition Examination Surveys. *medRxiv* 2023; : 2023.06.02.23290861. <https://www.medrxiv.org/content/10.1101/2023.06.02.23290861v1> (under review *Journal of Exposure Science and Environmental Epidemiology*)

Lee B, Wang J, **Hall MA**, Kim D, Stites SD, Shen L. (2023) Sex modifies predictive effects of imaging and CSF biomarkers on cognitive and functional outcomes: A study of Alzheimer's disease. *Neurobiology of Aging*, in press.

Aguilar MA, Ebanks S, Markus H, Lewis MM, Midya V, Vrana, Huang X, **Hall MA***, Kawasawa YI* (2023) Neuronally enriched microvesicle RNAs are differentially expressed in the serums of Parkinson's patients. *Front. Neurosci.* 12:1145923. *Co-Corresponding Authors

Qian F, Nettleford SK, Zhou J, Arner BE, **Hall MA**, Sharma A, Annageldiyev C, Rossi RM, Tukaramrao DB, Sarkar D, Hegde S, Gandhi UH, Finch ER, Goodfield L, Quickel MD, Claxton DF, Paulson RF, Prabhu SK (2023) Activation of GRP44 decreases severity of myeloid leukemia initiating stem cells. *Cell Reports* 42(112794).

Misra S, Lee T, Sebastian A, McGuigan J, Liao C, Koo I, Patterson AD, Rossi RM, **Hall MA**, Albert I, Prabhu KS. (2023) Loss of selenoprotein W in murine macrophages alters the hierarchy of selenoprotein expression, redox tone, and mitochondrial functions during inflammation. *Redox Biology* 59(102571).

Zhou J, Guare L, Rico ALG, Zarzar TG, Palmiero N, Assimes TL, Verma SS, and **Hall MA**. Flexibly encoded GWAS identifies novel nonadditive SNPs in individuals of African and European ancestry. *medRxiv* 2023; : 2023.06.01.23290857. <https://www.medrxiv.org/content/10.1101/2023.06.01.23290857v1>

Ruan B, Chen Y, Trimidal S, Koo I, Cai J, Mcguigan J, **Hall MA**, Patterson AD, Prabhu KS, Paulson RF. Itaconate promotes the differentiation of murine stress erythroid progenitors by increasing Nrf2 activity. *bioRxiv* 2023.03.11.532211; doi: 10.1101/2023.03.11.532211. Preprint. *Blood Advances* in revision.

Ruan B, Chen Y, Trimidal S, Koo I, Qian F, Cai J, Mcguigan J, **Hall MA**, Patterson AD, Prabhu KS, Paulson RF. Nitric oxide regulates metabolism in murine stress erythroid progenitors to promote recovery during inflammatory anemia. *bioRxiv*. 2023 Mar 11:2023.03.11.532207. doi: 10.1101/2023.03.11.532207. Preprint. *Blood* in revision.

González Zarzar T, Lee B, Coughlin R, Kim D, Shen L, **Hall MA**. (2022) Sex Differences in the Metabolome of Alzheimer's Disease Progression. *Frontiers in Radiology* 2(782864). *Imaging Genomics Special Issue <https://doi.org/10.3389/fradi.2022.782864>

Etzel L, Hastings WJ, **Hall MA**, Heim C, Meaney M, Noll JG, Rose E, Schreier H, Shenk C, Shalev I. (2022) Obesity and accelerated epigenetic aging in a high-risk cohort of children. *Scientific Reports* 12(8328). <https://www.nature.com/articles/s41598-022-11562-5>

Li L*, Zhou J*, Ma Z; Bensi M, **Hall MA**, Baecher GB. (2022) Dynamic assessment of the COVID-19 vaccine acceptance leveraging social media data. *Journal of Biomedical Informatics* 129(104054). *Co-first authors <https://doi.org/10.1016/j.jbi.2022.104054>

Hall MA, Wallace J, Lucas AM, Bradford Y, Verma SS, Müller Myhsok B, Passero K, Zhou J, McGuigan J, Jiang B, Pendergrass SA, Zhang Y, Peissig P, Brilliant M, Sleiman P, Hakonarson H, Harley JB, Kiryluk K, Van Steen K, Moore JH, Ritchie MD. (2021) Novel EDGE encoding method enhances ability to identify genetic interactions. *PLoS Genetics* 17(6): e1009534. <https://doi.org/10.1371/journal.pgen.1009534>

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Li JC, **Hall MA**, Shalev I, Schreier HMC, Gonzalez Zarzar T, Marcovici I, Putnam FW, Noll JG. (2021) Hypothalamic-pituitary-adrenal axis attenuation and obesity risk in sexually abused females. *Psychoneuroendocrinology* 129 1055254.

Passero K, Setia-Verma S, McAllister K, Manrai A, Patel C, **Hall MA**. (2021) What About the Environment? Leveraging Multi-Omic Datasets to Characterize the Environment's Role in Human Health. *Pac Symp Biocomput*, 26: 309-315. https://doi.org/10.1142/9789811232701_0029

Aguilar MA, McGuigan J, **Hall MA**. (2021) Semi-automated NMR Pipeline for Environmental Exposures: New Insights on the Metabolomics of Smokers versus Non-smokers. *Pac Symp Biocomput*, 26: 316-327. https://doi.org/10.1142/9789811232701_0030

Lingyao Li, Lei Gao, Jiayan Zhou, Zihui Ma, **Molly A. Hall**. (2021) Can social media be utilized to enhance early warning: Retrospective analysis of the U.S. COVID-19 pandemic outbreak. *medRxiv*. <https://doi.org/10.1101/2021.04.11.21255285>

Zhou J, Passero K, Palmiero N, Mueller-Myhsok B, Kleber M, Maerz W, **Hall MA**. (2020) Investigation of gene-gene interactions in cardiac diseases and serum fatty acid levels in LURIC cohort. *PLOS ONE* 15(9): e0238304. <https://doi.org/10.1371/journal.pone.0238304>

Passero K, He X, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, **Hall MA**. (2020). Phenome-wide association studies on cardiovascular health and fatty acids considering phenotype quality control practices for epidemiological data. *Pac Symp Biocomput*, 25: 659-670

Lucas AM*, Palmiero N*, McGuigan J, Passero K, Zhou J, Orie D, Ritchie MD, **Hall MA**. (2019) CLARITE facilitates the quality control and analysis process for EWAS of metabolic-related traits. *Frontiers in Genetics*, 10: 1240. <https://doi.org/10.3389/fgene.2019.01240> *Co-first authors

Manduchi E, Chesi A, **Hall MA**, Grant SFA, Moore JH. (2018) Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in type 2 diabetes GWAS. *Pac. Symp. Biocomput*. 23:548-558.

Hall MA, Cole B, Moore JH. (2018) Gene-Gene Interactions: An Essential Component to Modeling Complexity for Precision Medicine. *Encyclopedia of Bioinformatics and Computational Biology*: 171-177.

Cole B, **Hall MA**, Urbanowicz RJ, Gilbert-Diamond D, Moore JH (2018) Analysis of Gene-Gene Interactions. *Current Protocols in Human Genetics*: 95(1), 1-14.

Hall MA, Wallace J, Lucas A, Kim D, Basile AO, Verma SS, McCarty CA, Brilliant MH, Peissig PL, Kitchner TE, Verma A, Pendergrass S, Dudek S, Moore JH, Ritchie MD (2017) PLATO provides analytic framework for investigating complexity beyond genome-wide association studies. *Nature Communications*:1167.

Manrai AK, Cui Y, Bushel PR, **Hall MA** Karakitsios S, Mattingly CJ, Ritchie M, Schmitt C, Sarigiannis DA, Thomas DC, Wishart D, Balshaw DM, Patel CJ (2017) Informatics and data analytics to support exposome-based discovery for public health. *Annual Review of Public Health*: 38, 279-294.

Kim D, Volk H, Girirajan S, Pendergrass S, **Hall MA**, Verma SS, Schmidt RJ, Hansen RL, Ghosh D, Ludena-Rodriguez Y, Kim K, Ritchie MD, Hertz-Picciotto I, and Selleck SB (2017) The joint effect of air pollution and copy number variation on risk for autism. *Autism Research* 10(9): 1470-1480.

De R, Verma SS, Holzinger ER, **Hall MA**, Burt A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Lange LA, Lanktree MB, Larson EB, North KE, Reiner AP, Tragante V, Tromp G, Wilson JG, Asselbergs FW, Drenos F, Moore JH, Ritchie MD, Keating B, Gilbert-Diamond D (2017) Identifying gene-gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. *Human Genetics* 136(2): 165-178.

Holzinger ER, Verma SS, Moore CB, **Hall M**, De R, Gilbert-Diamond D, Lanktree MB, Pankratz N, Amuzu A, Burt A, Dale C, Dudek S, Furlong CE, Gaunt TR, Kim DS, Riess H, Sivapalaratnam S, Tragante V, van Iperen EPA, Brautbar A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Larson EB, Rasmussen-Torvik LJ, Tromp G, Baumert J, Cruickshanks KJ, Farrall M, Hingorani AD, Hovingh GK, Kleber ME, Klein BE, Klein R, Koenig W, Lange LA, März W, North KE, Charlotte Onland-Moret N, Reiner AP, Talmud PJ, van der Schouw YT, Wilson JG, Kivimaki M, Kumari M, Moore JH, Drenos F, Asselbergs FW, Keating BJ, Ritchie MD. Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Min.* 2017 Jul 24;10:25

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Hall MA, Moore JH, Ritchie MD (2016) Embracing complex associations in common traits: Critical considerations for precision medicine. *Trends in Genetics*: 32, 470-484

Li R, Dudek S, Kim D, **Hall MA**, Bradford Y, Peissig P, Brilliant B, Linneman JG, McCarty CA, Bao Le, Ritchie MD (2016) Identification of genetic interaction networks via an evolutionary algorithm evolved Bayesian network. *BioData Mining* 9:18.

Hall MA, Verma A, Brown-Gentry KD, Goodloe R, Boston J, Wilson S, McClellan B, Sutcliffe C, Dilks HH, Gillani NB, Jin H, Mayo P, Allen M, Schnetz-Boutaud N, Crawford DC, Ritchie MD, Pendergrass SA (2014) Detection of pleiotropy through and phenome-wide association study (PheWAS) of epidemiologic data as part of the Environmental Architecture for Genes Linked to Environment (EAGLE) study. *PLoS Genetics*: 10.

Hall MA, Verma SS, Wallace J, Lucas AM, Berg RL, Connolly J, Crawford DC, Crosslin DR, de Andrade M, Dohen KF, Haines JL, Harley JB, Jarvik GP, Kitchner T, Kuivaniemi H, Larson EB, Carrell DS, Tromp G, Vrabec TR, Pendergrass SA, McCarty CA, Ritchie MD (2015) Biology-driven gene-gene interaction analysis of age-related cataract in the eMERGE Network. *Genetic Epidemiology*: 39 376-384.

Hall MA, Verma SS, Wall DP, Moore JH Keating B, Campbell DB, Gibson G, Asselbergs FW, Pendergrass S (2015) Session Introduction: Characterizing the the importance of environmental exposures, interactions between the environment and genetic architecture, and genetic interactions. *Pac. Symp. Biocomput.*

Pendergrass SA, Verma A, Okula A, **Hall MA**, Crawford DC, Ritchie MD (2015) Phenome-wide association studies (PheWAS): Embracing complexity for discovery. *Human Heredity* 79:111-123.

De R, Verma SS, Drenos F, Holzinger ER, Holmes MV, **Hall MA**, Burt A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Lange LA, Lanktree MB, Larson EB, North KE, Reiner AP, Tragante V, Tromp G, Wilson JG, Asselbergs FW, Drenos F, Moore JH, Ritchie MD, Keating B, Gilbert-Diamond D. (2015) Identifying gene-gene interactions that are highly associated with body mass index using quantitative multifactor dimensionality reduction (QMDR) *BioData Mining* 8: 4.

Hall MA, Dudek SM, Goodloe R, Crawford DC, Pendergrass SA, Peissig P, Brilliant M, McCarty CA, Ritchie MD (2014) Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield Personalized Medicine Research Project Biobank. *Pac Symp Biocomput*: 200-211

Ritchie MD, Verma SS, **Hall MA**, Goodloe RJ, Berg RL, Carrell DS, Carlson CS, Chen L, Crosslin DR, Denny JC, Jarvik G, Li R, Linneman JG, Pathak J, Peissig P, Rasmussen LV, Ramirez AH, Wang X, Wilke RA, Wolf WA, Torstenson ES, Turner SD, McCarty CA (2014) Electronic medical records and genomics (eMERGE) network exploration in cataract: Several new potential susceptibility loci. *Molecular Vision*: 20.

Pendergrass SA, Verma SS, **Hall MA**, Holzinger ER, Moore CB, Wallace JR, Dudek SM, Huggins W, Kitchner T, Waudby C, Berg R, McCarty CA, Ritchie MD (2013) Next-generation analysis of cataracts: determining knowledge driven gene-gene interactions using Biofilter, and gene-environment interactions using the PhenX Toolkit. *Pac Symp Biocomput*: 147-58.

Funding

Active/Recent:

U2C OD023375-06

Hall (PI)

9/1/2021-8/31/2023

National Institutes of Health/NICHHD

Funding Title: Environmental Influences on Child Health Outcomes (ECHO) Opportunities and Infrastructure Fund (OIF)

Title: Integrative genome-exposome method to identify interactions between early life exposures and the genome

R01 CA239256

Peters, Patterson (MPI), Role: Co-Investigator

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12/01/2019-11/30/2024

National Institutes of Health/NCI

Title: Unique Targeting of Pparb/d Regulation for Cancer Prevention and Therapy

Administrative Supplement for U01 NS112008

6/01/2021-5/31/2024

Huang (PI), Role: Co-Investigator

National Institutes of Health/NINDS

Title: The impact of COVID-19 on cognitive and neuropathological process leading to Parkinson's Dementia and other ADRD

R01 DK138865-04

08/15/2023- 07/31/2026

Paulson (PI), Role: Co-Investigator

National Institutes of Health/NIDDK

Title: Metabolic Regulation of erythropoiesis

UH3OD023332-01

9/1/2021-8/31/2022

Blair (PI), Role: Co-Investigator

National Institutes of Health (ECHO Initiative)

Title: Early Life Stress and the Environmental Origins of Disease: a Population-based Prospective Longitudinal Study of Children in Rural Poverty (Family Life Project). Goals: To evaluate the role of early-life exposures on later health outcomes.

Penn State Frances Keesler Graham Early Career Professorship

Hall (PI)

10/1/2019-9/30/2022

Social Science Research Institute, Pennsylvania State University

Title: Longitudinal metabolomic profile of childhood maltreatment and its impact on neural development

Penn State Human Health and the Environment Seed Grant

Hall (PI)

6/1/2019-5/31/2025

Social Science Research Institute, Pennsylvania State University

Title: Leveraging metabolomics to identify environmental exposures and biomarkers associated with health disparities due to child maltreatment

Penn State Institute for Energy and the Environment Seed Grant

Hall (PI)

6/1/2020-3/31/2025

Institute for Energy and the Environment, Pennsylvania State University

Title: Linking Environmental Toxicants to Neurodegenerative Processes

L30HG010739 NIH Loan Repayment Program (LRP)

Hall (PI)

National Institutes of Health/NHGRI

Title: Software for integrated genome-metabolome analysis (SIGMA)

T32 DK120509-04

Patterson (PI), Role: Faculty

National Institutes of Health/NIDDK

Title: Integrative Analysis of Metabolic Phenotypes (IAMP) Predoctoral Training Program

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Pending:

R01
NHGRI
Scientific Review Group GHD
Hall (PI)
Title: Incorporating nonadditive and environmental effects in genetic associations to improve complex disease prediction for diverse populations
First Submission: February 5, 2022: Scored 45 (41st percentile)
Resubmitted November 5, 2022: Scored 36 (25th percentile)
New Submission: June 5, 2023 (to be reviewed October 2023)

R01
NIA
Scientific Review Group Special Emphasis Panel for PAR-22-093
Shen/Kim (UPenn) and Hall (MPI)
Title: Informatics strategies to enable AD precision medicine through unraveling sex-specific molecular mechanisms
First Submission: July 15, 2022: Scored 44 (37th percentile)
Submission: July 15, 2023 (to be reviewed October 2023)

R01
NIDDK
Scientific Review Group KNOD
Shalev and Hall (MPI)
Title: Elucidating biological mechanisms of obesity risk in a high-risk cohort: A multi-level multi-omics approach
Submission: June 5, 2023

R01
NIDDK
Paulson (PI), Role: Co-Investigator
Title: Role of Perk signaling in stress erythropoiesis
Resubmitted: July 2023 (scored/discussed during first submission)

Completed Research Support

F31HG008588
05/16/2015-09/30/15
NIH/NHGRI
Ruth L. Kirschstein National Research Service Award (NRSA) Individual Predoctoral Fellowship (Parent F31)
The primary goal of this project is to develop novel methods to identify and replicate complex interactions in common disease
Role: PI

PA Tobacco Settlement Fund (TSF), Commonwealth of Pennsylvania
Prabhu, Zheng (MPI), Role: Co-Investigator
6/1/2019-5/30/2020
Title: Integration of Differentially Regulated Pathways of Selective Targeting of Leukemia Stem Cells in Models of Human Acute Myeloid Leukemia

Conference Talks (current and former trainees/staff underlined):

González Zarzar T, Palmiero N, **Hall MA** (2022) Phenome-wide sex differences in environmental effects on health.

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American Society of Human Genetics. Los Angeles, CA. *Selected as one of 16 finalist for the 2022 ASHG Trainee Research Excellence Award (formerly Epstein Award)

Zhou J, Verma SS, **Hall MA** (2022) Identifying nonadditive genetic effects with flexible encoding in GWAS. American Society of Human Genetics. Los Angeles, CA.

Hall MA, Passero K, Zhou J, González Zarzar T (September 14, 2022) Research Talk with US Senator of Agriculture Tom Vilsack. College of Agricultural Sciences, Penn State University, University Park, PA.

Aguilar MA, McGuigan J, **Hall MA** (Jan 2021) Semi-automated NMR Pipeline for Environmental Exposures: New Insights on the Metabolomics of Smokers versus Non-smokers. Paper presented at the Pacific Symposium on Biocomputing. Virtual.

Passero K, Setia-Verma S, McAllister K, Manrai A, Patel C, **Hall MA** (Jan 2021) What About the Environment? Leveraging Multi-Omic Datasets to Characterize the Environment's Role in Human Health. Paper presented at the Pacific Symposium on Biocomputing. Virtual.

Hall MA, Dudek SM, Goodloe R, Crawford DC, Pendergrass SA, Ritchie MD (2014) Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield Personalized Medicine Research Project Biobank. *2014 Pacific Symposium on Biocomputing (PSB)*

Hall MA, Verma SS, Holzinger ER, Ritchie MD (2013) Replication of gene-gene interaction models associated with cataracts in the eMERGE Network. *American Society for Human Genetics (ASHG)*

Hall MA, Verma A, Brown-Gentry KD, Pendergrass SA (2012) A Phenome-Wide Association Study (PheWAS) using multiple National Health and Nutritional Surveys (NHANES) to identify pleiotropy. *2012 Translational Biology Conference (TBC)*

Invited Talks

Hall MA (Presenter & Author). (3/30/2022). "Modeling and analyzing complex relationships in biological big data". Department of Machine Learning and Data Processing, Masaryk University, Brno, Czech Republic. (International)

Hall MA (Presenter & Author). (3/23/2021). "Integrative genome-exposome method to identify interactions between early life exposures and the genome". The Family Life Project, University of North Carolina, Chapel Hill.

Hall MA (Presenter & Author). (3/18/2021). "Integrative genome-exposome method to identify interactions between early life exposures and the genome". Department of Environmental Health and Engineering, Johns Hopkins University.

Hall MA (Presenter & Author). (2/25/2021). "Knowledge-based gene-environment interaction modeling for neurodevelopmental outcomes". ECHO Cohort, Duke University.

Hall MA (Presenter & Author). (11/5/2020). "Computational approaches for modeling complexity in common disease". Animal Science Department Seminar, Penn State University

Hall MA (Presenter & Author). (12/6/2019). "Modeling the complexity of common disease". Roy C. Buck Faculty Award Bortree Seminar, Penn State University

Hall MA (Presenter & Author). (12/4/2019). "Modeling the complexity of common disease". KINES PhD program seminar 12/6/19, Penn State University

Hall MA (Presenter & Author). (February 25, 2019). "Methods for identifying complex associations predictive of common disease". Biobehavioral Health Seminar Series, Penn State University.

Hall MA (Presenter & Author). (November 15, 2018). "Methods for identifying complex associations with diet predictive of common disease". Big Data Workshop, Department of Nutritional Sciences, Penn State University.

Hall, MA (Presenter & Author). (November 14, 2018). "Big data genomics methods for identifying complex associations predictive of common disease". Genomics Seminar Series, Penn State University.

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Hall, MA (Presenter & Author). (September 21, 2018). “Leveraging the exposome in health data for identifying complex associations predictive of common disease”. Mechanism of Carcinogenesis Retreat, Penn State Cancer Institute, Penn State University.

Hall MA (Presenter & Author). (June 18, 2018). “Quality control is essential to ensuring reproducibility in genotype and non-genetic data”. Reproducibility Data Boot Camp, Bioinformatics & Genomics, Penn State University.

Hall MA, Noll J, Patterson A. (May 5, 2018) “Metabolomics: Bridging the divide between life and social sciences”. University Health Sciences Council, Penn State University.

Hall MA (Presenter & Author). (October 16, 2017). “Gene-environment interactions predictive of common disease”. Genomics Lecture, Department of Biochemistry and Molecular Biology, Penn State University.

Hall MA (Presenter & Author). (September 23, 2017). “Emerging methods for complex associations beyond GWAS”. Bioinformatics & Genomics Retreat, Penn State University.

Hall MA (Presenter & Author). (June 11, 2015). “Beyond GWAS: Emerging methods for complex associations for common disease”. Department of Biomedical Informatics, Harvard Medical School.

Hall MA (Presenter & Author). (May 5, 2015). “Beyond GWAS: Emerging methods for complex associations for common disease”. Institute for Biomedical Informatics, Perelman School of Medicine, University of Pennsylvania.

Posters (current and former trainees/staff underlined):

Passero K, Selin C, Noll JG, **Hall MA**. Evaluating the interaction of polygenic risk and child sexual abuse on longitudinal trajectories of PTSD. 2023 *American Society of Human Genetics (ASHG)*. Washington, DC.

Apsley A, Passero K, Noll JG, Shalev I, **Hall MA**. Metabolome-wide association study in a high-risk pediatric cohort. 2023 *American Society of Human Genetics (ASHG)*. Washington, DC.

Palmiero N, **Hall MA**. Phenomic environment-wide association study to evaluate the complexity of the exposome. 2023 *American Society of Human Genetics (ASHG)*. Washington, DC.

Aguilar M, **Hall MA**. Secondary NMR analysis of estrogen receptor positive breast cancer: diagnosis, histology, and years-to-relapse prediction. 2020 *MidAtlantic Bioinformatics Conference*.

Aguilar M, McGuigan J, **Hall MA**. Semi-automated environmental exposure phenotyping: a case for smoking. 2020 *American Medical Informatics Association (AMIA)*.

McGuigan J, Veturi Y, Li B, Verma A, Le T, Fu W, Haas D, Ritchie MD, **Hall MA***, Moore JH*. Automated machine learning for rare variant analysis of response to antiretroviral therapy in patients infected with HIV. 2020 *American Society of Human Genetics (ASHG)*. San Diego, CA.

Aguilar M, McGuigan J, **Hall MA**. Secondary metabolic analysis of breast cancer nanoparticle chemotherapy: fatty acid metabolism perturbation with newly quantified metabolites and high fidelity classification models. 2020 *American Society of Human Genetics (ASHG)*. San Diego, CA.

Hall MA, Palmiero NE, Zhou J, Aguilar M, McGuigan J, Kolli P, Brosius D, Vijay A, Tian Y, Koo I, Allman E, Patterson A, Noll J. Metabolomics reveals novel biomarkers in children who experienced maltreatment. 2020 *American Society of Human Genetics (ASHG)*.

Zhou J, Palmiero N, Passero K, McGuigan JR, Aguilar MA, and **Hall MA**. Interaction between genes and fatty acids for cardiac-related traits in LURIC cohort. 2020 *American Society of Human Genetics (ASHG)*.

Palmiero N, Passero K, Zhou J, McGuigan J, Aguilar M, Ludman A, and **Hall MA**. Environment-wide association study of the phenome to evaluate the complexity of the exposome. 2020 *American Society of Human Genetics (ASHG)*.

Palmiero N, Passero K, Zhou J, McGuigan J, Aguilar M, Ludman A, and **Hall MA**. Phenome-wide environment wide association study to evaluate the complexity of the exposome. 2020 *NYC Exposome Symposium*. New York, NY.

Curriculum Vitae: Molly Hall

Zhou J, Palmiero N, Passero K, McGuigan JR, Aguilar MA, Prabhu KS, and Hall MA. Risk assessments for the common types of anemia from exposome through a series of environment-wide association studies (EWASs) in NHANES 1999-2006. *2020 NYC Exposome Symposium*. New York, NY.

Zhou J, Palmiero N, Passero K, McGuigan JR, Aguilar MA, and Hall MA. Gene-environment interaction analysis for cardiac-related traits in the Ludwigshafen Risk and Cardiovascular (LURIC) Health Study. *2020 NYC Exposome Symposium*. New York, NY.

Passero K, Palmiero N, Gatzke-Kopp L, Hall MA. Leveraging Environment-wide, Longitudinal Data to Discern How Early-life Exposures Affect Child Health and Development. *2020 NYC Exposome Symposium*. New York, NY.

Aguilar M, McGuigan J, Hall MA. Automated NMR Preprocessing and Predictive Modeling of Smoking Exposure with Random Forests. *2020 NYC Exposome Symposium*. New York, NY.

Passero K, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, Hall MA. Establishing quality control practices for phenome-wide association studies (PheWAS). *2020 Pacific Symposium on Biocomputing*. Hawaii, HI.

Passero K, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, Hall MA. Establishing quality control practices for phenome-wide association studies (PheWAS). *2019 American Society for Human Genetics (ASHG)*. Houston, TX.

Passero K, He X, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, Hall MA. Phenome-wide association studies on cardiovascular health and fatty acids considering phenotype quality control practices for epidemiological data. *2019 American Society of Human Genetics (ASHG)*.

Zhou J, Passero K, Müller-Myhsok B, Kleber ME, Maerz W, Hall MA. Investigation of gene-gene interactions in cardiac diseases and fatty acids in LURIC. *2019 American Society of Human Genetics (ASHG)*.

Lucas AM, Palmiero N, Orié D, Ritchie MD, Hall MA. CLARITE facilitates the quality control and analysis process for EWAS of metabolic-related traits. *2018 American Society of Human Genetics Conference (ASHG)*.

Palmiero NE.*, Lucas A.*, Ritchie MD, Vazquez-Vidal I, Peter JH, Hall MA. The Utility of CLARITE While Prioritizing Environment-Environment Interactions Relating to HDL-C. *2018 American Society of Human Genetics (ASHG)*.

Hall MA, Wallace JR, Pendergrass SA, Ritchie MD. EWAS to GxE: A robust strategy for detecting gene-environment interaction models for age-related cataract. *2014 American Society for Human Genetics (ASHG)*.

Hall MA, Verma A, Brown-Gentry KD, Pendergrass SA. A Phenome-Wide Association Study (PheWAS) using multiple National Health and Nutritional Surveys (NHANES) to identify pleiotropy. *2012 American Society for Human Genetics (ASHG)*.

Trainees

Morris Aguilar (Bioinformatics & Genomics, MD/PhD) 2019-December 2023 (Defending October 30, 2023)

Kristin Passero, PhD (Molecular, Cellular, and Integrative Biosciences) 2018-September 2023 (Research Associate, Virginia Commonwealth University)

Jiayan Zhou, PhD (Pathobiology) 2018-January 2023 (Postdoctoral Fellow, Stanford University)

Co-Mentored: Abner Apsley (PhD Student MCIBS, Penn State, Mentor: Dr. Idan Shalev) – 2021-present

Tomás González Zarzar (Postdoctoral Fellow) 2021-March 2023 (Assistant Professor [tenure-track], Universidad Mayor, Chile)

Ph.D. Dissertation Committee Member

Polina Tikhonova (Bioinformatics & Genomics, Penn State, Mentor: Dr. Emily Davenport) 2023-present

Brenda Xiao (Penn Genomics and Computational Biology, UPenn, Co-mentors: Drs. Marylyn Ritchie and Dokyoon Kim) – 2022-present

Abner Apsley (PhD Student MCIBS, Penn State, Mentor: Dr. Idan Shalev) – 2021-present

Laura Etzel-House (BBH, Penn State, Mentor: Dr. Idan Shalev) – 2020-2022

Curriculum Vitae: Molly Hall

Latisha Franklin (BMMB, Penn State, Mentor: Dr. Wendy Hanna-Rose) 2017-2023

Corinna Moro (BMMB, Penn State, Mentor: Dr. Wendy Hanna-Rose) 2017-2022

Undergraduate and Other Supervision/Mentoring

Miran Rezhan (Undergraduate, Immunology & Infectious Disease – 2023-present

Ethan Glenn (Undergraduate, Pharmacology & Toxicology) – 2022-present

Chase Cunningham (Undergraduate, Data Sciences) – 2022-2023

Serina Blessing (Undergraduate, Pharmacology and Toxicology) – 2022-2022

Rory Coughlin (Undergraduate, Biochemistry and Molecular Biology) – 2021-2022

Deven Orié (Undergraduate, Dartmouth College) – Spring 2018

Bryan Almonte (Undergraduate, Bates College) – Summer 2018

Nicole Palmiero (Intern) – Summer 2018

Tuyen Pham (Graduate Intern, West Virginia University) – Summer 2018