

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)
- 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

- 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

Curriculum Vitae: Molly Hall

- 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
Genomics
Metabolomics
Gene-Environment Interactions
Environment-Wide Association Studies
Gene-Gene Interactions
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)

28. 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* (in press). *Imaging Genomics Special Issue

27. 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* (accepted). *Co-first authors
26. **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>
25. 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.
24. 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
23. 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
22. 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>
21. 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>
20. 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
19. 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
18. 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.
17. **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.
16. 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.
15. **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.
14. 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.

13. 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.
12. 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.
11. 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
10. **Hall MA**, Moore JH, Ritchie MD (2016) Embracing complex associations in common traits: Critical considerations for precision medicine. *Trends in Genetics*: 32, 470-484
9. 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.
8. **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.
7. **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.
6. **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.*
5. 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.
4. 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.
3. **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

Curriculum Vitae: Molly Hall

2. 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.

1. 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.

Submitted/Under Review:

Morris A. Aguilar, Shauna Ebanks, Mechelle Lewis, Vishal Midya, Vonn Walter, Kent Vrana, Xuemei Huang, **Molly A. Hall***, Yuka Imamura Kawasawa*. Neuronal Enriched Exosomal Small RNAs as Potential Biomarkers for Parkinson's Disease (*JAMA Neurology*). * Co-senior/corresponding authors

Etzel L, Hastings WJ, **Hall MA**, Heim C, Meaney M, Noll JG, Rose E, Schreier H, Shenk C, Shalev I. Obesity and accelerated epigenetic aging in a high-risk cohort of children (*Scientific Reports*).

Zhou X, Murray IA, Coslo D, Chakraborty D, Kehs Z, Zhou J, Ton C, **Hall MA**, and Perdew GH. Ah receptor activation coordinates intestinal epithelial cell programming.

Baiye Ruan, Yuanting Chen, Imhoi Koo, Jingwei Cai, John Mcguigan, **Molly A. Hall**, Andrew D. Patterson, Robert F. Paulson. Nitric oxide dependent metabolism regulates proliferation and differentiation of immature stress erythroid progenitors during inflammatory anemia (*Cell Metabolism*).

McKayla J. Nicol, John R. McGuigan, Imhoi Koo, Anastasia Tyryshkina, Andrew Patterson, Santhosh Girirajan, **Molly A Hall**, and Girish S. Kirimanjeswara. Integrated multi-omic approach to simultaneously elucidate host-pathogen responses (*eLife*).

Additional Information: Research Support and/or Scholastic Performance

Complete List of Published Work in MyBibliography

<https://www.ncbi.nlm.nih.gov/sites/myncbi/18sXnah7uHfQb/bibliography/46095730/public/?sort=date&direction=descending>

Funding

Active:

U2C OD023375-06

Hall (PI)

9/1/2021-8/31/2023

National Institutes of Health/NICHD

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

Goals: To develop a novel method for genome-exposome interaction analysis that identifies risk factors for development of autism spectrum disorder in the ECHO Program.

R01 CA239256

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

12/01/2019-11/30/2024

National Institutes of Health/NCI

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

Goals: To integrate metabolome and transcriptome data and determine the mechanisms that inhibit tumorigenesis in colon cancer models.

Curriculum Vitae: Molly Hall

Administrative Supplement for U01 NS112008

6/01/2021-5/31/2023

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

Goals: To test the impact of SARS-CoV2 infection on clinical as well as brain structural and functional changes leading to PD/ADRD, and to explore its multi-omic signatures associated with the AD/ADRD.

Penn State Institute for Energy and the Environment Seed Grant

Hall (PI)

6/1/2020-3/31/2021

Institute for Energy and the Environment, Pennsylvania State University

Title: Linking Environmental Toxicants to Neurodegenerative Processes

Goals: To collect metabolomics data in a high-risk chemical exposure population of farmers and welders and to evaluate metabolomic dysregulations associated with decline in neurocognitive function.

Penn State Human Health and the Environment Seed Grant

Hall (PI)

6/1/2019-5/31/2021

Social Science Research Institute, Pennsylvania State University

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

Goals: To collect metabolomics data on urine from the first 400 participants of the Penn State Child Health Study (P50 HD089922, PI: Noll) to evaluate metabolomic dysregulations associated with childhood obesity in a high-risk cohort.

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

Goals: To evaluate metabolomic dysregulations associated with adverse neural development in the first 400 participants of an at-risk cohort: the Penn State Child Health Study (P50 HD089922, PI: Noll).

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

Goals: To understand how LSCs isolated from either the humanized AML model as well as the murine model of AML differ from hematopoietic stem cells (HSCs) and identify the basis for the increased sensitivity of LSCs to PGJ₃.

L30HG010739 NIH Loan Repayment Program (LRP)

Hall (PI)

NHGRI

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

Pending

R01

NHGRI

Scientific Review Group GGG

Hall (PI)

Title: Incorporating nonadditive and environmental effects to improve polygenic risk prediction in diverse populations

Curriculum Vitae: Molly Hall

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

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

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.

Curriculum Vitae: Molly Hall

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.

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):

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.

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.

Curriculum Vitae: Molly Hall

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)*.

Ph.D. Dissertation Advisor

Morris Aguilar (Bioinformatics & Genomics, MD/PhD) 2019-Present

Kristin Passero (Molecular, Cellular, and Integrative Biosciences) 2018-Present

Jiayan Zhou (Pathobiology) 2018-Present

Ph.D. Dissertation Committee Member

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

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

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

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

Research Supervision/Mentoring

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

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