YOGASUDHA VETURI, Ph.D.
Postdoctoral Research Fellow
Department of Genetics
Perelman School of Medicine
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Education

Ph.D. Biostatistics, University of Alabama at Birmingham, Nov 2016
- Dissertation: *"Methods for analysis of genetic differences in sex and ethnicity for complex human traits"*, Advisor: Dr. Gustavo de los Campos

M.S. Plant and Soil Sciences, University of Delaware, Jul 2012
- Thesis: *"Development of a statistical framework for association mapping in recurrently selected populations"*, Advisor: Dr. Randall Wisser

M.S. Statistics, North Carolina State University, May 2009
B.Sc. (Honors) Statistics, Lady Shri Ram College for Women, University of Delhi, May 2006

Professional Experience

Pennsylvania State University, Departments of Biobehavioral Health and Statistics
Assistant Professor — Aug 2020 – present

University of Pennsylvania, Perelman School of Medicine, Department of Genetics
Postdoctoral Fellow, Ritchie Lab — Jan 2018 – Aug 2020
- *Lipid-EHR pleiotropy*:
  - Devised a comprehensive framework integrating genetics, gene expression, electronic health records, and plasma lipids to shed light on the landscape of genetic mechanisms linking plasma lipids to phenome-wide diseases in multiple large-scale cohorts.
  - Used an ensemble of methods including genome-wide, phenome-wide and transcriptome-wide association studies, statistical colocalization, fine-mapping, conditional analyses and Mendelian randomization.
  - Developed a tool to conduct statistical colocalization on a gene-by-gene basis https://github.com/RitchieLab/Gene-level-statistical-colocalization.
- Analyzed pleiotropy between cardiovascular and neurological diseases in the eMERGE and UK Biobank cohorts using a combination of univariate, bivariate and multivariate statistical methods.
- Devised a framework for integrating multi-modal brain imaging data (across ancestral groups) from UK Biobank cohort with genetics and electronic health records.

Geisinger, Department of Biomedical and Translational Informatics
Postdoctoral Fellow, Ritchie Lab — Jan 2017 – Dec 2017
- Conducted simulation analysis to examine power of a variety of methods used to conduct transcriptome-wide association studies under varying genetic architectures and sample sizes.
- Conducted quality control, genotype imputation and association analyses on plasma lipid traits within the eMERGE network using protocols developed by Global Lipids Genetics Consortium as part of their million-individual lipid GWAS.
- Evaluated risk for virologic failure and peripheral neuropathy with efavirenz-containing antiretroviral therapy regimens using gene binning approaches (burden and dispersion-based) on rare and common variants in whole exome sequencing data.
- Analyzed associations between fat-derived CT scans from Geisinger's MyCode and disease diagnoses from Geisinger's Electronic Health Records.

Michigan State University, Department of Epidemiology and Biostatistics
Intern in Biostatistics, QuantGen Lab Jul 2015 – Dec 2016

- Analyzed heterogeneity of marker effects between (a) Caucasians and African Americans from the Atherosclerosis Risk in Communities (ARIC). and (b) Caucasian males and females for anthropometric and obesity-related human traits from the UK Biobank dataset by modeling genotype-by-group random interactions using novel Bayesian and likelihood-based frameworks.

University of Alabama at Birmingham, Department of Biostatistics
Graduate Research Assistant, QuantGen Lab Aug 2012 – Dec 2016

- Estimated genomic heritability for body composition traits using whole genome regression methods in the multi–ethnic Training Interventions and Genetics of Exercise and Response (TIGER) study.
- Analyzed variable selection and shrinkage methods for complex trait prediction in distantly related humans in the Gene Environment Association Studies (GENEVA) dataset.
- Analyzed and predicted survival for breast cancer patients using multi-layer high-dimensional "omic" information from The Cancer Genome Atlas (TCGA).

University of Delaware, Department of Plant and Soil Sciences
Statistician and Graduate Research Assistant, Wisser Lab Oct 2009 – Jul 2012

- Developed a whole genome simulator for closed breeding populations under recurrent selection.
- Determined the influence of intense artificial selection vs. genetic drift on coancestry in recurrently selected populations.
- Examined the utility of multivariate analysis in plant pathology in achieving multiple scopes of temporal inference, using a multi–environment maize population recurrently selected for resistance to northern leaf blight disease.
- Performed statistical analyses for studying fungal morphology by evaluating traits indicative of pathogenesis of *Cochliobolus heterostrophus* on maize.
- Contributed to Maize ATLAS project (http://maizeatlas.org/) to analyze clinal variation in maize.

North Carolina State University, Department of Statistics
Statistical consultant Jan 2009 – May 2009

- Evaluated the influence of different fungal strains on lesion size in maize lines.
- Analyzed bicultural identity effects on assignment success for American expatriates.

Gilead Sciences Inc., Durham, NC
Biostatistician I Aug 2008 – May 2009

- Analyzed and reported data from clinical trials investigating chemical compounds used for the treatment of HCV and HPV in humans.
- Performed interim analyses of compounds for efficacy and futility endpoints; superiority/inferiority trials; sequential tests, multiple comparisons and simulations for power and sample size calculations; fixed allocation and adaptive randomization methods; summary tables and CRF SAS datasets.

Peer Reviewed Publications (***** - co-first author, † - corresponding author)

1. Yengo, L.*, Vedantam, S.*, …, **Veturi, Y.,** et al., … and Wood, A., Visscher, P., and Hirschhorn, J. *"A saturated map of common genetic variants associated with human height from 5.4 million individuals of diverse ancestries"* – https://www.biorxiv.org/content/10.1101/2022.01.07.475305v1 Accepted in *Nature*
2. Kanoni, S. *, Graham, S.E. *, Wang, Y. *, Surakka, I. *, Ramdas, S. *, Zhu*, X., Clarke, S.L., Bhatti, F.K., Vedantam, S., Winkler, T.W., Locke, Marouli, E., Zajac, G.J.M., Wu, K.H., Ntalla, I., Hui, Q. D., Klarin, D., Hilliard, A., Wang, Z., Xue, C., Thorleifsson, G., Helgadottir, A., Gudbjartsson, D.F., Holm, H., Olafsson, I., Hwang, M.Y., Han, S., Akiyama, M., Sakaue, S., Terao, C., Kanai, M., Zhou,

W., Brumpton, B.M., Rasheed, H., Havulinna, A.S., **Veturi, Y.,** et al. … and Willer C., Peloso G.M. *"Implicating genes, pleiotropy and sexual dimorphism at blood lipid loci through trans-ancestry meta-analysis"* – https://www.medrxiv.org/content/10.1101/2021.12.15.21267852v1 Accepted in *Genome Biology*

3. Ramdas, S.*, Judd, J.*, Graham, S.E.*, Kanoni S*, Wang Y., Surakka, I., Wenz, B., Clarke, S.L., Chesi, A., Wells, A., Bhatti, F.K., Vedantam, S., Winkler, T.W., Locke, Marouli, E., Zajac, G.J.M., Wu, K.H., Ntalla, I., Hui, Q. D., Klarin, D., Hilliard, A., Wang, Z., Xue, C., Thorleifsson, G., Helgadottir, A., Gudbjartsson, D.F., Holm, H., Olafsson, I., Hwang, M.Y., Han, S., Akiyama, M., Sakaue, S., Terao, C., Kanai, M., Zhou, W., Brumpton, B.M., Rasheed, H., Havulinna, A.S., **Veturi, Y.,** et al … and Willer C., Brown, C.,*"A multi-layer functional genomic analysis to understand noncoding genetic variation in lipids"* – *American Journal of Human Genetics* 109(8), 1366-1387 https://www.biorxiv.org/content/10.1101/2021.12.07.470215v1
4. Zhang, X, Lucas, A.M., **Veturi, Y.**, Drivas, T.G., Bone W.,Verma, A., Chung, W.K., Crosslin, D., Denny, J.C., Fasel, D., Hakonarson, H., Hebbring, S., Jarvik, G.P., Kullo, I., Larson, E.B., Pendergrass, S., Rasmussen-Torvik, L.J., Schaid, D.J., Sleiman, P., Smoller, J.W., Stanaway, I.B., Wei, W., Weng, C., Ritchie, M.D. *"Large-scale genomic analyses reveal insights into pleiotropy across circulatory system diseases and central nervous system disorders"* – *Nature Communications* 13, 3428 (2022) https://www.nature.com/articles/s41467-022-30678-w.pdf
5. Wen, J., Fu, H.Y.C., Tosun, D., **Veturi**, **Y**., Yang, Z., Abdulkadir, A., Mamourian, E., Srinivasan, D., Bao, J., Erus, G., Shou, H., Habes, M., Doshi, J., Varol, E., Mackin, S.R., Sotiras, A., Fan, Y., Saykin, A.J., Sheline, Y.I., Shen, L., Ritchie, M.D., Wolk, D.A., Albert, M., Resnick, S.M., Davatzikos, C. *"Multidimensional representations in late-life depression: convergence in neuroimaging, cognition, clinical symptomatology and genetics"* – *JAMA Psychiatry* 79(5), 464-474 (2022) https://jamanetwork.com/journals/jamapsychiatry/article-abstract/2789902
6. Graham, S., Clarke, S.L., Wu, K.H., Kanoni, S., Zajac, G.J.M., Ramdas,S., Surakka, I., Ntalla, I., Vedantam, S., Winkler, T., Locke, A.E., Marouli, E., Hwang, M.Y., Han, S., Narita, A., Verma, A., Trivedi, B., Martin, H.C., Hunt, K.A., Hui, Q., Klarin, D., Zhu, X., Thorleifsson, G., Helgadottir, A., Gudbjartsson, D.F., Holm, H., Olafsson, I., Akiyama, M., Sakaue, S., Terao, C., Kanai, M., Zhou, W., Brumpton, B.M., Rasheed, H., Ruotsalainen, S.E., Havulinna, A.S., **Veturi, Y.**, et al … and Willer, C. *"The power of genetically diverse individuals in genome-wide association studies of blood lipid levels"* – *Nature* 600, 675–679 (2021) https://www.nature.com/articles/s41586-021-04064-3
7. **Veturi, Y.**, Lucas, A., Bradford, Y., Hui, D., Dudek, S., Theusch, E., Verma, A., Miller, J.E., Kullo, I., Hakonarson, H., Sleiman, P., Schaid, D., Stein, C.M., Velez Edwards, D.R., Feng, Q., Wei, Q., Medina, M.W., Krauss, R., Hoffmann, T.J., Risch, N., Voight, B.F., Rader, D.J., Ritchie, M.D. *"Unified framework identifies novel replicating links between plasma lipids and diseases from Electronic Health Records across large-scale cohorts"*. *Nature Genetics* 53, 972–981 (2021) https://www.nature.com/articles/s41588-021-00879-y
8. Li, B., **Veturi, Y**., Verma, A., Bradford, Y., Daar, E.S., Gulick, R.M., Riddler, S.A., Robbins, G.K., Lennox, J.L., Haas, D.W., Ritchie, M.D. *"Tissue specificity-aware TWAS framework identifies novel associations with metabolic and virologic traits in HIV-positive adults"*. *PLOS Genetics* (2021) https://doi.org/10.1371/journal.pgen.1009464
9. Miller, J., **Veturi, Y.,** Ritchie, M.D. *"Innovative strategies for annotating the "relationSNP" between variants and molecular phenotypes"*. *BioData Mining* 12:10 (2019) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6518798/
10. **Veturi, Y.**†, Yi, N., Huang, W., Vazquez A.I., de los Campos, G. *"Modeling Heterogeneity in the Genetic Architecture of Ethnically Diverse Groups Using Random Effect Interaction Models"*. *Genetics* 211(4):1395-1407 (2019) https://www.genetics.org/content/genetics/211/4/1395.full.pdf
11. Zhang, X.*, **Veturi, Y.***, Verma, S.S., Bone, W., Verma, A., Lucas, A., Hebbring, S., Denny, D.C., Stanaway, I.B., Jarvik, G.P., Crosslin, D., Larson, E.B., Rasmussen-Torvik, L., Pendergrass, S.A., Smoller, J.W., Hakonarson H., Sleiman P., Weng C., Fasel D., Wei W., Kullo, I., Schaid, D. Chung, W.K., Ritchie, M.D. *"Detecting potential pleiotropy across cardiovascular and neurological diseases*

using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network", *Pacific Symposium on Biocomputing* 24:272-283 (2018) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6457436/

12. Li, B., **Veturi, Y.**, Bradford, Y., Verma S.S., Verma, A., Lucas, A.M., Haas, D.W., Ritchie, M.D. *"Influence of tissue context on gene prioritization for predicted transcriptome-wide association studies"*, *Pacific Symposium on Biocomputing* 24:296-307 (2018) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6417797/
13. Cha, E.D.*, **Veturi, Y.*,** Agarwal, C., Patel, A., Arbabshirani, M.R., Pendergrass, S.A. *"Using Adipose Measures from Health Care Provider-Based Imaging Data for Discovery"*, *Journal of Obesity* 10.1155/2018/3253096 (2018) https://www.hindawi.com/journals/jobe/2018/3253096/
14. Verma, S.S., Josyula, N., Verma, A., Zhang, X., **Veturi, Y**., Mukherjee, S., Gottesman O., Dewey, F.E., Hartzel, D.N., Lavage, D.R., Leader, J., Kirchner, H.L., Ritchie, M.D., Pendergrass, S.A., *"Phenome-Wide Gene Burden Analysis to Identify DrugBank Genes Associated with Patient Diagnoses", Scientific Reports* 8(1), 4624 (2018) https://www.nature.com/articles/s41598-018-22834-4
15. Verma, S. S., Lucas, A., Zhang, X., **Veturi, Y**., Dudek, S., Li, B., Li, R., Kim, D., Ritchie M. D. *"Collective feature selection to identify important variables for epistatic interactions" BioData Mining* 11(5) (2018) https://doi.org/10.1186/s13040-018-0168-6
16. **Veturi, Y**., and Ritchie, M.D. "*How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures?", Pacific Symposium in Biocomputing* 23:228-239 (2018) https://pubmed.ncbi.nlm.nih.gov/29218884/
17. Li, B., Verma, A., Verma, S., **Veturi, Y**., Bradford Y., and Ritchie, M.D., *"Evaluation of PrediXcan for GWAS prioritization and gene expression prediction", Pacific Symposium in Biocomputing* 23:448-459 (2018) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5749400/
18. Vazquez AI, **Veturi, Y**., Behring, M., Shrestha, S., Kirst, M., Resende Jr., M.F.R., de los Campos, G., *"Increased Proportion of Variance Explained and Prediction Accuracy of Survival of Breast Cancer with use of Whole Genome Multi–Omic Profiles", Genetics* 203(3) (2016) https://www.genetics.org/content/genetics/203/3/1425.full.pdf
19. de los Campos, G., **Veturi, Y.,** Vazquez, A I., Lehermeier, C., and Pérez–Rodríguez, P., *"Incorporating Genetic Heterogeneity in Whole Genome Regressions Using Interactions", Journal of Agricultural, Biological, and Environmental Statistics* 20(4) pp. 467–490 (2015) 10.1007/s13253–015–0222–5 **Meritorious Paper in JABES by an IBS Member** for 2015–2016.
20. Vazquez, A.I., Klimentidis, Y.C., Dhurandhar, E.J., **Veturi, Y.**, Perez–Rodriguez, P., *"Assessment of Whole Genome Regression for Type II Diabetes"*, *PLOS One*, 10(4):e0123818 (2015) DOI: 10.1371/journal.pone.0123818
21. Miller, S., Perez–Rodriguez, P., **Veturi, Y.**, Simianer, H., de los Campos, G., *"Effectiveness of Shrinkage and Variable Selection Methods for the Prediction of Complex Human Traits Using Data from Distantly Related Individuals", Annals of Human Genetics* 79(2), 122–135 (2015) DOI: 10.1111/ahg.12099
22. **Veturi, Y.**, Kump, K., Walsh, W., Ott, O., Poland, J., Kolkman, J.M., Balint–Kurti, P.J., Holland, J.B., and Wisser, R.J., *"Multivariate Mixed Linear Model Analysis of Longitudinal Data: An Information–Rich Statistical Technique for Analyzing Plant Disease Resistance"*. Phytopathology 102(11), 1016–1025 (2012) DOI:10.1094/PHYTO-10-11-0268 "**Top Papers of the Month**" in *Phytopathology* for Nov 2012.
23. D'Souza, M.J., Alabed, G.J., Wheatley, J.M., Roberts, N., **Veturi, Y.**, Bi, X., Continisio, C.H., *"A Database developed from Information Extracted from Chemotherapy Drug Package Inserts to Enhance Future Prescriptions"*, *Conference on Computer Vision and Pattern Recognition Workshops IEEE Computer Society*, 219–226 (2011) PMID:25302340 PMCID:pmc4187114

Manuscripts Under Review/In preparation

1. Wen, J., Nasrallah, I.M., Abdulkadir, A., Satterthwaite, T.D., Erus, G., Robert-Fitzgerald, T., Singh, S., Sotiras, A., Boquet-Pujadas, A., Yang, Z., Mamourian, E., Doshi, J., Cui, Y., Srinivasan, D., Bergman, M., Bao, J., **Veturi, Y**. … and Christos Davatzikos[1*], for the iSTAGING, the BLSA, the BIOCARD, the PHENOM, the ADNI studies, and the AI4AD consortium "*Mega-analysis of brain structural covariance, genetics, and clinical phenotypes*" - https://www.researchsquare.com/article/rs-1503113/v1 Under review in *Science Advances*
2. Li, B., **Veturi, Y.,** Lucas, A., Bradford, Y., Verma, S., Verma, A., Park, J., Wei, W., Feng, Q., Namjou, B., Kiryluk, K., Kullo, I., Luo, Y., Regeneron Genetics Center, Pividori, M., Im, H.K., Greene, C., Ritchie, M.D. *"The gene-trait landscape in multi-ancestry electronic health record (EHR)-linked biobank data"* – https://www.medrxiv.org/content/10.1101/2021.10.21.21265225v1 In preparation for *American Journal of Human Genetics*
3. Singhal, P., **Veturi, Y.,** Dudek, S., Lucas, A., Frase, A., Schrodi, S., Fasel, D., Weng, C., Pendergrass, R., Schaid, D.J., Kullo, I.J., Dikilitas, O., Sleiman, P., Hakonarson, H., Moore, J., Williams, S., Ritchie, M.D., and Verma, S.S "*Largest genome-wide long range interaction study identifies interchromosomal associations across 5 complex diseases in UK Biobank and eMERGE datasets*" – In preparation for *American Journal for Human Genetics*

Honors and Awards

1. Epstein Award postdoctoral finalist (18/700), American Society of Human Genetics (ASHG) 2022
2. Reviewers' choice designation, ASHG 2021
3. Reviewers' choice designation, ASHG 2019
4. Best abstract award, Pharmacogenomics Research Network session, ASHG 2017
5. USDA travel grant, Gordon Research Conference for Quantitative Genetics and Genomics, Italy (One of 11 abstracts selected for a short talk at the 2015 Gordon Research Seminar.)
6. Membership, Phi Kappa Phi Honor Society, University of Alabama at Birmingham, AL, 2015
7. Seng-jaw Soong award for excellence in Biostatistics and Bioinformatics, Comprehensive Cancer Center, University of Alabama at Birmingham, AL, 2014
8. Caroline P. Ireland Travel Scholarship, University of Alabama at Birmingham. Attended *Statistical Learning and Data Mining III – Trevor Hastie and Robert Tibshirani*, Stanford University, San Francisco, CA (Mar 20 – 21, 2014)
9. Graduate Fellowship, University of Alabama at Birmingham, 2012-2013
10. The University of Delaware Professional Development Award for Graduate Students, 2012
11. Best student poster award, 2nd Annual University of Delaware Bioinformatics and Systems Biology Research Symposium, 2012
12. Tuition scholarship, 16th Annual Summer Institute in Statistical Genetics, University of Washington, Seattle, WA, 2012
13. Travel grant, 23rd Annual Conference on Applied Statistics in Agriculture, 2010

Book chapter

1. McCauley, J., **Veturi, Y.**, Verma, S.S., and Ritchie, M.D. *Genome-wide Association Studies*, "Genetic Analysis of Complex Disease", 3rd edition, Wiley https://www.wiley.com/en-us/Genetic+Analysis+of+Complex+Disease%2C+3rd+Edition-p-9781118123911

Poster Presentations

1. **Veturi, Y.,** Davatzikos, C., and Ritchie, M.D. *"Neuroimaging-guided functional variant multi-ancestry PheWAS using electronic health records from UK Biobank"*, ASHG (virtual) 2021, Oct 18-22, 2021, Pacific Symposium in Biocomputing, Big Island HI, Jan 3-7, 2022

2. Verma, S. S., Singhal, P., Lucas, A., **Veturi, Y.,** Weng, C., Pendergrass, S., Kullo, I.J., Schrodi, S.J., Fasel, D., Schaid, D.J., Dikilitas, O., Sleiman, P., Hakonarson, H., Ritchie, M.D., *"Genome-wide inter-chromosomal epistatic associations identified across complex diseases in the ~300,000 participants from eMERGE and UK Biobank"*, ASHG (virtual) 2021, Oct 18-22, 2021
3. **Veturi, Y.**, Lucas, A., Bradford, Y., Dudek, S., Theusch, E., Verma, A., Miller, J.E., Kullo, I., Hakonarson, H., Sleiman, P., Schaid, D., Stein, C.M., Velez Edwards, D.R., Feng, Q., Wei, Q., Medina, M.W., Krauss, R., Hoffmann, T.J., Risch, N., Voight, B.F., Rader, D.J., Ritchie, M.D. *"Unified framework identifies novel replicating links between plasma lipids, tissue-specific gene expression and phenome-wide disease outcomes across large-scale cohorts"*, ASHG (virtual) 2020, Oct 27-30, 2020
4. McGuigan, J., Moore, J., **Veturi, Y.,** Li, B., Verma, A., Le, T., Fu, W., Haas, D.W., Ritchie, M.D., Hall, M.A., "*Automated machine learning for rare variant analysis of response to antiretroviral therapy in persons living with HIV"*, ASHG (virtual) 2020, Oct 27-30, 2020
5. **Veturi, Y.**, Lucas, A., Bradford, Y., Hoffmann, T., Theusch, E., Miller, J.E., Hakonarson, H., Kullo, I., Sleiman, P., Schaid, D., Wei, W., Stein, C.M., Velez Edwards, D.R., Feng, Q., Medina, M., Krauss, R., Risch, N., Ritchie, M.D. *"Integrative transcriptome-wide association framework identifies many novel replicating genes for lipid traits"*, ASHG 2019, Houston, TX, Oct 15-19, 2019; American Medical Informatics Association, Houston, TX, Mar 23-26, 2019
6. Li, B., **Veturi, Y**., Bradford, Y., Verma, S., Verma, A., Haas, D.W., Ritchie, M.D., *"Enhanced transcriptome-wide analytic framework identifies novel associations with metabolic and virologic traits in HIV-positive adults"*, ASHG 2019, Houston, TX, Oct 15-19, 2019
7. Zhang X.*, **Veturi, Y.***, Verma, S.S., Bone, W., Verma, A., Lucas, A., Hebbring, S., Denny, D.C., Stanaway, I.B., Jarvik, G.P., Crosslin, D., Larson, E.B., Rasmussen-Torvik, L., Pendergrass, S.A., Smoller, J.W., Hakonarson H., Sleiman P., Weng C., Fasel D., Wei W., Kullo, I., Schaid, D. Chung, W.K., and Ritchie, M.D. *"Identifying Potential Pleiotropy across Cardiovascular and Neurological Diseases in the eMERGE network"*, Penn Genetics Retreat, University of Pennsylvania, Philadelphia, PA, Sept 20, 2018; MidAtlantic Bioinformatics Conference, Philadelphia, PA, Oct 29, 2018 and Pacific Symposium for Biocomputing, Big Island HI, Jan 4-7, 2019; Pharmacogenomics Research Network Symposium, San Diego, CA, Oct 16, 2018 (**Won Honorable mention**)
8. **Veturi, Y.**, Haas, D.W., Bradford, Y., Verma, A., Verma, S.S., Eron, J.J., Gulick, R.M., Riddler, S.A., Sax, P.E., Daar, E.S., Morse, G.D., Acosta, E.P., and Ritchie, M.D. and the AIDS Clinical Trials Group *"Rare variant analysis for Efavirenz Central Nervous System Side Effects Using Whole Exome Sequencing Data"*, ASHG, San Diego, CA, Oct 16-20, 2018
9. **Veturi, Y.**, Hoffman, T., Theusch, E., Medina, M., Risch, N., Krauss, R., Ritchie, M.D. *"Identification of pathways strongly associated with lipid traits in mice and humans using gene expression and human GWAS data"*, Pharmacogenomics Research Network Symposium, San Diego, CA, Oct 16, 2018
10. Li, B., **Veturi, Y.**, Bradford, Y., Verma S.S., Verma, A., Lucas, A.M., Haas, D.W., Ritchie, M.D. *"Evaluation of PrediXcan Capabilities to Predict Gene Expression Levels and Prioritize Variant-Based Associations Using Datasets with Varied Population Background"*, American Medical Informatics Association, San Francisco, CA, Nov 3-7, 2018
11. **Veturi, Y.**, and Ritchie, M.D. *"Comparison of power of summary-based methods for identifying expression-trait associations"*, ASHG 2017, Orlando, FL, Oct 17-21, 2017
12. **Veturi, Y.**, and Ritchie, M.D. *"TWAS identification of gene-trait associations under varying genetic architectures - An examination using simulated and real data"*, Pharmacogenomics Research Network Symposium (PGRN Hub), Orlando FL, Oct 19, 2017
13. Verma, S. S., Lucas, A., Zhang, X., **Veturi, Y.**, Dudek, S., Li, B., Li, R., Kim, D., Ritchie M.D. *"Collective feature selection to identify important variables for epistatic interactions"*, 7th Annual Translational Bioinformatics in Precision Medicine Conference, Los Angeles, CA, Sep 29 - Oct 1, 2017 and ASHG 2017, Orlando, FL, Oct 17-21, 2017
14. **Veturi Y.**, Cha E.D., Arbabshirani M., Pendergrass S.A., *"Using Adipose Measures from Electronic Health Record Imaging Data for Discovery"*, 7th Annual Translational Bioinformatics in Precision

Medicine Conference, Los Angeles, CA, Sep 29-Oct 1, 2017 and ASHG 2017, Orlando, FL, Oct 17-21, 2017

15. **Veturi, Y.**, Yi, N., Huang, W., Vazquez A.I., de los Campos, G. *"Quantifying Effect Heterogeneity between Ethnic Groups and Sexes for Complex Human Traits"*, Grand Opening of BioEngineering Facility, Michigan State University, East Lansing, MI, Oct 27, 2016
16. **Veturi, Y.**, and de los Campos, G. *"Modeling Genetic Heterogeneity in Structured Human Populations using Random Effects Interactions"*, 2016 Graduate Student Research Day, UAB, Birmingham AL, Mar 10, 2016, International Biometric Conference, Victoria British Columbia, Canada, Jul 10-15, 2016, and Joint Statistical Meeting, Chicago, IL, Jul 30-Aug 4, 2016
17. de los Campos, G, **Veturi, Y.**, Vazquez, A I., Lehermeier, C., and Pérez–Rodríguez, P *"Incorporating Genetic Heterogeneity in Whole-Genome Regressions using Interactions"*, International Biometric Conference, Victoria British Columbia, Canada, Jul 10-15, 2016
18. A. Vazquez, A. Gonzalez, **Veturi**, **Y.,** G. de los Campos. *"Prediction of Years of Life after Diagnosis of Breast Cancer using Multi-Layer Omic and Clinically Relevant Covariates: Two Studies using METABRIC and TCGA"*, ASHG 2016, Vancouver, British Columbia, Oct 18-22, 2016
19. Vazquez, A.I., **Veturi. Y.,** Lunt S.Y., Behring, M., de los Campos. *"Inquiring Omics Data about Breast Cancer Patient Survival"*, 4th Annual MSU Conference on Women's Health Research, East Lansing, MI, Nov 10, 2015
20. **Veturi, Y.**, and de los Campos, G. *"Whole Genome Regression on Structured Human Populations using Interaction Models"*, 2015 Gordon Research Conference on Quantitative Genetics and Genomics, Lucca, Italy, Feb 22-27, 2015
21. **Veturi. Y.**, Wiener, H., de los Campos, G, Vazquez, A.I. *"Bayesian Models for Prediction of Breast Invasive Carcinoma using Gene Expression Data from The Cancer Genome Atlas"*, UAB Cancer Retreat, Birmingham, AL, Oct 6, 2014
22. Lebron, D., Vazquez, A.I., **Veturi, Y.,** Sorensen, I., Fernandez, J., Bray, M. *"Genetic Variance in BMI Associated with the FTO Gene in Young Adults"*, UAB Summer Research Expo, Birmingham, AL, Jul 24, 2014
23. **Veturi. Y.**, Wiener, H., Vazquez, A.I. *"Analysis of Breast Invasive Carcinoma using RNA–Seq Data from the Cancer Genome Atlas"*, UAB School of Public Health Research Day, Birmingham, AL, Apr 10, 2014
24. Wisser, R.J., De Leon, N., Flint–Garcia, S., Holland, J.B., Lauter, N., Murray, S., Xu, W., Weldekidan, T., Teixeira, J., **Veturi, Y.**, Kumar, N., Rogers, K., Kanchi, R., Peddicord, L., Lopez, M., and Sood, S. *"Maize ATLAS Project: Implementation of Experimental Framework for Studying Adaptation"*. Visions for a Sustainable Planet, Cincinnati, OH, Oct 24, 2012
25. **Veturi, Y.**, Wisser, R.J. *"Development of a Statistical Framework for Association Mapping in Recurrently Selected Populations"*. 2nd Annual University of Delaware Bioinformatics and Systems Biology Research Symposium, Newark, DE, May 24, 2012 and 54th Annual Maize Genetics, Portland, OR, Mar 15-18, 2012
26. Teixeira, J., De Leon, N., Flint–Garcia, S., Holland, J.B., Lauter, N., Murray S., Xu, W., Hessel, D., Weldekidan, T., Kleintop, A., **Veturi, Y.**, Wisser, R.J. *"A Decade of Tropical to Temperate Maize Adaptation Reveals a Potential Mechanism for Broad Adaptation"*, 54th Annual Maize Genetics Conference, Portland, OR, Mar 15-18, 2012
27. **Veturi, Y.**, Wisser, R.J. *"Characterizing Genetic Architecture in Recurrently Selected Populations – A New Estimator for Coancestry"*, International Plant and Animal Genome XX, San Diego, CA, Jan 14-18, 2012
28. Teixeira, J., **Veturi, Y.**, Rogers, K., Wisser, R.J. *"Use of RAS (Response to Artificial Selection) Mapping as an Experimental Approach for Characterizing the Genetic Architecture of Adaptation"*, International Plant and Animal Genome XX, San Diego, CA, Jan 14-18, 2012
29. Roy, S., Jackson, M., **Veturi, Y.**, Turgeon, G., Wisser, R.J. *"Efficient Workflows to Study Natural Genetic Variation in Fungal Populations"*, University of Delaware Research Foundation (UDRF) poster session, Newark, DE, Nov 16, 2011

30. **Veturi, Y.**, Wisser, R.J., Holland, J.B. *"Statistical Framework for Association Mapping in Recurrently Selected Populations"*, 23rd Annual Conference on Applied Statistics in Agriculture, Kansas State University, Manhattan, KS, May 1-5, 2011
31. **Veturi, Y.**, Wisser, R.J., Walsh, E., Poland, J., Kolkman, J.M., Nelson, R.J., Ott, O., Kump, K., Balint–Kurti, P.J., and Holland, J.B. *"Longitudinal Mixed Model Analysis of Plant Disease Resistance Data: An Examination of Northern Leaf Blight of Maize"*, Plant and Soil Sciences Research Symposium, University of Delaware, Newark, DE, May 5, 2010
32. Wisser, R. J., **Veturi**, **Y.**, Walsh, E., Poland, J., Kolkman, J.M., Nelson, R.J., Ott, O., Kump, K., Balint–Kurti P.J., and Holland, J.B. *"Development of an Efficient Genetic Framework for Studying Genomic Responses to Artificial Selection"*, 2nd International Symposium on Genomics of Plant Genetic Resources, Bologna, Italy, Apr 24-27, 2010

Invited Seminars

1. **Veturi, Y.**, et al and Ritchie, M.D *"Integrating genomics with Electronic Health Records to identify pleiotropy",* School of Biological Sciences, Georgia Tech University, Atlanta, GA, Jan 30, 2022
2. **Veturi, Y.**, et al and Ritchie, M.D *"Integrating genomics with Electronic Health Records to identify pleiotropy",* Department of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI, Feb 10, 2022
3. **Veturi, Y.**, et al and Ritchie, M.D *"Integrating genomics with Electronic Health Records to identify pleiotropy"*, Department of Epidemiology and Biostatistics, Michigan State University, East Lansing, MI, Mar 2, 2022
4. **Veturi, Y.**, et al and Ritchie, M.D *"Methods to integrate multi-omic data with Electronic Health Records across heterogeneous populations"*, Structural Biology and Department of Biomedical Sciences, St. Jude's Children's Research Hospital, Memphis, TN, Nov 13, 2021
5. **Veturi, Y.**, et al and Ritchie, M.D *"Integrative framework links plasma lipid to diseases from Electronic Health Records in large-scale cohorts"*, Institute for Quantitative Heath Science and Engineering, Michigan State University, East Lansing, MI, Sep 01, 2021
6. **Veturi, Y.**, and de los Campos, G. *"Whole Genome Regression Based Methods for Analyzing Effect Heterogeneity in Breeding and Human Populations"*, Department of Statistics and Department of Genetics, Development and Cell Biology, Iowa State University, Ames IA, Mar 10, 2016
7. **Veturi, Y.**, and de los Campos, G. *"Whole Genome Regression Based Methods for Analyzing Effect Heterogeneity in Ethnically Diverse Human Populations"*, Department of Biomedical and Translational Informatics, Geisinger and Department of Statistics, Penn State University, State College PA, Mar 17-18, 2016

Session Co-chair

Scalable Applications of clinical risk utility and prediction (SALUD) https://psb.stanford.edu/callfor/papers/salud/, Pacific Symposium on Biocomputing, Big Island, Hawai'i, January 2023

Oral Presentations

1. **Veturi, Y.**, and Ritchie, M.D *"Neuroimaging-guided PheWAS using electronic health records from UK Biobank and eMERGE cohorts yield novel associations between brain imaging and disease outcomes"*, accepted for **platform presentation at ASHG 2022**
2. **Veturi, Y.**, and Ritchie, M.D *"Integrating neuroimaging, genomics and diseases from Electronic Health Records to identify pleiotropy"*, Penn Genetics Research Talks, Philadelphia, PA, Dec 3, 2021
3. **Veturi, Y.**, and Ritchie, M.D *"Integrative transcriptome-wide association framework identifies many novel replicating genes for lipid traits"*, American Medical Informatics Association, Houston, TX, Mar 23-26, 2020 (canceled due to COVID-19)

4. **Veturi, Y.**, and Ritchie, M.D *"Integrative transcriptome-wide association framework identifies many novel replicating genes for lipid traits"*, Penn Genetics Research Talks, Philadelphia, PA, Dec 23, 2019
5. Zhang X*, **Veturi, Y.***, and Ritchie, M.D. *"Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network".* Platform Presentation, Pacific Symposium in Biocomputing – Big Island, HI, Jan 4-7, 2019
6. Zhang X*, **Veturi, Y.***, and Ritchie, M.D. *"Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network".* eMERGE Network Steering Committee Meeting, Rockville, MD, Oct 21, 2018
7. **Veturi, Y.**, and Ritchie, M.D. *"How powerful are summary-based methods for identifying expression-trait associations under different genetic architectures?"*, Platform Presentation, Pacific Symposium in Biocomputing – Big Island, HI, Jan 3-7, 2018
8. **Veturi, Y.**, and Ritchie, M.D. *"Power Analysis of summary-based methods for identifying expression-trait associations"*, Platform presentation, 7th Annual Translational Bioinformatics in Precision Medicine Conference, Los Angeles, CA, Sep 29-Oct 1, 2017
9. **Veturi, Y.**, and de los Campos, G. *"Genetic Analysis of Data from Structured Populations"*. 2015 Gordon Research Seminar on Quantitative Genetics and Genomics, Lucca, Italy, Feb 21 – 22, 2015
10. **Veturi, Y.**, Ferragina, A. *"Bayesian Approaches for Variable Selection and Shrinkage: An Investigation of Milk Composition Traits using Infrared Spectroscopy Analysis"*. Department of Biostatistics, UAB, Birmingham, AL, Feb 28, 2012
11. **Veturi Y.**, Vazquez A.I., Bray, M., de los Campos, G. *"Genomic Heritability and Likelihood Estimability using the Genomic Best Linear Unbiased Predictor"*. UAB Graduate Student Research Day, Birmingham, AL, Mar 3, 2014
12. **Veturi, Y.**, Wisser, R.J., *"Development of a Statistical Framework for Association Mapping in Recurrently Selected Populations"*. 2nd Annual University of Delaware Bioinformatics and Systems Biology Research Symposium, Newark, DE, May 24, 2012

Teaching and Mentoring Experience

University of Pennsylvania, Perelman School of Medicine, Department of Genetics

Co-instructor — Summer 2018

- **Human Genetics** (graduate level): Co-taught the crash course with Dr. Marylyn Ritchie (Jun-Jul 2018).

Mentor — Summer 2021

- Anni Moore, 1st year PhD student, Department of Genetics
- **Virtual Summer Research Program** (American Physician Scientists Association): Mentored Ms. Sumaya Hardi, Cornell University (sophomore), on her summer project integrating genetics, neuroimaging and cardiometabolic diseases. Sumaya won the Penn Center for Global Genomics and Health Equity Summer Student Intern Funding Award ($1000) for this summer program.

Michigan State University, Department of Epidemiology and Biostatistics

Guest lecturer — Fall 2016

- **Statistical Genetics** (graduate level): Conducted a one-hour *"Problem solving session on Bayesian Analysis Using Pedigree Data"* (Oct 25, 2016).
- **Analysis and Prediction of Complex Traits** (graduate level): Gave a three-hour lecture + lab using R on *"Genome Wide Association Studies in Humans"* (July 13, 2016).

Michigan State University, Department of Statistics and Probability

Guest lecturer — Fall 2016

- **Bayesian Statistical Methods** (undergraduate level): Gave a one-hour lecture on *"Ordinary Least Squares Estimation and the Normal Model"* (Oct 19, 2016).

University of Alabama at Birmingham, Department of Biostatistics
Mentor Summer 2013

- **Summer Internship for Training in Statistical Genetics**: Mentored Ms. Dayanara Lebron, Universidad Metropolitana, San Juan, PR (Summer 2013) on her project *"Analysis of genetic variance in BMI associated with the FTO gene in young adults using the TIGER dataset"*. Currently Bioinformatics Scientist at Tecan (MS Statistics from UC Davis).

North Carolina State University, Department of Statistics
Graduate Teaching Assistant Fall 2007-Summer 2008

- **SIBS-Summer Institute for training in Biostatistics**: NCSU and Duke Clinical Research Institute collaboration. Teaching assistant for high-school students interested in pursuing a career in Biostatistics, Summer 2008.
- **Introduction to Mathematical Statistics** (undergraduate level): Grading, holding problem-solving sessions, Spring 2008.
- **Experimental Statistics for Biological Sciences** (graduate level): Grading, holding problem-solving sessions, Fall 2007.

Academic service (referee)

- Heredity, Frontiers in Genetics, Frontiers in Cardiovascular Medicine, International Journal of Obesity, G3: Genes, Genomes, Genetics, Briefings in Bioinformatics, GigaScience, Pacific Symposium on Biocomputing 2019 "Pattern Recognition in Biomedical Data: Challenges in putting big data to work" 2017-2019, Conference proceedings for Applied Statistics in Agriculture, Kansas State University, 2011.

Professional Membership

- American Society for Human Genetics, 2016-
- International Biometric Society, 2016-2017
- American Statistical Association, 2007-2016
- Association for Women in Science, 2012-2014
- Genetics Society of America, 2011-

References

1. **Marylyn D. Ritchie, Ph.D.**
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