

## Mahlet G. Tadesse

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### EMPLOYMENT

- 2020 – present Chair, Department of Mathematics & Statistics, Georgetown University.
- 2016 – present Professor, Department of Mathematics & Statistics, Georgetown University.
- 2010 – 2016 Associate Professor, Department of Mathematics & Statistics, Georgetown University.
- 2012 – 2016 Adjunct Associate Professor, Department of Epidemiology, Harvard University.
- 2011 – 2012 Visiting Associate Professor, Department of Biostatistics, Harvard University;  
Department of Biostatistics & Computational Biology, Dana-Farber Cancer Institute.
- 2007 – 2010 Assistant Professor, Department of Mathematics, Georgetown University.
- 2004 – 2007 Assistant Professor, Department of Biostatistics & Epidemiology, University of Pennsylvania.
- 2002 – 2004 Research Assistant Professor, Department of Statistics, Texas A&M University.

### EDUCATION

- 2002 Sc.D. Biostatistics Harvard University
- 2000 M.S. Biostatistics Harvard University
- 1998 B.S. Mathematics University of the District of Columbia

### HONORS AND AWARDS

- Myrto Lefkopoulou Distinguished Lectureship, Harvard University, 2016.
- Fellow, American Statistical Association (ASA), elected 2013.
- Yerby Visiting Scholar, Harvard University, 2012.
- Elected Member, International Statistical Institute (ISI), elected 2006.
- Byar Young Investigator Award from the Biometric Section of ASA, 2004.
- ENAR Distinguished Student Paper Award from the International Biometric Society, 2002.
- Howard Hughes Medical Institute (HHMI) Predoctoral Fellow, 1999 – 2002.

**SELECTED PUBLICATIONS**

- **TADESSE, M.G.**, SHA, N. and VANNUCCI, M. (2005) Bayesian variable selection in clustering high-dimensional data. *Journal of the American Statistical Association*, 100: 602-617.
- KIM, S., **TADESSE, M.G.** and VANNUCCI, M. (2006) Variable selection in clustering via Dirichlet process mixture models. *Biometrika*, 93: 877-893.
- MARKOV, V., KUSUMI, K., **TADESSE, M.G.**, WILLIAM, D.A., HALL, D.M., LOUNEV, V., CARLTON, A., LEONARD, J., COHEN, R.I., RAPPAPORT, E.F. and SAITTA, B. (2007) Identification of cord blood-derived mesenchymal stem/stromal cell populations with distinct growth kinetics, differentiation potentials, and gene expression profiles. *Stem Cells and Development*, 16: 53-73.
- MONNI, S. and **TADESSE, M.G.** (2009) A stochastic partitioning method to associate high-dimensional responses and covariates (with discussion). *Bayesian Analysis*, 4: 413-436.
- TSAI, T-H., **TADESSE, M.G.**, DI POTO, C., PANNELL, L.K., MECHREF, Y., WANG, Y. and RESSOM, H.W. (2013) Multi-profile Bayesian alignment model for LC-MS data analysis with integration of internal standards. *Bioinformatics*, 29: 2774-2780.
- GELAYE, B., **TADESSE, M.G.**, WILLIAMS, M.A., FANN, J.R., STOEP, A.V. and ZHOU, X-H. A. (2014) Assessing validity of a depression screening instrument in the absence of a gold standard. *Annals of Epidemiology*, 24: 527-531.
- DENIS, M., ENQUOBAHRIE, D.A., **TADESSE, M.G.**, GELAYE, B., SANCHEZ, S.E., SALAZAR, M., ANANTH, M. and WILLIAMS, M.A. (2014) Placental genome and maternal-placental genetic interactions: A genome-wide and candidate gene association study of placental abruption. *PLoS ONE*, 9: e116346.
- GELAYE, B., **TADESSE, M.G.**, LOHSONTHORN, V., LERTMEHARIT, S., PENSUKSAN, W.C., SANCHEZ, S.E., LEMMA, S., BERHANE, Y., VÉLEZ, J.C., BARBOSA, C., ANDERADE, A. and WILLIAMS, M.A. (2015) Psychometric properties and factor structure of the general health questionnaire in a multi-national study of young adults. *Journal of Affective Disorders*, 187: 197-202.
- LEE, K.H., **TADESSE, M.G.**, BACCARELLI, A.A, SCHWARTZ, J. and COULL, B.A. (2017) Multivariate Bayesian variable selection exploiting dependence structure among outcomes: Application to air pollution effects on DNA methylation. *Biometrics*, 73: 232-241.
- VARGHESE, R.S., ZHOU, Y., BAREFOOT, M., CHEN, Y., DI POTO, C., BALLA, A.K., OLIVER, E., SHERIF, Z.A., KUMAR, D., KROEMER, A.H., **TADESSE, M.G.** and RESSOM, H.W. (2020) Identification of miRNA-mRNA associations in hepatocellular carcinoma using hierarchical integrative model. *BMC Medical Genomics*, 13: 56.