Grace Yoon   **Mathematical Statistician**

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CONTACT
INFORMATION

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EMPLOYMENT

Mathematical Statistician, USDA NASS   Sep 2020 - Present
Postdoctoral Research Associate, Biostatistics, Bioinformatics, Nutrition and Cancer Training Program, Texas A&M University   Sep 2017 - Aug 2020
     P.I. and mentors: Drs. Raymond J. Carroll, Robert S. Chapkin and Irina Gaynanova
Assistant Lecturer, Department of Statistics, Texas A&M University
     STAT 302: Statistical Methods ($\sim$100 students)   Fall 2019
Researcher, Department of Preventive Medicine, Northwestern University
                                  Apr 2015 - Aug 2017
Graduate Student Statistical Consultant, Feinberg School of Medicine, Northwestern University   Jun 2014
Graduate Teaching Assistant, Department of Statistics, Northwestern University
                                Fall 2013 - Spring 2016

EDUCATION

Northwestern University, Evanston, IL, USA
     Ph.D. in Statistics   Sep 2017
         Advisors: Drs. Wenxin Jiang and Lei Liu
         Dissertation: Topics of Variable Selection in Biomedical Data Mining
     M.S. in Statistics   Jun 2014
Yonsei University, Seoul, South Korea
     Graduate coursework in Applied Statistics   Mar 2011 - Jun 2012
     B.S. in Mathematics, minor in Applied Statistics   Feb 2011
         GPA: 4.15 out of 4.3 (*Graduated with high honors*)

AWARDS AND
HONORS

ENAR Regional Advisory Board's (RAB) Poster Award   Mar 2019
     ENAR (Eastern North American Region) Spring Meeting
Summer Institute Scholarship   Jul 2016
     Department of Biostatistics, University of Washington
Student Poster Honorable Mention Award   Oct 2015
     International Chinese Statistical Association (ICSA) Midwest Chapter Meeting
National Science & Technology Scholarship, Korea Student Aid Foundation
     Full-tuition scholarship for all 8 semesters   Spring 2007 - Fall 2010

PUBLICATIONS

Peer-reviewed manuscripts

- **Yoon G.**, Carroll RJ. and Gaynanova I. Sparse semiparametric canonical correlation analysis for data of mixed types. *Biometrika*, 107(3): 609-625.

- **Yoon G.**, Gaynanova I. and Müller C. (2019) Microbial networks in SPRING: Semiparametric rank-based correlation and partial correlation estimation for quantitative microbiome data. *Frontiers in Genetics*, 10:516.

- **Yoon G.**, Jiang W., Liu L. and Shih YCT. (2019) Simple quasi-Bayesian approach for modeling mean medical costs. *International Journal of Biostatistics*.

- **Yoon G.**, Zheng Y., Zhang Z., Zhang H., Gao T., Joyce B., Zhang W., Baccarelli A., Jiang W., Schwartz J., Vokonas P., Hou L. and Liu L. (2017). Ultra-high Dimensional Variable Selection with Application to Normative Aging Study: DNA Methylation and Metabolic Syndrome. *BMC Bioinformatics*, 18:156

- Han H., Davidson LA., Fan YY., Goldsby J.,**Yoon G.**, Jin UH., Wright GA., Landrock KK., Weeks BR., Allred CD., Jayaraman A., Ivanov I., Roper J., Safe SH. and Chapkin RS. (2020) Loss of aryl hydrocarbon receptor potentiates FoxM1 signaling to enhance self- renewal of colonic stem and progenitor cells. *EMBO journal*, e104319.

- Nannini DR., Joyce BT., Zheng Y., Gao T., Liu L., **Yoon G.**, Huan T., Ma J., Jacobs DR. Jr., Wilkins J., Ren J., Zhang K., Khan S., Allen NB., Horvath S., Lloyd-Jones DM., Greenland P. and Hou L. (2019). Epigenetic Age Acceleration and Metabolic Syndrome in Coronary Artery Risk Development in Young Adults Study. *Clinical Epigenetics*, 11:160.

- Zhang H., Zheng Y., **Yoon G.**, Zhang Z., Gao T., Joyce B., Zhang W., Schwartz J., Vokonas P., Colicino E., Baccarelli A., Hou L. and Liu L. (2017). Regularized Estimation in Sparse Multivariate Regression with High-dimensional Responses. *Statistical Applications in Genetics and Molecular Biology*, 16(3):159-171.

- Zhang H., Zheng Y., Zhang Z., Gao T., Joyce B., **Yoon G.**, Zhang W., Schwartz J., Just A., Colicino E., Vokonas P., Zhao L., Lv J., Baccarelli A., Hou L. and Liu L. (2016). Estimating and Testing High-dimensional Mediation Effects in Epigenetic Studies. *Bioinformatics*, 32(20): 3150-3154.

Manuscript under review

- **Yoon G.**, Müller C. and Gaynanova I. Fast computation of latent correlations. *arXiv*.

Manuscripts in preparation

- **Yoon G.**, Davidson LA., Goldsby JS., Mullens DA., Ivanov I., Chapkin RS. and Donovan SM. Exfoliated epithelial cell transcriptome reflects both small and large intestinal cell signatures in piglets .

SOFTWARE DEVELOPED	mixedCCA: an R package to perform sparse canonical correlation analysis for data of mixed types: continuous, binary or zero-inflated (truncated continuous), available from github.
	SPRING: an R package to perform Semi-Parametric Rank-based approach for INference in Graphical model, available from github.

CONFERENCES AND TALKS

Invited presentations:

ASA Joint Statistical Meeting, Philadelphia, PA	Aug 2020
CM Statistics, London, UK	Dec 2019

Contributed presentations:

IMS New Researchers Conference, Burnaby, BC, Canada	Jul 2018
ENAR Spring Meeting, Atlanta, GA	Mar 2018
ICSA Applied Statistics Symposium, Chicago, IL	Jun 2017
ASA Joint Statistical Meeting, Chicago, IL	Aug 2016

Contributed posters:

SETCASA poster session, College Station, TX	Apr 2019
ENAR Spring Meeting, Philadelphia, PA	Mar 2019
Bioinformatics and Cancer Symposium, College Station, TX	Sep 2018
ICSA Midwest Chapter Meeting, Mettawa, IL	Oct 2015

ADDITIONAL	NCI Summer Curriculum - Molecular Prevention Course, Rockville, MD	Aug 2018
PROFESSIONAL	NISS Writing Workshop for Junior Researchers, Vancouver, BC, Canada	Jul 2018
DEVELOPMENT	Software Carpentry Workshop (Unix Shell and Version Control with Git), College Station, TX	Mar 2018
	POWER Writing Workshop, College Station, TX	Jan 2018
	High Performance Research Computing Workshop, College Station, TX	Sep 2017
	Summer Institute Statistics for Big Data, University of Washington, Seattle, WA	Jul 2016