IAN S. ARRIAGA MACKENZIE

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EDUCATION

MS   University of Colorado Denver, Statistics   August 2021

BS   University of Colorado Denver, Mathematics   May 2020

INTERESTS

My recent work has been in statistical genetics and ancestry estimation, including optimization, parallel computing, algorithm design, and machine learning.

I enjoy exploring the intersection between big data and computing, particularly in delivering scalable and adaptable solutions to current research questions.

RESEARCH

University of Colorado Anschutz, Katerina Kechris, PhD   2021 to Present
Center for Innovative Design & Analysis
Andrew Monte, MD, PhD, Jack Pattee, PhD
- Gene and variant association testing for liver damage with acetaminophen use, assessing copy number variants within genome.
- Genomic data pre-processing, single and multi-variant models, checking CNVs, analysis of results.

University of Colorado Denver, Audrey Hendricks, PhD   2019 to 2021
Hendricks Research
- Estimation of ancestry in summary genetic data and adjusting allele frequency data to match ancestry of target population
- Genomic data cleaning and merging, sequential quadratic programming, cluster computing and algorithm optimization, Shiny Apps to interactively visualize data, fixation index between populations

University of Colorado Denver, Audrey Hendricks, PhD   2020
Women First Project
Sarah Borengasser, PhD, Chris Gignoux, PhD, Nancy Krebs, MD, Michael Hambidge, MD
- Genome wide association study (GWAS) on birth height in Guatemalan population
- Genomic data pre-processing, correction for kinship (relatedness), linear model with multiple covariates, analysis of results

University of Colorado Anschutz Medical Campus, Greg Kinney, PhD   2019
MS Consulting Course Project
- Cannabis sleep study to assess differences between intoxicated versus unintoxicated subjects in stage N2 sleep
- Electroencephalogram (EEG) analysis, applying Fast Fourier Transforms, signal processing and cleaning, ANOVA

PUBLICATIONS

Arriaga-MacKenzie IS, Matesi G, Chen S, Ronco A, Marker KM, Hall JR, Scherenberg R, Khajeh-Sharafabadi M, Wu Y, Gignoux CR, Null M, Hendricks AE. Summix: A method for detecting and adjusting for population structure in genetic summary data. *American Journal of Human Genetics* **2021** 108, 1270-1282

Monte AA, **Arriaga-MacKenzie IS**, Pattee J, Kaiser S, Willems E, Rumack B, Reynolds K, Dart RC, Heard KJ. Genetic Variants Associated with ALT Elevation from Therapeutic Acetaminophen. (In Progress, 2022)

Borengasser SJ, Murphy J, Null M, Jambal P, Jones KL, Yang IV, Friedman JE, Waldrop SW, Gilley SP, Saint-Cyr M, **Arriaga-MacKenzie IS**, Kemp J, Westcott J, Garces A, Figueroa L, Greally JM, Hambidge MK, Hendricks AE, Krebs NF. Role of a Preconception Maternal Nutrition Supplement and Pre-pregnancy BMI on Infant DNA Methylation at Birth in Guatemalan Mother-Infant Dyads: The Women First Trial. (In Progress, 2022)

TEACHING

University of Colorado Denver   Fall 2019
Learning Assistant, Statistical Theory 3382
- Developed learning activities, assisted students in theory and introductory R coding

University of Colorado Denver   Spring/Fall 2019
Grader, Pre-Calculus

AWARDS

CLAS Outstanding MS Graduate Award   2021
University of Colorado Denver

C.W. Cotterman Award   2021
American Journal of Human Genetics

Undergraduate Research Opportunity Program (UROP) Grant   2019/2020
University of Colorado Denver

Education Through Undergraduate Research and Creative Activities   2019
Work Study Award

University of Colorado Denver

PRESENTATIONS

Presentations

SUM-MIX: A method for detecting and adjusting for population structure in genetic summary data. **Speed Talk**
Joint Statistical Meetings, Virtual

August 2021

SUM-MIX: A method for detecting and adjusting for population structure in genetic summary data.
The Western North American Region of the International Biometric Society, Virtual

June 2021

Poster Presentations

SUM-MIX: A Method to Estimate and Adjust for Ancestry in Genetic Summary Data
American Society of Human Genetics, Virtual

October 2020

Estimation of non-Reference Ancestry Proportions in Genotype Frequency Data, **Selected for Lighting Presentation**
International Genetic Epidemiology Society, Virtual

July 2020

Efficient Estimation of Hidden Ancestry Substructure in Summary Genotype Frequency Data
Research and Creative Activities Symposium, Virtual

May 2020

Estimation of Hidden Ancestry Substructure Using a Least Squares Mixture Model with Summary Genotype Frequency Data
Society for the Advancement of Chicanos/Hispanics and Native Americans in Science, Honolulu HI

November 2019

Efficient Estimation of Hidden Ancestry Structure Using Summary Genotype Frequency Data, **Selected for Lighting Presentation**
International Genetic Epidemiology Society, Houston TX

October 2019

Estimating Hidden Ancestries in Real Data
Research and Creative Activities Symposium, Denver CO

April 2019

PROGRAMMING

R, Bash, Python, Linux, Matlab, SAS, git, Julia, C++, Jupyter, Docker, bedtools, Shiny Apps, Samtools, VCFtools, PLINK, ADMIXTURE, Galaxy, Ingenuity Pathway Analysis, PennCNV

PROFESSIONAL AFFILIATIONS

American Statistical Association (ASA), *Student member*
American Society of Human Genetics (ASHG), *Student member*
International Genetic and Epidemiology Society, *Student member*
The Western North American Region of The International Biometric Society, *Student member*
Society for the Advancement of Chicanos/Hispanics and Native Americans in Science, *Student member*

REFERENCES

Audrey E. Hendricks, PhD, Associate Professor
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