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* August 2021

*structure in genetic summary data.* **Speed Talk**

Joint Statistical Meetings, Virtual

*SUM-MIX: A method for detecting and adjusting for population* June 2021

*structure in genetic summary data.*

The Western North American Region of the International Biometric Society, Virtual

**Poster Presentations**

*SUM-MIX: A Method to Estimate and Adjust for Ancestry in Genetic* October 2020

*Summary Data*

American Society of Human Genetics, Virtual

*Estimation of non-Reference Ancestry Proportions in Genotype* July 2020

*Frequency Data,* **Selected for Lighting Presentation**

International Genetic Epidemiology Society, Virtual

*Efficient Estimation of Hidden Ancestry Substructure in Summary* May 2020

*Genotype Frequency Data*

Research and Creative Activities Symposium, Virtual

*Estimation of Hidden Ancestry Substructure Using a Least Squares* November 2019

*Mixture Model with Summary Genotype Frequency Data*

Society for the Advancement of Chicanos/Hispanics and Native Americans in Science, Honolulu HI

*Efficient Estimation of Hidden Ancestry Structure Using Summary* October 2019

*Genotype Frequency Data,* **Selected for Lighting Presentation**

International Genetic Epidemiology Society, Houston TX

*Estimating Hidden Ancestries in Real Data* April 2019

Research and Creative Activities Symposium, Denver CO

# 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

Mathematical and Statistical Sciences

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**Stephanie A. Santorico, PhD**, Professor

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**Erin E. Austin, PhD**, Assistant Professor

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