Albert Tucci, Ph.D.

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Education

Ph.D. in Bioinformatics, North Carolina State University **2020 – 2025**
Co-advised by Drs. Robert Franks and Jung-Ying Tzeng
Dissertation: *Efforts in Exposing Vulnerable Mechanisms: From Hybrid Seed Development to Alzheimer's Disease Analysis*

M.S. in Biology, East Carolina University **2018 – 2020**
Advised by Dr. John Stiller
Thesis: *Characterizing the Stigma Transcriptome of Leptosiphon jepsonii*

B.S. in Quantitative Biology, University of North Carolina at Chapel Hill **2013 – 2017**

Research Experience

Leveraging statistical and machine learning models to gain insights into biological systems.

- Identified candidate genetic mechanisms underlying hybrid seed development in monkeyflowers using kernel principal component regression with gradient boosting, and ensemble regression tree approaches for gene regulatory network inference. *First author publication available upon request.*
- Contributed to development of penalized regression method for performing copy number variant (CNV) association analysis. *Publication in preparation.*

Development, deployment, and assessment of bioinformatic analysis pipelines.

- Collaboratively developed pipeline for calling CNVs from WGS data provided by the Alzheimer's Disease Sequencing Project. *Co-first author publication available upon request.*
- Assessed comparative advantages and disadvantages of different pipelines for performing CNV association analyses. *First author publication in preparation.*
- Contributed to statistical analysis and result interpretations for project analyzing CNV haplotypes at 17q21.31 as genetic risk factors for progressive supranuclear palsy. *Publication available upon request.*

Genomic data analysis using a wide variety of next generation sequencing (NGS) data types.

- Lead bioinformatician in the Franks Lab in charge of NGS data analyses including (not limited to):
  - Variant calling and nuclear mitochondrial insertion mapping with WGS data.
  - Draft genome annotation including transposons and other repetitive elements.
  - Phylogenetic tree reconstruction and analysis of hybrid seed inviability in *Mimulus cardinalis - lewisii* complex.
- Collaborated with members of the Wan-Ping Lee Lab at the University of Pennsylvania's Perelman School of Medicine in handling and analyzing WGS data from the Alzheimer's Disease Sequencing Project.
  - Calculated relatedness statistics and performed in-group pincipal components analyses.
  - Prepared variant and covariate data upstream of association analyses.
- Assembled, annotated, and analyzed the transcriptome of the *Leptosiphon jepsonii* stigma.
  - Performed *de novo* transcriptome assembly using RNA-seq data.
  - Identified potentially conserved mechanism underlying transient self-incompatibility.
- Led consulting project for the James Holland Lab on a maize landrace resequencing analysis
  - Annotated functional regions and calculated sitewise diversity statistics for variant data.
  - Generated pipeline for performing association analysis upon completion of data collection.

Skills

Technical proficiency working in multiple programming languages and environments.

- R, Python, bash, Julia, MATLAB, SLURM job manager, GitHub, AWS Cloud computing, and more.

Adept communicator of analysis results and interpretation of findings.

- Track record of scientific writing and editing, including operating with LaTeX.
- *Reviewer's choice award* for poster presentation at ASHG 2021 Meeting.
- Presented findings at: Evolution 2023, ASHG 2023, ADSP Review 2024, and more.
- Use of Shiny WebApps to create data exploration dashboards.

Extensive experience operating with popular genomics tools and data repositories.

- STAR, GATK, samtools, bcftools, PLINK, DESeq2, BLAST, MAFFT, bioconda, bioconductor, and many more.
- NCBI GenBank, SRA, JGI and Ensembl genome databases, EMBL-EBI InterPro, and more.

Demonstrated the organization and collaboration skills necessary for thriving in dynamic research environments.

- While concurrently a member of two distinct labs with disparate research interests, I was productive in both labs. Work from both resulted in chapters for my dissertation.

Selected Teaching Experience

Orchestrated instruction session on developing pipelines and create data exploration tools for the Tzeng Lab.

- Workshop incorporated the {targets} pipeline package and app development with Shiny in R.

Taught 3 sections of anatomy and physiology lab at ECU each semester for two years.

- Handled all instruction and grading, and held weekly office hours and review sessions.

Selected Works

Publications

- **Tucci A**, Flores-Vergara MA, Franks RG. Machine Learning Inference of Gene Regulatory Networks in Developing Mimulus Seeds. Plants. 2024; 13(23):3297. *doi: 10.3390/plants13233297*
- Lee W-P*, **Tucci A***, Conery M, et al. Copy number variation identification on 3,800 Alzheimer's disease whole genome sequencing data from the Alzheimer's Disease Sequencing Project. Front Genet. 2021;12:752390. *doi:10.3389/fgene.2021.752390*
- Wang H, Chang TS, Dombroski BA, Cheng P-L, Si Y-Q, **Tucci A**, et al. Copy number variation and haplotype analysis of 17q21.31 reveals increased risk associated with progressive supranuclear palsy and gene expression changes in neuronal cells. Mov Disord. 2025 Mar 8. doi:10.1002/mds.30150doi:10.1002/mds.30150

In Preparation

- **Tucci A**, Wang H, Si Y, Cheng Y, Holloway S, Wang L-S, Schellenberger G, Lee W-P, Tzeng J-Y. Impact of different copy number variant region definitions on copy number variation association analysis with whole genome sequencing data – lessons learned from the Alzheimer's Disease Sequencing Project (ADSP). 2025.
- Si Y, Lu W, Holloway S, Wang H, **Tucci A**, Brucker A, Cheng Y, Wang LS, Schellenberger G, Lee WP, Tzeng JY CNV-profile regression: A new approach for copy number variant association analysis in whole genome sequencing data. bioRxiv. Published online November 25, 2024. doi:10.1101/2024.11.23.624994
- Wang H, Dombroski BA, Cheng P-L, Liu C, Lee WP, Lu W, **Tucci A**, et al. Structural variation detection and association analysis of whole-genome-sequence data from 16,905 Alzheimer's Disease Sequencing Project subjects. medRxiv. Published online September 13, 2023. doi:10.1101/2023.09.13.23295505
- Flores-Vergara MA, Oneal E, **Tucci A**, Honeycutt J, Willis J, Franks RG. Determining the strength and importance of hybrid seed lethality in the speciation process in the *Mimulus cardinalis–lewisii* complex. 2025.
- Flores-Vergara MA, **Tucci A**, Oneal E, Hunt L, Franks RG. Characterizing the medusa ovule mutant in *Mimulus nudatus*. 2025.

Notable Presentations

- **Tucci A**, Flores-Vergara M, and Franks RG, "Gene regulatory network inference in Mimulus hybrid endosperm," Evolution 2023.
- **Tucci A**, Wang H, Si Y, Cheng Y, Wang L-S, Schellenberger G, Tzeng J-Y, and Lee W-P, "Impact of different copy number variant region definitions on copy number variation association analysis with whole genome sequencing data – lessons learned from the alzheimer's disease sequencing project (adsp)," American Society of Human Genetics (ASHG) Annual Meeting 2023.
- **Tucci A**, Tzeng J-Y, Conery M, et al., "Copy number variation identification and association study on 3,800 alzheimer's disease whole genome sequencing data from the alzheimer's disease sequencing project (adsp)," American Society of Human Genetics (ASHG) Meeting 2021, **Reviewer's Choice Award**.

References

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