

Groves Dixon

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SKILLS

Programming Languages: Python, R, UNIX environment

Tools: Pandas, Sklearn, Tidyverse, Ggplot, PostgreSQL, High Performance Computing

Statistics: data visualization, logistic and linear regression, ensemble algorithms, PCA, clustering

Bioinformatics: Next-Generation Sequencing, mapping, variant calling, RNA-seq, methylomics

EXPERIENCE

Health Data Science Fellow, *Insight*, Boston

May 2020 - Present

- Developed a model to forecast and prevent hospital readmissions fitting criteria penalized by the Hospital Readmissions Reduction Program
- Utilized PostgreSQL, Pandas, Natural Language Toolkit, and Random Forests to wrangle structured and unstructured data from thousands of hospital visits to forecast rapid readmissions
- Built a Streamlit web application to assist in readmission reduction strategy development and provide user interface for applying predictive model

Postdoctoral Researcher, *University of Texas*, Austin

August 2018 - May 2020

- Leveraged PCA, correlation network analysis, and regression to synthesize over 1,000 RNA-seq profiles from 36 independent studies, establishing the theory of a general stress response in corals
- Developed a novel method in coral epigenomics, including a bioinformatic pipeline (Python, Unix environment), wetlands protocol, and wrangling of three distinct datasets (using R) for statistical corroboration; the method has since been adopted by two other laboratories
- Mentored an undergraduate computer science major in statistics, data visualization, and bioinformatics, cooperatively initiating and completing a project first-authored by the student

Postdoctoral Researcher, *University of Texas*, Austin

August 2017 - August 2018

- Advanced a novel approach for reconstructing evolutionary histories of sex chromosomes that was adopted by two co-workers and aided in the completion of three peer-reviewed projects
- Presented research and computational methodology at the competitively selected Gordon Research Conference in Ecological and Evolutionary Genomics for over 100 experts in the field
- Designed a bioinformatic pipeline (Python and high-performance computing) for molecular evolution tailored to sequences reconstructed from RNA-seq data; utilized to complete a collaborator's first project as a principal investigator

Graduate research fellow, *University of Texas*, Austin

August 2012 - August 2017

- Constructed the first genomic linkage map based on Next-Generation Sequencing in a reef-building coral, integrating data from a cohort of 400 individuals (Python, R, JoinMap) and establishing anchor points for the first chromosome-level coral reference genome
- Published first-author paper in *Science*, cited by 230 subsequent studies
- Pioneered the field of coral epigenomics using Python and R for data analysis; the laboratory was granted over one million dollars to continue studying the topic

EDUCATION

PhD in Cell and Molecular Biology, *University of Texas*, Austin, TX

2017

MS in Biology, *Western Carolina University*, Cullowhee, NC

2012

BS in Biology, *The University of the South*, Sewanee, TN

2010