MCKENZIE WALKER

Computational Biologist | Lead Computational Engineer | Teaching Assistant
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Summary

BIOLOGICAL SCIENTIST | COMPUTATIONAL ENGINEER | RECENT HARVARD BIOLOGY MASTERS GRAD | I am a driven scientist and programmer with a deep passion for advancing humanity's future at the intersection of biology and technology. As a co-first author published researcher in genomics with 10 publications and more pending peer review, I have gained extensive experience working as Consultant Research Scientist in Genomics and Computational Biology at Mass General Brigham Hospital in dry lab genomics research developing computational tools and pipelines for automated analytics pipelines. I also serve as the Lead Computational Engineer for the INT²GRATE Oncology Consortium with the aim of increasing diverse representation in genomic datasets specifically within rare cancer syndromes. I am self-motivated and fast-learning professional with a track record of independently mastering new skills—such as programming and languages—and consistently delivering high-quality results that exceed baseline requirements. With a strong foundation in both biology and computational sciences, I'm passionate about driving innovation and delivering meaningful contributions to both scientific progress and team success. I'm eager to bring my energy, initiative, and expertise to a new role and available to start immediately.

Experience

Mass General Brigham Hospital — Remote

Consultant Research Scientist - Genomics and Computational Biology — 12/2023 - Present

- Performing integrated analysis of germline and somatic genomic data analysis for the interpretation of genetic variant pathogenicity in selected cancer syndromes
- Enabling the simultaneous assessment of hundreds or thousands of genomic variants within an assessment framework by developing automated assessment pipelines, greatly saving time resource and reducing human error
- Creating automated pipelines and computational and bioinformatic tools for data analysis and processing to increase laboratory efficiency
- Analyzing genomic variants to assess disease origin and pathogencity
- Increasing diverse representation in genomic research by concentrating research on underrepresented global populations and rare diseases
- Modeling data and developing scientific figures for visualization and published scientific figure creation utilizing Python and R
- Preparing manuscripts for publications with both co-first authorship and middle authorship roles
- Developing computational and bioinformatic tools using languages such as Python, R, and JavaScript
- Analyzing genomic data and interpreting genetic variants
- Managing large data using Excel and database management tools such as SQL
- Developing websites including 3D modeling for graphic design to create user facing research products

Harvard University — Boston, Remote

Teaching Assistant (Introduction to Genomics) — 01/2024 - Present

- Assisting in teaching Introduction to Genomics Course for both graduate and undergraduate students
- Grading exams, essays, and quizzes over diverse and advanced genomics concepts
- Guiding students to become better authors by counseling them on best practice for scientific writing
- Exhibiting mastery level of course content to allow for teaching assistance with course material
- Utilizing thorough understanding of genomics from scientific and multidisciplinary perspectives
- Communicating with students regarding course content, genomics concepts, and course policies and procedures

INT²GRATE Oncology Consortium — Remote

Lead Computational Engineer and Senior Developer — 01/2023 - Present

- Automating pipelines for research workflows using Python
- Developing computational and bioinformatic tools and programs to assess large datasets
- Managing and analyzing large databases using statistics across various data strata
- Deriving scientifically important insights from large data in the context of cancer genomics
- Participating in cross institutional collaboration to increase global diversity in genomics and access to genomic insights
- Analyzing genomic data and interpreting genetic variants such as in the context of pathogenecity
- Preparing manuscripts for publication

Harvard University — Remote

Faculty Aide — 07/2024 - 12/2024

- Performing integrated germline and tumor genomics research in rare cancer syndromes utilizing computational tools
- Implementing computational biology practices performing research in the context of genomics
- Developing bioinformatic tools such as programs for genomic data management and interpretation
- Developing public facing, web based research tools to aid interaction with research product

Experience

Mass General Brigham Hospital
Remote

Research Trainee
08/2022 - 12/2023

- Using computational biology practices performing integrated germline and tumor genomics research in rare cancer syndromes such as Lynch syndrome related endometrial and colorectal cancers
- Analyzing genetic variants with emphasis on variants of unknown significance
- Preparing manuscripts for co-first authorship and middle authorship publications
- Developing computational and bioinformatic tools to aid research workflows and automated interpretation pipelines
- Genetic data analysis and variant interpretation
- Managing clinical data using tools such as Excel and Python for extracting data insights
- Programming in Python, R, and JavaScript
- Developing web based products for research tools including graphic design

ENCORE Research Center
Jacksonville, Florida

Clinical Research Coordinator
01/2017 - 01/2020

- Managing Phases I-IV Clinical Trials for investigational drug product in humans according to study protocol
- Recruiting patients high volume studies (large *n* numbers) and rare disease trials (highly selective inclusion criteria)
- Coordinating patient care and study visits and following clinical procedures and protocols
- Maintaining patient charts, records, and study data
- Charting patent data and symptomatology
- Performing vital signs and ECG
- Working collaboratively with study monitors, study sponsors, patient care team, and clinicians

Education

Harvard University
Boston, Remote

Master's Degree - Biology Extension Studies
06/2022 - 11/2024

University of Florida
Gainesville, Florida

Bachelor's Degree - Pre-Med & Gender Studies
01/2013 - 05/2017

Key Achievements

Dean's List / Summa Cum Laude - Master's Degree

Journal Title Story in Cancers MDPI for co-first authorship publication

Abstract selected for poster presentation at the American Association for Molecular Pathology (AMP) meeting

Languages

English Native ●●●●●

Spanish Fluent (Native level) ●●●●●

Skills

BIOLOGY · Research · Genomic Evaluation · Data Interpretation · Analysis of Large Genomic Datasets · Population Genetics Assessment · Genomic Variant Assessment in the Context of Oncology · Scientific Figure Creation · Manuscript Preparation · Scientific Publication · Database Management · Applying Statistical Methods for Data Interpretation · Literature Review · Scientific Framework Development · Identifying Areas of Workflow Automation · Utilizing Excel and Excel formulas to interact with genomic data · Rare Cancer Syndromes · Multidisciplinary Approach to Science · Increasing Diverse Representation in Genomic Research · Git · GitHub · GitLab

COMPUTATION · Python for computational biology workflows and interacting with genomic datasets · Web development utilizing JavaScript HTML and CSS · R / R Studio for scientific figure creation and data visualization · Graphic design · Interacting with APIs for computational biology tools · SQL for database creation and management

Find me online

My AI Resume Website - Chat with the AI chatbot I trained on my resume and publications
mckenziewalker.com

Ghazani Lab
https://ghazani-lab.bwh.harvard.edu/index.php/team/

LinkedIn
https://www.linkedin.com/in/mckenzie-walker-4480361b6/

Certification

IBM Artificial Intelligence (AI) Developer Professional Certificate (In progress)

Systems Biology and Biotechnology Specialization (In progress)

Publications

Genes — https://www.mdpi.com/2073-4425/16/2/120 01/2025

Novel TBR1 c.1303C>T Variant Led to Diagnosis of Intellectual Developmental Disorder with Autism and Speech Delay: Application of Comprehensive Family-Based Whole-Genome Analysis

Authors / Co-authors

Genes — https://www.mdpi.com/2073-4425/15/10/1300 10/2024

Novel Variant in ANO5 Muscular Dystrophy: Identification by Whole Genome Sequencing and Quad Analysis

Ćuk, M.; Unal, B.; Lovrenčić, L.; Walker, M.; Hayes, C.P.; Abraamyan, F.; Prutki, M.; Krakar, G.; Srkoč-Majčica, L.; Ghazani

Journal of Personalized Medicine 08/2024
— https://pubmed.ncbi.nlm.nih.gov/39338155/

Novel RAI1:c.2736delC Variant in Smith–Magenis Syndrome: Identification by Whole Genome Sequencing and Joint Analysis

Ćuk M, Unal B, Jandric N, Hayes CP, Walker M, Abraamyan F, Gornik KC, Ghazani AA.

Cancer Genetics — https://pubmed.ncbi.nlm.nih.gov/39067332/ 07/2024

Whole genome joint analysis reveals ATM:C.1564_1565del variant segregating with Ataxia-Telangiectasia and breast cancer

Ćuk M, Unal B, Hayes CP, Walker M, Bevanda A, Antolović V, Ghazani AA.

Genes — https://pubmed.ncbi.nlm.nih.gov/39062725/ 07/2024

Diagnosis of Two Unrelated Syndromes of Prader-Willi and Calpainopathy: Insight from Trio Whole Genome Analysis and Isodisomy Mapping

Ćuk M, Unal B, Bevanda A, Hayes CP, Walker M, Abraamyan F, Beluzic R, Gornik KC, Ozretic D, Prutki M, Nie Q, Reddi HV, Ghazani AA

The American Journal of Case Reports 07/2024
— https://pubmed.ncbi.nlm.nih.gov/38995884/

Novel de Novo Nonsense Variants in AGO3 and KHSRP: Insights into Global Developmental Delay and Autism Spectrum Disorders through Whole Genome Analysis

Ćuk M, Lovrenčić L, Unal B, Walker M, Hayes CP, Krakar G, Beluzić R, Sansović I, Pavliša G, Ghazani AA

Cancers — https://pubmed.ncbi.nlm.nih.gov/38473309/ 02/2024

Advancing Precision Oncology in Hereditary Paraganglioma-Pheochromocytoma Syndromes: Integrated Interpretation and Data Sharing of the Germline and Tumor Genomes

Rana HQ, Koeller DR, Walker M, Unal B, Levine AS, Chittenden A, Isidro RA, Hayes CP, Manam MD, Buehler RM, Manning DK, Barletta JA, Hornick JL, Garber JE, Ghazani AA

Journal Title Story in Cancers MDPI

Cancer Medicine — https://pubmed.ncbi.nlm.nih.gov/38308423/ 02/2024

Genomic disparity impacts variant classification of cancer susceptibility genes in Turkish breast cancer patients

Agaoglu NB, Unal B, Hayes CP, Walker M, Ng OH, Doganay L, Can ND, Rana HQ, Ghazani AA

Frontiers in Oncology — https://pubmed.ncbi.nlm.nih.gov/38344144/ 01/2024

Development and evaluation of INT²GRATE: a platform for comprehensive assessment of the role of germline variants informed by tumor signature profile in Lynch syndrome

Isidro RA, Chittenden A, Walker M, Schwartz A, Koeller DR, Hayes CP, Unal B, Manam MD, Buehler RM, Manning DK, Sholl LM, Redston MS, Yurgelun MB, Rana HQ, Garber JE, Ghazani AA

Abstract

INT²GRATE Oncology Consortium: A Novel Variant Evidence Framework for Cancer Syndromes and Data-Sharing Platform for Integrated Germline and Tumor Variants

Abstract selected for poster presentation at the American Association for Molecular Pathology (AMP) meeting

Publications

Harvard University ProQuest Dissertations & Theses 11/2024

_ https://www.proquest.com/openview/640de0fd3802db336d8552c1bbd1cd7c/1?pq-origsite=gscholar&cbl=18750&diss=y

Genetic Evaluation of Rare Cancer Syndromes Using a Combined Analysis of the Germline and Tumor Genome Data

Walker, McKenzie