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 through technology and biology. As a co-first author published researcher in genomics with 10 publications total to date, I have gained extensive experience working as a consultant biological scientist and computational engineer at Mass General Brigham Hospital in dry lab research using computational tools. I also serve as the Lead Computational Engineer for the INT²GRATE Oncology Consortium. I am a self-starter with ambitious visions, swift execution, and keen attention to detail. With a strong foundation in biology and computation, I am driven to advance innovation and make meaningful contributions to my company's team and to science. I am eager to bring my energetic approach and expertise to a new role, and I am ready to start immediately.

Experience

Mass General Brigham — Remote

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

- Use computational biology practices to perform integrated germline and tumor genomics research in rare cancer syndromes such as Lynch syndrome related endometrial and colorectal cancers
- Genomic variant analysis
- Data modeling and scientific visualization for published scientific figure creation (utilizing Python and R)
- Manuscript preparation and co-first authorship publications
- Computational and bioinformatic tool development
- Genetic data analysis and variant interpretation
- Data management (Excel, SQL)
- Programming (Python, R, JavaScript)
- Web development and graphic design for research tools
- Increasing diverse representation in genomic research in creating global population genomic databases

Harvard University — Boston, Remote

Teaching Assistant (Introduction to Genomics) — 12/2024 - Present

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

INT²GRATE Oncology Consortium — Remote

Lead Computational Engineer — 01/2023 - Present

- Cross institutional collaboration to increase global diversity in genomics and access to genomic insights
- Deriving scientifically important insights from large data in the context of cancer genomics
- Database management and statistics in population stratification
- Computational and bioinformatic tool development
- Manuscript preparation
- Genetic data analysis and variant interpretation
- Data manipulation using a variety of computational tools such as Python and R
- Using APIs from external institutions to obtain for analysis and report data for data sharing

Harvard University — Remote

Faculty Aide — 07/2024 - 12/2024

- Integrated germline and tumor genomics research in rare cancer syndromes utilizing computational tools
- Implementation of computational biology practices to perform research
- Bioinformatic tool development such as programs for genomic data management and interpretation
- Web development for public facing research tools to aid interaction with research product

Experience

Mass General Brigham
Remote

Research Trainee
08/2022 - 12/2023

- Integrated analysis of germline and somatic genomic data for the interpretation of genetic variant pathogenicity in selected cancer syndromes
- Genomic variant analysis
- Manuscript preparation and co-first authorship publications
- Computational and bioinformatic tool development
- Genetic data analysis and variant interpretation
- Data management (Excel)
- Programming (Python, R, JavaScript)
- Web development and graphic design for research tools

ENCORE Research Center
Jacksonville, Florida

Clinical Research Coordinator
01/2017 - 01/2020

- Managed 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)
- Managing patient care, study visits, and following clinical procedures and protocols
- Maintenance of patient charts and records
- Patient charting and symptomatology
- Vital signs and ECG
- Work 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 Native ●●●●●

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

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

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

INT²GRATE Oncology Consortium
https://int2grateoncology.org/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