

Savannah Hutchinson

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 Detroit, MI 48226

SUMMARY

Analytical Bioinformatics Scientist with a Ph.D. in Computational Biology and over 4 years of experience in genomic data analysis and computational workflow development. Proven ability to analyze high-throughput sequencing datasets and contribute to multi-omics studies. Skilled in Python and R programming within Linux environments. Strong collaborator, bridging gaps between computational analyses and clinical applications. Committed to advancing genomic research through innovative solutions and data integration.

EXPERIENCE

Bioinformatics Scientist
Genomic Insights Inc.

June 2025 - Present
Ann Arbor, MI

- Oversaw large-scale whole-genome sequencing analyses and developed bioinformatics workflows driving impactful results. Responsible for cross-functional collaboration with teams for data integration.
- Led comprehensive analysis of large-scale whole-genome sequencing datasets, assuring quality throughout the evaluation.
 - Worked effectively with multidisciplinary teams, integrating genomic findings with clinical and epidemiological intelligence, which enhanced research outputs.
 - Created and improved bioinformatics pipelines responsible for short-read and long-read analysis, increasing overall examination efficiency.
 - Executed differential expression and trajectory studies on single-cell RNA-seq datasets, contributing meaningful content to prominent scientific publications.
 - Introduced reproducible computational strategies via Nextflow, bridging gaps in data management practices while enhancing workflow precision.
 - Presented significant findings at various scientific venues, heightening visibility for ongoing genomic research endeavors.

Computational Biologist
Precision Genomics Lab

January 2024 - May 2025
Grand Rapids, MI

- Focused on analyzing high-throughput sequencing data while developing analytical workflows that fostered project completion efficiency.
- Analyzed extensive high-throughput sequencing datasets emphasizing variant discovery and structural variation in genomic investigations.
 - Built analytical frameworks that trimmed down processing times, promoting faster report generation.
 - Collaborated closely with external research institutions leading to co-authored works circulated in respected journals.
 - Set higher standards for reproducibility within analyses by defining rigorous best practices evident in documentation.
 - Facilitated educational workshops aimed at young scientists, ensuring knowledge transmission in bioinformatics methods.
 - Drafted future grant requests and project outlines distinctly conveying research ambitions and methodologies.

Research Assistant
Bioinformatics Research Center

August 2022 - December 2023
Lansing, MI

- Supported genomic examinations by performing essential data cleanup and fostering greater access to visualization tools.
- Provided crucial support to genomic initiatives through data normalization procedures addressing sequencing abnormalities.
 - Assisted in developing software solutions that enhanced data visualization capabilities, making analyses more accessible.
 - Engaged collaboratively, offering bioinformatics insights aimed at augmenting experimental designs informed by data.
 - Conducted thorough literature explorations, maintaining currency with trends within genomic evaluations.
 - Authored process documentation guiding analytical protocols adhering to established research regulations.
 - Actively participated in team meetings, sharing updates and insights to maintain a consistent push towards goals.

LEADERSHIP & AWARDS

- Dean's List - University of Michigan, 2024
- Best Paper Award - Genomic Research Conference, 2025

EDUCATION

Ph.D. in Computational Biology
University of Michigan GPA: 4.0

2026
Ann Arbor, MI

Coursework: Genomics, Biostatistics, Data Analysis, Bioinformatics

CERTIFICATIONS

- Certified Bioinformatics Analyst  2025

- Python Programming Certification 📅 2025

TECHNICAL SKILLS

- **Programming Languages:** Python, R, JavaScript
- **Data Analysis Tools:** RStudio, Pandas, NumPy
- **Version Control Systems:** Git, GitHub, SVN
- **Linux/Unix Systems:** Ubuntu, CentOS, Red Hat
- **Bioinformatics Applications:** Galaxy, GATK, BEDTools
- **Cloud Computing Platforms:** AWS, Google Cloud, Azure
- **Workflow Management Tools:** Nextflow, Snakemake, WDL
- **Statistical Software:** SAS, SPSS, R Stats
- **Visualization Tools:** Tableau, Matplotlib, ggplot
- **Training & Mentorship:** Workshop Facilitation, Peer Tutoring, Team Collaboration

SKILLS

- | | | | |
|-------------------------|---------------------------|---------------------------|-------------------------|
| • Bioinformatics | • Single-Cell RNA-seq | • Linux/Unix | • Structural Variation |
| • Genomic Data Analysis | • Whole-Genome Sequencing | • Statistical Analysis | • Emerging Technologies |
| • Python | • Data Integration | • Haplotype Analysis | • Data Processing |
| • R | • Workflow Development | • Differential Expression | • Reproducibility |

PROFESSIONAL AFFILIATIONS

- American Society of Human Genetics (ASHG)
- International Society for Computational Biology (ISCB)

LANGUAGES

- English (Native)
- Spanish (Proficient)

ADDITIONAL INFORMATION

Work Status : Authorized to work in United States. No sponsorship required.

REFERENCES

AVAILABLE ON REQUEST