

Savannah Hutchinson

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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 June 2025 - Present
Genomic Insights Inc. *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 January 2024 - May 2025
Precision Genomics Lab *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 August 2022 - December 2023
Bioinformatics Research Center *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 2026
University of Michigan GPA: 4.0 *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

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|-------------------------|---------------------------|---------------------------|-------------------------|
| • 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