

Audrey Dillon

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SUMMARY

Dedicated Computational Biologist with over 6 years of experience specializing in large-scale data analysis and multi-omics datasets. Proven expertise in statistical modeling, machine learning, and bioinformatics tailored to cancer biology, particularly breast cancer. Holds a PhD in Computational Biology and is proficient in R, Python, and shell scripting, with a strong commitment to delivering high-quality results and insights. Excellent communicator and collaborator with a passion for advancing cancer research through innovative analytical approaches. Eager to contribute to cutting-edge research at HealthTech Innovations and propel its clinical objectives.

EXPERIENCE

Computational Biologist March 2020 - Present
Data Analysis Solutions Los Angeles, CA

Lead team efforts in analyzing large-scale RNA and WES datasets, enabling breakthroughs in cancer research. This role emphasizes collaboration across scientific disciplines and standardization of workflows to ensure efficiency and accuracy.

- Led the analysis of large-scale RNA and WES datasets to provide actionable insights for ongoing cancer research projects.
- Developed and implemented advanced multivariate statistical models to enhance understanding of disease mechanisms.
- Collaborated with cross-functional teams to interpret complex data and present findings in a clear, concise manner.
- Standardized analytical workflows, improving efficiency in data processing and documentation practices.
- Conducted training sessions for junior team members on best practices in computational biology and data analysis.
- Authored several research papers based on findings that contributed to advancements in clinical oncology.

Research Scientist June 2017 - February 2020
Bioinformatics Corp San Francisco, CA

Played a pivotal role in harnessing clinical omics data through predictive analyses, collaborating closely with clinical teams to fulfill research goals. Presented findings nationally, fostering organization visibility.

- Analyzed clinical omics data utilizing predictive and prognostic methodologies to support hypothesis-driven research.
- Collaborated with oncology teams to interpret results and deliver insights that aligned with clinical objectives.
- Automated data processing pipelines using R and Python, significantly reducing analysis time.
- Maintained version control and documentation of all coding and analytical processes using Git.
- Engaged in continuous learning and development to stay updated on advancements in computational biology.
- Presented findings at national conferences, enhancing the visibility of the organization's research initiatives.

Data Scientist January 2016 - May 2017
Innovative BioSolutions San Jose, CA

Supported complex data analyses with an emphasis on novel methods and software, contributing significantly in high-performance computing environments focused on cancer research.

- Supported large-scale data analysis projects with a focus on cancer research, utilizing high-performance computing environments.
- Developed scripts for data cleaning and preprocessing, ensuring data integrity and quality for subsequent analyses.
- Participated in team meetings to discuss project objectives, outcomes, and next steps, contributing to collaborative decision-making.
- Investigated novel analytical techniques to enhance data interpretation and visualization capabilities.
- Documented all analytical processes for compliance and reproducibility in research studies.
- Fostered a collaborative environment by mentoring interns and new hires in data analysis techniques.

LEADERSHIP & AWARDS

- Certified Bioinformatics Analyst, 2025
- R Programming for Data Science Certification, 2025

EDUCATION

PhD in Computational Biology 2016
University of California, San Diego GPA: 3.9 San Diego, CA
Coursework: Computational Genomics, Machine Learning, Statistical Analysis, Data Visualization

CERTIFICATIONS

- Certified Bioinformatics Analyst 📅 2025
- R Programming for Data Science Certification 📅 2025

TECHNICAL SKILLS

- **Statistical Analysis Tools:** R, Python
- **Scripting Languages:** Shell Scripting
- **Workflow Management:** Git
- **Data Processing Techniques:** Pipelines, Automation Tools, High-Performance Computing
- **Analysis Methodologies:** Multivariate Statistics, Predictive Modeling
- **Biological Databases:** Omics Data Repositories, Clinical Records
- **Visualization Frameworks:** ggplot2, matplotlib, Seaborn
- **Project Coordination Tools:** Trello, Asana, JIRA
- **Machine Learning Platforms:** scikit-learn, TensorFlow, Keras
- **Documentation Standards:** Markdown, LaTeX

SKILLS

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|-------------------|-------------------------------------|------------------------------|------------------|
| • R | • Multivariate Statistical Analysis | • Git | • Cancer Biology |
| • Python | • Predictive Modeling | • High-Performance Computing | |
| • Shell Scripting | • Bioinformatics Pipelines | • Data Visualization | |

PROFESSIONAL AFFILIATIONS

- Member of the American Society for Biochemistry and Molecular Biology
- Contributor to local educational outreach programs related to science and technology

LANGUAGES

- English (Native)
- Spanish (Intermediate)

ADDITIONAL INFORMATION

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

REFERENCES

AVAILABLE ON REQUEST