

**BIOGRAPHICAL SKETCH**

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NAME: Chaffer, James

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Software Developer and Data Wrangler

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
University of Rochester, Rochester, New York	BS	05/2021	Computational Biology
Stanford University, Palo Alto, California	Other training	2024	Large Language Models for Business with Python

**A. Personal Statement**

The thorough understanding of both biological and computational concepts I received while during my undergraduate studies has provided a solid foundation to gain further understanding of genomics research initiatives. Early on as an undergraduate, I was able to gain initial wet and dry lab research experience while assisting in research of centromere-associated retroelement evolution in the Larracuenta Lab at the University of Rochester. Starting towards the end of my time as an undergraduate, and continuing after graduation, I built upon my research experience working with the Yule Lab at the University of Rochester Medical Center. While simultaneously performing wet lab experiments, I developed new analysis software techniques to analyze in vivo and in vitro calcium imaging data. To do this required being the main communicator between Yule Lab members and computer science and statistics colleagues in New Zealand. This communication experience, as well as the software development experience, has proved to be invaluable in my current role as a Software Developer and Data Wrangler for the Lattice data coordination team at Stanford University. I look forward to continuing my important work with the Lattice team and continuing to explore the endless possibilities of computational biology.

1. John Rugis, James Chaffer, James Sneyd, David Yule. Tools for Quantitative Analysis of Calcium Signaling Data Using Jupyter-Lab Notebooks. 2023 June. Available from: <https://doi.org/10.1101/2023.06.13.544740> DOI: 10.1101/2023.06.13.544740
2. Shibli Abdulla, Brian Aevermann, Pedro Assis, Seve Badajoz, Sidney M. Bell, Emanuele Bezzi, Batuhan Cakir, Jim Chaffer, Signe Chambers, J. Michael Cherry, Tiffany Chi, Jennifer Chien, Leah Dorman, Pablo Garcia-Nieto, Nayib Gloria, Mim Hastie, Daniel Hegeman, Jason Hilton, Timmy Huang, Amanda Infeld, Ana-Maria Istrate, Ivana Jelic, Kuni Katsuya, Yang Joon Kim, Karen Liang, Mike Lin, Maximilian Lombardo, Bailey Marshall, Bruce Martin, Fran McDade, Colin Megill, Nikhil Patel, Alexander Predeus, Brian Raymor, Behnam Robotmili, Dave Rogers, Erica Rutherford, Dana Sadgat, Andrew Shin, Corinn Small, Trent Smith, Prathap Sridharan, Alexander Tarashansky, Norbert Tavares, Harley Thomas, Andrew Tolopko, Meghan Urisko, Joyce Yan, Garabet Yeretssian, Jennifer Zamanian, Arathi Mani, Jonah Cool, Ambrose Carr. CZ CELLxGENE Discover: A single-cell data platform for scalable exploration, analysis and modeling of aggregated data. 2023 November. DOI: 10.1101/2023.10.30.563174
3. Lucas Hemmer, Sherif Negm, Xuewen Geng, Cécile Courret, Beatriz María Navarro Domínguez, Iain Speece, Xiaolu Wei, Eddyson Altidor, James Chaffer, John Sproul, Amanda Larracuenta. Centromere-associated retroelement evolution in *Drosophila melanogaster* reveals an underlying conflict. 2022 November. Available from: <https://doi.org/10.1101/2022.11.25.518008> DOI: 10.1101/2022.11.25.518008

## B. Positions, Scientific Appointments and Honors

### Positions and Scientific Appointments

- 2022 - Software Developer and Data Wrangler, Stanford University, Department of Biomedical Data Sciences, GECKO Group, Lattice Team, Palo Alto, CA
- 2021 - 2022 Laboratory Technician, University of Rochester Medical Center, Department of Pharmacology and Physiology, Yule Lab, Rochester, NY
- 2021 - 2021 Undergraduate Research Assistant, University of Rochester Medical Center, Department of Pharmacology and Physiology, Yule Lab, Rochester, NY
- 2019 - 2020 Computational Biology Research Assistant, University of Rochester, Larracuenta Lab, Rochester, NY

## C. Contribution to Science

1. As an undergraduate, I Collaborated with researchers in the Larracuenta Lab in their research in identifying centromeres contained in islands rich in retroelements. Specifically, the retroelement G2/Jockey3. I designed multiple primers using Primer3, IDT, and BLAST. I Ran these primers using short and long PCRs, gradient PCRS, and gel electrophoresis with multiple different DNA strains. I also served as a teaching assistant in a "Introduction to Programming" course. I aided with care of naked mole rats used for aging research in the Gorbunova Lab. Finally, I assisted with a nutritional intake study on mice at the Rochester Medical Center. I was responsible for accurate measurement taking and following of strict protocols.
  - a. Lucas Hemmer, Sherif Negm, Xuewen Geng, Cécile Courret, Beatriz María Navarro Domínguez, Iain Speece, Xiaolu Wei, Eddyson Altidor, James Chaffer, John Sproul, Amanda Larracuenta. Centromere-associated retroelement evolution in *Drosophila melanogaster* reveals an underlying conflict. 2022 November. Available from: <https://doi.org/10.1101%2F2022.11.25.518008> DOI: 10.1101/2022.11.25.518008
2. Continuing through graduation, I mediated between Dr. Yule of the Department of Pharmacology and Physiology, and his computer science and statistics colleagues in New Zealand to improve and develop Python scripts deployed in JupyterLab Notebooks for identification of peaks and latencies in pixel intensity data representing Calcium signals. I created new imaging analysis software techniques to rapidly analyze bulk in vitro calcium imaging data, allowing for results in minutes rather than days. I developed new techniques to analyze and measure in vivo calcium signal responses within mouse pancreas cells, providing rapid, accurate, and most importantly unbiased, results. I performed various wet lab tasks and experiments including but not limited to cell culturing, western blots, cell transfections, and in vitro microscope imaging.
  - a. John Rugis, James Chaffer, James Sneyd, David Yule. Tools for Quantitative Analysis of Calcium Signaling Data Using Jupyter-Lab Notebooks. 2023 June. Available from: <https://doi.org/10.1101%2F2023.06.13.544740> DOI: 10.1101/2023.06.13.544740
3. In my current role as a Software Developer and Data Wrangler I have assisted numerous researchers by curating the data of their studies for upload to CELLxGENE Discover, a visualization and analysis platform for single-cell data developed by the Chan Zuckerberg Initiative. Simultaneously to this data wrangling work, I have assisted in QA efforts for updates to the CELLxGENE schema, updating and testing various scripts as needed to maintain schema formatting. I have significantly assisted in continual improvement of a large script used to transform a contributor matrix, raw count data, and Lattice Database metadata in JSON format into an AnnData file that can be uploaded to CELLxGENE. One of these improvements in the script was utilizing object oriented approach for increased code readability and ease of future updates. I have also performed uploads of large quantities of Fastq files to the Gene Expression Omnibus.
  - a. Shibli Abdulla, Brian Aevertmann, Pedro Assis, Seve Badajoz, Sidney M. Bell, Emanuele Bezzi, Batuhan Cakir, Jim Chaffer, Signe Chambers, J. Michael Cherry, Tiffany Chi, Jennifer Chien, Leah Dorman, Pablo Garcia-Nieto, Nayib Gloria, Mim Hastie, Daniel Hegeman, Jason Hilton, Timmy

Huang, Amanda Infeld, Ana-Maria Istrate, Ivana Jelic, Kuni Katsuya, Yang Joon Kim, Karen Liang, Mike Lin, Maximilian Lombardo, Bailey Marshall, Bruce Martin, Fran McDade, Colin Megill, Nikhil Patel, Alexander Predeus, Brian Raymor, Behnam Robotmili, Dave Rogers, Erica Rutherford, Dana Sadgat, Andrew Shin, Corinn Small, Trent Smith, Prathap Sridharan, Alexander Tarashansky, Norbert Tavares, Harley Thomas, Andrew Tolopko, Meghan Urisko, Joyce Yan, Garabet Yeretssian, Jennifer Zamanian, Arathi Mani, Jonah Cool, Ambrose Carr. CZ CELLxGENE Discover: A single-cell data platform for scalable exploration, analysis and modeling of aggregated data. 2023 November. DOI: 10.1101/2023.10.30.563174