

JAYARAM KANCHERLA

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Institution & Affiliation

Current Position

Senior Research Software Engineer
GENENTECH, A Member of the Roche Group
South San Francisco, California

Education

- Masters in Computer Science Aug 2009 - May 2011
North Carolina State University, Raleigh
- Bachelors in Computer Science and Engineering Oct 2005 - Apr 2009
V.R. Siddhartha Engineering College
Affiliated to Nagarjuna University, India

MOOC Courses

- Introduction to Big Data with Apache Spark - [edX](#) Jul 2015
- Scalable Machine Learning - [edX](#) Aug 2015

Conferences, Workshops, and Talks

Publications

1. **[Preprint]** Mohamed K. Gunady, **Jayaram Kancherla**, Héctor Corrada Bravo, Soheil Feizi. scGAIN: Single Cell RNA-seq Data Imputation using Generative Adversarial Networks. *bioRxiv* 837302; doi: [10.1101/837302](https://doi.org/10.1101/837302)
2. BRAIN Initiative Cell Census Network, et al. A multimodal cell census and atlas of the mammalian primary motor cortex. *bioRxiv* 2020.10.19.343129; doi: [10.1101/2020.10.19.343129](https://doi.org/10.1101/2020.10.19.343129)
3. Bakken, Trygve E., et al. Comparative cellular analysis of motor cortex of human, marmoset monkey, and mouse. *bioRxiv* 2020.03.31.016972; doi: [10.1101/2020.03.31.016972](https://doi.org/10.1101/2020.03.31.016972)
4. Zizhen Yao., et al. A transcriptomic and epigenomic cell atlas of mouse primary motor cortex. 2020.02.29.970558; doi: [10.1101/2020.02.29.970558](https://doi.org/10.1101/2020.02.29.970558)
5. Orvis, Joshua, Brian Gottfried, **Jayaram Kancherla**, Ricky S. Adkins, Yang Song, Amiel A. Dror, Dustin Olley et al. "gEAR: gene Expression Analysis Resource portal for community-driven, multi-omic data exploration." *Nature methods* (2021): 1-2.
6. **Jayaram Kancherla**, Yifan Yang, Hyeyun Chae, Hector Corrada Bravo, Epiviz File Server: Query, transform and interactively explore data from indexed genomic files, *Bioinformatics*, Volume 36, Issue 18, 15 September 2020, Pages 4682–4690, doi: [10.1093/bioinformatics/btaa591](https://doi.org/10.1093/bioinformatics/btaa591)

7. Wagner J, **Kancherla J**, Braccia D et al. Interactive exploratory data analysis of Integrative Human Microbiome Project data using Metaviz. *F1000Research* 2020, 9:601. doi: [10.12688/f1000research.24345.1](https://doi.org/10.12688/f1000research.24345.1)
8. **[*equal contribution]** **Jayaram Kancherla***, Shruti Rao*, Krithika Bhuvaneshwar, Rebecca B. Riggins, Robert A. Beckman, Subha Madhavan, Héctor Corrada Bravo, Simina M. Boca. An evidence-based network approach to recommending targeted cancer therapies. *JCO Clinical Cancer Informatics* no. 4 (2020) 71-88; doi: [10.1200/CCI.19.00097](https://doi.org/10.1200/CCI.19.00097)
9. Z. Cui, **J. Kancherla**, H. C. Bravo and N. Elmqvist, Sherpa: Leveraging User Attention for Computational Steering in Visual Analytics. 2019 IEEE Visualization in Data Science (VDS), Vancouver, BC, Canada, 2019, pp. 48-57. doi: [10.1109/VDS48975.2019.8973384](https://doi.org/10.1109/VDS48975.2019.8973384)
10. **[*equal contribution]** Zhe Cui*, **Jayaram Kancherla***, Kyle W Chang, Niklas Elmqvist, Héctor Corrada Bravo, Proactive visual and statistical analysis of genomic data in Epiviz, *Bioinformatics*, btz883, doi: [10.1093/bioinformatics/btz883](https://doi.org/10.1093/bioinformatics/btz883)
11. Nathan D Olson, Nidhi Shah, **Jayaram Kancherla**, Justin Wagner, Joseph N Paulson, Héctor Corrada Bravo. metagenomeFeatures: an R package for working with 16S rRNA reference databases and marker-gene survey feature data, *Bioinformatics*, btz136, doi: [10.1093/bioinformatics/btz136](https://doi.org/10.1093/bioinformatics/btz136)
12. **Kancherla J**, Zhang A, Gottfried B and Bravo HC. Epiviz Web Components: reusable and extensible component library to visualize functional genomic datasets. *F1000Research* 2018, 7:1096; doi: [10.12688/f1000research.15433.1](https://doi.org/10.12688/f1000research.15433.1)
13. **[*equal contribution]** Justin Wagner*, Florin Chelaru*, **Jayaram Kancherla***, Joseph N Paulson*, Alexander Zhang, Victor Felix, Anup Mahurkar, Niklas Elmqvist, Héctor Corrada Bravo; Metaviz: interactive statistical and visual analysis of metagenomic data, *Nucleic Acids Research*, Volume 46, Issue 6, 6 April 2018, Pages 2777–2787, doi: [10.1093/nar/gky136](https://doi.org/10.1093/nar/gky136)
14. Gary Ginsberg, Suryanarayana V Vulimiri, Yu-Sheng Lin, **Jayaram Kancherla**, Brenda Foos & Babasaheb Sonawane (2017) A framework and case studies for evaluation of enzyme ontogeny in children’s health risk evaluation, *Journal of Toxicology and Environmental Health, Part A*, 80:10-12, 569-593, doi: [10.1080/15287394.2017.1369915](https://doi.org/10.1080/15287394.2017.1369915)
15. Mansouri, Kamel et al. Collaborative Estrogen Receptor Prediction Project for EDSP Prioritization. *Environmental Health Perspectives* (2016); doi: [10.1289/ehp.1510267](https://doi.org/10.1289/ehp.1510267)
16. Richard M.A. et al. The ToxCast Chemical Landscape: Paving the Road to 21st Century Toxicology. *Chemical Research in Toxicology* (2016) doi: [10.1021/acs.chemrestox.6b00135](https://doi.org/10.1021/acs.chemrestox.6b00135)

Book Chapters

- **[Under Review]** Electronic Waste: Public Health and Environmental Risk. Bob Sonawane, Abdel Kadry and **Jayaram Kancherla**
- Kanchana Padmanabhan, Brent Harrison, Kevin Wilson, Michael L. Warren, **Jayaram Kancherla**, Katie Bright, Justin Mosiman, Hieu Phung, Benjamin Miller, and Sam Shamseldin, 2013. Cluster-Analysis, Practical Graph Mining with R, CRC Press. ISBN: [9781118398608](https://doi.org/10.1002/9781118398608)

Presentations & Posters

1. Jayaram Kancherla, Kazi Tasnim Zinat, Hector Corrada Bravo, Stephanie Hicks. Hierarchical interactive exploration and analysis of single cell RNA-seq datasets, BioVis, *International Society for Molecular Biology* (ISMB/ECCB 2021), July 25-20, 2021 (Presentation & Poster)
2. B. Fowler, B. Sonawane, A. M. Kadry, and J. Kancherla. Health Risk Assessment Challenges of Handling and Disposal of Electronic Waste (E-waste) Society of Toxicology, March 12-26 2021 (Poster)

3. Jayaram Kancherla, Kazi Zinat Tasnim, Hector Corrada Bravo, Hierarchical interactive exploration and analysis of single cell RNA-seq datasets, Biological Data Science, November 4-6 2020. CSHL BDS (Presentation & Poster)
4. Jayaram Kancherla, Héctor Corrada Bravo. Quickly compose custom interactive genomic visualization apps in R/Bioc with epiviz components. BioC 2020, July 29 - 31, 2020. (Presentation)
5. Jayaram Kancherla, Héctor Corrada Bravo. Quickly compose custom interactive genomic visualization apps in R/Bioc with epiviz components. *BioC* 2020, July 29 - 31, 2020. [10.7490/f1000research.1118127.1](https://doi.org/10.7490/f1000research.1118127.1) (Presentation)
6. Chrysostomou, Elena, Katherine E. Prater, Yang Song, Joshua Orvis, Jayaram Kancherla, Brian Herb, Seth Ament et al. "NeMO Analytics-AD: The Neuroscience Multi-Omic Visualization and Analysis Platform, now extended to support Alzheimer's Disease." In 2020 *Alzheimer's Association International Conference*. ALZ, 2020. (Poster)
7. Prioritizing targeted therapies in an evidence-based manner, integrating biological context and functional precision medicine. Simina Boca, Krithika Bhuvaneshwar, Vireliz Fernandez-Vega, Jayaram Kancherla, Shruti Rao, Subha Madhavan, Rebecca Riggins, Robert A. Beckman, Hector Corrada Bravo, Louis Scampavia, and Timothy Spicer *Journal of Clinical Oncology* 2020 38:15_suppl, e14065-e14065 (Presentation) [10.1200/JCO.2020.38.15_suppl.e14065](https://doi.org/10.1200/JCO.2020.38.15_suppl.e14065)
8. Jayaram Kancherla, Yifan Yang, Héctor Corrada Bravo. Epiviz File Server – Query, Compute and Interactive Exploration of data from Indexed Genomic Files, BOSC, *International Society for Molecular Biology* (ISMB/ECCB), July 21-25, 2019, Basel, Switzerland [10.7490/f1000research.1117422.1](https://doi.org/10.7490/f1000research.1117422.1) (Presentation & Poster)
9. Jayaram Kancherla, Zhe Cui, Héctor Corrada Bravo. Proactive Visual and Statistical Analysis of Genomic Data in Epiviz, BioVis, *International Society for Molecular Biology* (ISMB/ECCB 2019), July 21-25, 2019, Basel, Switzerland [10.7490/f1000research.1117423.1](https://doi.org/10.7490/f1000research.1117423.1) (Presentation & Poster)
10. Jayaram Kancherla, Bob Sonawane, Bruce Fowler. Determination of Permissible Daily Exposures in Human Drug Products for Elemental Impurities via the Transdermal Delivery Route. *Society of Toxicology* 2019, March 10-14, Baltimore, MD (Presentation) [link](#)
11. B.R. Sonawane, G. Ginsberg, and J. Kancherla, 2018. Role on Enzyme Ontogeny in Evaluation of Acetaminophen Metabolism and Hepatotoxicity in Children. *Society of Toxicology* 2018. March 11-15, San Antonio, TX (Presentation)
12. Richard, A., C. Grulke, I. Thillainadarajah, K. Mansouri, J. Kancherla, R. Judson, A. Williams., 2015. EPA DSSTox Chemical Database: Resource for the Non-Targeted Testing Community. *NTA workshop*. August 18-19, RTP, NC [10.23645/epacomptox.5077765](https://doi.org/10.23645/epacomptox.5077765)
13. Mansouri, K., Kancherla J., Richard A., Judson R., 2015. EDSP Prioritization: Collaborative Estrogen Receptor Activity Prediction (CERAPP). *Society of Toxicology 54th Annual Meeting*. March 22-26, San Diego, CA. (Presentation & Poster) [10.23645/epacomptox.5178844](https://doi.org/10.23645/epacomptox.5178844)
14. Mansouri K, Kancherla J, Judson R.S., 2014. CERAPP - Collaborative Estrogen Receptor Activity Prediction Project. *US EPA Chemical Safety Research: Second Toxcast Data Summit*, September 29-30, Durham, NC 27711. [Weblink](#)
15. Cory Strobe, Kamel Mansouri, Jayaram Kancherla, Caroline Stevens, John Wambaugh., 2014. High Throughput Pharmacokinetic Modeling Using Computationally Predicted Parameter Values: Dissociation Constants. *US EPA Chemical Safety Research: Second Toxcast Data Summit*, September 29-30, Durham, NC 27711. [Weblink](#)
16. Strobe C.L., Mansouri K., Kancherla J., Stevens C., Wambaugh J.F., 2014. Throughput Pharmacokinetic Modeling Using Computationally Predicted Parameter Values: Dissociation Constants. *US EPA –NCCT, Second ToxCast Data Summit*, September 29-30, Durham, NC [10.23645/epacomptox.5197147](https://doi.org/10.23645/epacomptox.5197147)

17. Kancherla J., Mansouri K., Truong H., Richard A.M., Judson R., 2014. ACToR Chemical Structure processing using Open Source Cheminformatics Libraries. *Society of Toxicology, Future Tox II National Meeting*. January 16-17, Chapel Hill, NC. (Poster) [10.23645/epacomptox.5197126](https://doi.org/10.23645/epacomptox.5197126)
18. Vulimiri S.V., Kancherla J., Lin YS., Ginsberg G., Foos B., Sonawane B., 2014. Scoping the need for PBPK modeling of Child-Adult Metabolism Differences: Case Studies Applying an Enzyme Ontogeny Database. *Society of Toxicology 53rd Annual Meeting*. March 23-27, Phoenix, AZ. (Poster)
19. Watford S., Edwards J., Linnenbrink M., Kancherla J., Martin M., 2014. Web Application Supporting Chemical Safety Decisions. *Society of Toxicology 53rd Annual Meeting*. March 23-27, Phoenix, AZ. (Poster)

Accepted Bioconductor Packages

- Kancherla J, Gottfried B, Corrada Bravo H. epivizrChart: R interface to epiviz web components. R package. doi: [10.18129/B9.bioc.epivizrChart](https://doi.org/10.18129/B9.bioc.epivizrChart)
- Bravo HC, Chelaru F, Smith L, Goldstein N, Kancherla J, Walter M, Gottfried B. epivizr: R Interface to epiviz web app. R package. doi: [10.18129/B9.bioc.epivizr](https://doi.org/10.18129/B9.bioc.epivizr)
- Corrada Bravo H, Chelaru F, Wagner J, Kancherla J, Paulson J (2020). metavizr: R Interface to the metaviz web app for interactive metagenomics data analysis and visualization. R package. doi: [10.18129/B9.bioc.metavizr](https://doi.org/10.18129/B9.bioc.metavizr).
- Kancherla J, Bravo HC. epivizrStandalone: Run Epiviz Interactive Genomic Data Visualization App within R. R package. doi: [10.18129/B9.bioc.epivizrStandalone](https://doi.org/10.18129/B9.bioc.epivizrStandalone)
- Corrada Bravo H, Chelaru F, Wagner J, Kancherla J, Paulson J. metavizr: R Interface to the metaviz web app for interactive metagenomics data analysis and visualization. R package. doi: [10.18129/B9.bioc.epivizrChart](https://doi.org/10.18129/B9.bioc.epivizrChart)

Workshops

- BICCN Omics Workshop - *Jan 20 & 27, 2021*
<https://nemoarchive.org/biccn-omics-workshop/>
- Interactive visualization and data analysis with Epiviz web - *Jul 27-28, 2017*
components (Differential Gene Expression analysis using minfi)
Jayaram Kancherla, Brian Gottfried, Héctor Corrada Bravo
[BioC 2017](#), Dana Farber Cancer Institute, Boston, MA
- Metaviz Interactive Statistical and Visual Analysis using data *Jun 2017*
from Human Microbiome Project
Justin Wagner, Jayaram Kancherla, Héctor Corrada Bravo
[University of Maryland Institute of Genomic Science](#), Baltimore, MD
- Interactive visualization of microbiome data using Metaviz *Nov 1-2, 2016*
Jayaram Kancherla, Héctor Corrada Bravo
[Mid Atlantic Microbiome Conference](#), College Park, MD
- Interactive visualization with epiviz *Jun 25-26, 2016*
Héctor Corrada Bravo, Jayaram Kancherla, Justin Wagner, Deok Park
[BioC 2016](#), Stanford University, Stanford, CA
- Interactive Genomic Data Analysis and Visualization using Epiviz *Jun 15, 2016*
Jayaram Kancherla
[International Society for Computational Biology](#), DC RSG

Research Grants, Fellowships & Awards

Grants

- Integrative Visual and Computational Exploratory Analysis of Genomics Data
Grant # R01GM114267-02
Role: Scholar
Jan 2016 - Present
- Integration of 3D primary tumor drug-profiling with patient-specific drug gene networks for recommending targeted cancer therapies
Grant # R21CA220398-02
Role: Co-investigator
Jun 2016 - May 2018

Fellowships

- Oakridge Science Research Fellowship (ORISE)
National Center for Computational Toxicology (NCCT)
U.S. Environmental Protection Agency
Research Triangle Park, Durham, NC
Fellowship #EPA-ORD/NCCT-2012-19
Aug 2013 - Dec 2015
Title: Design and Development of Computational Decision Support Systems
The overall goal of the project is to integrate High Throughput Screening (HTS) data from the ToxCast project & the Tox21 initiative with other EPA data sources and, build interactive tools and applications to visualize HTS data and for characterizing risk assessment and prioritization of chemicals.
- Student Research Trainee
National Center for Environmental Assessment (NCEA)
U.S. Environmental Protection Agency
Crystal City, Arlington, VA
Fellowship #EP-11-H-001649
Sep 2011 - Aug 2013
Title: Sustainable Community Assessment platform
I worked with the US Census & sustainable communities to create a platform to share environmental data. Identified use cases and created an ideation platform to engage stakeholders and communities to make sustainable decisions. Developed tools to visualize data shared through the platform.
Enzyme Ontogeny: Text mining to collect metabolism & enzyme ontogeny data from published literature. Visualize time series data for enzyme expression across different life stages.

Honors & Awards

- Level III EPA Scientific and Technological Achievement Award
2019
- Travel Fellowship, ISMB/ECCB 2019
Jul 2019
- Travel Fellowship, Society of Toxicology (SOT), Future Tox II
Jan 2014
- STARS (Students & Technology in Academia, Research and Service)
Student Volunteer Award, North Carolina State University
Feb 2011

Service & Outreach

Reviewer

- Journal of Open Source Software (JOSS)

- American Medical Informatics Association (AMIA) 2020, 2021 Informatics Summit
- RECOMB CCB 2019
- ACM-BCB 2016

Research Experience

Positions

- Sr. Research Software Engineer *Jul 2021 - Present*
 Bioinformatics Software Engineer III *Oct 2020 - Jul 2021*
 Genentech, *A Member of Roche Group*
 South San Francisco, CA
 My research focuses on development of tools and methods for interactive and integrative exploration and visualization of genetic, epigenetic and transcriptomic data
- Faculty Specialist (with *Dr. Hector Corrada Bravo*) *Sep 2019 - Present*
 Faculty Research Assistant *Jan 2016 - Sep 2019*
 University of Maryland, College Park, MD
 My research focuses on development of tools and methods for interactive statistical exploration and visualization of large scale genomic datasets. I primarily work as on the development of the Epiviz (<http://www.epiviz.org>) and Metaviz (<http://www.metaviz.org>) suite of tools.
- Oakridge Science Research Fellow (with *Dr. Richard Judson*) *Aug 2013 - Dec 2015*
 National Center for Computational Toxicology (NCCT)
 U.S. Environmental Protection Agency, Durham, NC

Dashboards & Tools

Dashboard systems are developed to interactively explore and visualize High Throughput Screening (HTS) data from the ToxCast program (1800 chemicals tested in 700 assays). I designed and developed the framework for building interactive dashboards, and was also responsible for managing and integrating the HTS data with existing EPA datasets (ExpoCast, PhysChem, ToxRef etc) for building QSAR models and analysis. I worked on the following publicly available dashboards

- EPA ToxCast Dashboard (<http://actor.epa.gov/dashboard>)
- Endocrine Disruptor Screening Program (<http://actor.epa.gov/edsp21/>)

ACToR (<http://actor.epa.gov>)

Aggregated Chemical Toxicology Resource (ACToR) is a widely used data repository that aggregates publicly available chemical structure data and toxicity information from over 3000 sources. I worked on developing and optimizing this repository, parsing, curating and validating chemical structures with various public domains (DSSTox, PubChem, SRS, HPVIS and ChemIDplus), calculating structural properties (RDKit) and fingerprints for structure search (jChem).

Data Mining & Other Contributions

- **PhysChemDB** – created a physico-chemical properties database by mining data from published literature and publicly available databases. It is available as a web service and is used by the dashboards
- **DSSTox chemical curation** – text mining and scripts to extract/clean chemical names, synonyms and CAS registry numbers from STN record documents and public databases

- Student Research Trainee
National Center for Environmental Assessment (NCEA)
U.S. Environmental Protection Agency, Arlington, VA

Sep 2011 - Aug 2013

Sustainable Community Assessment Platform (Mentor: Rick Ziegler)

I worked with the US Census & sustainable communities to create a platform to share environmental data. Identified use cases and created an ideation platform to engage stakeholders and communities to make sustainable decisions. Developed tools to visualize data shared through the platform.

Enzyme Ontogeny (Mentors: Dr. Bob Sonawane & Dr. Suryanarayana Vulimiri)

Text mining to collect metabolism & enzyme ontogeny data from published literature. Visualize time series data for enzyme expression across different life stages.

Research Software and Applications

(Complete list available on GitHub [id: jkanche])

- Kana: Single-Cell RNA-seq analysis in the browser
GitHub: <https://github.com/jkanche/kana>
Application: <https://www.jkanche.com/kana/>
- scTreeViz: Interactive Hierarchical exploration of single cell RNA-seq expression datasets
GitHub: <https://github.com/HCBravoLab/scTreeViz>
- Epiviz File Server: Query and Transform directly from indexed genomic files
GitHub: <https://github.com/epiviz/epivizFileParser>
Published to PyPI: <https://pypi.org/project/epivizFileServer>
doi: [10.5281/zenodo.3841643](https://doi.org/10.5281/zenodo.3841643)
- Epiviz Feed: Proactive interactive and statistical visualization of genomic data
The Epiviz Feed application for the cancer epigenetics use case is hosted on an AWS instance and is available at <http://54.157.53.251/browser>
User Interface: https://github.com/epiviz/epiviz_feed_polymer
Computational Server: <https://github.com/epiviz/epiviz-feed-computation>
doi: [10.5281/zenodo.3373762](https://doi.org/10.5281/zenodo.3373762)
- CDGnet: Network visualization for precision medicine
The CDGnet tool is hosted at <http://epiviz.cbcb.umd.edu/shiny/CDGnet>
<https://github.com/jkanche/nfpmShinyComponent>
- Epiviz Components: Web Components for interactive visualization of genomic data
Epiviz Chart - <https://github.com/epiviz/epiviz-chart>
R package - Epivizr - <https://github.com/epiviz/epivizrChart>
- Interactive visualization of metagenomic data
Metaviz - <https://github.com/epiviz/metaviz>
R package - Metavizr - <https://github.com/epiviz/metavizr>
- Interactive visualization of functional genomics data
Epiviz - <https://github.com/epiviz/epiviz>
R package - Epivizr - <https://github.com/epiviz/epivizr>
- EPA ToxCast Dashboard - <http://actor.epa.gov/dashboard>
- EPA Endocrine Disruptor Screening Program - <http://actor.epa.gov/edsp21/>

Skills

Programming - JavaScript, Python, R, Go
Data Management - MySQL, Neo4j
Frameworks - Polymer, Flask, Sanic, d3Js
Chemo Informatics - RDKit, Indigo, KNIME

Work Experience

- Web Developer *Oct 2010 - May 2011*
North Carolina State University, NC
- STARS Website Developer (Volunteer) *Aug 2010 - Mar 2011*
STARS Student Leadership Corps (SLC)
North Carolina State University, NC
- Transcriber *Nov 2009 - Apr 2010*
University Disability Services,
North Carolina State University, NC

Teaching & Mentoring

Guest Lectures

- Next Generation Toxicology and Computational Toxicology Databases *Apr 30, 2019*
EMAP 514 – Introduction to Environmental Health Risk Assessment & Management
Environmental Metrology and Policy Program
Georgetown University, Washington DC

Co-supervised Students

Interns (at Genentech)

- Samuel Rosen, Math, *Summer 2021*

Undergraduate (at UMD)

- Lan Tran, CS, *Graduated 2016*
- Alexander Zhang, CS, *Graduated 2018*
- Brian Gottfried, CS, *Graduated 2018*
- Hyeyun Chae, Intern, *Summer 2019*
- Yifan Yang, CS, *Spring 2020*
- Kyle Chang, CS, *Spring 2020*

Mentoring Activities

- CSC 116 Tutor *Aug 2010 - Mar 2011*
North Carolina State University, NC
- Mentor for STARS Student Leadership Corps (SLC) *Aug 2010 - Mar 2011*
STARS Student Leadership Corps (SLC)
North Carolina State University, NC