

**Curriculum Vitae**

Name Guangyuan(Frank) Li  
Address 334 E 25th St, Apt 512, New York, NY, 10010  
Email [guangyuan.li@nyulangone.org](mailto:guangyuan.li@nyulangone.org)  
Blog <https://frankligy.medium.com/>  
GitHub <https://github.com/frankligy>  
LinkedIn <https://www.linkedin.com/in/guangyuan-li-399617173/>

**Skill Sets**

1. *Deep Learning (Pytorch, Tensorflow, Keras) and probabilistic modeling*
2. *Single-Cell Multimodal analysis (scRNA-Seq, CITE-Seq, scATAC-Seq, TCR, Spatial)*
3. *Neoantigen pipeline, Immune Repertoire, Cancer Immunotherapy*
4. *Gene Regulatory Network, Splicing Regulatory Network [[Poster](#)]*
5. *Web development (HTML, CSS, JavaScript, Flask, Dash, MySQL). [[Demo1](#), [Demo2](#), [Code1](#), [Code2](#)]*
6. *Python, Linux, R, Matlab, C, Data Visualization. [[Tutorials authored by me](#), [Code](#)]*
7. *Code Documentation [[Example1](#), [Example2](#)]*
8. *Docker, Singularity [[Example1](#), [Example2](#)]*
9. *Quick and continual Learner.*

**Education**

08/2019 - 08/2023 PhD student, Division of Biomedical Informatics  
Cincinnati Children's Hospital Medical Center, United States

09/2018 - 04/2019 Exchange Student, Biodesign Institute  
Arizona State University, United States

09/2015 - 06/2019 Bachelor of Science, Division of Life Science  
Wuhan University, China

**Working Experience**

09/2023 - present Postdoctoral Researcher, New York University, New York, NY, United States

- Developing next generation peptide-centric CAR-T therapy (PC-CAR)

05/2022 - 08/2022 Bioinformatics Intern, Sanofi, Cambridge, MA, United States

- Evaluating spatial deconvolution methods on 10x Visium data to guide the drug target selection and validation
- Developing standardized spatial analysis framework on AWS server to support bench scientists analysis

**First-Author Publications**

1. **Guangyuan Li\***, Balaji Iyer, V.B. Surya Prasath, YiZhao Ni, Nathan Salomonis. 2021. "DeepImmuno: Deep Learning-Empowered Prediction and Generation of Immunogenic Peptides for T-Cell Immunity." *Briefings in Bioinformatics* 22 (6). <https://doi.org/10.1093/bib/bbab160>.
2. **Guangyuan Li\***, Baobao Song, Harinder Singh, V.B. Surya Prasath, H. Leighton Grimes, Nathan Salomonis. 2022. "Decision level integration of unimodal and multimodal single cell data with scTriangulate" *Nature Communications* 14. <https://doi.org/10.1038/s41467-023-36016-y>
3. **Guangyuan Li\***, Shweta Mahajan\*, Siyuan Ma, Erin D. Jeffery, Xuan Zhang, Anukana Bhattacharjee, Meenakshi Venkatasubramanian et al. 2024. "Splicing Neoantigen Discovery with SNAF Reveals Shared Targets for Cancer Immunotherapy." *Science Translational Medicine* January. <https://doi.org/10.1126/scitranslmed.ade2886>.
4. **Guangyuan Li\***, Anukana Bhattacharjee, Nathan Salomonis. 2023 "Quantifying Tumor Specificity Using Bayesian Probabilistic Modeling for Drug Target Discovery and Prioritization." *BioRxiv*. <https://www.biorxiv.org/content/10.1101/2023.03.03.530994v1>
5. **Guangyuan Li\***, Amir Bayegan, Joon Sang Lee, Donald Jackson, Jack Pollard. 2022. "Evaluating diverse deconvolution methods for tumor spatial transcriptomic datasets." *Journal for ImmunoTherapy of Cancer* 2022;10 <https://doi.org/10.1136/jitc-2022-SITC2022.0926>

### **Collaborative Publications**

6. Minzhe Guo, Michael P. Morley, Cheng Jiang, Yixin Wu, **Guangyuan Li**, Yina Du, Shuyang Zhao et al. 2023. "Guided Construction of Single cell Reference for Human and Mouse Lung." *Nature Communications* 14 (1): 1-20. <https://www.nature.com/articles/s41467-023-40173-5>
7. Kang Jin, Daniel Schnell, **Guangyuan Li**, Nathan Salomonis, V.B. Surya Prasath, Rhonda Szczesniak, Bruce J. Aronow. 2022 "CellDrift: Inferring Perturbation Responses in Temporally-Sampled Single Cell Data." *Briefing in Bioinformatics*. <https://doi.org/10.1093/bib/bbac324>
8. Zhang Xuan, Baobao Song, Maximillian J. Carlino, **Guangyuan Li**, Kyle Ferchen, Mi Chen, Evrett N. Thompson, et al. 2024. "An Immunophenotype-Coupled Transcriptomic Atlas of Human Hematopoietic Progenitors." *Nature Immunology*, March, 1–13. <https://www.nature.com/articles/s41590-024-01782-4>
9. L. Lambourne, K. Mattioli, C. Santoso, G. Sheynkman, S. Inukai, B. Kaundal, A. Berenson, K. Spirohn-Fitzgerald, A. Bhattacharjee, E. Rothman, S. Shrestha, F. Laval, Z. Yang, D. Bisht, J. A. Sewell, **G. Li**, A. Prasad, S. Phanor, R. Lane, D. M. Campbell, T. Hunt, D. Balcha, M. Gebbia, J.-C. Twizere, T. Hao, A. Frankish, J. A. Riback, N. Salomonis, M. A. Calderwood, D. E. Hill, N. Sahni, M. Vidal, M. L. Bulyk, J. I. Fuxman Bass, 2024 "Widespread variation in molecular interactions and regulatory properties among transcription factor isoforms". *bioRxiv*, <https://www.biorxiv.org/content/10.1101/2024.03.12.584681v2>