

Education

University of Virginia (Ming Li lab, UVa) Ph.D., Biomedical Sciences (Bioinformatics) Dissertation URL: http://libra.virginia.edu/catalog/libra-oa:11462	2013-2016
University of Wisconsin-Madison (UW-Madison) Master, Information Science	2009-2011
Renmin University of China (Renmin U) Bachelor, Information Management and Information System	2005-2009

Research Experience

Assistant Professor at Rutgers University Department of Genetics & Human Genetics Institute of New Jersey

2024-

- Perform CRISPR screening in mouse and human dendritic cells to identify key regulators for dendritic cell maturation and immune-regulation
- Investigate spatial distributions of dendritic cells and their interactions with neighboring cells in metastatic melanoma using spatial transcriptomics and single-cell assays
- Identify transcriptional signatures for aging microglia using different statistical and machine learning methods
- Develop accurate cell segmentation methods for sequencing-based spatial transcriptomics data
- Build mathematical and deep learning models to understand gene regulatory network rewiring in single cells within their spatial contexts

Research Scientist (Manolis Kellis lab) at MIT Computer Science & Artificial Intelligence Lab and Broad Institute

2019-2023

- *Cancer*: Investigated cell-type-specific and cell communication alterations underlying heterogeneous responses of metastatic melanoma to immune checkpoint inhibitors
- *Obesity*: Dissected single-cell multi-tissue multi-omics obesity-exercise interaction
- *Down Syndrome*: Determined susceptible cell types, genes, pathways, and master regulators for Alzheimer's Disease in Down Syndrome (DS) using single-cell dissection of postmortem human brains
- *Deep learning*: Inferred sample-specific contextualized graphical models using clinical, genetics and transcriptomics data to reveal gene regulatory network heterogeneity in cancer
- *Leadership*: Strategic planning of projects and grant writing with collaborators from Joslin Diabetes Center, Massachusetts General Hospital, Dana-Farber Cancer Institute, MD Anderson, University of California-Irvine, Novo Nordisk & Takeda
- *Mentorship*: Mentored graduate and undergraduate students for cancer, metabolism, DS, and method development projects

Postdoctoral Research Fellow (Sunney Xie lab) at Boston Children's Hospital and Harvard Medical School

2019 (PI moved to China)

- Developed a single-cell mass spectrometry project, designed synthetic peptides and conducted preliminary data analysis
- Wrote a computational program for a novel single-cell methylation technique
- Collaborated on computational analysis for non-invasive preimplantation genetic tests of mono- and poly-genic diseases

Postdoctoral Researcher (Mazhar Adli lab) at UVa Biochemistry and Molecular Genetics

2016-2019

- Conceived, developed, and conducted independent research on the association between transcription factor

- (TF) binding and somatic mutations in breast and prostate cancers, which generated a \$25K grant award
- Co-led studies of pancreatic and ovarian cancers by focusing on hypothesis generation using ChIP-seq, ATAC-seq, RNA-seq, and CROP-seq data
 - Designed CRISPR-STOP and CRISPR screening libraries and optimized screening strategies

Research Specialist (Ming Li lab) at UVa Psychiatry and Neurobehavioral Sciences

2011-2013

- Designed analytical and computational pipelines for terabyte-scale genetic datasets
- Conceived and performed statistical analysis for family and case-control studies with thousands of subjects

Teaching Experience

Genomes, Department of Genetics Elective

Spring 2026

Grants and Fellowships

Rutgers Cancer Institute Collaborative/Translational Research Pilot Award	2025-2026
School of Arts and Sciences Seed Grant	2025-2027
Busch Biomedical Grant	2024-2026
NIH T32-DK110919	2020-2021
Alana Postdoctoral Fellowship, MIT	2019-2020
UVa Cancer Center Trainee Grant	2018-2019

Honors and Awards

Rutgers Cancer Institute New Investigator Award	2024
Outstanding Student Award of Biochemistry & Molecular Genetics, UVa	2016

Publications

* co-first author, † co-corresponding author, **people from my lab**

29. **Sun, C.***, Thomas, R.*, Stringer, C.*, Galani, K., Ho, L.-L., Sun, N., Renfro A., Wright, S., Firenze, R., Tsai, L.-H., Head, E.#, Kellis, M.#, **Yang, J.#**, 2026. Epigenetically constrained astrocyte states underlie prefrontal cortex vulnerability in Down syndrome associated Alzheimer disease. <https://www.biorxiv.org/content/10.64898/2026.04.17.719050v1> (bioRxiv)
28. **Wu, L.C.***, **Hu, X.***, **Zhan, F.**, **Sun, C.**, **Gonzales, J.**, Ofer, R., Tran, T., Verzi, M.P., Liu, L.#, **Yang, J.#**, 2026. STCS: A Platform-Agnostic Framework for Cell-Level Reconstruction in Sequencing-Based Spatial Transcriptomics. <https://www.biorxiv.org/content/10.64898/2026.02.26.708370v2> (bioRxiv)
27. Han, X., Shen, J., Yan, J., **Tacke, R.**, Dai, W., Mao, Q., Daguplo, H.Q., Liu, S., Islam, A., Liu, T., Koch, M.C., Lin, R.Z., Li, H., Anthony, T., Xie, P., Zhang, L., Gao, S., Simon, M.C., Chen, X., **Yang, J.**, Su, X., Zong, W., 2026. Impaired nitrogenous waste clearance promotes hepatocellular carcinoma. *Science Advances*. <https://doi.org/10.1126/sciadv.aec0766>
26. **Asnani, M.**, **Yang, J.**, 2025. Optimized Ex Vivo Differentiation of CD103+ Dendritic Cells and High-Efficiency Retroviral Transduction of Mouse Bone Marrow HSCs. <https://doi.org/10.1101/2025.09.21.677651> (bioRxiv)
25. Ofer, R., Tran, T., He, P., Qiu, X., **Hu, X.**, Zachariah, E., Krier, C., Saxena, A., **Yang, J.**, Verzi, M.P., 2025. A Spatial and Temporal Transcriptomic Atlas of Mouse Intestinal Regeneration. *Nature Communications* (under review). <https://doi.org/10.1101/2025.08.06.668727> (bioRxiv)
24. Middelbeek, R.J.W.*, **Yang, J.***, Nigro, P., James, B., Papadopoulos, D., Simpson, L.K., Park, J., Vamvini, M., Ho, L.-L., Zhang, H., Carbone, N.P., Hirshman, M.F., Kellis, M., Goodyear, L.J., 2025. Type 2 Diabetes

- and Obesity Alter Exercise Training-Induced Transcriptional Adaptations to Subcutaneous White Adipose Tissue. *Cell Metabolism* (under review). <https://doi.org/10.1101/2025.10.11.681273> (bioRxiv)
23. Huang, A.Y.*, Burke, K.P.*, Porter, R., Fatouros, P., Vokes, N., Ricker, C., Robitschek, E., Tarantino, G., Aprati, T.J., Glettig, M.C., Chen, J., He, Y., **Yang, J.**, Wang, C., Ho, L.-L., Galani, K., Freeman, G., Van Allen, E.M., Kellis, M., Boland, G.M., Sharpe, A.H., Liu, D., 2025. Immune infiltrate predicts response to α PD1/ α CTLA4 but not α PD1 and distinguishes programs of primary resistance in metastatic melanoma. *Science Translational Medicine* (under review). <https://doi.org/10.1101/2024.10.29.620300> (bioRxiv)
 22. Qiu, M., Hu, X., Zhan, F., Yun, S., Peng, J., Zhang, R., Kailkhura, B., **Yang, J.**, Chen, T., 2025. GRNFormer: A biologically-guided framework for integrating gene regulatory networks into RNA foundation models. In *Findings of the Association for Computational Linguistics: ACL 2025*, pages 3805–3819, Vienna, Austria. Association for Computational Linguistics. <https://doi.org/10.18653/v1/2025.findings-acl.196>
 21. **Yang, J.*†**, Wang, C.*, Fu, D.*, Ho, L.-L., Galani, K., Chen, L., Gonzalez, J., Fu, J., Huang, A.Y., Frederick, D.T., He, L., Asnani, M., Tacke, R., Robitschek, E.J., Yadav, S.K., Deng, W., Burke, K.P., Sharova, T., Sullivan, R.J., Weiss, S., Rai, K., Liu, D., Boland, G.M.†, Kellis, M.†, 2025. Mature and migratory dendritic cells promote immune infiltration and response to anti-PD-1 checkpoint blockade in metastatic melanoma. *Nature Communications*. <https://doi.org/10.1038/s41467-025-62878-5>
 20. Babu, S., Chen, J., Baron, C.S., Sun, K., Robitschek, E., McConnell, A., Wu, C., Dedeilia, A., Sade-Feldman, M., Modhurima, R., Manos, M.P., Chen, K.Y., Cox, A.M., Ludwig, C.G., Kellis, M., Buchbinder, E.I., Hacohen, N., **Yang, J.**, Boland, G.M., Abraham, B.J., Liu, D., Zon, L.I., Insko, M.L., 2025. Specific oncogene activation of the cell of origin in mucosal melanoma. *Nature Communications* 16, 6750. <https://doi.org/10.1038/s41467-025-61937-1>
 19. Revach, O., Cicerchia, A.M., Shorer, O., Palin, C.A., Petrova, B., Anderson, S., Liu, B., Park, J., Chen, L., Mehta, A., Wright, S.J., McNamee, N., Tal-Mason, A., Cattaneo, G., Tiwari, P., Xie, H., Sweere, J.M., Cheng, L., Sigal, N., Enrico, E., Milijakovic, M., Evans, S.A., Nguyen, N., Whidden, M.E., Srinivasan, R., Spitzer, M.H., Sun, Y., Sharova, T., Lawless, A., Michaud, W.A., Rasmussen, M.Q., Fang, J., Brook, J.R., Chen, F., Wang, X., Ferrone, C.R., Lawrence, D.P., Sullivan, R.J., Liu, D., Sachdeva, U.M., Sen, D.R., Flaherty, K.T., Manguso, R.T., Bod, L., Kellis, M., Boland, G.M., Yizhak, K., **Yang, J.**, Kanarek, N., Sade-Feldman, M., Hacohen, N., Jenkins, R.W., 2025. Overcoming resistance to immunotherapy by targeting CD38 in human tumor explants. *Cell Reports Medicine* 6, no. 7. <https://doi.org/10.1016/j.xcrm.2025.102210>.
 18. Ellington, C.N., Lengerich, B.J., Watkins, T.B.K., **Yang, J.**, Adduri, A.K., Mahbub, S., Xiao, H., Kellis, M., Xing, E.P., 2025. Learning to estimate sample-specific transcriptional networks for 7,000 tumors. *Proceedings of the National Academy of Sciences* 122(21). <https://doi.org/10.1073/pnas.2411930122>
 17. Pujadas Liwag, E.M., Wei, X., Acosta, N., Carter, L.M., **Yang, J.**, Almossalha, L.M., Jain, S., Daneshkhah, A., Rao, S.S.P., Seker-Polat, F., MacQuarrie, K.L., Ibarra, J., Agrawal, V., Aiden, E.L., Kanemaki, M.T., Backman, V., Adli, M., 2024. Depletion of lamins B1 and B2 promotes chromatin mobility and induces differential gene expression by a mesoscale-motion-dependent mechanism. *Genome Biol* 25, 77. <https://doi.org/10.1186/s13059-024-03212-y>
 16. Wang, C., Chen, L., Fu, D., Liu, W., Puri, A., Kellis, M., **Yang, J.**, 2024. Antigen presenting cells in cancer immunity and mediation of immune checkpoint blockade. *Clin Exp Metastasis*. <https://doi.org/10.1007/s10585-023-10257-z>
 15. Liu, W., Puri, A., Fu, D., Chen, L., Wang, C., Kellis, M., **Yang, J.**, 2023. Dissecting the tumor microenvironment in response to immune checkpoint inhibitors via single-cell and spatial transcriptomics. *Clin Exp Metastasis*. <https://doi.org/10.1007/s10585-023-10246-2>
 14. Nigro, P.*, Vamvini, M.*, **Yang, J.**, Caputo, T., Ho, L., Carbone, N.P., Papadopoulos, D., Conlin, R., He, J., Hirshman, M.F., White, J.D., Robidoux, J., Hickner, R.C., Nielsen, S., Pedersen, B.K., Kellis, M.,

- Middelbeek, R.J.W., Goodyear, L.J., 2023. Exercise Training Remodels Inguinal White Adipose Tissue through Adaptations in Innervation, Vascularization, and the Extracellular Matrix. *Cell Reports* 42, no. 4. <https://doi.org/10.1016/j.celrep.2023.112392>
13. **Yang, J.***, Vamvini, M.*, Nigro, P.*, Ho, L.-L., Galani, K., Alvarez, M., Tanigawa, Y., Renfro, A., Carbone, N.P., Laakso, M., Agudelo, L.Z., Pajukanta, P., Hirshman, M.F., Middelbeek, R.J.W., Grove, K., Goodyear, L.J., Kellis, M., 2022. Single-cell dissection of the obesity-exercise axis in adipose-muscle tissues implies a critical role for mesenchymal stem cells. *Cell Metabolism* 34, 1578-1593.e6. <https://doi.org/10.1016/j.cmet.2022.09.004>
 12. Maitituoheti, M., Shi, A., Tang, M., Ho, L.-L., Terranova, C., Galani, K., Keung, E.Z., Creasy, C.A., Wu, M., Chen, J., Chen, N., Singh, A.K., Chaudhri, A., Anvar, N.E., Tarantino, G., **Yang, J.**, Sarkar, S., Jiang, S., Malke, J., Haydu, L., Burton, E., Davies, M.A., Gershenwald, J.E., Hwu, P., Lazar, A., Cheah, J.H., Soule, C.K., Levine, S.S., Bernatchez, C., Saladi, S.V., Liu, D., Wargo, J., Boland, G.M., Kellis, M., Rai, K., 2022. Enhancer Reprogramming in Melanoma Immune Checkpoint Therapy Resistance. *Nature Communications* (under review). <https://doi.org/10.1101/2022.08.31.506051>
 11. Ozturk, H.*, Cingoz, H.*, Tufan, T.*, **Yang, J.***, Adair, S.J., Tummala, K.S., Kuscü, C., Kinali, M., Comertpay, G., Nagdas, S., Goudreau, B.J., Luleyap, H.U., Bingul, Y., Ware, T.B., Hwang, W.L., Hsu, K., Kashatus, D.F., Ting, D.T., Chandel, N.S., Bardeesy, N., Bauer, T.W., Adli, M., 2022. ISL2 is a putative tumor suppressor whose epigenetic silencing reprograms the metabolism of pancreatic cancer. *Developmental Cell* 57, 1331-1346.e9. <https://doi.org/10.1016/j.devcel.2022.04.014>
 10. Wei, X.*, **Yang, J.***, Adair, S.J., Ozturk, H., Kuscü, C., Lee, K.Y., Kane, W.J., O'Hara, P.E., Liu, D., Demirlenk, Y.M., Habieb, A.H., Yilmaz, E., Dutta, A., Bauer, T.W., Adli, M., 2020. Targeted CRISPR screening identifies PRMT5 as synthetic lethality combinatorial target with gemcitabine in pancreatic cancer cells. *Proceedings of the National Academy of Sciences* 117, 28068–28079. <https://doi.org/10.1073/pnas.2009899117>
 9. Shang, S., **Yang, J.**, Jazaeri, A.A., Duval, A.J., Tufan, T., Fischer, N.L., Benamar, M., Guessous, F., Lee, I., Campbell, R.M., Ebert, P.J., Abbas, T., Landen, C.N., Difeo, A., Scacheri, P.C., Adli, M., 2019. Chemotherapy-Induced Distal Enhancers Drive Transcriptional Programs to Maintain the Chemoresistant State in Ovarian Cancer. *Cancer Res* 79, 4599–4611. <https://doi.org/10.1158/0008-5472.CAN-19-0215>
 8. **Yang, J.**, Adli, M., 2019. Mapping and Making Sense of Noncoding Mutations in the Genome. *Cancer Research* 79, 4309–4314. <https://doi.org/10.1158/0008-5472.CAN-19-0905>
 7. **Yang, J.***, Wei, X.*, Tufan, T., Kuscü, C., Unlu, H., Farooq, S., Demirtas, E., Paschal, B.M., Adli, M., 2018. Recurrent mutations at estrogen receptor binding sites alter chromatin topology and distal gene expression in breast cancer. *Genome Biology* 19, 190. <https://doi.org/10.1186/s13059-018-1572-4>
 6. Szlachta, K., Kuscü, C., Tufan, T., Adair, S.J., Shang, S., Michaels, A.D., Mullen, M.G., Fischer, N.L., **Yang, J.**, Liu, L., Trivedi, P., Stelow, E.B., Stukenberg, P.T., Parsons, J.T., Bauer, T.W., Adli, M., 2018. CRISPR knockout screening identifies combinatorial drug targets in pancreatic cancer and models cellular drug response. *Nature Communications* 9, 4275. <https://doi.org/10.1038/s41467-018-06676-2>
 5. Kuscü, C., Parlak, M., Tufan, T., **Yang, J.**, Szlachta, K., Wei, X., Mammadov, R., Adli, M., 2017. CRISPR-STOP: gene silencing through base-editing-induced nonsense mutations. *Nat Meth* 14, 710–712. <https://doi.org/10.1038/nmeth.4327>
 4. **Yang, J.**, Li, M.D., 2016. Converging findings from linkage and association analyses on susceptibility genes for smoking and other addictions. *Molecular Psychiatry* 21, 992–1008. <https://doi.org/10.1038/mp.2016.67>
 3. **Yang, J.***, Wang, S.*, Yang, Z., Hodgkinson, C.A., Iarikova, P., Ma, J.Z., Payne, T.J., Goldman, D., Li, M.D., 2015. The contribution of rare and common variants in 30 genes to risk nicotine dependence. *Mol Psychiatry* 20, 1467–1478. <https://doi.org/10.1038/mp.2014.156>

2. **Yang, J.**, Li, M.D., 2014. Association and interaction analyses of 5-HT₃ receptor and serotonin transporter genes with alcohol, cocaine, and nicotine dependence using the SAGE data. *Hum Genet* 133, 905–918. <https://doi.org/10.1007/s00439-014-1431-7>
 1. Cui, W.Y., Wang, S., **Yang, J.**, Yi, S.G., Yoon, D., Kim, Y.-J., Payne, T.J., Ma, J.Z., Park, T., Li, M.D., 2013. Significant association of CHRNA3 variants with nicotine dependence in multiple ethnic populations. *Molecular Psychiatry* 18, 1149–1151. <https://doi.org/10.1038/mp.2012.190>
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Invited Talks

12. Learning Cells in Space: Spatial AI, Multi-Omics Modeling, and the Vision of a Virtual Immune Twin. Rutgers Health AI Virtual Seminar. January 8, 2026.
11. Serendipity, Resilience, and Data-Driven Biology: My Path to Biomedical Science. Rutgers Women in Biomedical Sciences (WIBS) club event, Rutgers University, Newark, NJ. November 20, 2025.
10. Decoding Dendritic Cell in Cancer: Integrating Single-Cell Multiomics, Spatial Transcriptomics, and AI-Driven Models. Institute of Quantitative Biomedicine Seminar, Rutgers University, Piscataway, NJ. October 22, 2025.
9. Dissecting Dendritic Cell Regulation and Tumor Immunity: From mregDC Biology to New Spatial Transcriptomics Approaches. Department of Microbiology, Biochemistry & Molecular Genetics and Public Health Research Institute Seminar, New Jersey Medical School, Newark, NJ. October 14, 2025.
8. Dissecting Dendritic Cell Regulation and Tumor Immunity: From mregDC Biology to New Spatial Transcriptomics Approaches. Cancer Metabolism and Immunology Seminar, Rutgers Cancer Institute, New Brunswick, NJ. September 17, 2025.
7. Decoding Immune Cell Fate in Cancer: Integrating Single-Cell Multiomics, Spatial Transcriptomics, and AI-Driven Models. Center for Biomedical Informatics and Health AI (BMIHAI) Annual Symposium, New Brunswick, NJ. May 13, 2025.
6. Single-Cell Dissection Across Tissue and Disease: Insights into Obesity and Cancer. Child Health Institute of New Jersey, New Brunswick, NJ. October 22, 2024.
5. Single-cell dissection of metastatic melanoma: Mature and migratory dendritic cells promote immune infiltration and response to anti-PD-1 checkpoint blockade. Systems Biology, Cancer Institute of New Jersey, New Brunswick, NJ. May 1, 2024.
4. Using single-cell computation and biology to overcome tissue and disease boundaries. Department of Biomedical Engineering, Tianjin Medical University, Tianjin, China. September 11, 2023.
3. Single-cell transcriptomic and epigenomic landscapes of innate and adaptive immune cells in metastatic melanoma treated with immunotherapy. 2nd Rutgers Chinese Faculty Cancer Symposium, Piscataway, NJ. June 17, 2023.
2. Single-cell epigenomic and transcriptomic dissection of melanoma immunotherapy response. 9th International Cancer Metastasis Congress, San Francisco, CA. May 4, 2023.
1. Using Single-cell computation and biology to overcome tissue and disease boundaries. INSERM MD PHD program conference (virtual). March 19, 2023.

Poster Presentations from Yang Lab at National and International Conferences

2. Hu, X., Zhan, F., Wu, L.C., Gonzalez, J., Sun, C., Ofer, R., Tran, T., Verzi, M., Yang, J. (2026). STCS: Spatial Transcriptomics Cell Segmentation Outperforms Existing Methods On Multiple Slides. Presented at AACR Annual Meeting, April 17-22.

1. Asnani, M., Yang, J. (2026). Defining The Immunoregulatory Molecular Drivers Of Dendritic Cells Using CRISPR Screens In Ex-Vivo Models. Presented at AACR Annual Meeting, April 17-22.

Conference Oral Presentations

6. Ellington, C., Lengerich, B., Watkins, T., **Yang, J.**, Kellis, M., Xing, E. (2023). Contextualized Networks Reveal Heterogeneous Transcriptomic Regulation in Tumors at Sample-Specific Resolution. Presented at the NeurIPS Generative AI and Biology workshop, December 16.
5. Ellington, C., Lengerich, B., Watkins, T., **Yang, J.**, Kellis, M., Xing, E. (2022). Sample-specific contextualized graphical models using clinical and molecular data reveal transcriptional network heterogeneity across 7000 tumors. Presented at CSHL Biological Data Science, November 9-12.
4. **Yang, J.***, Vamvini, M.*, Nigro, P.*, Galani, K., Ho, L., Agudelo, L., Middelbeek, R., Goodyear, L., and Kellis, M. (2022). Single-cell dissection of the obesity-exercise axis in adipose-muscle tissues infers a critical role for mesenchymal stem cells. Presented at Keystone Symposia Adipose Tissue and Metabolic Health, August 7-10.
3. **Yang, J.***, Vamvini, M.*, Nigro, P.*, Galani, K., Ho, L., Agudelo, L., Middelbeek, R., Goodyear, L., and Kellis, M. (2021). Single-cell multi-tissue dissection of obesity-exercise circuitry in mouse. Presented at CSHL The Biology of Genomes, May 11-14.
2. **Yang, J.***, Vamvini, M.*, Nigro, P.*, Galani, K., Ho, L., Agudelo, L., Middelbeek, R., Goodyear, L., and Kellis, M. (2020). Single-cell dissection of obesity-exercise interaction across four tissues. Presented at Annual Meeting of the American Society of Human Genetics (ASHG), October 27-30.
1. **Yang, J.** (2016). Determination of genetic mechanisms underlying smoking addiction. Presented at Graduate Biosciences Society (GBS) Symposium, Charlottesville, Virginia, March 21.

Professional Activities/Scientific Leadership

- External Reviewer for *Nature Reviews*, *Nature Communications*, *Advanced Science*, *Frontiers Immunology*, *Discover Oncology*, *Cell Death Discovery*
- Ad Hoc Early Career Reviewer for NIH Neurobiology of Motivated Behavior Study Section, 2025
- Scientific Editor for Science China, Nature Publishing Group, 2024-2025