

Stanford



Melissa Ko

Postdoctoral Research Fellow, Bioengineering

Bio

BIO

Melissa Ko earned an S.B. in biology from MIT and a PhD in cancer biology from Stanford University. Her graduate research developed novel computational pipelines to make sense of single-cell high-dimensional data collected by biologists. Using visualizations and modeling, Melissa revealed mechanisms of drug resistance in cancer and identified more effective treatment combinations. During her graduate career, Melissa received support from the National Science Foundation (NSF) Graduate Research Fellowship, Stanford's Diversifying Academia, Recruiting Excellence (DARE) Fellowship, and the National Cancer Institute F99/K00 Fellowship.

After transitioning to an education-focused career track, Melissa taught various workshops and courses at Stanford University, Santa Clara University, and Foothill College. During her time as a Thinking Matters Fellow, Melissa also taught Breaking Codes, Living with Viruses, Our Genome, and The Cancer Problem. Melissa is now the Science and Engineering Education Fellow (SEEF) for the Bioengineering department, working on broader educational research projects and curricular change to better understand and support student development as ethical and quantitative thinkers.

Over the years, Melissa has been involved with numerous educational outreach programs including the Splash program at MIT, Stanford, and Berkeley. Through these programs and related efforts, she has taught middle school and high school students in a variety of subjects, from cancer biology to personal finance to poetry. Melissa is dedicated to improving the experience of underrepresented students in all STEM disciplines. She served as a mentor and program leader for numerous Stanford Bioscience programs including SSRP and ADVANCE. Through work with Stanford's Center for Teaching and Learning (CTL), Melissa has also developed diversity and inclusion content for instructors of in-person, online, and hybrid format classes. Melissa continues to serve as a teaching consultant with CTL and focuses on projects relating to equity.

Outside of work, Melissa enjoys cooking, playing video games, reading poetry, and going on family walks with her dog in the park.

HONORS AND AWARDS

- Diversifying Academia, Recruiting Excellence (DARE) Fellowship, Stanford University (2016-2018)
- F99/K00 Predoctoral to Postdoctoral Fellow Transition Award, National Cancer Institute (2016-2018)
- Graduate Research Fellowship, National Science Foundation (2013-2016)

PROFESSIONAL EDUCATION

- Bachelor of Science, Massachusetts Institute of Technology , Biology (2012)
- Doctor of Philosophy, Stanford University , CANBI-PHD (2018)
- SB, Massachusetts Institute of Technology , Biology (2012)

- PhD, Stanford University , Cancer Biology (2018)

STANFORD ADVISORS

- Drew Endy, Postdoctoral Faculty Sponsor

LINKS

- Website: <http://mesako.github.io/>
- LinkedIn: <https://www.linkedin.com/in/mesako/>

Teaching

COURSES

2019-20

- Our Genome: THINK 68 (Win)
- The Cancer Problem: Causes, Treatments, and Prevention: THINK 23 (Spr)

2018-19

- Breaking Codes, Finding Patterns: THINK 3 (Aut)
- Living with Viruses: THINK 61 (Win)
- The Cancer Problem: Causes, Treatments, and Prevention: THINK 23 (Spr)

Publications

PUBLICATIONS

- **Undergraduate Biology Education Research Gordon Research Conference: A Meeting Report.** *CBE life sciences education*
Dolan, E. L., Borrero, M., Callis-Duehl, K., Musgrove, M. M., de Lima, J., Ero-Tolliver, I., Gerhart, L. M., Goodwin, E. C., Hamilton, L. R., Henry, M. A., Herrera, J., Huot, B., Kiser, et al
2020; 19 (2): mr1
- **Deep profiling of apoptotic pathways with mass cytometry identifies a synergistic drug combination for killing myeloma cells.** *Cell death and differentiation*
Teh, C. E., Gong, J., Segal, D., Tan, T., Vandenberg, C. J., Fedele, P. L., Low, M. S., Grigoriadis, G., Harrison, S. J., Strasser, A., Roberts, A. W., Huang, D. C., Nolan, et al
2020
- **FLOW-MAP: a graph-based, force-directed layout algorithm for trajectory mapping in single-cell time course datasets.** *Nature protocols*
Ko, M. E., Williams, C. M., Fread, K. I., Goggin, S. M., Rustagi, R. S., Fragiadakis, G. K., Nolan, G. P., Zunder, E. R.
2020
- **Multi-omic single-cell snapshots reveal multiple independent trajectories to drug tolerance in a melanoma cell line.** *Nature communications*
Su, Y., Ko, M. E., Cheng, H., Zhu, R., Xue, M., Wang, J., Lee, J. W., Frankiw, L., Xu, A., Wong, S., Robert, L., Takata, K., Yuan, et al
2020; 11 (1): 2345
- **Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen** *NATURE COMMUNICATIONS*
Menden, M. P., Wang, D., Mason, M. J., Szalai, B., Bulusu, K. C., Guan, Y., Yu, T., Kang, J., Jeon, M., Wolfinger, R., Nguyen, T., Zaslavskiy, M., Jang, et al
2019; 10: 2674
- **CDX2 is an amplified lineage-survival oncogene in colorectal cancer** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Salari, K., Spulak, M. E., Cuff, J., Forster, A. D., Giacomini, C. P., Huang, S., Ko, M. E., Lin, A. Y., van de Rijn, M., Pollack, J. R.
2012; 109 (46): E3196-E3205

PRESENTATIONS

- FLOWMAPR—A graph-based visualization tool for single-cell omics data across time. - Cold Spring Harbor Laboratory Meeting: Single Cell Analyses 2017

- High-Dimensional Single-Cell Data Elucidates the Role of Bcl-2 Family Proteins in Drug Sensitivity in Multiple Myeloma. - CYTO 2017