

EDUCATION

PhD in Physiology, Biophysics and Systems Biology Weill Cornell Medicine (Cornell University), New York, NY	September 2013 - August 2019
MA in Biomedical Informatics Columbia University, New York, NY	September 2010 - May 2012
MS in Pharmaceutical Science National Taiwan University, Taipei, Taiwan	September 2005 - May 2007
Dual Bachelor of Science in Chemistry, Information Management National Taiwan University, Taipei, Taiwan	September 1999 - May 2005

RELATED EXPERIENCE

Postdoctoral associate. Massachusetts Institute of Technology. Boston, MA 2026 April - Present
Advisor: Dr. Devavrat Shah. Department of Electrical Engineering and Computer Science

- Apply cutting-edge machine learning, statistics, and AI methods for improving diagnostics, risk stratification, and outcomes analyses in cancers.

Bioinformatics scientist. Dana-Farber Cancer Institute. Boston, MA 2024 Oct – 2026 March
Advisor: Dr. Michael Tolstorukov. Department of Informatics and Analytics, bioinformatics service core

- Developed and implemented computational pipelines for analyzing whole-exome sequencing (WES), whole-genome sequencing (WGS), bulk RNA-seq, ATAC-seq, and CUT&RUN data in T-cell lymphoma research.
- Performed single-cell transcriptomics and single-cell immune repertoire sequencing (TCR-seq) analysis to investigate anti-KLRG1 antibody (mAb208) therapy in NK/T-cell lymphoma pilot study.
- Developed and optimized NGS data analysis pipelines on high-performance computing (HPC) and cloud-based platforms (DNAnexus) to enable large-scale computational oncology studies.

Postdoctoral fellow. Memorial Sloan Kettering Cancer Center. New York, NY 2020 - 2024 Sep
Advisor: Dr. Ed Reznik. Department of Computational Oncology

- Developed a multi-modal pipeline integrating spatial metabolomics (MALDI) and multiplexed immunofluorescence imaging data to characterize the interactions among metabolites, immune cells, and cancer cells in a breast cancer mouse model with anti-PD-1 treatment resistance.
- Performed single-cell RNA-seq analysis to delineate the functional consequences of mitochondrial DNA mutations on immunotherapy response in melanoma.
- Employed a concordance-based meta-analysis to reveal gene-metabolite covariations across 988 tumors from 11 different cancer types.
- Conducted integrated analysis and consensus clustering of genomics, bulk RNA-seq, and metabolomics to nominate and characterize subtypes in a rare form of thyroid cancer.

Graduate Research Assistant. Weill Cornell Medicine. New York, NY 2013 - 2019
Advisor: Dr. Ekta Khurana. Department of Physiology, Biophysics, and Systems Biology

- Developed the statistical inference algorithm (CNCDriver) to analyze single nucleotide variants (SNVs) from whole-genome sequencing data to identify cancer drivers in protein-coding and non-coding regions.
- Interrogated cancer driver candidates from 40 TB of multi-omics data, including RNA-seq and copy number.
- Collaborated with wet-lab scientists to design CRISPR experiments for the functional validation of SNVs.
- Delivered presentations at The Cancer Genome Atlas (TCGA) and PanCancer Analysis of Whole Genomes (PCAWG) consortium meetings.

Graduate Research Assistant. Columbia University. New York, NY
Advisor: Dr. Raul Rabadan. Department of Biomedical Informatics

2011 - 2012

- Assessed data quality and analyzed exome-sequencing data from The Cancer Genome Atlas (TCGA) to identify the *FGFR3-TACC3* fusion event in brain tumor (GBM), which occurred in 10% of pan-cancer cases.
- Developed a new gene-fusion detection method from whole-exome sequencing data, which was subsequently integrated into the Rabadan Lab's genomics analysis pipeline.

BIOINFORMATICS SOFTWARE

Non-Coding Cancer Driver Web App (CNCDatabase)

March 2019

• github.com/mil2041/CNCDatabase

- Designed a relational database system storing the non-coding cancer driver evidence curated from the literature.
- Developed a front-end web application that offers summary statistics and data visualizations for non-coding cancer evidence across 28 cancer types.

Cancer Driver Detection Package in R (CNCDriver)

September 2017

• github.com/mil2041/CNCDriver

- Developed a new statistical inference method to identify coding and non-coding cancer drivers from 1,962 whole-genome sequencing tumor samples. The package also incorporated parallel computing to reduce the run time by 80%.
- Integrated analysis of genomic datasets from WGS, WXS, 1000 genome, ENCODE, Roadmap Epigenomics, ChIP-seq, Hi-C, and ChIA-PET.

Integrated Pathway Analysis Package in R (NetBoxr)

October 2015

• github.com/mil2041/netboxr

- Implemented the “NetBox” algorithm in R and prepared technical documentations to facilitate cellular pathway discovery tutorial.
- Contributed the integrated pathway analysis in three TCGA publications, including sarcoma, mesothelioma, and testicular germ cell tumors, under the supervision of Professor Chris Sander.

Key SKILLS

Primary languages: proficient in Python, R, UNIX environment, Scripting languages, SQL, Git

AI/ML Framework: PyTorch, TensorFlow

Bioinformatics tools: igraph, DESeq2, Kallisto, Samtools, BWA, Bowtie, ASCAT, starAligner, FunSeq2, bedtools

Cloud computing: high-performance computing environment

Databases: MySQL, PostgreSQL

Selected PUBLICATIONS

5. Mahnoor Mahmood, **Eric Minwei Liu**, Amy L. Shergold, Elisabetta Tolla, Jacqueline Tait-Mulder, Alejandro Huerta-Uribe, Engy Shokry, et al. “[Mitochondrial DNA Mutations Drive Aerobic Glycolysis to Enhance Checkpoint Blockade Response in Melanoma.](#)” *Nature Cancer*, January, 1–14. 10.1038/s43018-023-00721-w. (2024)
4. Elisa Benedetti*, **Eric Minwei Liu***, Cerise Tang*, Fengshen Kuo, Mustafa Buyukozkan, Tricia Park, Jinsung Park, et al. “[A Multimodal Atlas of Tumour Metabolism Reveals the Architecture of Gene–Metabolite Covariation.](#)” *Nature Metabolism* 5 (6): 1029–44. 10.1038/s42255-023-00817-8. (2023)
3. Ian Ganly*, **Eric Minwei Liu***, Fengshen Kuo, Vladimir Makarov, Yiyu Dong, Jinsung Park, Yongxing Gong, Alexander N Gorelick, Jeffrey A Knauf, Elisa Benedetti, Jacqueline Tait-Mulder, Luc GT Morris, James A Fagin, Andrew M Intlekofer, Jan Krumsiek, Payam A Gammage, Ronald Ghossein, Bin Xu, Timothy A Chan, Ed Reznik “[Mitonuclear genotype remodels the metabolic and microenvironmental landscape of Hürthle cell carcinoma](#)”. *Sci. Adv.* 8, eabn9699. 10.1126/sciadv.abn9699. (2022)

2. **Eric Minwei Liu***, Alexander Martinez-Fundichely, Rajesh Bollapragada, Maurice Spiewack, Ekta Khurana
“[CNCDatabase: a database of non-coding cancer drivers](#)”, *Nucleic Acids Res.* 49, D1094–D1101 (2021)

1. **Eric Minwei Liu***, Alexander Martinez-Fundichely*, Bianca Jay Diaz*, Boaz Aronson, Tawny Cuykendall, Matthew MacKay, Priyanka Dhingra, Elissa WP Wong, Ping Chi, Effie Apostolou, Neville E Sanjana, Ekta Khurana
“[Identification of Cancer Drivers at CTCF Insulators in 1,962 Whole Genomes](#)”, *Cell Systems*, 8,4460455. e8 (2019)

PUBLICATIONS

21. Mahnoor Mahmood, **Eric Minwei Liu**, Amy L. Shergold, Elisabetta Tolla, Jacqueline Tait-Mulder, Alejandro Huerta-Uribe, Engy Shokry, et al. “[Mitochondrial DNA Mutations Drive Aerobic Glycolysis to Enhance Checkpoint Blockade Response in Melanoma](#).” *Nature Cancer*, January, 1–14. 10.1038/s43018-023-00721-w. (2024)

20. Cerise Tang, Amy X. Xie, **Eric Minwei Liu**, Fengshen Kuo, Minsoo Kim, Renzo G. DiNatale, Mahdi Golkaram, et al. “[Immunometabolic Coevolution Defines Unique Microenvironmental Niches in ccRCC](#).” *Cell Metabolism* 35 (8): 1424-1440.e5. 10.1016/j.cmet.2023.06.005. (2023)

19. Elisa Benedetti*, **Eric Minwei Liu***, Cerise Tang*, Fengshen Kuo, Mustafa Buyukozkan, Tricia Park, Jinsung Park, et al. “[A Multimodal Atlas of Tumour Metabolism Reveals the Architecture of Gene–Metabolite Covariation](#).” *Nature Metabolism* 5 (6): 1029–44. 10.1038/s42255-023-00817-8. (2023)

* These authors have contributed equally to this work.

18. Ian Ganly*, **Eric Minwei Liu***, Fengshen Kuo, Vladimir Makarov, Yiyu Dong, Jinsung Park, Yongxing Gong, Alexander N Gorelick, Jeffrey A Knauf, Elisa Benedetti, Jacqueline Tait-Mulder, Luc GT Morris, James A Fagin, Andrew M Intlekofer, Jan Krumsiek, Payam A Gammage, Ronald Ghossein, Bin Xu, Timothy A Chan, Ed Reznik
“[Mitonuclear genotype remodels the metabolic and microenvironmental landscape of Hürthle cell carcinoma](#)”. *Sci. Adv.* 8, eabn9699. 10.1126/sciadv.abn9699. (2022)

* These authors have contributed equally to this work.

17. Fanying Tang, Duo Xu, Shangqian Wang, Chen Khuan Wong, Alexander Martinez-Fundichely, Cindy J Lee, Sandra Cohen, Jane Park, Corinne E Hill, Kenneth Eng, Rohan Bareja, Teng Han, **Eric Minwei Liu**, Ann Palladino, Wei Di, Dong Gao, Wassim Abida, Shaham Beg, Loredana Puca, Maximiliano Meneses, Elisa de Stanchina, Michael F Berger, Anuradha Gopalan, Lukas E Dow, Juan Miguel Mosquera, Himisha Beltran, Cora N Sternberg, Ping Chi, Howard I Scher, Andrea Sboner, Yu Chen, Ekta Khurana “[Chromatin profiles classify castration-resistant prostate cancers suggesting therapeutic targets](#)”, *Science* 376, eabe1505. 10.1126/science.abe1505. (2022)

16. David Danko, Daniela Bezdán, Evan E Afshin, Sofia Ahsanuddin, Chandrima Bhattacharya, Daniel J Butler, Kern Rei Chng, Daisy Donnellan, Jochen Hecht, Katelyn Jackson, Katerina Kuchin, Mikhail Karasikov, Abigail Lyons, Lauren Mak, Dmitry Meleshko, Harun Mustafa, Beth Mutai, Russell Y Neches, Amanda Ng, Olga Nikolayeva, Tatyana Nikolayeva, Eileen Png, Krista A Ryon, Jorge L Sanchez, Heba Shaaban, Maria A Sierra, Dominique Thomas, Ben Young, Omar O Abudayyeh, Josue Alicea, Malay Bhattacharyya, Ran Blekhman, Eduardo Castro-Nallar, Ana M Cañas, Aspasia D Chatziefthimiou, Robert W Crawford, Francesca De Filippis, Youping Deng, Christelle Desnues, Emmanuel Dias-Neto, Marius Dybwad, Eran Elhaik, Danilo Ercolini, Alina Frolova, Dennis Gankin, Jonathan S Gootenberg, Alexandra B Graf, David C Green, Iman Hajirasouliha, Jaden JA Hastings, Mark Hernandez, Gregorio Iraola, Soojin Jang, Andre Kahles, Frank J Kelly, Kaymisha Knights, Nikos C Kyrpides, Paweł P Łabaj, Patrick KH Lee, Marcus HY Leung, Per O Ljungdahl, Gabriella Mason-Buck, Ken McGrath, Cem Meydan, Emmanuel F Mongodin, Milton Ozorio Moraes, Niranjan Nagarajan, Marina Nieto-Caballero, Houtan Noushmehr, Manuela Oliveira, Stephan Ossowski, Olayinka O Osuolale, Orhan Özcan, David Paez-Espino, Nicolás Rascovan, Hugues Richard, Gunnar Räscher, Lynn M Schriml, Torsten Semmler, Osman U Sezerman, Leming Shi, Tielu Shi, Rania Siam, Haruo Suzuki, Denise Syndercombe Court, Scott W Tighe, Xinzhao Tong, Klas I Udekwu, Juan A Ugalde, Brandon Valentine, Dimitar I Vassilev, Elena M Vayndorf, Thirumalaisamy P Velavan, Jun Wu, María M Zambrano, Jifeng Zhu, Sibozhu, Christopher E Mason, and **The International MetaSUB Consortium*** “[A global metagenomic map of urban microbiomes and antimicrobial resistance](#)” *Cell*, 184, 3376-3393.e17. 10.1016/j.cell.2021.05.002. (2021)

*One of the members of The International MetaSUB Consortium

15. Jian Carrot-Zhang, Xiaotong Yao, Siddhartha Devarakonda, Aditya Deshpande, Jeffrey S Damrauer, Tiago Chedraoui Silva, Christopher K Wong, Hyo Young Choi, Ina Felau, A Gordon Robertson, Mauro AA Castro, Lisui Bao, Esther Rheinbay, ***Eric Minwei Liu***, Tuan Trieu, David Haan, Christina Yau, Toshinori Hinoue, Yuexin Liu, Ofer Shapira, Kiran Kumar, Karen L Mungall, Hailei Zhang, Jake June-Koo Lee, Ashton Berger, Galen F Gao, Binyamin Zhitomirsky, Wen-Wei Liang, Meng Zhou, Sitapriya Moorthi, Alice H Berger, Eric A Collisson, Michael C Zody, Li Ding, Andrew D Cherniack, Gad Getz, Olivier Elemento, Christopher C Benz, Josh Stuart, JC Zenklusen, Rameen Beroukhim, Jason C Chang, Joshua D Campbell, D Neil Hayes, Lixing Yang, Peter W Laird, John N Weinstein, David J Kwiatkowski, Ming S Tsao, William D Travis, Ekta Khurana, Benjamin P Berman, Katherine A Hoadley, Nicolas Robine, Kanika Arora, Minita Shah, Jennifer Shelton, Reanne Bowlby, Verena Friedl, Mary Goldman, Brian Craft, David I Heiman, Iman Hajirasouliha, Camir Ricketts, Pavana Anur, Kami E Chiotti, Samantha J Caesar-Johnson, John A Demchok, Martin L Ferguson, Anab Kemal, Roy Tarnuzzer, Zhining Wang, Liming Yang, Paul T Spellman, Benjamin Raphael, Rehan Akbani, Jingchun Zhu, Steven JM Jones, Hui Shen, Matthew Meyerson, Ramaswamy Govindan, Marcin Imielinski “[Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway](#)”, *Cell Rep.* 34, 108707. 10.1016/j.celrep.2021.108707 (2021)

14. ***Eric Minwei Liu****, Alexander Martinez-Fundichely, Rajesh Bollapragada, Maurice Spiewack, Ekta Khurana “[CNCDatabase: a database of non-coding cancer drivers](#)”, *Nucleic Acids Res.* 49, D1094–D1101 (2021)

13. ***Eric Minwei Liu****, Augustin Luna*, Guanlan Dong, Chris Sander “[netboxr: Automated discovery of biological process modules by network analysis in R](#)”, *PLoS One* 15, e0234669 (2020)

* These authors have contributed equally to this work.

12. ***Eric Minwei Liu****, Alexander Martinez-Fundichely*, Bianca Jay Diaz*, Boaz Aronson, Tawny Cuykendall, Matthew MacKay, Priyanka Dhingra, Elissa WP Wong, Ping Chi, Effie Apostolou, Neville E Sanjana, Ekta Khurana “[Identification of Cancer Drivers at CTCF Insulators in 1,962 Whole Genomes](#)”, *Cell Systems*, 8,4460455. e8 (2019)

* These authors have contributed equally to this work.

11. Julija Hmeljak, Francisco Sanchez-Vega, Katherine A. Hoadley, Juliann Shih, Chip Stewart, David Heiman, Patrick Tarpey, Ludmila Danilova, Esther Drill, Ewan A. Gibb, Reanne Bowlby, Rupa Kanchi, Hatice U. Osmanbeyoglu, Yoshitaka Sekido, Jumpei Takeshita, Yulia Newton, Kiley Graim, Manaswi Gupta, Carl M. Gay, Lixia Diao, David L. Gibbs, Vesteinn Thorsson, Lisa Iype, Havish Kantheti, David T. Severson, Gloria Ravegnini, Patrice Desmeules, Achim A. Jungbluth, William D. Travis, Sanja Dacic, Lucian R. Chiriac, Françoise Galateau-Sallé, Junya Fujimoto, Aliya N. Husain, Henrique C. Silveira, Valerie W. Rusch, Robert C. Rintoul, Harvey Pass, Hedy Kindler, Marjorie G. Zauderer, David J. Kwiatkowski, Raphael Bueno, Anne S. Tsao, Jenette Creaney, Tara Lichtenberg, Kristen Leraas, Jay Bowen, ***TCGA Research Network****, Ina Felau, Jean Claude Zenklusen, Rehan Akbani, Andrew D. Cherniack, Lauren A. Byers, Michael S. Noble, Jonathan A. Fletcher, A. Gordon Robertson, Ronglai Shen, Hiroyuki Aburatani, Bruce W. Robinson, Peter Campbell and Marc Ladanyi “[Integrative molecular characterization of malignant pleural mesothelioma](#)”, *Cancer Discovery*, 8,1548-1565 (2018)

* One of the members of The Cancer Genome Atlas Research Network

10. Hui Shen, Juliann Shih, Daniel P Hollern, Linghua Wang, Reanne Bowlby, Satish K Tickoo, Vesteinn Thorsson, Andrew J Mungall, Yulia Newton, Apurva M Hegde, Joshua Armenia, Francisco Sánchez-Vega, John Pluta, Louise C Pyle, Rohit Mehra, Victor E Reuter, Guilherme Godoy, Jeffrey Jones, Carl S Shelley, Darren R Feldman, Daniel O Vidal, Davor Lessel, Tomislav Kulis, Flavio M Cárcano, Kristen M Leraas, Tara M Lichtenberg, Denise Brooks, Andrew D Cherniack, Juok Cho, David I Heiman, Katayoon Kasaian, ***Minwei Liu***, Michael S Noble, Liu Xi, Hailei Zhang, Wandong Zhou, Jean C Zenklusen, Carolyn M Hutter, Ina Felau, Jiashan Zhang, Nikolaus Schultz, Gad Getz, Matthew Meyerson, Joshua M Stuart, Rehan Akbani, David A Wheeler, Peter W Laird, Katherine L Nathanson, Victoria K Cortessis, Katherine A Hoadley, Cancer Genome Atlas Research Network “[Integrated Molecular Characterization of Testicular Germ Cell Tumors](#)”, *Cell Reports*, 23,3392-3406 (2018)

9. Matthew H Bailey, Collin Tokheim, Eduard Porta-Pardo, Sohini Sengupta, Denis Bertrand, Amila Weerasinghe,

- Antonio Colaprico, Michael C Wendl, Jaegil Kim, Brendan Reardon, Patrick Kwok-Shing Ng, Kang Jin Jeong, Song Cao, Zixing Wang, Jianjiong Gao, Qingsong Gao, Fang Wang, **Eric Minwei Liu**, Loris Mularoni, Carlota Rubio-Perez, Niranjana Nagarajan, Isidro Cortés-Ciriano, Daniel Cui Zhou, Wen-Wei Liang, Julian M Hess, Venkata D Yellapantula, David Tamborero, Abel Gonzalez-Perez, Chayaporn Suphavitai, Jia Yu Ko, Ekta Khurana, Peter J Park, Eliezer M Van Allen, Han Liang, Michael S Lawrence, Adam Godzik, Nuria Lopez-Bigas, Josh Stuart, David Wheeler, Gad Getz, Ken Chen, Alexander J Lazar, Gordon B Mills, Rachel Karchin, Li Ding, MC3 Working Group, Cancer Genome Atlas Research Network “[Comprehensive Characterization of Cancer Driver Genes and Mutations](#)”, *Cell* 173, 371–385.e18 (2018).
8. Ed Reznik, Augustin Luna, Bülent Arman Aksoy, **Eric Minwei Liu**, Konnor La, Irina Ostrovnaya, Chad J Creighton, A Ari Hakimi, Chris Sander, “[A Landscape of Metabolic Variation across Tumor Types](#)”, *Cell Systems* 6, 301–313.e3 (2018).
 7. Priyanka Dhingra, Alexander Martinez-Fundichely, Adeline Berger, Franklin W Huang, Andre Neil Forbes, **Eric Minwei Liu**, Deli Liu, Andrea Sboner, Pablo Tamayo, David S Rickman, Mark A Rubin, Ekta Khurana “[Identification of novel prostate cancer drivers using RegNetDriver: a framework for integration of genetic and epigenetic alterations with tissue-specific regulatory network](#)”, *Genome Biology* 18 (1), 141 (2017)
 6. **The Cancer Genome Atlas Research Network*** “[Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas](#)”, *Cell* 171, 950–965.e28 (2017).
 - * One of the members of The Cancer Genome Atlas Research Network
 5. A Ari Hakimi, Ed Reznik, Chung-Han Lee, Chad J Creighton, A Rose Brannon, Augustin Luna, B. Arman Aksoy, **Eric Minwei Liu**, Ronglai Shen, William Lee, Yang Chen, Steve M Stirdivant, Paul Russo, Ying Bei Chen, Satish K Tickoo, Victor E Reuter, Emily H. Cheng, Chris Sander, and James J. Hsieh “[An Integrated Metabolic Atlas of Clear Cell Renal Cell Carcinoma](#)”; *Cancer Cell* 29 (1), 104-116 (2016).
 4. Devendra Singh, Joseph Chan, Pietro Zoppoli, Francesco Niola, Ryan Sullivan, Angelica Castano, **Eric Minwei Liu**, Jonathan Reichel, Paola Porrati, Serena Pellegatta, Kunlong Qin, Zhibo Gao, Michele Ceccarelli, Riccardo Riccardi, Daniel J. Brat, Abhijit Guha, Ken Aldape, John G. Golfinos, David Zagzag, Tom Mikkelsen, Gaetano Finocchiaro, Anna Lasorella, Raul Rabadan, Antonio Iavarone “[Transforming and recurrent fusions of FGFR and TACC genes in glioblastoma](#)”; *Science* 337 (6099), 1231-1235 (2012)
 3. Jih-Bin Chen*, **Eric Minwei Liu***, Ting-Rong Chern, Chieh-Wen Yang, Chia-I Lin, Nai-Kuei Huang, Yun-Lian Lin, Yijuang Chern, Jung-Hsin Lin, and Jim-Min Fang “[Design and Synthesis of Novel Dual-Action Compounds Targeting Adenosine A_{2A} Receptor and Adenosine Transporter for Neuroprotection](#)”; *ChemMedChem* 6, 1390-1400 (2011)
 - * These authors have contributed equally to this work.
 2. Nai-Kuei Huang, Jung-Hsin Lin, Jiun-Tsai Lin, Chia-I Lin, **Eric Minwei Liu**, Chun-Jung Lin, Wan-Ping Chen, Yuh-Chiang Shen, Hui-Mei Chen, Jih-Bin Chen, Hsing-Lin Lai, Chieh-Wen Yang, Ming-Chang Chiang, Yu-Shuo Wu, Jiang-Fan Chen, Jim-Min Fang, Yun-Lian Lin, and Yijuang Chern “[A new drug design targeting the adenosinergic system for Huntington’s disease](#)”; *PLoS ONE* 6(6), e20934 (2011)
 1. Po-Hsien Lee, Kuei-Ling Kuo, Pei-Ying Chu, **Eric Minwei Liu**, and Jung-Hsin Lin “[SLITHER: a web server for generating contiguous conformations of substrate molecules entering into deep active sites of proteins or migrating through channels in membrane transporters](#)”; *Nucleic Acids Research* 37: W559–W564 (2009)

