Yosuke Tanigawa, Ph.D.

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Personal Website:	https://yosuketanigawa.com/
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Google Scholar:	9hVh3nQAAAAJ

Education and postdoctoral training

Massachusetts Institute of Technology, 2021 -
Postdoctoral Associate, Computational Biology Group
Research advisor: Dr. Manolis Kellis

Stanford University
Ph.D. in Biomedical Informatics, 2016 - 2021 (GPA: 4.21 / 4.30)
Dissertation: Large-scale genomic inference of multiple phenotypes (link)
Research advisors: Dr. Manuel Rivas (primary) and Dr. Gill Bejerano (secondary)

University of Tokyo, Japan
B.S. in Bioinformatics and Systems Biology, 2012 - 2016 (GPA: 3.93 / 4.00)
Research advisor: Dr. Shinichi Morishita

Publications

You can also find my articles and recent preprints on my Google Scholar profile. In the following list of publications and presentations, the '*' symbol indicates equal contribution, and the '+' symbol indicates correspondence.

Select publications

1. N. Sinnott-Armstrong*+, **Y. Tanigawa*+**, D. Amar, N. J. Mars, C. Benner, M. Aguirre, G. R. Venkataraman, M. Wainberg, H. M. Ollila, T. Kiiskinen, A. S. Havulinna, J. P. Pirruccello, J. Qian, A. Shcherbina, FinnGen, F. Rodriguez, T. L. Assimes, V. Agarwala, R. Tibshirani, T. Hastie, S. Ripatti, J. K. Pritchard, M. J. Daly, M. A. Rivas*+, Genetics of 35 blood and urine biomarkers in the UK Biobank. *Nat Gen*. **53**(2), 185-194 (2021). https://doi.org/10.1038/s41588-020-00757-z
    - Full text: https://rdcu.be/cdMmM
    - Featured as Research Highlights in *Nature Reviews Nephrology*: Allison, S.J. Biomarker genetics. *Nat Rev Nephrol*. **17**, 222 (2021). https://doi.org/10.1038/s41581-021-00400-y
    - Recommended in Faculty Opinions: Borgwardt K: Faculty Opinions Recommendation of [Sinnott-Armstrong N et al., Nat Genet 2021 53(2):185-194]. In Faculty Opinions, 25 Feb 2021; https://doi.org/10.3410/f.739382438.793583091
2. **Y. Tanigawa**, M. Wainberg, J. Karjalainen, T. Kiiskinen, G. Venkataraman, S. Lemmelä, J. A. Turunen, R. R. Graham, A. S. Havulinna, M. Perola, A. Palotie, FinnGen, M. J. Daly, M. A. Rivas, Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. *PLoS Genet*. **16**, e1008682 (2020). https://doi.org/10.1371/journal.pgen.1008682
    - Highlighted as Editors' Choice in *Science* journal: Vignieri, S. et al. Editors' Choice. *Science* **368**, 962–963 (2020). https://doi.org/10.1126/science.2020.368.6494.twil
3. **Y. Tanigawa***, J. Li*, J. M. Justesen, H. Horn, M. Aguirre, C. DeBoever, C. Chang, B. Narasimhan, K. Lage, T. Hastie, C. Y. Park, G. Bejerano, E. Ingelsson, M. A. Rivas, Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. *Nat Commun*. **10**, 4064 (2019). https://doi.org/10.1038/s41467-019-11953-9

  - Recommended in *Faculty Opinions*: I. Barroso, E. Wheeler, Faculty Opinions Recommendation of [Tanigawa Y et al., Nat Commun 2019 10(1):4064], In *Faculty Opinions*, (2019). https://doi.org/10.3410/f.736565849.793565082

Recent Preprints

Preprints are provided for rapid sharing of the data, results, and knowledge among the scientific community and have not finished the peer-review process. We welcome comments and feedback.

- G. R. Venkataraman, **Y. Tanigawa**, M. Pirinen, M. A. Rivas, Bayesian mixture model for clustering rare-variant effects in human genetic studies. *bioRxiv*, 2021.08.03.454967 (2021). https://doi.org/10.1101/2021.08.03.454967
- A. Lavertu*, G. M. McInnes*, **Y. Tanigawa**, R. B. Altman, M. A. Rivas, LPA and APOE are associated with statin selection in the UK Biobank. *bioRxiv*, 2020.08.28.272765 (2020). https://doi.org/10.1101/2020.08.28.272765
- G. R. Venkataraman, J. E. Olivieri, C. DeBoever, **Y. Tanigawa**, J. M. Justesen, M. A. Rivas, Pervasive additive and non-additive effects within the HLA region contribute to disease risk in the UK Biobank. *bioRxiv*, 2020.05.28.119669 (2020). https://doi.org/10.1101/2020.05.28.119669
- C. DeBoever, A. J. Venkatakrishnan, J. M. Paggi, F. M. Heydenreich, S.-A. Laurin, M. Masureel, **Y. Tanigawa**, G. Venkataraman, M. Bouvier, R. Dror, M. A. Rivas, Medical relevance of common protein-altering variants in GPCR genes across 337,205 individuals in the UK Biobank study. *bioRxiv*, 2019.12.13.876250 (2019). https://doi.org/10.1101/2019.12.13.876250

Peer-reviewed journal publications

4. J. Yang*, M. Vamvini*, P. Nigro*, L.-L. Ho, K. Galani, M. Alvarez, **Y. Tanigawa**, A. Renfro, N. P. Carbone, M. Laakso, L. Z. Agudelo, P. Pajukanta, M. F. Hirshman, R. J.W. Middelbeek, K. Grove, L. Goodyear, M. Kellis, Single-cell dissection of the obesity-exercise axis in adipose-muscle tissues implies a critical role for mesenchymal stem cells. *Cell Metab.* **34**(10),1578-1593.e6 (2022). https://doi.org/10.1016/j.cmet.2022.09.004
5. **Y. Tanigawa***, E. S. Dyer*, G. Bejerano, WhichTF is dominant in your open chromatin data? *PLOS Comput Biol* **18**(8): e1010378. (2022). https://doi.org/10.1371/journal.pcbi.1010378
6. V. N. Parikh*, A. G. Ioannidis*, D. Jimenez-Morales, J. E. Gorzynski, H. N. D. Jong, X. Liu, J. Roque, V. P. Cepeda-Espinoza, K. Osoegawa, C. Hughes, S. C. Sutton, N. Youlton, R. Joshi, D. Amar, **Y. Tanigawa**, D. Russo, J. Wong, J. T. Lauzon, J. Edelson, D. M. Montserrat, Y. Kwon, S. Rubinacci, O. Delaneau, L. Cappello, J. Kim, M. J. Shoura, A. N. Raja, N. Watson, N. Hammond, E. Spiteri, K. C. Mallempati, G. Montero-Martin, J. Christle, J. Kim, A. Kirillova, K. Seo, Y. Huang, C. Zhao, S. Moreno-Grau, S. Hershman, K. P. Dalton, J. Zhen, J. Kamm, K. Bhatt, A. Isakova, M. Morri, T. Ranganath, C. A. Blish, A. J. Rogers, K. Nadeau, S. Yang, A. Blomkalns, R. O’Hara, N. F. Neff, C. DeBoever, S. Szalma, M. T. Wheeler, C. Gates, K. Farh, G. P. Schroth, P. Febbo, F. deSouza, O. Cornejo, M. Fernandez-Vina, A. Kistler, J. Palacios, B. A. Pinsky, C. D. Bustamante, M. A. Rivas, E. A. Ashley, Deconvoluting complex correlates of COVID19 severity with a multi-omic pandemic tracking strategy. *Nat Commun*. **13**, 5107 (2022). https://doi.org/10.1038/s41467-022-32397-8
7. J. Qian, **Y. Tanigawa**, R. Li, R. Tibshirani, M. A. Rivas, T. Hastie, Large-Scale Sparse Regression for Multiple Responses with Applications to UK Biobank. *Ann. Appl. Stat*. **16**(3), 1891-1918 (2022). https://doi.org/10.1214/21-AOAS1575
8. C. Smail, N. M. Ferraro, Q. Hui, M. G. Durrant, M. Aguirre, **Y. Tanigawa**, M. R. Keever-Keigher, A. S. Rao, J. M. Justesen, X. Li, M. J. Gloudemans, T. L. Assimes, C. Kooperberg, A. P. Reiner, J. Huang, C. J. O'Donnell, Y. V. Sun, Million Veteran Program, M. A. Rivas, S. B. Montgomery, Integration of rare

expression outlier-associated variants improves polygenic risk prediction. *Am J Hum Genet*. **109**(6), 1055-1064 (2022). https://doi.org/10.1016/j.ajhg.2022.04.015
   - Full text: https://authors.elsevier.com/c/1f5cZ_4GsWG3Z
9. R. Li, C. Chang, J. M. Justesen, **Y. Tanigawa**, J. Qiang, T. Hastie, M. A. Rivas, R. Tibshirani, Fast Lasso method for large-scale and ultrahigh-dimensional Cox model with applications to UK Biobank. *Biostatistics*. **23**(2), 522-540 (2022). https://doi.org/10.1093/biostatistics/kxaa038
10. **Y. Tanigawa**, J. Qian, G. R. Venkataraman, J. M. Justesen, R. Li, R. Tibshirani, T. Hastie, M. A. Rivas, Significant Sparse Polygenic Risk Scores across 813 traits in UK Biobank. *PLOS Genet*. **18**(3), e1010105 (2022). https://doi.org/10.1371/journal.pgen.1010105
11. G. R. Venkataraman, C. DeBoever, **Y. Tanigawa**, M. Aguirre, A. G. Ioannidis, H. Mostafavi, C. C. A. Spencer, T. Poterba, C. D. Bustamante, M. J. Daly, M. Pirinen, M. A. Rivas, Bayesian model comparison for rare-variant association studies. *Am J Hum Genet*. **108**(12), 2354-2367 (2021). https://doi.org/10.1016/j.ajhg.2021.11.005
    - Full text: https://authors.elsevier.com/c/1e863geW~j2B
12. **COVID-19 Host Genetics Initiative**, Mapping the human genetic architecture of COVID-19. *Nature* **600**(7890), 472-477 (2021). https://doi.org/10.1038/s41586-021-03767-x
    - This consortia flagship manuscript has 2000+ authors. I have been fortunate to be part of the participating study of the COVID-19 Host Genetics Initiative.
13. S. Sakaue*, M. Kanai*, **Y. Tanigawa**, J. Karjalainen, M. Kurki, S. Koshiba, A. Narita, T. Konuma, K. Yamamoto, M. Akiyama, K. Ishigaki, A. Suzuki, K. Suzuki, W. Obara, K. Yamaji, K. Takahashi, S. Asai, Y. Takahashi, T. Suzuki, N. Sinozaki, H. Yamaguchi, S. Minami, S. Murayama, K. Yoshimori, S. Nagayama, D. Obata, M. Higashiyama, A. Masumoto, Y. Koretsune, F. Gen, K. Ito, C. Terao, T. Yamauchi, I. Komuro, T. Kadowaki, G. Tamiya, M. Yamamoto, Y. Nakamura, M. Kubo, Y. Murakami, K. Yamamoto, Y. Kamatani, A. Palotie, M. A. Rivas, M. Daly, K. Matsuda, Y. Okada, A cross-population atlas of genetic associations for 220 human phenotypes. *Nat Gen*. **53**(10), 1415-1424 (2021). https://doi.org/10.1038/s41588-021-00931-x
    - Full text: https://rdcu.be/cyG6p
    - Highlighted as the cover *Nature Genetics*: https://www.nature.com/ng/volumes/53/issues/10
14. S. Goyal, **Y. Tanigawa**, W. Zhang, J. Chai, M. Almeida, X. Sim, M. Lerner, J. Chainakul, J. G. Ramiu, C. Seraphin, B. Apple, A. Vaughan, J. Muniu, J. Peralta, D. M. Lehman, S. Ralhan, G. S. Wander, J. R. Singh, N. K. Mehra, E. Sidorov, M. D Peyton, P. R. Blackett, J. E. Curran, E. S. Tai, R. van Dam, C. Cheng, R. Duggirala, J. Blangero, J. C. Chambers, C. Sabanayagam, J. S. Kooner, M. A. Rivas, C. E. Aston, D. Sanghera, APOC3 genetic variation, serum triglycerides, and risk of coronary artery disease in Asian Indians, Europeans, and other ethnic groups. *Lipids Health Dis*. **20**, 113 (2021). https://doi.org/10.1186/s12944-021-01531-8
15. M. Aguirre, **Y. Tanigawa**, G. R. Venkataraman, R. Tibshirani, T. Hastie, M. A. Rivas, Polygenic risk modeling with latent trait-related genetic components. *Eur J Hum Genet*. **29**(7), 1071–1081 (2021), https://doi.org/10.1038/s41431-021-00813-0
    - Full text: https://rdcu.be/ceXyy
16. R. Li, C. Chang, **Y. Tanigawa**, B. Narasimhan, T. Hastie, R. Tibshirani, M. A. Rivas, Fast Numerical Optimization for Genome Sequencing Data in Population Biobanks. *Bioinformatics* **37**(22), 4148-4155 (2021). https://doi.org/10.1093/bioinformatics/btab452
17. R. Li, **Y. Tanigawa**, J. M. Justesen, J. Taylor, T. Hastie, R. Tibshirani, M. A. Rivas, Survival Analysis on Rare Events Using Group-Regularized Multi-Response Cox Regression. *Bioinformatics* **37**(23), 4437-4443 (2021). https://doi.org/10.1093/bioinformatics/btab095
18. E. Flynn, **Y. Tanigawa**, F. Rodriguez, R. B. Altman, N. Sinnott-Armstrong, M. A. Rivas, Sex-specific genetic effects across biomarkers. *Eur J Hum Genet*. **29**(1), 154-163 (2021). https://doi.org/10.1038/s41431-020-00712-w
    - Full text: https://rdcu.be/b6DJF

19. A. Córdova-Palomera, C. Tcheandjieu, J. Fries, P. Varma, V. Chen, M. Fiterau, K. Xiao, H. Tejeda, B. Keavney, H. Cordell, **Y. Tanigawa**, G. Venkataraman, M. Rivas, C. Re, E. Ashley, J. R. Priest, Cardiac Imaging of Aortic Valve Area from 34,287 UK Biobank Participants Reveal Novel Genetic Associations and Shared Genetic Comorbidity with Multiple Disease Phenotypes. *Circ Genom Precis Med*. **13**, e003014 (2020). https://doi.org/10.1161/CIRCGEN.120.003014
20. J. Qian, **Y. Tanigawa**, W. Du, M. Aguirre, C. Chang, R. Tibshirani, M. A. Rivas, T. Hastie, A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. *PLOS Genet*. **16**, e1009141 (2020). https://doi.org/10.1371/journal.pgen.1009141
21. D. M. Ruderfer, C. G. Walsh, M. W. Aguirre, **Y. Tanigawa**, J. D. Ribeiro, J. C. Franklin, M. A. Rivas, Significant shared heritability underlies suicide attempt and clinically predicted probability of attempting suicide. *Mol Psychiatry*. **25**(10), 2422-2430 (2020). https://doi.org/10.1038/s41380-018-0326-8
22. C. DeBoever, **Y. Tanigawa**, M. Aguirre, G. McInnes, A. Lavertu, M. A. Rivas, Assessing Digital Phenotyping to Enhance Genetic Studies of Human Diseases. *Am J Hum Genet*. **106**(5), 611-622 (2020). https://doi.org/10.1016/j.ajhg.2020.03.007
23. G. McInnes, **Y. Tanigawa**, C. DeBoever, A. Lavertu, J. E. Olivieri, M. Aguirre, M. A. Rivas, Global Biobank Engine: enabling genotype-phenotype browsing for biobank summary statistics. *Bioinformatics*. **35**(14), 2495-2497 (2019). https://doi.org/10.1093/bioinformatics/bty999
24. T. Ohta, T. Kawashima, N. O. Shinozaki, A. Dobashi, S. Hiraoka, T. Hoshino, K. Kanno, T. Kataoka, S. Kawashima, M. Matsui, W. Nemoto, S. Nishijima, N. Suganuma, H. Suzuki, Y. Taguchi, Y. Takenaka, **Y. Tanigawa**, M. Tsuneyoshi, K. Yoshitake, Y. Sato, R. Yamashita, K. Arakawa, W. Iwasaki, Collaborative environmental DNA sampling from petal surfaces of flowering cherry Cerasus × yedoensis 'Somei-yoshino' across the Japanese archipelago. *J Plant Res*. **131**, 709–717 (2018). https://doi.org/10.1007/s10265-018-1017-x
25. C. DeBoever, **Y. Tanigawa**, M. E. Lindholm, G. McInnes, A. Lavertu, E. Ingelsson, C. Chang, E. A. Ashley, C. D. Bustamante, M. J. Daly, M. A. Rivas, Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study. Nat Commun. 9, 1612 (2018). https://doi.org/10.1038/s41467-018-03910-9

Peer-reviewed conference papers (12 pages)

26. S. Anand*, L. Kalesinskas*, C. Smail*, **Y. Tanigawa*+**, SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. Pac Symp Biocomput. 2019, **24**, 184-195 (World Scientific, 2018). https://doi.org/10.1142/9789813279827_0017

Review article (with peer review)

27. **Y. Tanigawa**, Large-scale human genetic statistical inference with multiple phenotypes. *JSBi Bioinformatics Review*. **1**(2), 47-59 (2021). https://doi.org/10.11234/jsbibr.2021.4 (invited review article written in Japanese)

Ph.D. thesis

- Y. Tanigawa, Large-scale genomic inference of multiple phenotypes. Stanford University, CA, U.S.A. (2021). https://purl.stanford.edu/sb956xt8745

Other manuscripts

- J. E. Gorzynski*, H. N. D. Jong*, D. Amar, C. R. Hughes, A. Ioannidis, R. Bierman, D. Liu, **Y. Tanigawa**, A. Kistler, J. Kamm, J. Kim, L. Cappello, N. F. Neff, S. Rubinacci, O. Delaneua, M. J. Shoura, K. Seo, A. Kirillova, A. Raja, S. Sutton, C. Huang, M. K. Sahoo, K. C. Mallempati, G. Montero-Martin, K. Osoegawa, N. Watson, N. Hammond, R. Joshi, M. Fernandez-Vina, J. W. Christle, M. T. Wheeler, P. Febbo, K. Farh, G. Schroth, F. Desouza, J. Palacios, J. Salzman, B. A. Pinsky, M. A. Rivas, C. D. Bustamante, E. A. Ashley, V. N. Parikh, High-throughput SARS-CoV-2 and host genome sequencing from single nasopharyngeal swabs, *medRxiv*, 2020.07.27.20163147 (2020). https://doi.org/10.1101/2020.07.27.20163147
- **Y. Tanigawa**, M. Rivas, Initial Review and Analysis of COVID-19 Host Genetics and Associated Phenotypes. *Preprints.org* (2020). https://doi.org/10.20944/preprints202003.0356.v1
- **Y. Tanigawa**, M. A. Rivas, Reported CCR5-Δ32 deviation from Hardy-Weinberg equilibrium is explained by poor genotyping of rs62625034. *bioRxiv*, 791517 (2019). https://doi.org/10.1101/791517
    - Other research groups also reported similar issues. The original paper was retracted. https://doi.org/10.1038/s41591-019-0710-1

Teaching and Mentoring Experience

Teaching Assistant

- BIODS 215: “Topics in Biomedical Data Science -- Large scale inference” (Jan.-Mar., 2018), Stanford University.
    - The TA duties included a TA lecture, office hours, creating and grading homework, guided class projects, and maintaining the class website.
    - Class website: https://biods215.github.io/class_website/2020.html
- BIOMEDIN 210 / CS 270 “Modeling Biomedical Systems: Ontology, Terminology, Problem Solving” (Jan.-Mar., 2019), Stanford University.
    - The TA duties included a TA lecture, office hours, creating and grading homework, and guided class projects
- BIODS 215: “Topics in Biomedical Data Science -- Large scale inference” (Jan.-Mar., 2018), Stanford University.
    - The TA duties included a TA lecture, office hours, creating and grading homework, guided class projects, and maintaining the class website.
    - Class website: https://biods215.github.io/class_website/2018.html

Research (co-)mentor

- MIT
    - Hannah Kirsten Ramcharan (PhD. rotation student at the Kellis lab 2022 Jan.)
    - William F Li (6.883 class project mentoring)
    - Di Kang (6.883 class project mentoring)
- Stanford Summer Research Program (SSRP)-Amgen Scholars Program, Stanford University.
    - Robert Minneker (2018 summer, the Rivas Lab)
        - Note: I was a co-mentor w/ Matthew Aguirre.
- Stanford, Undergraduate Research Internship in CS (CURIS).
    - Ruchir Rastogi (2019, the Bejerano Lab)
    - John Dalloul (2019, the Bejerano Lab)
    - David Wei Wu (2018, the Bejerano Lab)

Thesis reader

- Dalla Lana School of Public Health, University of Toronto
    - Amin Kharaghani (MSc Thesis Defense External Reviewer) (2022)

Awards and Travel Grants

Awards

1. Innovators Under 35 Japan Award, MIT Technology Review, 2022
    - https://www.innovatorsunder35.com/the-list/yosuke-tanigawa/
2. Winner (postdoctoral), Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research, the American Society of Human Genetics, 2022
    - https://doi.org/10.1016/j.ajhg.2023.01.014
3. Selected as Finalist (unfunded), The Life Sciences Research Foundation Postdoctoral Fellowship, February 2022
4. Reviewers' Choice Abstract Award, the American Society of Human Genetics 2021 Annual Meeting (virtual)
5. The Best Oral Presentation Award, Informatics in Biology, Medicine, and Pharmacology conference (IIBMP2020), September 2020
6. Reviewers' Choice Abstract Award, the American Society of Human Genetics 2018 Annual Meeting
7. Helmsley Interdisciplinary Fellowship, The Helmsley Charitable Trust, July 2016
8. The Faculty of Science Study Award, University of Tokyo, March 2016
    - The best student in the department receives this award
9. Funai Overseas Scholarship (pre-doctoral fellowship), Funai Foundation for Information Technology, November 2015.
    - The Funai fellowship supports ~12 Japanese students across all disciplines every year for their graduate training.
10. Excellence in Technical Execution, European Innovation Academy, July 2015.
11. Global Leadership Award, Friends of UTokyo, Inc., June 2014.
    - Around 20 students in the university receive this award.
12. Silver Medal. Japan Biology Olympiad National Competition, August 2011.
13. Bronze Medal. Japan Biology Olympiad National Competition, August 2010.

Travel Grants

1. Alzheimer's Association International Conference 2023 Conference Fellowship, Alzheimer's Association, 2023
2. International Congress of Human Genetics 2023 Travel Grant, the American Society of Human Genetics, 2022
3. Biosciences office of the graduate education travel grant. Stanford University., Jan. 2019
4. Biosciences office of the graduate education travel grant. Stanford University., Oct. 2018
5. Biosciences office of the graduate education travel grant. Stanford University., Oct. 2017
6. Cold Spring Harbor Laboratory Meetings and Courses, July 2016
7. Students and Researchers Exchange Program in the Faculty of Sciences, University of Tokyo, June 2015.
8. Hands-on Activity Program, University of Tokyo, June 2015.
9. Pre-Global Education for Innovation & Leadership program, University of Tokyo, March 2015.
10. Study and Visit Abroad Program, School of Science, University of Tokyo, Feb. 2015.

    a. About 10 students in the School of Science receive this award.
11. Elite Science Student Visit Abroad Program (Summer Program), School of Science, University of Tokyo, February 2014.
    a. 3 students in the School of Science received this award.
12. University of Tokyo Short-Term Summer Study Abroad Programs with Scholarships, University of Tokyo, May 2014.

Presentations

Invited talks, lectures, and seminars (Research)

- Invited Talk. Single-cell Transcriptional Hallmarks and Individual Subtyping for Alzheimer's Disease across 427 Subjects. The potential role of astrocytes and microglia in neurodegeneration. International Conference on Alzheimer's and Parkinson's Diseases and related neurological disorders (ADPD 2023). Gothenburg, Sweden. 2023/4/1
- Invited Seminar. Computational Genomics for Precision Medicine: Therapeutics, Polygenic Modeling, and Disease Subtypes. The Novo Nordisk Foundation Center for Basic Metabolic Research. University of Copenhagen. Copenhagen, Denmark. 2023/3/26
- Invited Talk. Computational Genomics for Precision Medicine. Immunotherapy and Immunobiology (CCII) and Center for Genomic Medicine (CGM) Joint Symposium – Genomics and Omics Study and Application to Human Biology –. Kyoto University. Kyoto, Japan. 2023/3/4
- Invited Seminar. Computational Genomics for Precision Medicine: Therapeutics, polygenic modeling, and disease subtypes. Research seminar at the Sydney Brenner Institute for Molecular Bioscience. University of Witwatersrand. Johannesburg, South Africa. 2023/2/20
- Invited Seminar. Computational Genomics for Precision Medicine: Inclusive polygenic scores, biomedical knowledge, and disease subtype. Okada Lab, Dept. Genome Informatics, Graduate School of Medicine, The University of Tokyo. Tokyo, Japan. 2023/1/5
- Invited Seminar. Computational Genomics for Precision Medicine: Therapeutics, polygenic modeling, and disease subtypes. Morishita Lab, Dept. Computational Biology, Graduate School of Frontier Sciences, The University of Tokyo. Tokyo, Japan. 2022/12/23
- Invited Seminar. Computational Genomics for Precision Medicine: Therapeutics, polygenic modeling, and disease subtypes. 17th meeting, Genomic Medicine Subcommittee. 17th meeting, Genomic Medicine Subcommittee, 21st Century Advanced Medical Consortium in Japan. Zoom. 2022/12/12
- Invited oral presentation. Single-cell Transcriptional Hallmarks and Individual Subtyping for Alzheimer's Disease across 427 Subjects. the Genetics and Genomics Digital Forum 2022 by ASHG. Zoom. 2022/11/16
- Invited oral presentation. Single-cell Transcriptional Hallmarks and Individual Subtyping for Alzheimer's Disease across 427 Subjects. Society for Neuroscience Annual Meeting 2022. San Diego, CA. 2022/11/15
- Invited oral presentation. Power of Inclusion: up to a 50-fold increase in polygenic score transferability with admixed individuals. the 14th annual RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges (RSGDREAM 2022). Las Vegas, NV, U.S.A. 2022/11/11
- Invited oral presentation. Single-cell Transcriptional Hallmarks and Individual Subtyping for Alzheimer's Disease across 427 Subjects. American Society of Human Genetics 2022. Los Angeles, CA. 2022/10/27
- Invited seminar. Multi-trait modeling in polygenic scores (複数の表現型を考慮したポリジェニック・スコア解析). Bioinformatics seminar, Graduate School of Medicine, Osaka University, Japan (via zoom), 2022/3/2
- Invited presentation. Multi-trait modeling in polygenic scores, Journal Club meeting at Debora Marks's lab, Harvard Medical School, Boston, MA (via zoom), 2022/1/28
- Invited lecturer. Statistical genetics summer school, Osaka University, 2019/8/26
- Invited speaker. Dept. Bioinformatics and Systems Biology, University of Tokyo, 2018/12/21

- Invited participant. Y. Tanigawa, et al. Transcription factor ontology, NBDC/DBCLS Biohackathon 2018, Japan, 2018/12/9
- Invited seminar. Y. Tanigawa. Decomposition of genetic effects across biomarkers, lifestyle measures, and disease outcomes, Eisai, Inc., Tokyo, 2017/12/22
- Invited seminar. Y. Tanigawa. Decomposition of genetic effects across biomarkers, lifestyle measures, and disease outcomes, Morishita Lab., University of Tokyo, 2017/12/15
- Invited speaker. Dept. Bioinformatics and Systems Biology, University of Tokyo, 2017/12/13

Invited talks and lectures (Teaching)

- Invited Lecture. Genetic prediction of complex traits. The 8th McGill-Kyoto training courses. Kyoto University. Kyoto, Japan. 2023/3/2
- Invited speaker “ENGR159Q: Japanese Companies and Japanese Society”, Stanford University, 2021/4/21
- Invited speaker “ENGR159Q: Japanese Companies and Japanese Society”, Stanford University, 2019/5/1
- Invited speaker “ENGR159Q: Japanese Companies and Japanese Society”, Stanford University, 2018/4/25

Other research talks

- Y. Tanigawa, N. Sun, C. A. Boix, K. Galani, H. Mathys, D. A. Bennett, LH Tsai, M Kellis. “Single-cell transcriptional hallmarks and individual subtyping for Alzheimer’s disease across 427 individuals”. Medical and Population Genetics seminar. Broad Institute. Cambrdige, MA, U.S.A. 2023/3/9
- Y. Tanigawa, E. S. Dyer, and G. Bejerano. “WhichTF is functionally important in your open chromatin data?”, Rapid Talks Session. GREGoR Stanford Sitewide Meeting. Stanford, CA, U.S.A. (Zoom). 2023/1/25
- Y. Tanigawa et al. “Single-cell transcriptional hallmarks and patient subtyping for Alzheimer’s disease”, 12th Annual Rush Alzheimer’s Disease Center ROSMAP Investigator’s Meeting 2022. Rush University Medical Center. Chicago, IL. 2022/7/11
- Y. Tanigawa, E. S. Dyer, and G. Bejerano. “WhichTF is open in your open chromatin data?”, the Research Roundtable meeting at the Stanford Cardiovascular Institute, Zoom, 2021/5/13
- Y. Tanigawa, “Genetics of 35 biomarkers in the UK Biobank”, Japanese San Francisco Bay Area Seminar (BAS) 2020 Annual Joint Seminar, Zoom, 2020/12/5
- Y. Tanigawa, “Large-scale genetic inference from population cohorts”, Iitomo seminar, Zoom, 2020/11/1
- Y. Tanigawa. “Sparse polygenic risk scores in hundreds of diseases elucidate their biological basis”, Biomedical Informatics research in progress talk, Zoom ~~Stanford, CA~~, 2020/10/13
- Y. Tanigawa and M. A. Rivas, “Multi-trait analysis informs genetic disease studies”, Informatics in Biology, Medicine, and Pharmacology conference, Zoom ~~Kitakyushu, Fukuoka, Japan~~, 2020/9/1
- Y. Tanigawa, D. Amar, and M. A. Rivas, “Genetics of 35 blood and urine biomarkers in the UK Biobank”, Workshop in Biostatistics, Stanford, CA, 2020/5/28
- Y. Tanigawa. “Genetic risk modeling based on L1-penalized regression”, Biomedical Informatics research in progress talk, Stanford, CA, 2019/11/12
- Y. Tanigawa. “Summary statistic-based large-scale inference for genomic disease studies”, Biomedical Informatics training program thesis pre-proposal talk, Stanford, CA, 2019/5/13
- Y. Tanigawa et al. "WhichTF is dominant in your open chromatin data?", Biomedical Informatics research in progress talk, Stanford, CA, 2018/11/27
- Y. Tanigawa*, J. Li*, et al. "Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight novel adipocyte biology", Japanese San Francisco Bay Area Seminar, San Francisco, CA, 2018/10/27
- R. Minneker, M. Aguirre, Y. Tanigawa, and M. Rivas. “Characterizing Non-Additive Genetic Effects in the UK Biobank”, SSRP-Amgen Scholars Program Final presentation, Stanford, 2018/8/22

- Y. Tanigawa. "Compressed representation of personal genomes and its application for real-time haplotype inference", Funai Foundation Annual Retreat, Los Angeles, 2018/7/27
- Y. Tanigawa. "Mapping components of genetic effects across 2,138 phenotypes from UK Biobank", Biomedical Informatics research in progress talk, Stanford, 2018/2/13
- Y. Tanigawa. "Compressed representation of personal genomes and its application for real-time haplotype inference", Funai Foundation Annual Retreat, Boston, 2017/7/29
- Y. Tanigawa, et al. "GRISM: An informatics tool to identify context-specific functions and cooperatively binding cis-regulatory elements of transcription factors", Biomedical Informatics research in progress talk, Stanford, 2017/5/9
- Y. Tanigawa. "Structural Metagenomics of Cerasus × yedoensis using co-occurrence relationship of species," 4th Annual Workshop in Next Generation Sequencing, Tsukuba, Japan, July 2015.
- H. Kume*, H. Matsuda*, T. Sugiyama*, Y. Tanigawa*, and Y. Nakazato. "Gene expression pattern of Drosophila Melanogaster in embryonic development," Japan Super Science Fair, Biwako, Japan, November 2011.

Poster presentations

- Y. Tanigawa, N. Sun, C. A. Boix, K. Galani, H. Mathys, D. A. Bennett, LH Tsai, M Kellis. "Single-cell transcriptional hallmarks and individual subtyping for Alzheimer's disease across 427 individuals" (poster), International Congress of Human Genetics 2023. Cape Town, South Africa, 2023/2/23
- Y. Tanigawa, N. Sun, C. A. Boix, K. Galani, H. Mathys, D. A. Bennett, LH Tsai, M Kellis. "Single-cell transcriptional hallmarks of Alzheimer's disease across 427 individuals" (poster), the Broad Institute 17th Annual Retreat. Boston, MA, U.S.A., 2022/12/12
- Y. Tanigawa, N. Sun, D. von Maydell, C. A. Boix, L. A. Akay, K. Galani, H. Mathys, D. A. Bennett, LH Tsai, M Kellis. "Single-cell transcriptional hallmarks of Alzheimer's disease across 427 individuals" (poster), the Broad Institute Poster Day 2022, Cambridge, MA, 2022/6/7
- Y. Tanigawa, N. Sun, D. von Maydell, C. A. Boix, L. A. Akay, K. Galani, H. Mathys, D. A. Bennett, LH Tsai, M Kellis. "Single-cell transcriptional hallmarks of Alzheimer's disease across 427 individuals" (poster), Biology of the Genomes 2022. Cold Spring Harbor, NY, 2022/5/13
- Y. Tanigawa, J. Qian, Ruilin Li, Guhan R. Venkataraman, Johanne M Justesen, Robert Tibshirani, T. Hastie, and M. A. Rivas. "Significant Sparse Polygenic Risk Scores in 813 traits in UK Biobank" (poster), the Broad Institute annual retreat 2021, Cambridge, MA, 2021/12/16
- Y. Tanigawa, J. Qian, Ruilin Li, Guhan R. Venkataraman, Johanne M Justesen, Robert Tibshirani, T. Hastie, and M. A. Rivas. "Significant Sparse Polygenic Risk Scores in 428 traits in UK Biobank" (poster), American Society of Human Genetics annual meeting 2021 (virtual), 2021/10/18-22
- Y. Tanigawa, J. Qian, Ruilin Li, Guhan R. Venkataraman, Johanne M Justesen, Robert Tibshirani, T. Hastie, and M. A. Rivas. "Significant Sparse Polygenic Risk Scores in 428 traits in UK Biobank" (poster), CSH Biology of Genomes Meeting, Zoom, 2021/5/11-14
- Y. Tanigawa, J. Qian, T. Hastie, and M. A. Rivas. "Sparse polygenic risk scores in hundreds of diseases elucidate their biological basis", the Japanese Society of Human Genetics 2020 Annual Meeting, Zoom, 2020/11/18
- Y. Tanigawa, E. S. Dyer, and G. Bejerano. "WhichTF is open in your open chromatin data?", the RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenge, Zoom, 2020/11/16
- Y. Tanigawa, J. Qian, T. Hastie, and M. A. Rivas. "Sparse polygenic risk scores in hundreds of diseases elucidate their biological basis", the American Society of Human Genetics 2020 Annual Meeting, Zoom, 2020/10/27
- Y. Tanigawa, et al. "Multi-trait genome-wide multivariate polygenic risk score improves disease prediction of complex traits", the American Society of Human Genetics 2019 Annual Meeting, 2019/10/18

- Y. Tanigawa*, J. Li*, et al. "Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight novel adipocyte biology", Center for Computational, Evolutionary, and Human Genomics Annual Symposium 2019, Stanford, 2019/2/25
- S. Anand*, L. Kalesinskas*, C. Smail*, Y. Tanigawa*. “SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs”, Pacific Symposium on Biocomputing 2019, Big Island, HA, 2019/1/5
- Y. Tanigawa*, J. Li*, et al. “Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight novel adipocyte biology”, American Society of Human Genetics Annual Meeting 2018, San Diego, CA, 2018/10/18
- Y. Tanigawa, et al. "Mapping components of genetic effects across 2,138 phenotypes from UK Biobank", Stanford Bioscience Association Symposium, Stanford, CA, 2018/9/27
- Y. Tanigawa, et al. "Mapping components of genetic effects across 2,138 phenotypes from UK Biobank", Biomedical Informatics Program Annual Retreat, Asilomar, CA, 2018/9/17
- Y. Tanigawa, et al. "Mapping components of genetic effects across 2,138 phenotypes from UK Biobank", Department of Biomedical Data Science Annual Symposium, Stanford, CA, 2018/9/13
- D. Wu, Y. Tanigawa, and G. Bejerano. “A comprehensive high-quality library of transcription factors”, Stanford, Undergraduate Research Internship in CS (CURIS) Final presentation, Stanford, 2018/8/30
- Y. Tanigawa, et al. "Mapping components of genetic effects across 2,138 phenotypes from UK Biobank", Stanford Data Science Initiative Spring 2018 Workshop, Stanford, 2018/5/30
- Y. Tanigawa, et al. "Mapping components of genetic effects across 2,138 phenotypes from UK Biobank", Big Data in Precision Health Conference 2018, Stanford, 2018/5/23
- Y. Tanigawa, et al. "Mapping components of genetic effects across 2,138 phenotypes from UK Biobank", Center for Computational, Evolutionary, and Human Genomics Annual Symposium 2018, Stanford, 2018/2/26
- Y. Tanigawa, et al. "Decomposition of genetic effects across biomarkers, lifestyle measures, and disease outcomes", Stanford-EMBL Personalized Health Conference, Stanford, 2017/11/2
- Y. Tanigawa, et al. "Large-scale inference in population cohorts," the American Society of Human Genetics Annual Meeting 2017, Orlando, FL, 2017/10/19
- Y. Tanigawa. "Biomedical inference with large-scale population cohorts," Biomedical Informatics Program Annual Retreat, Asilomar, CA, 2017/9/18
- Y. Tanigawa and M. A. Rivas. "Compressed representation of personal genomes and its application for real-time haplotype inference", Stanford Bio-X Symposium, Stanford, 2017/8/24
- Y. Tanigawa and M. A. Rivas. "Compressed representation of personal genomes and its application for real-time haplotype inference", 23andMe Research day, Mountain View, CA, 2017/6/1
- Y. Tanigawa and M. A. Rivas. "Compressed representation of personal genomes and its application for real-time haplotype inference", Big Data in Biomedicine Symposium, Stanford, 2017/5/24
- Oliver Bear Don't Walk IV*, Y. Tanigawa*, et al. "Emerging Technologies for Efficient Clinical, Genetic, and Omics Inference", Stanford Bio-X Symposium, Stanford, 2017/3/1.

Work Experience

- Technical Assistant, Department of Computational Biology, Graduate School of Frontier Sciences, The University of Tokyo, Japan (2016/4-2016/8)
    - Research advisor: Dr. Shinichi Morishita
- Tetsuryoku-kai (Cram School), Tokyo, Japan (2013-15)
    - Part-time lecturer for high-school biology class (2014-15)
        - This cram school educates motivated and talented high-school students targeting the top Japanese universities and medical schools.
    - Textbook author for high-school biology class (2013-15)
        - I was one of the four members of the textbook writing group, where we prepared a new version of textbooks for the entire high-school biology curriculum and problem sets.

Community Service

- Peer review (ad hoc reviewer)
  - Journal:
    - Scientific Reports
    - IEEE/ACM Transactions on Computational Biology and Bioinformatics
    - BMC Medical Genomics
    - BMC Nephrology
  - Conference
    - American Society of Human Genetics (2021)
    - Pacific Symposium on Biocomputing (2020, 2021)
    - Intelligent Systems for Molecular Biology (ISMB) (2022)
- Symposium Organizer, Biomedical Computation at Stanford (BCATS) (2018)
  - http://bcats.stanford.edu/previous_bcats/bcats18/index.html
- Research meeting organizer, Biobank Method development seminar (2018-2020)
- Teacher, Stanford Splash (outreach opportunity) (2018)
- Seminar series organizer, Life Science in Japan (LSJ) (2017-2021)
- Member and Officer (2018-2020), Stanford Japanese Association (SJA) (2016-2021)
- Member, The Japanese Graduate Student Association in the United States (2016-)
  To promote international academic exchange, we hold information sessions about degree-seeking graduate programs outside of Japan in Japanese universities.
  - 2021/7/10: Information session panelist, Nagoya University
  - 2018/7/15: Information session organizer and speaker, the University of Tokyo
  - 2017/12/25: Information session panelist, the University of Tokyo
  - 2016/12/22: Information session speaker, Waseda University
- Member and Chair (2012-2013), Piano Society at the University of Tokyo (2012-2016)
- Science outreach talks to high school students
  - 2021/3/21: Tokai High School
  - 2020/8/2: Nishiyamato High School
  - 2020/7/24: Junior & Senior High School at Komaba, University of Tsukuba
  - 2019/10/25: Fukui Prefectural Koshi Junior and Senior High School
  - 2019/9/16: Kobe Ryukoku High School
  - 2019/8/6: Dokkyo High School
  - 2019/8/3: Kaichi High School
  - 2019/8/3: St. Margaret's High School
  - 2018/8/2: Takigawa High School
  - 2019/7/29: Kagoshima La Salle High School
  - 2019/7/25: Shutoken Rengo High schools
  - 2019/7/23: Otemae High School
  - 2019/7/12: Shuyukan High School
  - 2019/3/8: Nagano Prefecture Suwa Seiryo Senior High School
  - 2018/11/15-16: Otsuma Ranzan Junior and Senior High School
  - 2018/8/2: Osaka Prefectural Tennoji High School