CURRICULUM VITAE
RUI YAMAGUCHI

CURRENT POSITION
Associate Professor, Laboratory of DNA Information Analysis,
Human Genome Center, The Institute of Medical Science, The
University of Tokyo
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RESEARH INTERESTS
One of my main research interests is to develop computational
methodologies to extract useful information for medicine from various kinds of massive
biological and medical data with supercomputers, especially for cancer immune genomics.
I am also interested in building cancer clinical sequence systems augmented with artificial
intelligence. Currently I am studying how to develop such a system for future medicine as
a member of the clinical sequencing team in the Institute of Medical Science, the
University of Tokyo.

ACADEMIC QUALIFICATION
- 2000 — 2003 Doctor of Philosophy, Department of Earth and Planetary Sciences, Graduate School of Sciences, Kyushu University, Japan
- 1998 — 2000 Master of Science, Department of Earth and Planetary Sciences, Graduate School of Sciences, Kyushu University, Japan
- 1994 — 1998 Bachelor of Science, Department of Earth and Planetary Sciences, School of Sciences, Kyushu University

CAREER HISTORY
- Nov., 2015 — Present **Associate Professor**, Laboratory of DNA Information Analysis, Human Genome Center, The Institute of Medical Science, The University of Tokyo
- 2009 — 2015 **Lecturer**, Laboratory of Sequence Analysis, Human Genome Center, The Institute of Medical Science, The University of Tokyo
- 2007 — 2009 **Project Lecturer**, Laboratory of DNA Information Analysis, Human Genome Center, The Institute of Medical Science, The University of Tokyo
- 2006 — 2007 **Project Lecturer**, Laboratory of Biostatistics, Human Genome Center, The Institute of Medical Science, The University of Tokyo
- Oct., 2003 — Mar., 2006 **Postdoctoral Fellow**, Department of Mathematics, Faculty of Sciences, Kyushu University
- Apr., 2003 — Sep., 2003 **Postdoctoral Fellow**, Institute of Statistical Mathematics, Japan

PUBLICATIONS (ONLY 2016-2017; TOTAL 105)

1. Zhang Y-Z, Imoto S, Miyano S, Yamaguchi R. Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep learning. Proceedings of International Workshop on Deep Learning in Bioinformatics, Biomedicine, and Healthcare Informatics (DLB2H 2017), (in press).

2. Kiyotani K, Mai TH, Yamaguchi R, Yew PY, Kulis M, Orgel K, Imoto S, Miyano S, Burks AW, Nakamura Y. Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy, Journal of Human Genetics, (in press).
3. Kobayashi M, Yokoyama K, Shimizu E, Yusa N, Ito M, Yamaguchi R, Imoto S, Miyano S, Tojo A. Phenotype-based gene analysis allowed successful diagnosis of X-linked neutropenia associated with a novel WASp mutation. Ann Hematol. doi: 10.1007/s00277-017-3134-3, (2017).
4. Miyamoto T, Tanikawa C, Yodsurang V, Zhang YZ, Imoto S, Yamaguchi R, Miyano S, Nakagawa H, Matsuda K. Identification of a p53-repressed gene module in breast cancer cells. Oncotarget. 8(34):55821-55836. doi: 10.18632/oncotarget.19608, (2017).
5. Sato R, Shibata T, Tanaka Y, Kato C, Yamaguchi K, Furukawa Y, Shimizu E, Yamaguchi R, Imoto S, Miyano S, Miyake K. Requirement of glycosylation machinery in Toll-like receptor responses revealed by CRISPR/Cas9 screening. Int Immunol. doi: 10.1093/intimm/dxx044, (2017).
6. Tsuda Y, Tanikawa C, Miyamoto T, Hirata M, Yodsurang V, Zhang Y-Z, Imoto S, Yamaguchi R, Miyano S, Takayanagi H, Kawano H, Nakagawa H, Tanaka S, Matsuda K. Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. Sci Rep 7, 10739, (2017).
7. Tanikawa C, Zhang Y-Z, Yamamoto R, Tsuda Y, Tanaka M, Funauchi Y, Mori J, Imoto S, Yamaguchi R, Nakamura Y, Miyano S, Nakagawa H, Matsuda K. The Transcriptional Landscape of p53 Signalling Pathway, EBioMedicine. 20:109-119. doi: 10.1016/j.ebiom.2017.05.017, (2017).
8. Ikeda Y, Kiyotani K, Yew PY, Sato S, Imai Y, Yamaguchi R, Miyano S, Fujiwara K, Hasegawa K, Nakamura Y. Clinical significance of T cell clonality and expression levels of immune-related genes in endometrial cancer. Oncol Rep. 37(5):2603-2610, doi: 10.3892/or.2017.5536, (2017).
9. Onuki R, Yamaguchi R, Shibuya T, Kanehisa M, Goto S. Revealing phenotype-associated functional differences by genome-wide scan of ancient haplotype blocks, PLoS ONE. 12:e0176530. doi: 10.1371/journal.pone.0176530, (2017).
10. Moriyama T, Shiraishi Y, Chiba K, Yamaguchi R, Imoto S, Miyano S. OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads, IEEE Transactions on NanoBioscience. 16(2):116-122, doi: 10.1109/TNB.2017.2670601, (2017).
11. Fujii K, Miyahara Y, Harada N, Muraoka D, Komura M, Yamaguchi R, Yagita H, Nakamura J, Sugino S, Okumura S, Imoto S, Miyano S, Shiku H. Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors. OncoImmunology, 6(5):e1306617. doi: 10.1080/2162402X.2017.1306617, (2017).
12. Zhang Y-Z, Yamaguchi R, Imoto S, Miyano S. Sequence-specific bias correction for RNA-seq data using recurrent neural networks. BMC Genomics 18:1044, doi: 10.1186/s12864-016-3262-5, (2017).
13. Yoshino T, Katayama K, Horiba Y, Munakata K, Yamaguchi R, Imoto S, Miyano S, Mima H, Watanabe K. Predicting Japanese Kampo Formulas by Analyzing Database of Medical Records: A Preliminary Observational Study, BMC Medical Informatics and Decision Making. 16(1):118, (2016).
14. Sugimachi K, Yamaguchi R, Eguchi H, Ueda M, Niida A, Sakimura S, Hirata H, Uchi R, Shinden Y, Iguchi T, Morita K, Yamamoto K, Miyano S, Mori M, Maehara

Y, Mimori K. 8q24 Polymorphisms and Diabetes Mellitus Regulate Apolipoprotein A-IV in Colorectal Carcinogenesis. Ann Surg Oncol. 23(Suppl 4):546-551, (2016).

15. Yamaguchi K, Nagayama S, Shimizu E, Komura M, Yamaguchi R, Shibuya T, Arai M, Hatakeyama S, Ikenoue T, Ueno M, Miyano S, Imoto S, Furukawa Y. Reduced expression of APC-1B but not APC-1A by the deletion of promoter 1B is responsible for familial adenomatous polyposis. Scientific Reports. 6: 26011, (2016).

16. Moriyama T, Shiraishi Y, Chiba K, Yamaguchi R, Imoto S, Miyano S. OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads. Lecture Notes in Bioinformatics. 9683: 40-51, (2016).

17. Chapman CG, Yamaguchi R, Tamura K, Weidner J, Imoto S, Kwon J, Marino SR, Miyano S, Nakamura Y, Kiyotani K. Characterization of T Cell Receptor Repertoire in Inflamed Tissues of Crohn's Disease through Deep Sequencing. Inflammatory Bowel Diseases. 22(6): 1275-1285, (2016).

18. Muramatsu T, Kozaki K, Imoto S, Yamaguchi R, Tsuda H, Kawano T, Fujiwara N, Morishita M, Miyano S, Inazawa J. The hypusine cascade promotes cancer progression and metastasis through the regulation of RhoA in squamous cell carcinoma. Oncogene. 35(40): 5304-5316, (2016).

19. Tamura K, Hazama S, Yamaguchi R, Imoto S, Takenouchi H, Inoue Y, Kanekiyo S, Shindo Y, Miyano S, Nakamura Y, Kiyotani K. Characterization of T cell repertoire in tumor tissues and blood in advanced colorectal cancers through deep T cell receptor sequencing. Oncology Letters. 11(6): 3643-3649, (2016).

20. Yoshino T, Katayama K, Horiba Y, Munakata K, Yamaguchi R, Imoto S, Miyano S, Mima H, Kenji Watanabe K, Mimura M. The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study. Evid Based Complement Alternat Med, 2016:3159617, (2016).

21. Kayano M, Matsui H, Yamaguchi R, Imoto S, Miyano S. Gene set differential analysis of time course expression profiles via sparse estimation in functional logistic model with application to time-dependent biomarker detection. Biostatistics. 17(2):235-248, (2016).

22. Hasegawa T, Niida A, Mori T, Shimamura T, Yamaguchi R, Miyano S, Akutsu T, Imoto S, A Likelihood-free Filtering Method via Approximate Bayesian Computation in Evaluating Biological Simulation Models. Computational Statistics & Data Analysis. 94:63-74, (2016).