

CURRICULUM VITAE SEIYA IMOTO

CURRENT POSITION

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ACADEMIC QUALIFICATION

- 1998-2001 Doctor of Philosophy, Graduate School of Mathematics, Kyushu University
- 1996-1998 Master of Science, Graduate School of Mathematics, Kyushu University
- 1992-1996 Undergraduate School, Department of Mathematics, Kyushu University

CAREER HISTORY

- April 1, 2017 – current: Director, Health Intelligence Center, Institute of Medical Science, The University of Tokyo
- October 1, 2016 – current: Advisor (Medical Statistics), Ministry of Health, Labour and Welfare
- May 1, 2015 – current: Professor, Division of Health Medical Data Analysis, Health Intelligence Center, Institute of Medical Science, The University of Tokyo
- February 15, 2007 – April 30, 2015: Associate Professor, Laboratory of DNA Information Analysis, Human Genome Center, Institute of Medical Science, The University of Tokyo
- December 1, 2001 – February 14, 2007: Assistant Professor, Laboratory of DNA Information Analysis, Human Genome Center, Institute of Medical Science, The University of Tokyo
- April 1, 2001 – November 30, 2001: Postdoctoral Fellow, Laboratory of DNA Information Analysis, Human Genome Center, Institute of Medical Science, The University of Tokyo
- January 1, 1999 – March 31, 2001: Young Research Fellow (DC2: Statistical Science), Japanese Society of Promotion of Science (JSPS)

PUBLICATIONS (ONLY 2016-2017; TOTAL 190)

1. Fujita K, Chen X, Homma H, Tagawa K, Amano M, Saito A, Imoto S, Akatsu H, Hashizume Y, Kaibuchi K, Miyano S, Okazawa H. (2017) Targeting Tyro3 signals ameliorates PGRN-mutant FTLD-TDP model via tau-mediated synapse pathology, Nature Communications, in press.
2. Different clonal dynamics of chronic myeloid leukaemia between bone marrow and the central nervous system, British Journal of Haematology, in press.
3. 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, International Workshop on Deep Learning in Bioinformatics, Biomedicine, and Healthcare Informatics, in press.

4. 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.* (2017) Sep 27. doi: 10.1007/s00277-017-3134-3. [Epub ahead of print]
5. Kiyotani K, Mai T, Yamaguchi R, Yew P-Y, Kulis M, Orgel K, Imoto S, Miyano S, Burks A.W, Nakamura Y. Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy, *Journal of Human Genetics*, in press.
6. 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 TLR responses revealed by CRISPR/Cas9 screening, *International Immunology*, in press.
7. Tanikawa C, Zhang YZ, 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.* 2017 Jun;20:109-119.
8. Miyamoto T, Tanikawa C, Yodsurang V, Zhang Y-Z, Imoto S, Yamaguchi R, Miyano S, Nakagawa H, Matsuda K. Identification of a p53-repressed gene module in breast cancer cells, *Oncotarget*, 2017 Jul 26;8(34):55821-55836.
9. Nagata H, Kozaki K, Muramatsu T, Hiramoto H, Tanimoto K, Fujiwara N, Imoto S, Ichikawa D, Otsuji E, Miyano S, Kawano T, Inazawa J. Genome-wide screening of DNA methylation associated with lymph node metastasis in esophageal squamous cell carcinoma, *Oncotarget*, in press.
10. 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, *Oncolmmunology*, in press.
11. 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):1-7 (2017) 10.1109/TNB.2017.2670601
12. Tsuda Y, Tanikawa C, Miyamoto T, Hirata M, Yodsurang V, Zhang YZ, 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.* 2017 Sep 6;7(1):10739. doi: 10.1038/s41598-017-11208-x.
13. Zhang Y-Z, Yamaguchi R, Imoto, S, Miyano S, Sequence-specific bias correction for RNA-seq data using recurrent neural networks, *BMC Genomics* 18(Suppl 1):1044 (2017).
14. Park H, Niida A, Imoto S, Miyano S, Interaction based feature selection for uncovering cancer driver genes via copy number driven expression level, *Journal of Computational Biology*, 24:138-152 (2017)
15. Park H, Shiraishi Y, Imoto S, Miyano S. A novel adaptive penalized logistic regression for uncovering biomarker associated with anti-cancer drug sensitivity, *IEEE IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14:771-782 (2017)
16. 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, *Sci Rep.* 6:26011 (2016) doi: 10.1038/srep26011.

17. Chapman CG, Yamaguchi R, Tamura K, Weidner J, Imoto S, Kwon J, Fang H, Yew PY, Marino SR, Miyano S, Nakamura Y, Kiyotani K. Characterization of T-cell receptor repertoire in inflamed tissues of patients with Crohn's disease through deep sequencing, *Inflamm Bowel Dis.* 22(6):1275-85 (2016)
18. Hasegawa T, Hayashi S, Shimizu E, Mizuno S, Yamaguchi R, Miyano S, Nakagawa H, Imoto S. An in silico automated pipeline to identify tumor specific neoantigens from whole genome and exome sequencing data. *Proc. 12th International Symposium on Bioinformatics Research and Applications*, 2016.
19. 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*, 16:118 (2016)
20. Mao Y, Tamura T, Yuki Y, Abe D, Tamada Y, Imoto S, Tanaka H, Homma H, Miyano S, Okazawa H. The hnRNP-Htt axis regulates necrotic cell death induced by transcriptional repression through impaired RNA splicing, *Cell Death & Disease*, 7:e2207 (2016)
21. Muramatsu T, Kozaki K-i, 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)
22. 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 Computer Science*, 9683, 40-51 (2016).
23. Kato T, Inoue H, Imoto S, Tamada Y, Miyamoto T, Matsuo Y, Nakamura Y, Park JH. Oncogenic roles of TOPK and MELK, and effective growth suppression by small molecular inhibitors in kidney cancer cells, *Oncotarget*, 7, 17652-17664 (2016).
24. 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).
25. Hasegawa T, Niida A, Moria 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 and Data Analysis*, 94, 63-74 (2016).
26. Yoshino T, Katayama K, Horiba Y, Munakata K, Yamaguchi R, Imoto S, Miyano S, Mima H, Watanabe K, Mimura M. The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study, *Evidence-Based Complementary and Alternative Medicine*, Article ID 3159617 (2016)
27. 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) DOI: 10.3892/ol.2016.4465
28. Park H, Imoto S, Miyano S. Recursive random lasso (RRLasso) for identifying anti-cancer drug targets, *PLoS ONE*, 10, e0141869 (2015).