Masahiro Kanai

Curriculum Vitae

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Education

Keio University   **Yokohama, Japan**
B.S. in Bioinformatics (expected), Department of Biosciences and Informatics   *Apr. 2013–present*

Senior High School at Komaba, University of Tsukuba   **Tokyo, Japan**
High School   *Apr. 2010–Mar. 2013*

Research Experience

Keio University   **Yokohama, Japan**
Undergraduate Researcher, Laboratory for Bioinformatics   *Apr. 2016–present*
Advisor: Dr. Yasubumi Sakakibara
Bachelor thesis: Integrative multi-omics analysis of renal cell carcinoma

RIKEN Center for Integrative Medical Sciences   **Yokohama, Japan**
Research Assistant, Laboratory for Statistical Analysis   *May 2015–present*
Advisor: Dr. Yoichiro Kamatani & Dr. Yukinori Okada
Research theme:

- Genome-wide association study (GWAS) of ~200,000 individuals in the BioBank Japan Project.
- Interpretation of GWAS polygenic signals using epigenomic data.
- Population genetics analysis of 1,037 Japanese whole-genome sequences.

Tokyo Medical and Dental University   **Tokyo, Japan**
Technical Assistant, Department of Human Genetics and Disease Diversity   *Apr. 2014–Mar. 2016*
Advisor: Dr. Yukinori Okada & Dr. Toshihiro Tanaka
Research theme:

- Empirical estimation of genome-wide significance thresholds based on GWAS simulations.
- HLA imputation analysis using the Japanese-specific reference panel.

Certification

The Certification for Bioinformatics Engineers
certificated by *the Japanese Society of Bioinformatics*   *2015*

Awards and Scholarships

The Nakajima Foundation Scholarship   **Tokyo, Japan**
                                                                                     2017–2019+

The 3rd place, Worldwide Finals   **New York, USA**
Microsoft Imagine Cup 2011 Windows 7 Touch Challenge   *2011*

The 1st place, National Finals & Worldwide Finalist   **Japan & Poland**
Microsoft Imagine Cup 2010 Software Design Competition   *2010*

Technical Skills

Programming Language: C/C++, C#, Python, R, Java, Matlab, Unix shell, sed/awk
Analysis: GWAS, Genotype Imputation, HLA Imputation, Polygenic analysis using GCTA and LDSC

Publications

1. Okada, Y., Suzuki, A., Ikari, K., Terao, C., Kochi, Y., Ohmura, K., Higasa, K., Akiyama, M., Ashikawa, K., **Kanai, M.**, Hirata, J., Suita, N., Teo, Y.-Y., Xu, H., Bae, S.-C., Takahashi, A., Momozawa, Y., Matsuda, K., Momohara, S., Taniguchi, A., Yamada, R., Mimori, T., Kubo, M., Brown, M. A., Raychaudhuri, S., Matsuda, F., Yamanaka, H., Kamatani, Y. & Yamamoto, K. Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. *The American Journal of Human Genetics* **99,** 366–374 (2016).

2. **Kanai, M.**, Tanaka, T. & Okada, Y. Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project data set. *Journal of Human Genetics* **61,** 861–866 (2016).

3. Okada, Y., Muramatsu, T., Suita, N., **Kanai, M.**, Kawakami, E., Iotchkova, V., Soranzo, N., Inazawa, J. & Tanaka, T. Significant impact of miRNA–target gene networks on genetics of human complex traits. *Scientific Reports* **6,** 22223 (2016).

4. Okada, Y., Momozawa, Y., Ashikawa, K., **Kanai, M.**, Matsuda, K., Kamatani, Y., Takahashi, A. & Kubo, M. Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. *Nature Genetics* **47,** 798–802 (2015).

Reviews (in Japanese)

1. **Kanai, M.** & Okada, Y. HLA imputation: construction of a population-specific reference panel in Japanese. *Journal of Clinical and Experimental Medicine (IGAKU NO AYUMI)* **257,** 939–940 (2016).

Presentations

International Conference

1. **Kanai, M.**, Akiyama, M., Okada, Y., Ikeda, M., Iwata, N., Kubo, M. & Kamatani, Y. Trans-ethnic comparison of partitioned heritability reveals shared cell-type specific enrichment between East Asian and European genome-wide association studies. *The 66th Annual Meeting of the American Society of Human Genetics, Poster Session* (2016).

2. Akiyama, M., **Kanai, M.**, Okada, Y., Takahashi, A., Momozawa, Y., Ikeda, M., Iwata, N., Ikegawa, S., Hirata, M., Matsuda, K., Yamaji, T., Iwasaki, M., Sobue, K., Yamamoto, M., Kubo, M. & Kamatani, Y. Genetic study of body mass index in 173,430 Japanese identifies 76 new loci and highlights shared heritability with broad spectrum of complex diseases. *The 66th Annual Meeting of the American Society of Human Genetics, Oral Session* (2016).

3. **Kanai, M.**, Tanaka, T. & Okada, Y. Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project. *The 13th International Congress of Human Genetics, Oral Session* (2016).

4. **Kanai, M.**, Okada, Y., Muramatsu, T., Suita, N., Kawakami, E., Iotchkova, V., Soranzo, N., Inazawa, J. & Tanaka, T. Significant impact of miRNA–target gene networks on genetics of human complex traits. *The 13th International Congress of Human Genetics, Oral Session* (2016).

Domestic Conference (in Japan)

1. **Kanai, M.**, Tanaka, T. & Okada, Y. Empirical estimation of a genome-wide significance threshold based on the 1000 Genomes Project. *The 60th Annual Meeting of the Japan Society of Human Genetics, Oral Session* (2015).

2. Suita, N., **Kanai, M.**, Higuchi, C., Tanaka, T. & Okada, Y. Comprehensive pathway analysis for 23 large-scale genome-wide association studies. *The 60th Annual Meeting of the Japan Society of Human Genetics, Poster Session* (2015).

3. **Kanai, M.**, Yamane, K., Higuchi, C., Tanaka, T. & Okada, Y. Performance evaluation of PLINK v.1.90: a next version of a tool set for genome-wide association study. *The 59th Annual Meeting of the Japan Society of Human Genetics, Poster Session* (2014).

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