

## Curriculum Vitae

# Shunsuke A Sakai

Department of Integrated Bioscience, Graduate School of  
Frontier Science, The University of Tokyo

JSPS Research Fellow (DC2)

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Github: <https://github.com/shusakai>



Currently, I am a member of Division of Translational Informatics, Exploratory  
Oncology Research & Clinical Trial Center, National Cancer Center:  
[https://www.ncc.go.jp/en/epoc/division/translational\\_informatics/kashiwa/index.html](https://www.ncc.go.jp/en/epoc/division/translational_informatics/kashiwa/index.html)

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## Research Interest

My research interest lies in applying cutting-edge omics technologies to clinical specimens from patient with cancer. By integrating the resulting high-resolution data with bioinformatics approaches, I aim to uncover the biological and medical rationales of patient heterogeneity—particularly differences related to treatment response or resistance. While maintaining a strong focus on clinical output, I also seek to translate these insights into new knowledge in biology and informatics.

## Skills

Languages Japanese (native), English (limited working proficiency)

Programming Python, R, and Shell

### Single-cell & spatial omics analysis

Basic Cell annotation, pathway, neighborhood, ligand-receptor analysis

Advanced Custom algorithm SpatialKNifeY (<https://github.com/shusakai/skny>)  
for microenvironment analysis

### Microbiome analysis

Basic Taxonomic and functional annotation.

Advanced Custom tool QINDAO (<https://qindao.hgc.jp>) for taxonomy, function,  
phenotype, and diversity analysis

### Software development

Basic Web application development with Flask and deployment via Apache;  
creation and release of Python libraries

## Education

- 2023 Apr. Started doctor course, Department of Integrated Bioscience, Graduate School of Frontier Science, The University of Tokyo
- 2023 Mar. Master of Science, Department of Integrated Bioscience, Graduate School of Frontier Science, The University of Tokyo
- 2021 Mar. Bachelor of Science, Department of Biological Science and Technology, Faculty of Industrial Science and Technology, Tokyo University of Science

## Work Experiences

- 2024–Today JSPS Research Fellow (DC2)
- 2023–Today Project Researcher, Department of Radiation Oncology, National Cancer Center Hospital East

## Grants and Funding

- 2024.04–2026.03 JSPS Research Fellowship (DC2) Japan Society for the Promotion of Science
- 2024.06–2025.03 GSFS Challenging New Area Doctoral Research Grant (GSFS Challenge Fund)
- 2023.04–2024.03 Doctoral Student Support: "Fostering Advanced Human Resources to Lead Green Transformation (GX)" (SPRING GX)

## Publications

- 1-\* Sawada K\*, Yamashita R\*, **Sakai SA**\*, Horasawa S, Yoshikawa A, Fujisawa T, Kadowaki S, Kato K, Ueno M, Oki E, Komatsu Y, Chiyoda T, Horita Y, Yasui H, Denda T, Satake H, Esaki T, Satoh T, Takahashi N, Yamazaki K, Matsuhashi N, Nishina T, Takeda H, Ohtsubo K, Ohta T, Tsuji A, Goto M, Kato T, Bando H, Tsuchihara K, Nakamura Y, Yoshino T. (2025) Microbiome landscape and association with response to immune checkpoint inhibitors in advanced solid tumors: a SCRUM-Japan MONSTAR-SCREEN study. *Cancer Research Communications*, <https://doi.org/10.1158/2767-9764.CRC-24-0543>
- 2-\* **Sakai SA**, Nomura R, Nagasawa S, Chi S, Suzuki A, Suzuki Y, Imai M, Nakamura Y, Yoshino T, Ishikawa S, Tsuchihara K, Kageyama S, Yamashita R (2025) SpatialKNifeY (SKNY): Extending from spatial domain to surrounding area to identify microenvironment features with single-cell spatial omics data, *PLOS Computational Biology*, 18;21(2):e1012854. 10.1371/journal.pcbi.1012854
- 3-\* **Sakai SA**, Saeki K, Chi SG, Hamaya Y, Du J, Nakamura M, Hojo H, Kojima T, Nakamura Y, Bando H, Kojima M, Suzuki A, Suzuki Y, Akimoto T, Tsuchihara K,

- Haeno H, Yamashita R, Kageyama S-I (2025) Mathematical Modeling Predicts Optimal Immune Checkpoint Inhibitor and Radiotherapy Combinations and Timing of Administration. *Cancer Immunology Research*, <https://doi.org/10.1158/2326-6066.CIR-24-0610>
- 4-\* Okazawa-Sakai M\*, **Sakai SA**\*, Hyodo I, Horasawa S, Sawada K, Fujisawa T, Yamamoto Y, Boku S, Hayasaki Y, Isobe M, Shintani D, Hasegawa K, Egawa-Takata T, Ito K, Ihira K, Watari H, Takehara K, Yagi H, Kato K, Chiyoda T, Harano K, Nakamura Y, Yamashita R, Yoshino T, Aoki D (2024) Gut microbiome associated with PARP inhibitor efficacy in patients with ovarian cancer, *Journal of Gynecologic Oncology*, <https://doi.org/10.3802/jgo.2025.36.e38>
- 5- Oyoshi H, Du J, **Sakai SA**, Yamashita R, Okumura M, Motegi A, Hojo H, Nakamura M, Hirata H, Sunakawa H, Kotani D, Yano T, Kojima T, Nakamura Y, Kojima M, Suzuki A, Zenkoh J, Tsuchihara K, Akimoto T, Shibata A, Suzuki Y, Kageyama SI (2023) Comprehensive single-cell analysis demonstrates radiotherapy-induced infiltration of macrophages expressing immunosuppressive genes into tumor in esophageal squamous cell carcinoma, *Science Advances*, 9, eadh9069. doi:10.1126/sciadv.adh9069
- 6-\* **Sakai SA**, Aoshima M, Sawada K, Horasawa S, Yoshikawa A, Fujisawa T, Kadowaki S, Denda T, Matsushashi N, Yasui H, Goto M, Yamazaki K, Komatsu Y, Nakanishi R, Nakamura Y, Bando H, Hamaya Y, Kageyama S-I, Yoshino T, Tsuchihara K and Yamashita R (2022) Fecal microbiota in patients with a stoma decreases anaerobic bacteria and alters taxonomic and functional diversities. *Frontiers in Cellular and Infection Microbiology*, 12:925444. doi: 10.3389/fcimb.2022.925444

## Poster Presentations

- 7-\* **Sakai SA**, Nomura R, Nagasawa S, Chi S, Suzuki A, Suzuki Y, Ishikawa S, Tsuchihara K, Kageyama S, Yamashita R, SKNY (SpatialKNifeY) : SKNY (SpatialKNifeY): Construction of a microenvironment analysis algorithm based on cancer cell clusters and its application to single cell spatial omics data of breast cancer, *The 47th Annual Meeting of the Molecular Biology Society of Japan*, 1P-851, Fukuoka, 2024
- 8-\* **Sakai SA**, Nomura R, Nagasawa S, Chi S, Suzuki A, Suzuki Y, Tsuchihara K, Kageyama S, Yamashita R, SpatialKNifeY detects tumor microenvironments and estimates the progression trajectory using spatial transcriptomics, *The 83th Annual Meeting of the Japanese Cancer Association*, P-1336, Fukuoka, 2024
- 9-\* **Sakai SA**, Iida N, Sawada K, Horasawa S, Fujisawa T, Yoshikawa A, Nakamura Y, Yoshino T, Kageyama S-I, Tsuchihara K, Yamashita R, Gut microbiota change under anticancer drugs and concomitant medications: SCRUM-Japan MONSTAR-

SCREEN project, *The 46th Annual Meeting of the Molecular Biology Society of Japan*, 3P-661, Kobe, 2023

- 10-\* **Sakai SA**, Sawada K, Horasawa S, Yoshikawa A, Fujisawa T, Nakamura Y, Tsuchihara K, Yamashita R, Analysis of gut microbiota of multiple types of cancer using the diversity analysis tool QINDAO, *Informatics in Biology, Medicine, and Pharmacology 2023*, P-77, Kashiwa, 2023
- 11-\* **Sakai SA**, Aoshima M, Tsuchihara K, and Yamashita R, Quantitative Index Alpha diversity Overview (QINDAO): Building a web application for computing microbiome diversity based on gene function, *The 45th Annual Meeting of the Japanese Cancer Association*, 3P-628, Chiba, 2022
- 12-\* **Sakai SA**, Aoshima M, Sawada K, Horasawa S, Yoshikawa A, Fujisawa T, Kadowaki S, Denda T, Matsushashi N, Yasui H, Goto M, Yamazaki K, Komatsu Y, Nakanishi R, Nakamura Y, Bando H, Hamaya Y, Kageyama S-I, Yoshino T, Tsuchihara K and Yamashita R, Fecal microbiota in patients with a stoma decreases anaerobic microbes and alters various diversities, *The 81th Annual Meeting of the Japanese Cancer Association*, P-1048, Yokohama, 2022
- 13-\* **Sakai SA**, Aoshima M, Tsuchihara K, and Yamashita R, Quantitative Index Alpha diversity Overview (QINDAO): Building a web application for computing microbiome diversity based on gene function, *Informatics in Biology, Medicine, and Pharmacology 2022*, P-23, Osaka, 2022

## Talks

- 14-\* **Sakai SA**, Nomura R, Nagasawa S, Chi S, Suzuki A, Suzuki Y, Tsuchihara K, Kageyama S, Yamashita R, Development of SKNY (SpatialKNifeY), a spatial omics analysis algorithm focusing on cancer cell clusters, and its application to breast cancer Xenium data, *The 6th Annual Meeting of Japanese Association for Medical Artificial Intelligence*, G-14, Nagoya, 2024
- 15-\* **Sakai SA**, Iida N, Sawada K, Horasawa S, Fujisawa T, Yoshikawa A, Nakamura Y, Yoshino T, Kageyama S-I, Tsuchihara K, Yamashita R, Gut microbiota change under anticancer drugs and concomitant medications: SCRUM-Japan MONSTAR-SCREEN project, *The 46th Annual Meeting of the Molecular Biology Society of Japan*, 2PS-14-1, Kobe, 2023
- 16-\* **Sakai SA**, Sawada K, Horasawa S, Yoshikawa A, Fujisawa T, Nakamura Y, Tsuchihara K, Yamashita R, Analysis of gut microbiota of multiple types of cancer using the diversity analysis tool QINDAO, *Informatics in Biology, Medicine, and Pharmacology 2022*, OS-4, Kashiwa, 2023
- 17-\* **Sakai SA**, Aoshima M, Tsuchihara K, and Yamashita R, Construction of QINDAO, a multi-perspective microbiome analysis tool, *The 17th Annual Meeting of Society for Genome Microbiology*, 3O2-04, Chiba, 2023

- 18-\* **Sakai SA**, Aoshima M, Tsuchihara K, and Yamashita R, Quantitative Index Alpha diversity Overview (QINDAO): Building a web application for computing microbiome diversity based on gene function, *The 45th Annual Meeting of the Japanese Cancer Association*, 3PW-18-6, Chiba, 2022

## Teaching Experience

1. JSPS Seminar, jointly held by 8 Young Researchers Associations, 2025
2. Data Science Human Resource Development Seminar, National Cancer Center Hospital East, 2024
3. Data Science Human Resource Development Seminar, National Cancer Center Hospital East, 2023
4. Exercise of Data Science for Drug Development., The University of Tokyo, 2023
5. Exercise of Data Science for Drug Development, The University of Tokyo, 2022

## Awards and Honors

1. MBSJ-EMBO Poster Award, The Molecular Biology Society of Japan, 2024
2. JCA Young Researcher Poster Award, The Japanese Cancer Association, 2024
3. JMAI AWARD, Japanese Association for Medical Artificial Intelligence, 2024
4. Best Oral Presentation Award, Japanese Society for Bioinformatics, 2023

## Professional Service

1. Reviewing for *Bioinformatics Advances*, *Frontiers in Immunology* (total: 3 reviews in 2025)
2. Program committee, Informatics in Biology, Medicine, and Pharmacology 2023 (IIBMP2023)