

Curriculum Vitae

Shunsuke A Sakai

Division of Translational Informatics, Exploratory Oncology
Research & Clinical Trial Center, National Cancer Center Japan

Research Scientist (Ph.D. in Life Sciences)

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

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I also hold a cross-appointment as Visiting Researcher at the Physiological Function and Data Analysis Research Team, Self-Care Implementation Research Center, National Institute of Advanced Industrial Science and Technology (AIST). My primary laboratory: https://www.ncc.go.jp/en/epoc/division/translational_informatics/index.html

Research Interest

My research interest lies in applying cutting-edge omics technologies to clinical specimens from patients 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 algorithms SpatialKNifeY (<https://github.com/shusakai/skny>) for microenvironment analysis and SPATNIC for cancer/normal cell classification

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

- 2026 Mar. Ph.D. in Life Sciences, Department of Computational Biology and Medical Sciences (Advanced Life Science Program), Graduate School of Frontier Sciences, The University of Tokyo (Mentor: Prof. Katsuya Tsuchihara)
- 2023 Mar. Master of Science, Department of Integrated Bioscience, Graduate School of Frontier Sciences, The University of Tokyo
- 2021 Mar. Bachelor of Engineering, Department of Biological Science and Technology, Faculty of Industrial Science and Technology, Tokyo University of Science

Work Experiences

- 2026.07–Today Visiting Researcher, Physiological Function and Data Analysis Research Team, Self-Care Implementation Research Center, National Institute of Advanced Industrial Science and Technology (AIST)
- 2026.04–Today Research Scientist, Division of Translational Informatics, Exploratory Oncology Research & Clinical Trial Center, National Cancer Center Japan
- 2024.04–2026.03 JSPS Research Fellow (DC2), Japan Society for the Promotion of Science
- 2023.05–2026.03 Project Researcher, Department of Radiation Oncology, National Cancer Center Hospital East

Grants and Funding

- 2026.07–2027.03 AIST Kakusei Project (FY2026 Deep-Tech Talent Development Program), National Institute of Advanced Industrial Science and Technology: "Development of a cell–cell interaction simulator to predict the efficacy of anticancer drugs" (PI)
- 2024.04–2026.03 JSPS Research Fellowship (DC2), Grant-in-Aid for JSPS Fellows, Japan Society for the Promotion of Science: "AI models predicting cancer treatment response from the gut microbiota for combination-therapy development" (PI)

- 2024.06–2025.03 GSFS Challenging New Area Doctoral Research Grant (GSFS Challenge Fund), The University of Tokyo: "Cataloging the tumor microenvironment toward a treatment-optimization system" (PI)
- 2023.04–2026.03 JST SPRING, The University of Tokyo SPRING GX Program ("Fostering Advanced Human Resources to Lead Green Transformation"): "A gut-microbiota database of cancer patients and AI-based treatment optimization" (PI)

Publications (peer-reviewed)

- 1- Nagaoka KH, Yamashita H, Mashima C, Zhang G, Saito H, Minamide T, Nakatsuru T, Kamata R, **Sakai SA**, Yamamoto G, Morita TY, Nakai K, Hakozaiki Y, Kinoshita K, Takahashi Y, Nakayama I, Kawazoe A, Pulukuri SM, Ishii Y, Haeno H, Kashima Y, Shitara K, Yano T, Saito T, Ohashi A. (2026) Neutrophil–Macrophage Interactions Shape Inflammatory Macrophage Remodeling in Gastric Cancer During Chemo–Immunotherapy. *Cancer Science*, 117(8):2115-2131. doi: 10.1111/cas.70384
- 2- Nakatsuru T, Yamashita H, Mashima C, Zhang G, Saito H, Minamide T, Nagaoka KH, Kamata R, **Sakai SA**, Yamamoto G, Morita TY, Nakai K, Hakozaiki Y, Kinoshita K, Takahashi Y, Nakayama I, Kawazoe A, Ishii Y, Pulukuri SM, Haeno H, Kashima Y, Shitara K, Yano T, Saito T, Ohashi A. (2026) A cDC1–NK/T–Malignant Cell Circuit Drives Immunogenic Remodeling Under PD-1 Blockade in Gastric Cancer. *Cancer Science*, 117(8):2098-2114. doi: 10.1111/cas.70381
- 3- Nakamura M, Kageyama SI, Hirata H, Ohira M, **Sakai SA**, Hakozaiki Y, Hojo H, Fujisawa T, Yamashita R, Haeno H, Kanai A, Suzuki Y, Yamaguchi M, Tsuchihara K, Zenda S. (2025) Tumor-Agnostic Circulating Tumor DNA Analysis as a Comprehensive Predictive Biomarker of Recurrence after Ablative Radiotherapy for Early-Stage Non-Small Cell Lung Cancer. *Clinical Lung Cancer*, 26(8):671-679. doi: 10.1016/j.clcc.2025.09.013
- 4-* **Sakai SA**, Oyoshi H, Nakamura M, Taki T, Nomura K, Hojo H, Hirata H, Motegi A, Nakamura Y, Zenkoh J, Aokage K, Hamada A, Kojima M, Kuwata T, Tsuchihara K, Akimoto T, Soh J, Mitsudomi T, Tsuboi M, Ishii G, Suzuki Y, Suzuki A, Yamashita R, Kageyama SI. (2025) Single-cell spatial analysis with Xenium reveals anti-tumour responses of CXCL13+ T and CXCL9+ cells after radiotherapy combined with anti-PD-L1 therapy. *British Journal of Cancer*, 133(6):795-808. doi: 10.1038/s41416-025-03088-0
- 5-* 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. (*equal contribution) (2025) Microbiome

- landscape and association with response to immune checkpoint inhibitors in advanced solid tumors: a SCRUM-Japan MONSTAR-SCREEN study. *Cancer Research Communications*, 5(5):857-870. doi: 10.1158/2767-9764.CRC-24-0543
- 6-* **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*, 21(2):e1012854. doi: 10.1371/journal.pcbi.1012854
- 7-* **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*, 13(3):353-364. doi: 10.1158/2326-6066.CIR-24-0610
- 8-* 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. (*equal contribution) (2025) Gut microbiome associated with PARP inhibitor efficacy in patients with ovarian cancer. *Journal of Gynecologic Oncology*, 36(3):e38. doi: 10.3802/jgo.2025.36.e38
- 9- 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(50):eadh9069. doi: 10.1126/sciadv.adh9069
- 10-* **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, 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

Preprints

- 11- Boku S, **Sakai S**, Sawada K, Horasawa S, Yoshikawa A, Nakamura Y, Fujisawa T, Yamashita R, Satake H, Komatsu Y, Nishina T, Shiozawa M, Kudo T, Matsushashi N, Yamazaki K, Yamaguchi T, Yasui H, Takahashi N, Kadowaki S, Denda T,

- Yoshino T. (2026) Distinct Gut Microbiome Landscape of PIK3CA-Mutated Colorectal Cancer: A Nationwide Pan-Cancer Genomic and Microbial Profiling Study (MONSTAR-SCREEN). *Research Square*, doi: 10.21203/rs.3.rs-9627410/v1
- 12- Horaguchi T, Nomura R, **Sakai SA**, Saito N, Kurihara K, Ohira M, Takaha R, Mitsui N, Hatanaka Y, Yokoi R, Kuno M, Hayashi H, Fukada M, Sato Y, Yasufuku I, Asai R, Bando H, Yamashita R, Matsuhashi N. (2026) Development of a Deep Learning Model Integrating CT Images and Blood Data for the Diagnosis of Acute Cholecystitis. *medRxiv*, doi: 10.64898/2026.05.08.26352724
- 13- Kurihara K, **Sakai SA**, Sawada K, Iida N, Horasawa S, Fujisawa T, Nakamura Y, Kageyama SI, Bando H, Yoshino T, Tsuchihara K, Yamashita R. (2026) Catalog of gut microbiota alterations associated with anticancer therapies across multiple cancer types. *bioRxiv*, doi: 10.64898/2026.05.08.723707
- 14-* **Sakai SA**, Okumura M, Morinaga Y, Kato K, Kojima M, Hofmann F, Reichholf B, Garcia PV, Nakamura Y, Sakashita S, Nakamura M, Hojo H, Tsukada Y, Ito M, Shitara K, Bando H, Kojima T, Zenkoh J, Tatekawa S, Katsuki S, Ogawa K, Takahashi Y, Suzuki A, Suzuki Y, Tsuchihara K, Gremel G, Yamashita R, Kageyama SI. (2026) Single-cell spatial multiomics identifies POSTN+ CAFs mediating chemoradiotherapy resistance in rectal cancer. *bioRxiv*, doi: 10.64898/2026.04.30.721803
- 15- Nomura R, **Sakai SA**, Kageyama SI, Tsuchihara K, Yamashita R. (2026) SpatialCompassV (SCOMV): De novo cell and gene spatial pattern classification and spatially differential gene identification. *bioRxiv*, doi: 10.64898/2026.02.26.707418

Review Articles (in Japanese)

- 16- Kageyama SI, **Sakai S**, Nomura R, Fujisawa T, Bando H, Yamashita R. (2026) Significance of AI/Radiomics in medical oncology practice (腫瘍内科診療における AI/Radiomics の意義). *Clinical Oncology (腫瘍内科)*, 37(6):613-618 (Kagaku-Hyoronsha)
- 17- Kageyama SI, **Sakai S**, Fujisawa T, Yamashita R. (2026) Drug discovery by spatial transcriptomics (空間トランスクリプトーム解析による創薬). *BIO Clinica*, 41(7):611-616 (Hokuryukan)

Poster Presentations

- 18-* **Sakai SA**, Nomura R, Ohira M, Kurihara K, Chi S, Matsubara H, Morinaga Y, Kato K, Kojima M, Suzuki A, Suzuki Y, Tsuchihara K, Kageyama S, Yamashita R, Construction of a classification model for cancer and normal epithelium using

spatial transcriptomics of colorectal cancer tissue, *The 48th Annual Meeting of the Molecular Biology Society of Japan*, P-888, Yokohama, 2025

- 19-* **Sakai SA**, Nomura R, Chi S, Nagasawa S, Suzuki A, Suzuki Y, Ishikawa S, Tsuchihara K, Kageyama S, Yamashita R, SpatialKNifeY analyses tumor microenvironment features from spatial transcriptomics, *ICGC 22nd Scientific Workshop and 9th ARGO Meeting*, P58, Yokohama, 2025
- 20-* **Sakai SA**, Nomura R, Chi S, Nagasawa S, Suzuki A, Suzuki Y, Ishikawa S, Tsuchihara K, Kageyama S, Yamashita R, SpatialKNifeY (SKNY): Detection of the Tumor Microenvironment and Estimation of Tumor Progression Trajectory Using Spatial Transcriptomics of Breast Cancer, *Informatics in Biology, Medicine, and Pharmacology 2025 (IIBMP2025)*, PO-111, Nagoya, 2025
- 21-* **Sakai SA**, Nomura R, Nagasawa S, Chi S, Suzuki A, Suzuki Y, Ishikawa S, Tsuchihara K, Kageyama S, Yamashita R, 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
- 22-* **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 83rd Annual Meeting of the Japanese Cancer Association*, P-1336, Fukuoka, 2024
- 23-* **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
- 24-* **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 (IIBMP2023)*, P-77, Kashiwa, 2023
- 25-* **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 Molecular Biology Society of Japan*, 3P-628, Chiba, 2022
- 26-* **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 81st Annual Meeting of the Japanese Cancer Association*, P-1048, Yokohama, 2022

- 27-* **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 (IIBMP2022)*, P-23, Osaka, 2022

Talks

- 28-* **Sakai SA**, Nomura R, Ohira M, Kurihara K, Morinaga Y, Kato K, Kojima M, Sakashita S, Suzuki A, Suzuki Y, Tsuchihara K, Kageyama S, Yamashita R, SPATNIC: Cancer cell classification and identification of rare cancer cell populations in single-cell and spatial transcriptomics, *Informatics in Biology, Medicine, and Pharmacology 2026 (IIBMP2026)*, O7-1, Sagamihara, 2026
- 29-* **Sakai SA**, SPATNIC: Development of an automated cancer/normal epithelium classification method for colorectal cancer based on spatial transcriptomics, *The 8th Annual Meeting of Japanese Association for Medical Artificial Intelligence*, G2-5, Tokyo, 2026
- 30-* **Sakai SA**, Nomura R, Ohira M, Kurihara K, Chi S, Matsubara H, Morinaga Y, Kato K, Kojima M, Suzuki A, Suzuki Y, Tsuchihara K, Kageyama S, Yamashita R, Construction of a classification model for cancer and normal epithelium using spatial transcriptomics of colorectal cancer tissue, *The 48th Annual Meeting of the Molecular Biology Society of Japan*, 1AS-17-07, Yokohama, 2025
- 31-* **Sakai SA**, Nomura R, Kojima M, Suzuki A, Suzuki Y, Tsuchihara K, Kageyama S, Yamashita R, Application of SpatialKNifeY to Spatial Transcriptomics for Extracting Tissue Structure and Cataloging Microenvironment, *The 84th Annual Meeting of the Japanese Cancer Association*, J-2071, Kanazawa, 2025
- 32-* **Sakai SA**, Analysis of the surrounding areas of tissue structures: an approach using spatial omics (invited workshop talk), *Informatics in Biology, Medicine, and Pharmacology 2025 (IIBMP2025)*, WS-105, Nagoya, 2025
- 33-* **Sakai SA**, Nomura R, Nagasawa S, Chi S, Suzuki A, Suzuki Y, Ishikawa S, Tsuchihara K, Kageyama S, Yamashita R, SpatialKNifeY (SKNY): Detection of the Tumor Microenvironment and Estimation of Tumor Progression Trajectory Using Spatial Transcriptomics of Breast Cancer (selected poster presentation), *Informatics in Biology, Medicine, and Pharmacology 2025 (IIBMP2025)*, PO-111, Nagoya, 2025
- 34-* **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
- 35-* **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

- 36-* **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 (IIBMP2023)*, OS-4, Kashiwa, 2023
- 37-* **Sakai SA**, Aoshima M, Tsuchihara K, and Yamashita R, Construction of QINDAO, a multi-perspective microbiome analysis tool, *The 17th Annual Meeting of the Society for Genome Microbiology*, 3O2-04, Chiba, 2023
- 38-* **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 Molecular Biology Society of Japan*, 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. Dean's Award, Graduate School of Frontier Sciences, The University of Tokyo, 2026
- 2. Doctoral Dissertation Special Encouragement Award, Advanced Life Science Program, The University of Tokyo, 2026
- 3. Excellent Poster Presentation Award (IIBMP2025), Japanese Society for Bioinformatics, 2025
- 4. MBSJ-EMBO Poster Award, The Molecular Biology Society of Japan, 2024
- 5. JCA Young Researcher Poster Award, The Japanese Cancer Association, 2024
- 6. JMAI Award (Excellent Presentation Award), Japanese Association for Medical Artificial Intelligence, 2024
- 7. Excellent Oral Presentation Award (IIBMP2023), Japanese Society for Bioinformatics, 2023

Professional Service

1. Reviewing for *Bioinformatics Advances*, *Frontiers in Immunology*, *Molecular and Cellular Biochemistry*, *Cell Communication and Signaling* (total: 5 reviews in 2025)
2. Organizer and chair, Young Researchers' Association for Bioinformation Science session "Bioinformatics and the future of AI coding", Informatics in Biology, Medicine, and Pharmacology 2026 (IIBMP2026), 2026
3. Organizer and chair, Young Researchers' Association for Bioinformation Science session "Bioinformatics Research Collaboration Guild", Informatics in Biology, Medicine, and Pharmacology 2025 (IIBMP2025), 2025
4. Organizer and chair, Young Researchers' Association for Bioinformation Science session "Let's talk about laboratory management", Informatics in Biology, Medicine, and Pharmacology 2023 (IIBMP2023), 2023
5. Program committee, Informatics in Biology, Medicine, and Pharmacology 2023 (IIBMP2023)
6. Staff member, Young Researchers' Association for Bioinformation Science (生命情報科学若手の会)

Professional Memberships

1. The Molecular Biology Society of Japan
2. The Japanese Cancer Association
3. Japanese Society for Bioinformatics
4. Japanese Association for Medical Artificial Intelligence
5. Young Researchers' Association for Bioinformation Science