講座名（専門科目名）	データマネジメント・インテグレーション	特任教授氏名	Imad Abugessaisa
学生への指導方針 Teaching policy for students	The laboratory is engaged in joint research with other laboratories within WPI-PRIMe and the Graduate School of Medicine, the system is in place to receive guidance from the PI members of those laboratories and to proceed with research. At WPI-PRIMe, there is a lot of interaction with other laboratories, and there are frequent opportunities to interact with other members at seminars, meetings and social events, so students can exchange opinions and gather information with students and researchers from other laboratories, and the environment is set up so that they can promote cutting-edge research and develop new ideas.		
学生に対する要望 Requests for students	We expect students to: **Take** responsibility for their own projects under the guidance of the lab head. | **Take** an active role in conducting their research withing the thesis timeframe. | **Participate** in relevant seminars, symposiums, workshops and lectures organized by WPI-PRIMe and UOsaka. | **Contributes** to the development of the laboratory.		
問合せ先	(Tel)06-6210-8303 (Email) koumekawa-t@office.osaka-u.ac.jp	担当者	小梅川
その他出願にあたっての注意事項等 Notes on application	Applicants are encouraged to meet the lab leader to discuss ideas before official application to join the lab.		

Laboratory name: Laboratory for Bio-digital Twin Data Management and Integration

The main mission of the laboratory is to enable metaverse-based medical research by fully utilizing biomedical data. Under this theme, graduate and undergraduate students will gain the necessary research skills and knowledge that stimulate students to engage in clinical and basic research in their careers.

Research output { *For full list of publications visit Google scholar profile from here*}

scRNA-seq method development and analysis

Abugessaisa I, et al. Computational approach to evaluate scRNA-seq data quality and gene body coverage with SkewC. STAR Protoc. (2023). [PMID]: 36853658. | Abugessaisa I, et al. SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. iScience. (2022). [PMID]: 35146392. | Woogeng IN, et al. Inducing human retinal pigment epithelium-like cells from somatic tissue. Stem Cell Reports. (2022). [PMID]: 35030321.

Genome annotation and gene regulation

Abugessaisa I, et al. FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. Nucleic Acids Res. (2021). [PMID]: 33211864 | Abugessaisa I, et al. refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. J Mol Biol. (2019). [PMID]: 31075273. | de Rie D, Abugessaisa I, et al. An integrated expression atlas of miRNAs and their promoters in human and mouse. Nat Biotechnol. (2017). [PMID]: 28829439.

Integration of clinical and molecular data

Abugessaisa I*, et al. OVCH1 Antisense RNA 1 is differentially expressed between non-frail and frail old adults. Geroscience. (2024). [PMID]: 37817005 | Gomez-Cabrero D, Walter S, Abugessaisa I, et al. A robust machine learning framework to identify signatures for frailty: a nested case-control study in four aging European cohorts. Geroscience. (2021). [PMID]: 33599920.