

IMSUT International Joint Usage/Research Center
International Project-completion Report (FY2022 ver.)

Date of submission: **05 / 10 / 2023**

Principal Investigator	Position, Institution: Professor, Shandong University
	Name: Leyi Wei
IMSUT Host Researcher	Division: Lab. Of Functional Analysis in silico
	Name: Kenta Nakai
Project Title	Dual learning based generative adversarial networks for imputation of single-cell RNA-seq data
Duration	From 4/1/2022 to 3/31/2023 *Please enter the entire research period.
Project Members	*Please enter all of your project members, including IMSUT members.
Name	Position, Institution
Fengsheng Wang	Master student, Shandong University
Kenta Nakai	Professor, IMSUT
Project-completion Report on achievements/progress through the entire project period	
*Since this report will be published on the website of IMSUT , please submit it with particular attention to matters related to intellectual property .	
<p>With the advent of single-cell RNA sequencing (scRNA-seq), one major challenging is the so-called ‘dropout’ events that distort gene expression and remarkably influence downstream analysis in single-cell transcriptome. To address this issue, much effort has been done and several scRNA-seq imputation methods were developed with two categories: model-based and deep learning-based. However, comprehensively and systematically comparing existing methods are still lacking. In this project, we use six simulated and two real scRNA-seq datasets to comprehensively evaluate and compare a total of 12 available imputation methods from the following four aspects: (i) gene expression recovering, (ii) cell clustering, (iii) gene differential expression, and (iv) cellular trajectory reconstruction. We demonstrate that deep learning-based approaches generally exhibit better overall performance than model-based approaches under major benchmarking comparison, indicating the power of deep learning for imputation. Importantly, we built <i>scIMC</i> (single-cell Imputation Methods Comparison platform), the first online platform that integrates all available state-of-the-art imputation methods for benchmarking comparison and visualization analysis, which is expected to be a convenient and useful tool for researchers of interest. It is now freely accessible via https://server.wei-group.net/scIMC/.</p>	

Research Results from the Project during FY2022

<Publications>

Dai, C., Jiang, Y., Yin, C., Su, R., Zeng, X., Zou, Q., Nakai, K. & Wei, L. (2022). scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. *Nucleic Acids Research*, 50(9), 4877-4899.

<Patent Applications>

Days of visits to IMSUT during FY2022

*Please include visits without travel allowances.

*If the project members could not visit IMSUT due to the pandemic of COVID-19 during FY2022, please present how many days in total your project has held online meetings, discussions via e-mail or communication tools such as Slack, etc. among your project members since April 1st, 2022.

*For the "Sex" and "Age" sections, the information shall be used only for statistical purposes.

*Please select the age range based on the age at the end of FY2022.

Name	Position, Institution	Sex	Age	Visits to IMSUT (Days)
Leyi Wei	Professor, Shandong U	Male	36 to 39	10 times communication
		Pull-down ▼	Pull-down ▼	
		Pull-down ▼	Pull-down ▼	
		Pull-down ▼	Pull-down ▼	
Name	Position, Institution	Sex	Age	Online Meetings (Days)
		Pull-down ▼	Pull-down ▼	
		Pull-down ▼	Pull-down ▼	
		Pull-down ▼	Pull-down ▼	
		Pull-down ▼	Pull-down ▼	
Name	Position, Institution	Sex	Age	Discussions via E-mail, Slack, etc. (Days)
Kenta Nakai	Professor, University of Tokyo	Male	40 or older	Via E-mail, 40+ times
		Pull-down ▼	Pull-down ▼	
		Pull-down ▼	Pull-down ▼	

		Pull-down ▼	Pull-down ▼	
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Usage of Facilities/Equipment during FY2022

*Please enter '0' or 'N/A' if you have not used any facilities.

*For this fiscal year only, if the project members could not visit IMSUT due to the pandemic of COVID-19, please include the uses by IMSUT faculty members to conduct this joint research project.

Name of Facility	Equipment	Number of Use (Times)	Usage time (Hours)
FACS Core Laboratory	e.g.) FACS Aria (BD)		
Medical Proteomics Laboratory	e.g.) Orbitrap QSTAR Elite		
Imaging Core Laboratory	e.g.) Zeiss Multiphoton Microscopy (LSM710NLO)		
Gene Manipulated Mouse Section	Creation and cryopreservation embryo of Knockout mouse		
Human Genome Center	Supercomputer		
Amami Laboratory of Injurious Animals	Experimental lab		
Other			

Usage of Scientific Resources *Please enter '0' or 'N/A' if you have not used any.

Name of Scientific Resource	Number of Samples/Lines
Serum (BioBank Japan)	
DNA (BioBank Japan)	
Knockout mouse	
Pathogenic bacteria	
Other	

Usage of Database *Please enter '0' or 'N/A' if you have not used any.

Name of Database	Number of Use (Times)