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Current Research Topic

- Developing high-speed variant calling methods for genomic data
- Investigating misidentification and contamination in global cell line data
- Designing real-time diagnostic platforms using nanopore sequencing
- Developing tools for RNA modification detection in nanopore sequencing

Education

Mar. 2017 – Feb. 2024	**PhD in Life Science**, Hanyang University, Seoul, Republic of Korea Thesis title: "Development of Fast Callers for Genomic Variants Using *k*-mer and Adaptive Sampling" Advisor: Prof. Jin-Wu Nam
Mar. 2012 – Feb. 2017	**BA in Life Science**, Hanyang University, Seoul, Republic of Korea Thesis title: "A New Computational Method to Classify Coding and Non-Coding Transcripts" Advisor: Prof. Jin-Wu Nam

Positions

Mar. 2024 – Present	**Postdoctoral Fellow**, Hanyang University, Seoul, Republic of Korea

Publications

- "Toward the functional interpretation of somatic structural variations: bulk- and single-cell approaches." **Dohun Yi**, Jin-Wu Nam, Hyobin Jeong. ***Briefings in Bioinformatics***, 24, 5 (2023). https://doi.org/10.1093/bib/bbad297
- "Ultrafast prediction of somatic structural variations by filtering out reads matched to pan-genome *k*-mer sets." Jang-il Sohn*, Min-Hak Choi*, **Dohun Yi***. et al. ***Nat. Biomed. Eng*** 7, 853–866 (2023). https://doi.org/10.1038/s41551-022-00980-5

* denotes equal contribution

Presentations

- "An Evaluation of Global Human Cell Line Contamination via the Fast and Efficient Cell Line Identifier" **HY-IBB Bio-BigData Center Symposium**, Seoul, Republic of Korea, May. 2024.
- "An Evaluation of Global Human Cell Line Contamination via the Fast and Efficient Cell Line Identifier" **KSMCB**, Pyeongchang, Republic of Korea, Feb. 2024**.** ***Selected as Young Investigator Award***

Awards & Honors

- Young Investigator Award, Korean Society for Molecular and Cellular Biology (KSMCB), Feb. 2024

Patent & Copyrights

- **Patent** (Republic of Korea, #10-2018-0139875, 2018.11.14)
  "Detection Method and Detection Apparatus for DNA Structural Variations Based on Multi-Reference Genome"

Languages

- Korean (native)
- English (intermediate)

Skills

- **Programming Languages:** Proficient in Python, R, Bash script
- **Data Analysis:** Skilled in optimizing computational analyses and applications. Experience in analyzing large-scale data (~200,000 samples), including expression data (RNA-seq), epi-transcriptomic data (m6A-seq, direct RNA-seq), and variant data (WGS, WES, targeted-panel). Proficient in data analysis using Illumina and Nanopore sequencing platforms.
- **Technical Skills:** Skilled in managing and maintaining high-performance Linux cluster environment, with 7 years of experience in cluster management
- **Cloud Computing:** Experienced in large-scale analysis on Amazon Web Service (AWS)
- **Machine Learning:** Experienced in developing applications based on large language model and retrieval-augmented generation