

Martin L. Putra

CONTACT

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RESEARCH INTERESTS

Areas: Systems Support for Genomics, Cluster Resource Management, Operating Systems, Storage Systems
Focus: Design and build novel genomics data processing systems to achieve

1. Performance: data- & task- parallelism for increased throughput and cluster utilization
2. Efficiency: scheduling based on novel workload characterization for improved time- and cost-efficiency
3. Scalability: reliable execution on large-scale fleet of (possibly transient) hybrid cloud machines

EDUCATION

University of Chicago Chicago, IL
Ph.D in Computer Science (*M.S. conferred in 2022*) 2020 - Present
Advisors: [Robert L. Grossman](#), [Haryadi S. Gunawi](#)
Bandung Institute of Technology (ITB) Bandung, Indonesia
B.Eng. in Computer Science 2015-2019

EXPERIENCES

Center for Translational Data Science (CTDS), Chicago, IL 2020 - Present
Working to optimize Genomics Data Commons (GDC)'s pipeline automation system by:

1. Characterizing Workload: I analyzed a **large-scale, 2-years-long production trace** to characterize GDC's workload and **build prediction models** for GDC's genomics workflows execution time.
2. Building a Hybrid Cloud Simulator: I integrated results from (1) into a high fidelity simulator which supports investigation of novel **high-throughput & cost-efficient scheduling policies**.
3. Migrating into State-of-Art Workflow Engine: I built an **semi-automatic translator** to migrate existing CWL production workflows into Nextflow [[C1](#)]. Experimental results showed up to **72% speedup of exec. time**.
4. Investigating Novel Workload Features: My extensive communication with domain experts suggests that there is an **understudied workload feature(s)** that can lead to **tail latency**.

CONFERENCE PUBLICATIONS

Bibliometrics on [Google Scholar](#) and [DBLP](#)

BIBE'23

[C1] [Martin L. Putra](#), In Kee Kim, Haryadi S. Gunawi, Robert L. Grossman. [CNT: Semi-Automatic Translation from CWL to Nextflow for Genomic Workflows](#). In The 23rd IEEE International Conference on Bioinformatics and BioEngineering (BIBE), 2023.
Artifact available upon request.

SOSP'21

[C2] Huaicheng Li, [Martin L. Putra](#), Ronald Shi, Xing Lin, Gregory R. Ganger, Haryadi S. Gunawi. [IODA: A Host/Device Co-Design for Strong Predictability Contract on Modern Flash Storage](#). In the Proceedings of the 28th Symposium on Operating Systems Principles (SOSP), 2021.
Pre-accepted sans discussion at the PC meeting; Artifact Available, Functional and Results Reproduced

JOURNAL PUBLICATIONS

TOS'23

[J1] Huaicheng Li, [Martin L. Putra](#), Ronald Shi, Fadhil I. Kurnia, Xing Lin, Jaeyoung Do, Achmad I. Kistijantoro, Gregory R. Ganger, Haryadi S. Gunawi. [Extending and Programming the NVMe I/O Determinism Interface for Flash Arrays](#). ACM Transactions on Storage (TOS), Volume 19, Issue 1, February 2023. [Extended version of [C2](#)]

TALKS

CNT: Semi-Automatic Translation from CWL to Nextflow for Genomic Workflows.
Conference Talk, BIBE'23, Online 2023

TECHNICAL SKILLS

Programming Languages: Bash, C, C++, Python, JavaScript, Groovy
Data Science Toolkit: NumPy, Pandas, Scikit-learn, Matplotlib, Gnuplot
Testbed / Cloud Platform: OpenStack, ChameleonCloud, Emulab, AWS, Azure Cloud, GCP
Systems Toolkit & Experiences: UNIX Tools, QEMU, FEMU, Linux Kernel (storage & md subsystems)
Bioinformatics Toolkit: CWL, Nextflow, bwa, STAR, FastQC, Picard, GATK

SERVICE

Secondary / Sub-reviewer

ASPLOS'24: The 29th ACM Intl' Conf. on Architectural Support for PL and OS 2023
OSDI'24: The 18th USENIX Symposium on Operating Systems Design and Implementation 2023
FAST'24: The 22nd USENIX Conference on File and Storage Technologies 2023

Artefact Evaluation Committee (AEC)

ATC'23: The 2023 USENIX Annual Technical Conference 2023

Other Activities

UC Santa Cruz's [Summer of Reproducibility](#) Project [Co-lead](#) 2023
UChicago's [Data Science Institute \(DSI\) Summer Lab](#) Mentor 2022