Andrew J. Mikalsen

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Research Interests

I am interested in applied algorithms and data structures for managing massive volumes of data in resource constrained environments. My research focuses on problems with applications to scientific computing, especially those problems important to computational biologists. My goals are to both (i) develop the theoretical tools needed by system designers and (ii) apply these tools by implementing full-scale systems for scientific applications. My current focus is on edge computing for real-time DNA analytics.

Education

Aug. 2021 – May 2027	**Doctor of Philosophy, Computer Science and Engineering**, *University at Buffalo, the State University of New York*, GPA 4.0 Advised by Dr. Jaroslaw Zola.
Jan. 2020 – May 2021	**Bachelor of Science, Computer Science**, *University at Buffalo, the State University of New York*, GPA 3.96

Professional Experience

May 2021 – Present	**Research Assistant in Scalable Computing Research Group (SCoRe)**, *University at Buffalo*, Amherst, NY
Aug. 2024 – May 2025	**Teaching Assistant for Operating Systems (CSE 421/521)**, *University at Buffalo*, Amherst, NY
Sep. 2020 – May 2021	**Research Aide in Scalable Computing Research Group (SCoRe)**, *University at Buffalo*, Amherst, NY
Aug. 2020 – Dec. 2020	**Undergraduate Teaching Assistant for Data Structures (CSE 250)**, *University at Buffalo*, Amherst, NY
May 2020 – Aug. 2020	**Research Intern (NSF REU) in Scalable Computing Research Group (SCoRe)**, *University at Buffalo*, Amherst, NY

Honors and Awards

Dec. 2022	**Russell L. Agrusa CSE Student Innovation Competition (Second Place)**, *University at Buffalo*
Dec. 2022	**CSE PhD Poster Competition (First Place)**, *University at Buffalo*
Aug. 2021	**Presidential Fellowship**, *University at Buffalo*

Publications

A.J. Mikalsen and J. Zola. "Coriolis: Enabling Metagenomic Classification on Lightweight Mobile Devices". In: *Intelligent Systems for Molecular Biology (ISMB)*. 2023, pp. i66–i75

Open Source Software

DNAsbt: *C++ library for exact pattern matching in external storage.*
`https://gitlab.com/SCoRe-Group/dnasbt`

○ Designed the compacted string B-tree data structure and formally proved its theoretical properties, such as I/O optimality, generality to multiple sequences, and alphabet independence.
○ Implemented the compacted string B-tree as a C++ library, featuring a parallel construction algorithm, on-the-fly compression and decompression, and a concurrent LFU cache.
○ Introduced abstractions enabling DNAsbt to work with numerous interchangeable data managers, including different caching policies, memory mapping, and direct I/O.
○ Demonstrated empirically that compacted string B-trees are extremely effective in practice, easily achieving 30× speedup over the competing methods (e.g,. FM-Index).

SMARTEn: *Programming model and C++ framework for mobile DNA analytics.*
`https://cse.buffalo.edu/~jzola/smarten/`

○ Co-designed and co-implemented SMARTEn's parallel runtime system for automatically parallelizing and optimizing algorithms written in our framework.
○ Utilized compacted string B-trees to design and implement Coriolis, a metagenomic classifier capable of performing DNA analytics on mobile devices.
○ Demonstrated that Coriolis can run in-step with DNA sequencing and basecalling with only MBs of memory, enabling real-time and in the field DNA analytics for the first time.

OneDataShare: *Distributed SaaS for optimized data transfers over WAN*
`https://onedatashare.org/`

○ Redesigned the service's REST API in collaboration with other project members to decouple the REST API from the front-end and enable effective programmatic use.
○ Developed an abstract, high-level design for the service's SDK to be used for both C++ and Python implementations, as well as by the Python CLI.
○ Implemented the service's C++ SDK.

Service

Reviewer, *International Parallel and Distributed Processing Symposium (IPDPS)*, 2024

Reviewer, *International Conference on Parallel Computing (ICPP)*, 2023

Skills

Languages: C++, C, Bash, Go, Rust, Python

Development Tools: Git, CMake, Vim, Neovim, VS Code, Jupyter

Operating Systems: Linux, Unix, macOS

Technical Knowledge: Parallel Computing, Distributed Systems, Internet of Things, Big Data, Edge Computing, Operating Systems, Algorithms, Data Structures, Databases, Bioinformatics, Machine Learning