TUDelft

ZygosDB: An efficient read-only database for Genome-Wide Association Studies (GWAS)

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1 INTRODUCTION & OBJECTIVE

- Genome-Wide Association Studies (GWAS): Identify associations between genetic variants and traits.
- snpXplorer: Website for visualising SNPs (single-base mutations) and SVs (multi-base mutations) in GWAS summaries.
- Tabix: Popular genomic indexing tool, currently in use by snpXplorer.
- Challenge: Querying genomic datasets is slow.
- Solution: Developed a custom specialized read-only database optimized for query throughput.

How can an efficient read-only database be designed and implemented for querying chromosomal, positional data?

Figure 1: An example B-tree.

2 METHOD

1. Implement database in Rust

- Custom binary format.
- Store all data sequentially.
- Encode positions using variable-length integers.
- Indices using B-trees for fast lookup.

2. Optimise query throughput

- Compress database using Gzip or LZ4.
- Resolve queries in parallel using multiple threads.
- 3. Measure performance



1

When returning small numbers of results, ZygosDB with Gzip compression is the fastest. As the window size increases, query throughput increases as well, with a not compressed ZygosDB database returning up to 7 million rows per second.

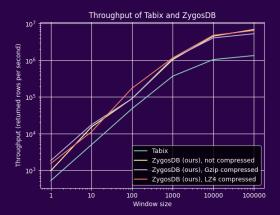


Figure 2: The query throughput, measured in the number of rows returned per window size, for both Tabix and our

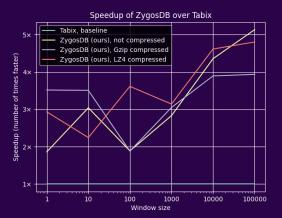


Figure 3: The speedup of ZygosDB over Tabix.

2

In a worst-case scenario, ZygosDB is approximately 2 times faster than Tabix. By increasing the window size, ZygosDB can reach throughputs that are over 5 times faster than Tabix.

3

The maximum query thoughput is reached when using 3-5 threads. Using more threads decreases performance, eventually reaching throughputs lower than when using a single thread.

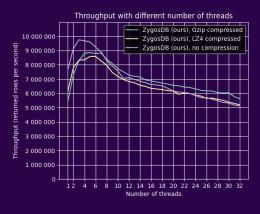


Figure 4: The multi-threaded query throughput with a window size of 100 000, measured with thread counts of 1-32.

4 CONCLUSION

ZygosDB, our read-only database, specialised for storing and querying genomic datasets, has a **2-5 times higher query throughput** than Tabix.