Compressed Suffix Arrays for Automata

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Some new content as well.

Collections of individual genomes or different versions of documents compress extremely well. With them, $o(n)$ bits of overhead information in a CSA can be too much.

CSAs where overhead scales with compressed size.
The story begins...

- Veli visited Richard Durbin at Sanger in late 2009.
- 1000 genomes project was not planning to assemble individual genomes.
- They were going to store the reads as de Bruijn graphs.
- I misunderstood the problem.
This is what I imagined
What I thought

- They wanted to index recombinations of individual genomes in addition to the genomes themselves.
- We can probably use bit vectors to split and join paths in the automaton.
- RLCSA analysis: Substrings between SNPs are usually unique.
# Backward searching

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<tr>
<th>Suffixes</th>
<th>BWT</th>
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- **Suffixes matching pattern AC**
- **Suffixes starting with T**
## Backward searching

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Suffixes matching pattern **AC**

Suffixes matching pattern **TAC**
Nodes with label c must be in the same order as nodes having a predecessor with label c.
Requirements for the automaton

- Multiple suffixes can be recognized from most nodes.
- We should get the same order for the nodes, regardless of which suffix we use as a sort key.
- Each node should correspond to a lexicographic range of suffixes.
Definition.

Let $A = (V, E)$ be a finite automaton, and let $v \in V$ be a node. Let $\text{rng}(v)$ be the smallest lexicographic range containing all suffixes that can be recognized from node $v$. Automaton $A$ is \textit{prefix-range-sorted}, if $\text{rng}(v) \cap \text{rng}(v') = \emptyset$ for all $v' \neq v$. 
Prefix-doubling

• Find a prefix-range-sorted automaton equivalent to the original automaton.

• Nodes are paths in the original automaton.

• \((u, v, r) \oplus (v, w, r') \longmapsto (u, w, (r, r'))\)

• If all paths sharing a rank start from the same original node, we merge them.
Creating the edges

- We first merge paths with adjacent ranks starting from the same original node.

- \((u, v) + (v, v', r') \leadsto (u, (v, v'))\)

- Sort edges by \((l(u), r')\) and scan the lists.

- \((u, u', r) + (u, (v, v')) \leadsto ((u, u'), (v, v'))\)

- The edges were sorted by \(r\).
We propose a biologically motivated generalization of the XBW transform for labeled trees. This automaton is transformed into an equivalent tree accepting the input language.

A simple generalization is used to index the transformed automaton.

We take the suffix array over plausible recombinations of the reference sequence and a set of mutations, and build the index.

For reasonable mutation frequencies, basic operations are about 2 times slower than in regular BWT-based indexes.
Index construction

- Human genome and genetic variation in the Finnish subpopulation of the 1000 genomes project.
- 4x Xeon X7550 (32 cores + HT, used 24 cores) and 1 TB of memory.
- Index construction took 10 hours, 181 GB.
- Final index takes 2.8 gigabytes.
Analysis

• Assume a random sequence of length $n$ and random mutations with probability $p$.

• The expected number of paths of length $k$ starting from a given position is $(1+p)^k$.

• For reasonable values of $p$, the expected number of nodes is $n(1+p)^{O(\log_\sigma n)} + O(1)$.

• This is $O(n)$ for $p = O(1 / \log_\sigma n)$. 
Search performance

- Backward searching requires one extra bit vector operation per character.
- `locate()` can be slow due to duplicates.
- Theoretically 2x slower than a similar CSA.
- In approximate matching, GCSA is 1.5 to 2.5 times slower than RLCSA using the same algorithm.
Multiple automata

• We can index multiple automata in the same way as multiple sequences.
• Indexing two identical automata results in exponential growth, as end markers are required to distinguish the paths.
• Maybe we can solve this by aligning the automata.
Class of languages

- Prefix-range-sorted automata exist for all finite languages (consider tries).
- Some infinite languages can also be recognized.
Theorem. Not all regular languages can be recognized by prefix-range-sorted automata.

Consider the language $L = \{a, b\}^* \cup \{a, c\}^*$ and its suffixes of type $B_n = a^n b$ and $C_n = a^n c$.

If $B_n$ and $C_n$ can be recognized from the same node, then $bC_n \in L$ – a contradiction.

As $C_{n+1} < B_n < C_n$, there must be separate nodes to recognize suffixes $C_i$ for all $i$ – the automaton must be infinite.
De Bruijn graphs?
An order-\(k\) de Bruijn graph is a prefix-range-sorted automaton, where \(\text{rng}(v)\) is defined by a prefix of length \(k\).

De Bruijn graphs with $m$ edges in $m(\log \sigma + 2) + o(m)$ bits. Based on the XBW transform. Different terminology and different design choices, but the core combinatorial structure is essentially GCSA.

I had solved the right problem already in 2009, but nobody noticed!
THANK YOU!