Scalable String Similarity Search/Join with Approximate Seeds and Multiple Backtracking

Enrico Siragusa, David Weese, Knut Reinert
FU Berlin, Algorithmic Bioinformatics

String Similarity Search/Join Competition, 22 March 2013

Overview

- This work is a variation of our new DNA read mapper[1]
- We follow the seminal work of Navarro and Baeza-Yates[2]
- We combine multiple methods

online	Banded Myers bit-vector algorithm
indexed	Multiple backtracking
filtering	Approximate seeds

- We preprocess both database and query strings
- Our approach solves search and join

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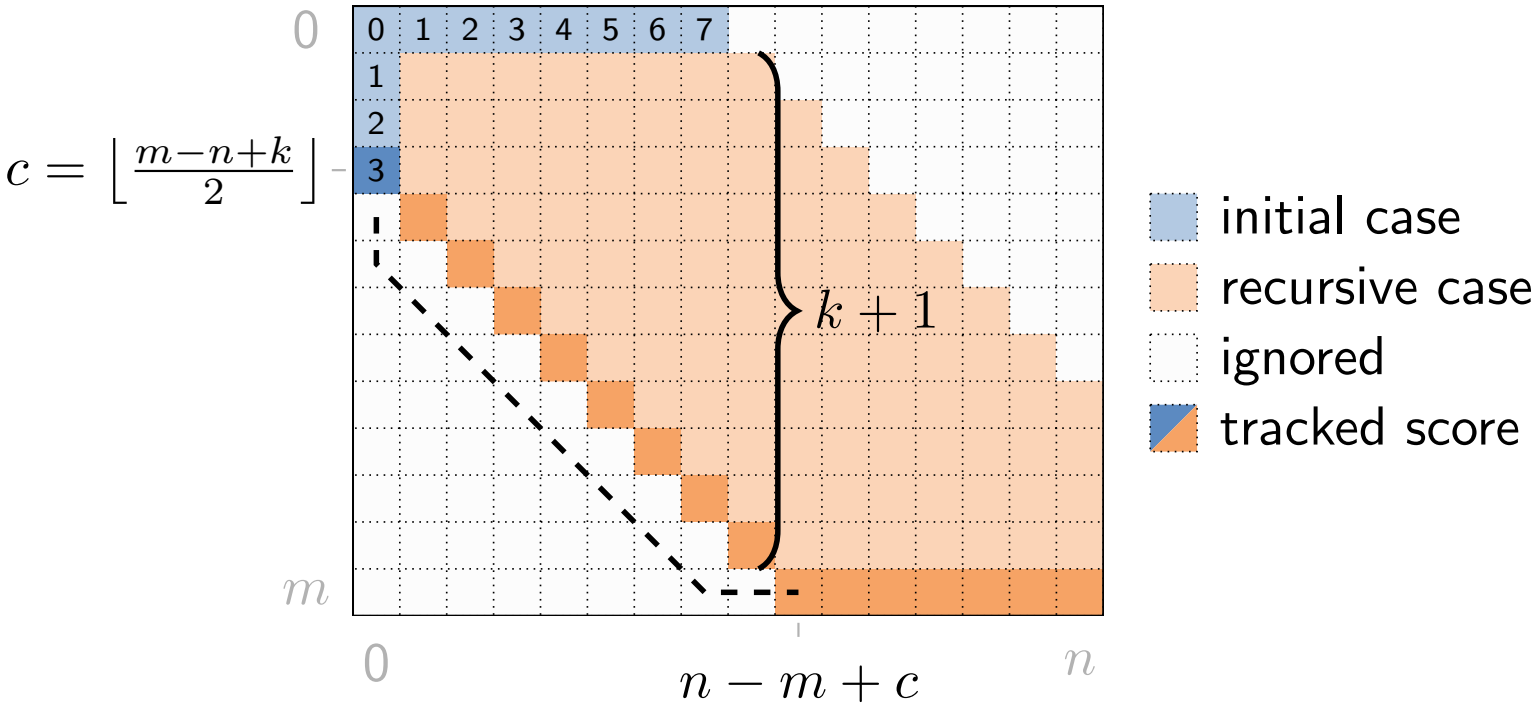
[1] Enrico Siragusa, David Weese, and Knut Reinert. "Fast and accurate read mapping with approximate seeds and multiple backtracking". In: **Nucleic Acids Res.** (2013).

[2] Gonzalo Navarro and Rircardo A. Baeza-Yates. "A hybrid indexing method for approximate string matching". In: **Journal of Discrete Algorithms** 1.1 (2000), pp. 205–239.

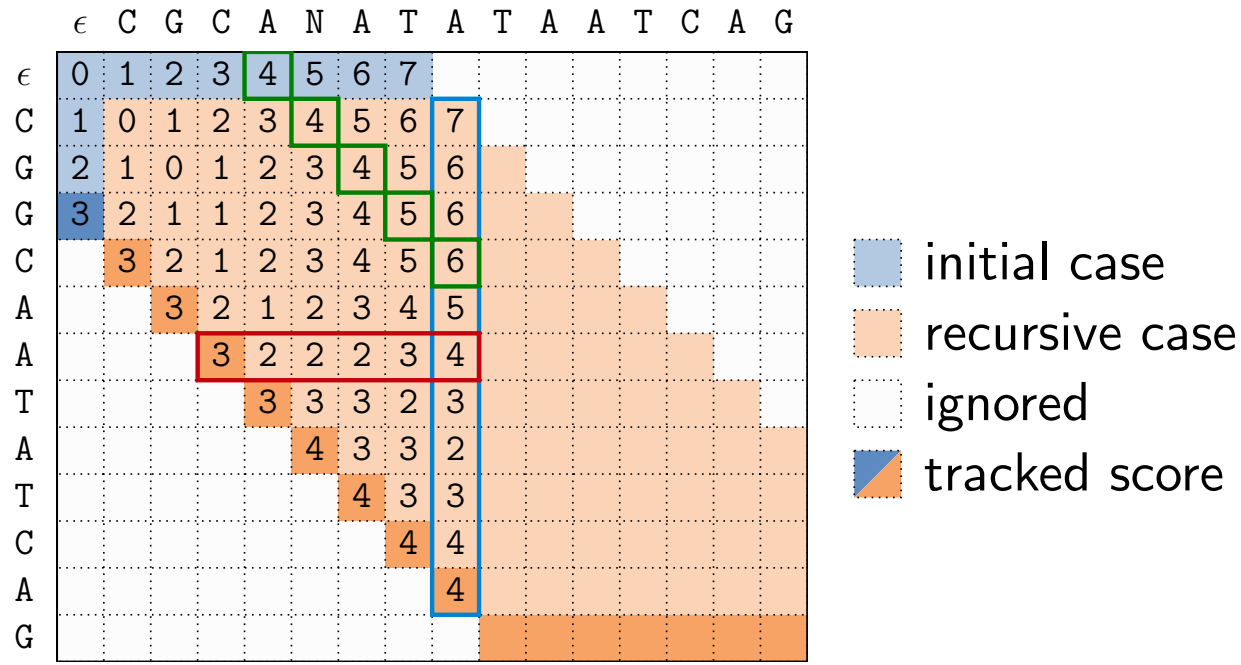
Online solution

- Check the edit distance between each query and any database string: **global k-differences problem**
- A band of $k+1$ cells is sufficient



Banded Myers bit-vector algorithm

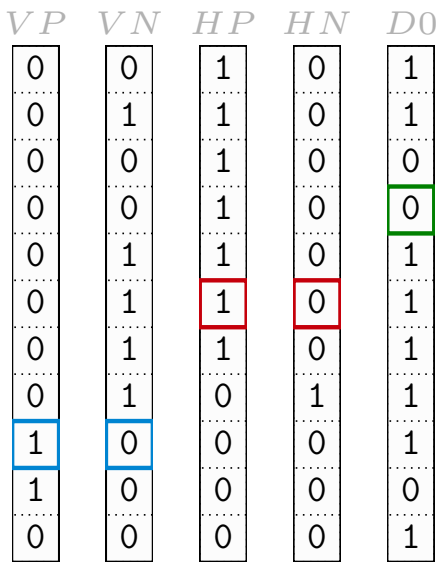
- The DP matrix has **diagonal** & **adjacency** properties

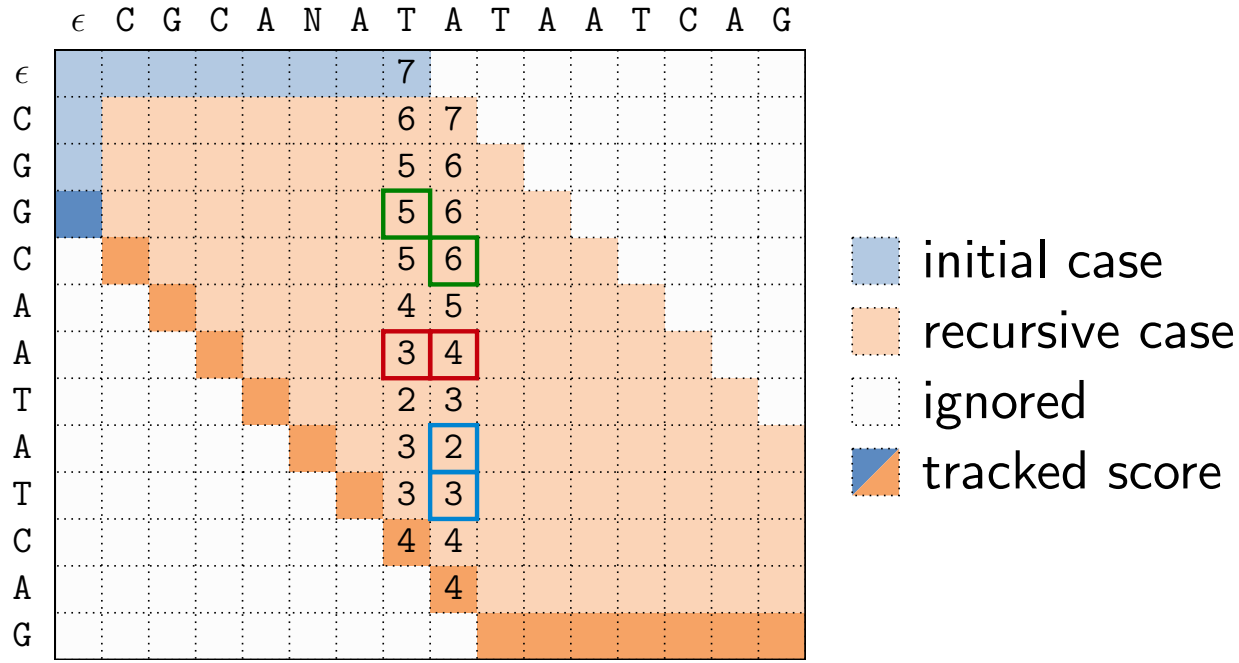


[3] Gene Myers. "A fast bit-vector algorithm for approximate string matching based on dynamic programming". In: **J. ACM** 46.3 (1999), pp. 395–415.

Banded Myers bit-vector algorithm

- The DP matrix has **diagonal** & **adjacency** properties
- Myers algorithm[3] encodes each column as **bit-vectors**





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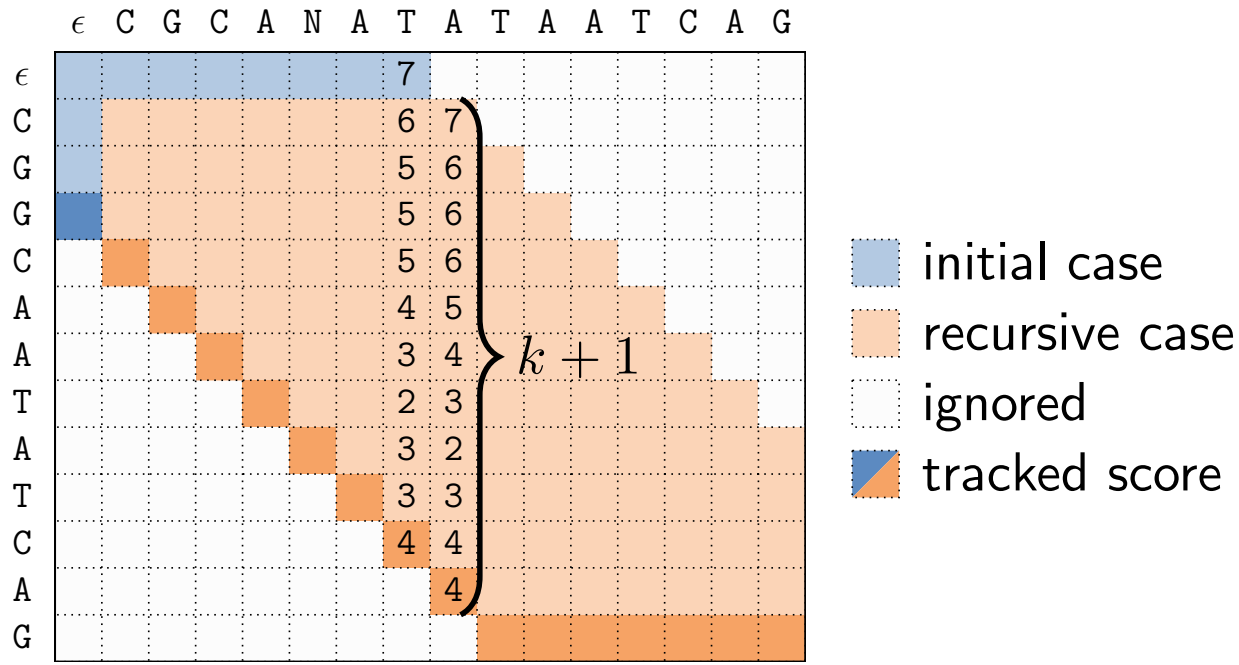
Banded Myers bit-vector algorithm

- The DP matrix has **diagonal** & **adjacency** properties
- Myers algorithm[3] encodes each column as **bit-vectors**
- Our banded version computes a column in time $\mathcal{O}(k/w)$

VP	VN	HP	HN	$D0$
0	0	1	0	1
0	1	1	0	1
0	0	1	0	0
0	0	1	0	0
0	1	1	0	1
0	1	1	0	1
0	1	1	0	1
0	1	0	1	1
1	0	0	0	1
1	0	0	0	0
0	0	0	0	1



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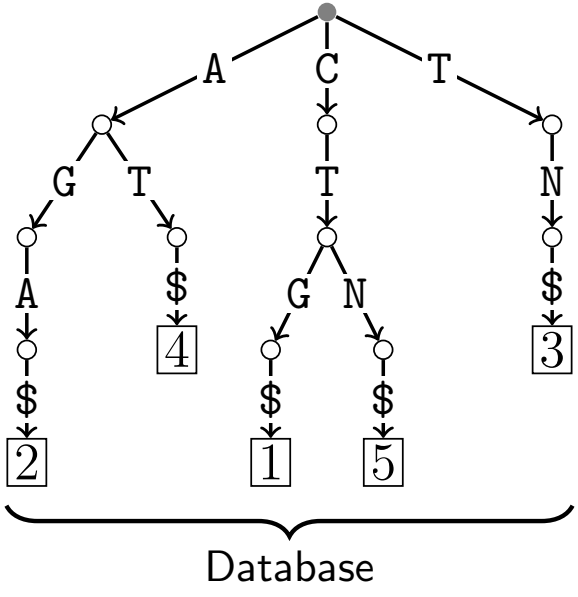
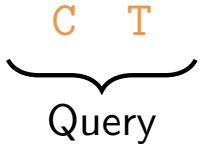
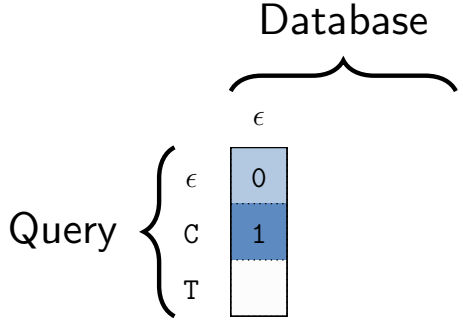
Backtracking

- Index database strings using a **radix tree**
- Perform a **top-down traversal** on the radix tree







Backtracking

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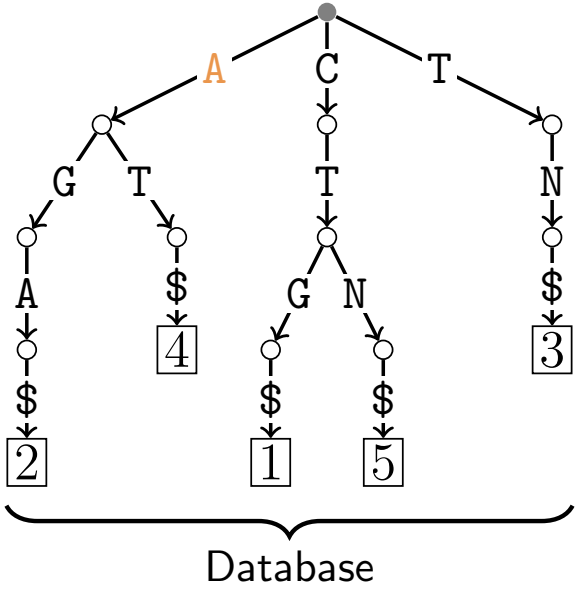
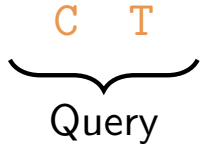
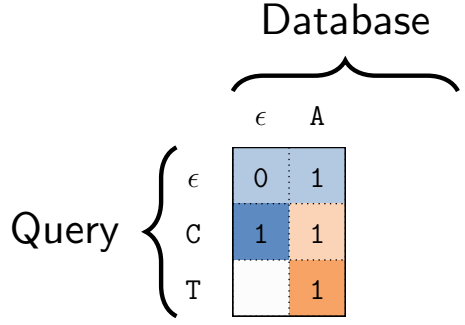
- Compute the distance between query and edge labels

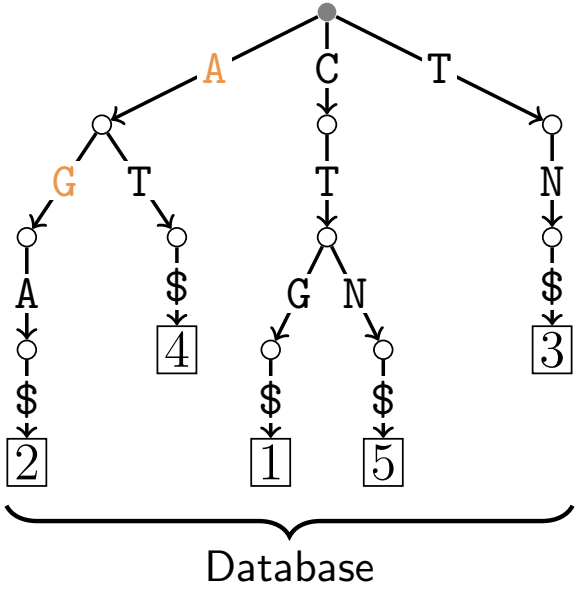


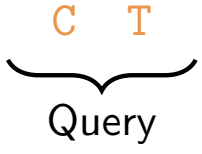


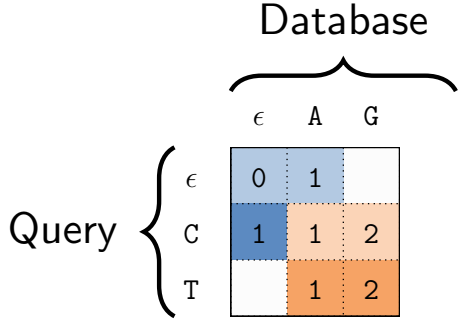


Backtracking

- Index database strings using a **radix tree**
- Perform a **top-down traversal** on the radix tree
- Compute the distance between query and edge labels
- **Cut** a branch when the minimum distance exceeds *k*







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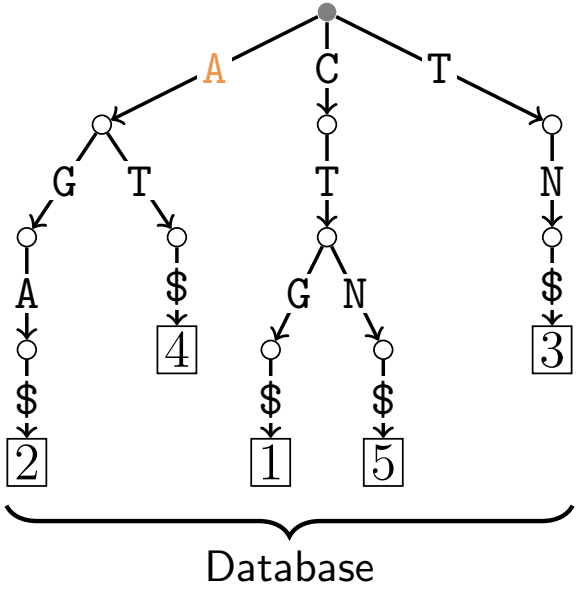
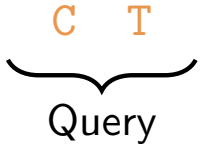
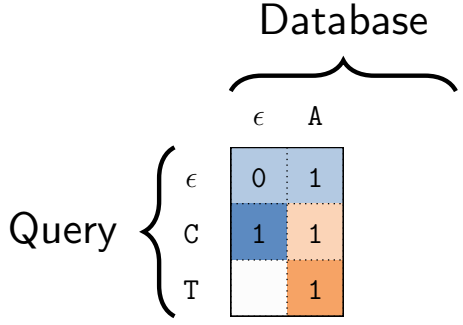
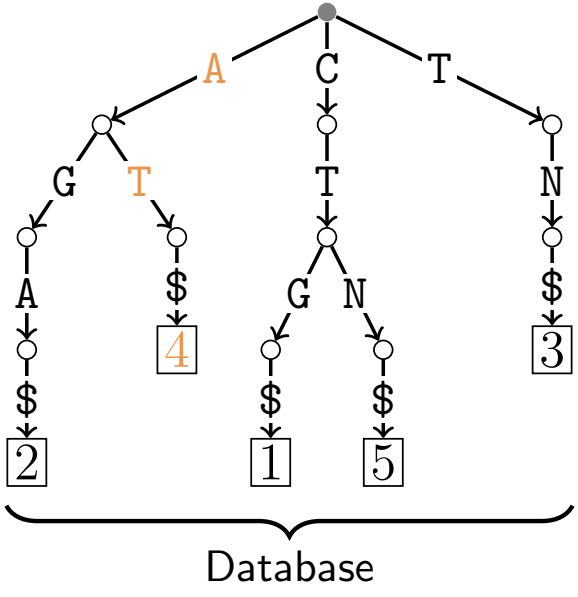


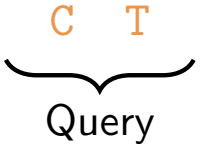


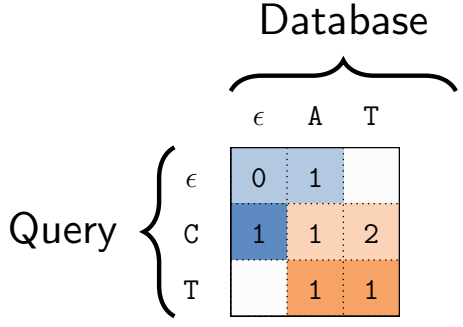


Backtracking

- Index database strings using a **radix tree**
- Perform a **top-down traversal** on the radix tree
- Compute the distance between query and edge labels
- **Cut** a branch when the minimum distance exceeds k
- Backtracking takes time **exponential** in k

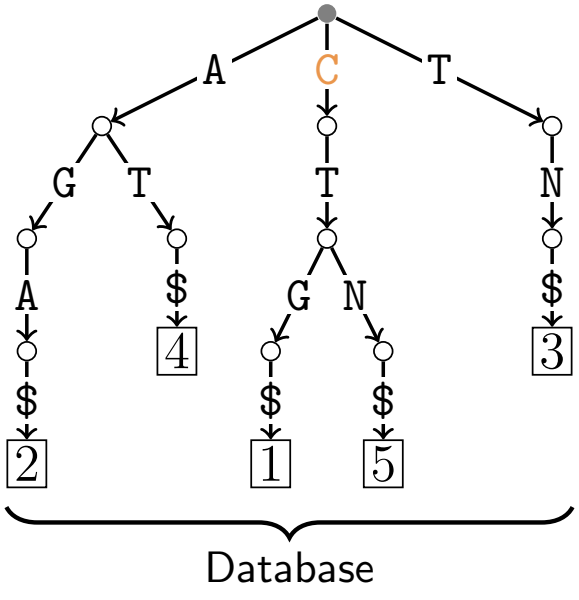


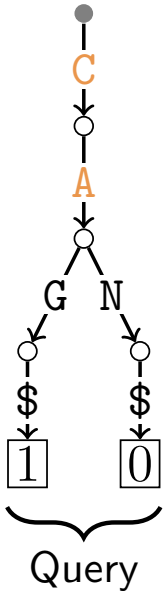


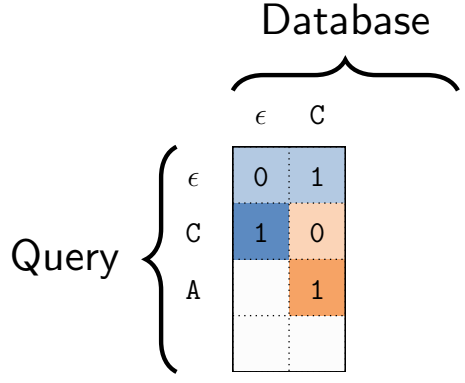


Multiple backtracking I

- Any two queries sharing a common prefix also share part of their backtracking
- Index the queries using another **radix tree**
- Backtrack the query tree in the database tree







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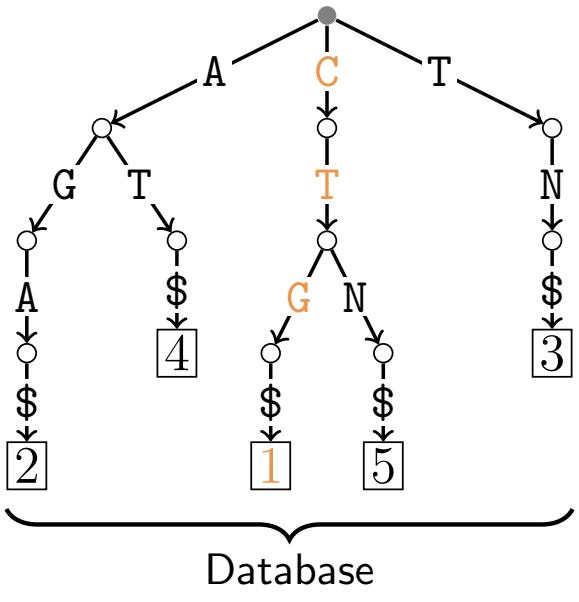

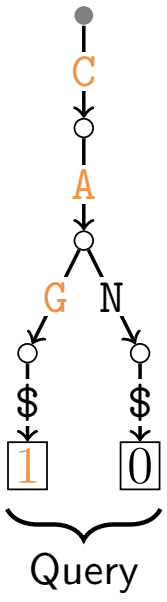

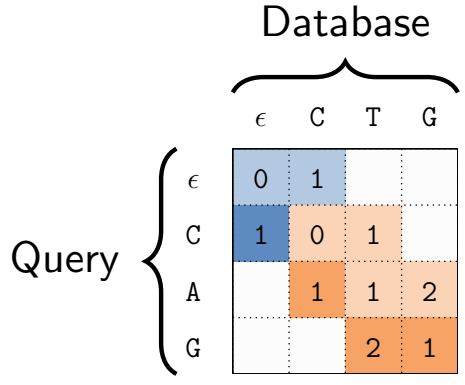

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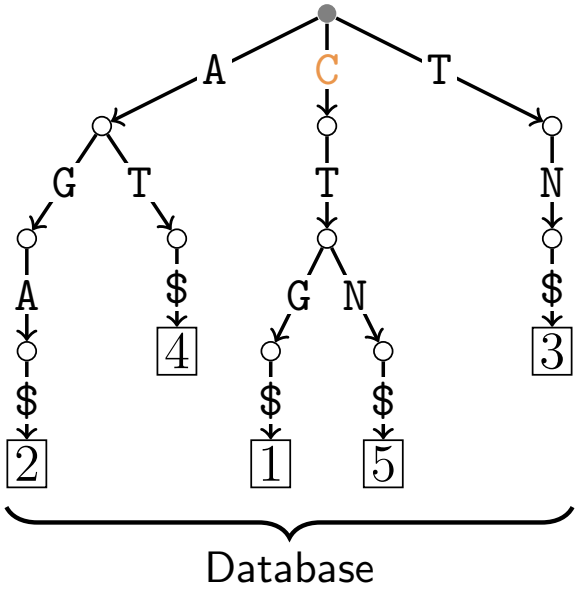

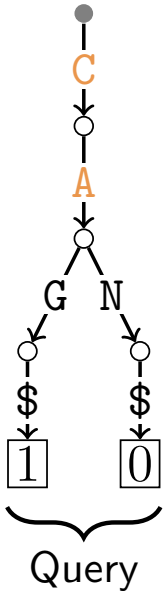

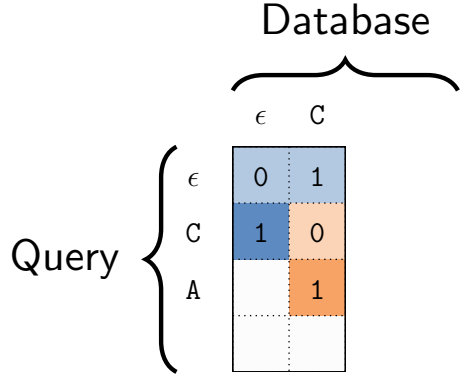

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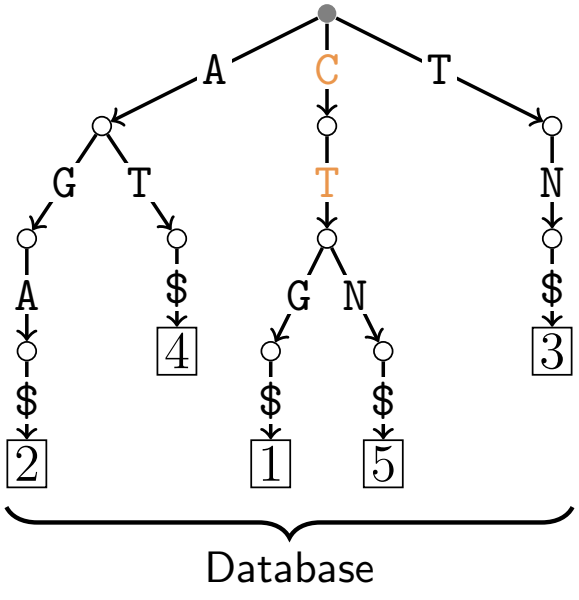
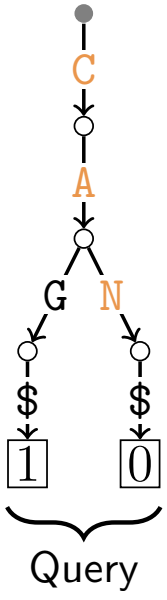
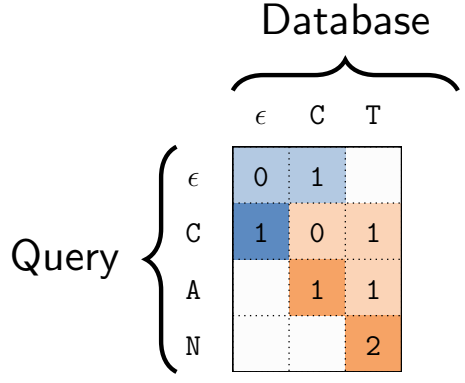


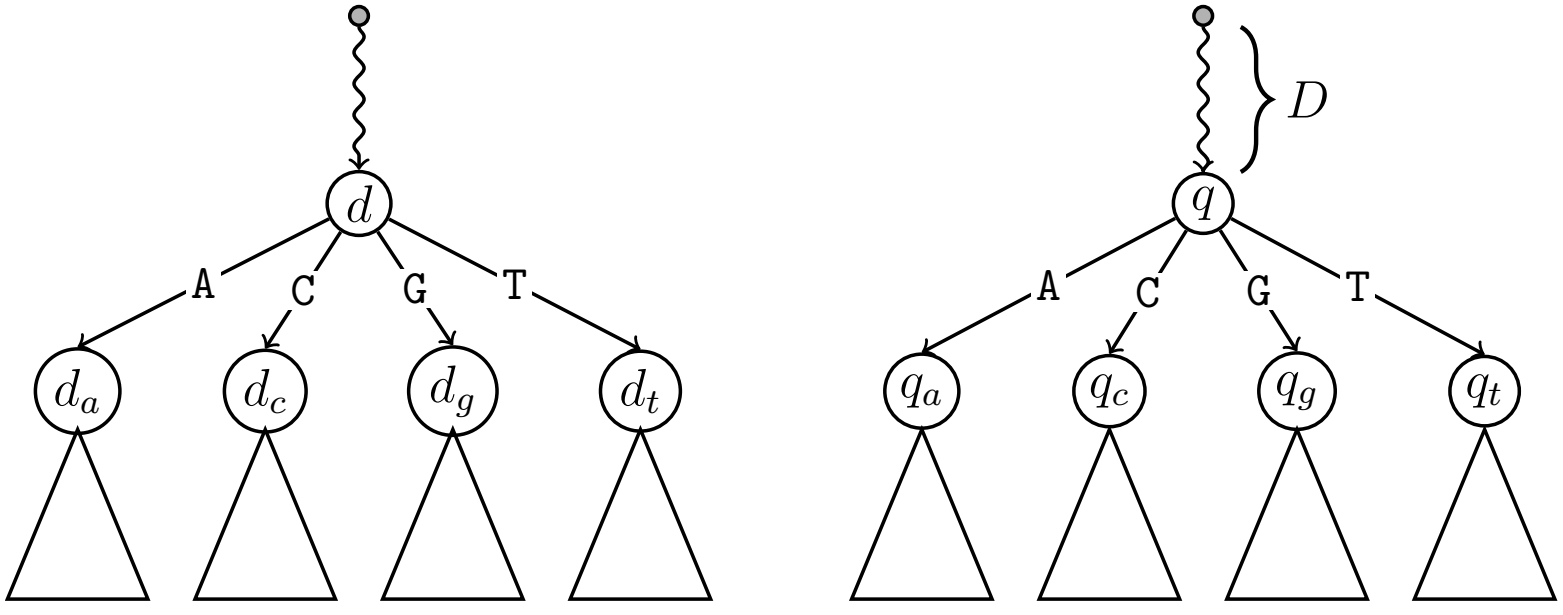




Multiple backtracking II

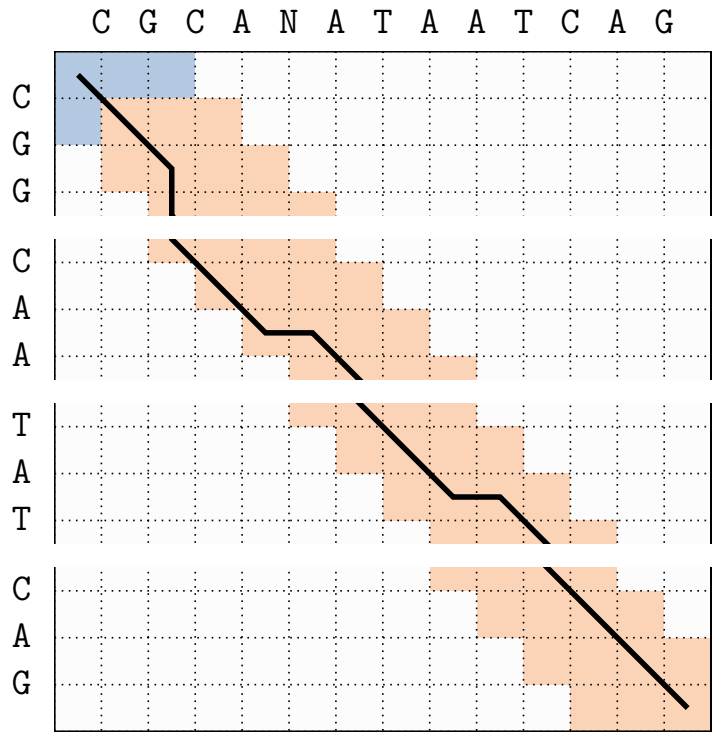
- Parallelization of multiple backtracking is non-trivial
- We collect pairs of subtrees at fixed depth D
- Each pair can be processed independently

$$\mathcal{Q} \leftarrow \mathcal{Q} \bigcup \left\{ (d_a, q_a), (d_a, q_c), (d_a, q_g), \ldots, (d_t, q_t) \right\}$$



Exact seeds

- Partition query $\mathcal{Q}$ in $k+1$ seeds
- One seed occurs without errors



Exact seeds

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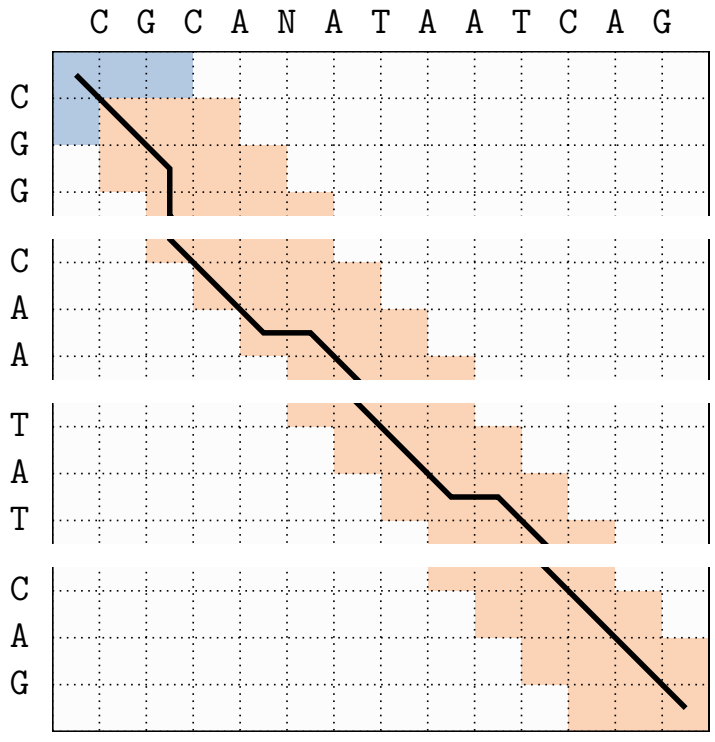
1. Index database strings with a **generalized suffix tree**
2. Search all seeds
3. Verify seeds inside a k-band



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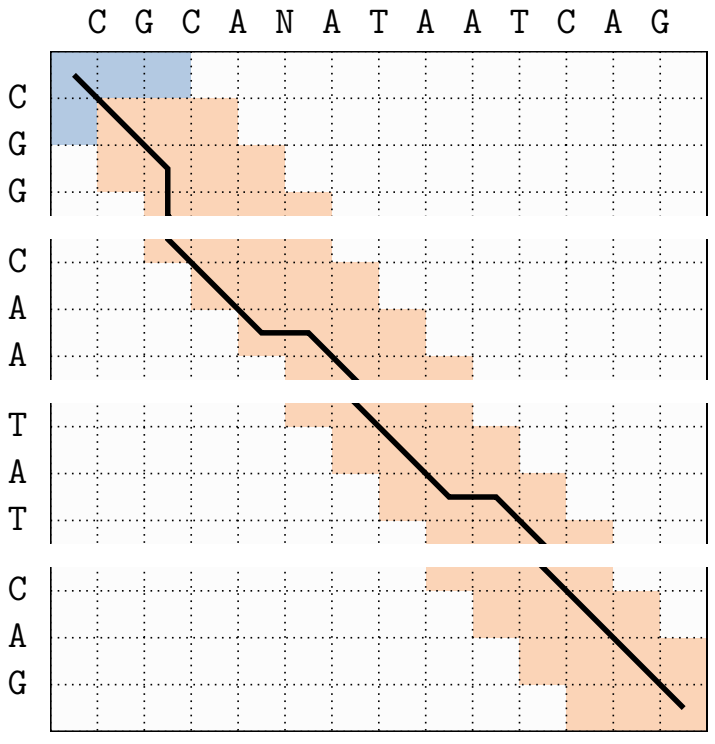
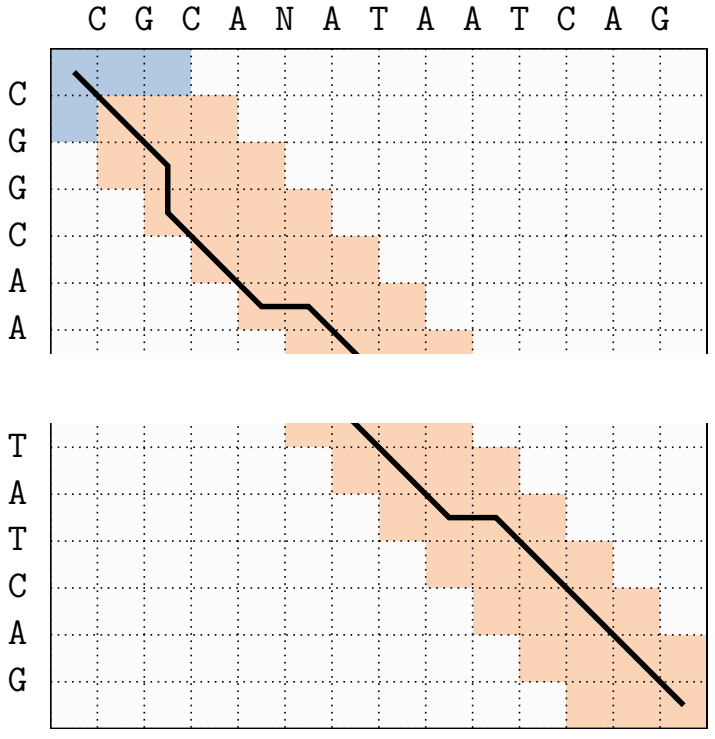
- Seed length $L = \frac{|\mathcal{Q}|}{k+1}$



Approximate seeds

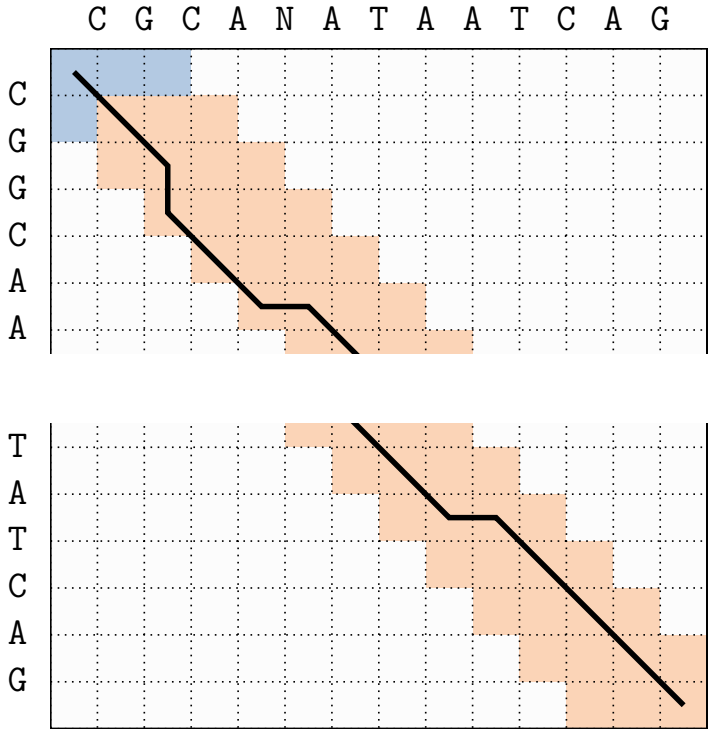
- Partition query $\mathcal{Q}$ in s seeds
- One seed is within $\lfloor k/s \rfloor$ errors



Approximate seeds

- Partition query $\mathcal{Q}$ in s seeds
- One seed is within $\lfloor k/s \rfloor$ errors

- Seed length $L = |\mathcal{Q}|/s$
- The seed length is a parameter



Implementation

- Implemented in C++ using SeqAn and OpenMP
- Indices implemented as generalized suffix arrays
- Index construction combines bucket sort and quicksort
- Backtracking implemented with banded DP

Acknowledgements

David Weese & Knut Reinert

The SeqAn team

References I

- Gene Myers. “A fast bit-vector algorithm for approximate string matching based on dynamic programming”. In: **J. ACM** 46.3 (1999), pp. 395–415.
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