DEVELOPMENT OF ALGORITHM LIBRARY FOR STRING MATCHING SUPPORTED BY VISUALIZATION AND PERFORMANCE COMPARISON USING BENCHMARKS FOR BIOLOGICAL SEQUENCE DATASETS

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Introduction
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Conclusion

Introduction: String searching and applications

Definition.

Pattern E X A

Text S T R I N G S E A R C H I N G E X A M P L E

Well-known algorithms.

Brute Force, Knuth-Morris-Pratt, Boyer-Moore, Karp-Rabin, etc.

Applications.

Text editors (search help, spell check),
Plagiarism detection,
Web search engines,
System intrusion detection,
DNA/ Biological sequence matching,
…

Introduction: Purpose of the thesis

Observations.

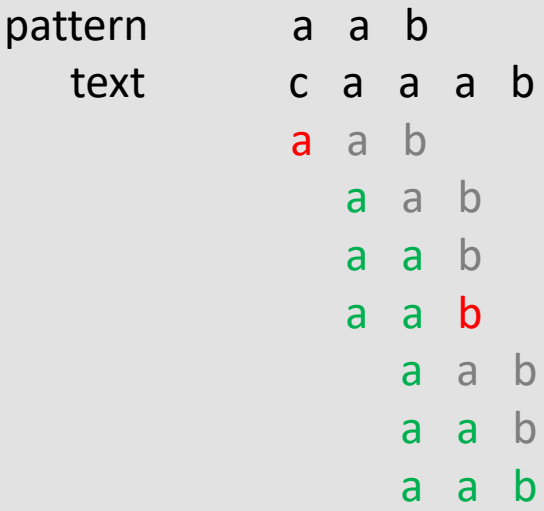
- Over 80 algorithms since 1970.
- Best algorithm in all cases does not exist; each thrives in different scenarios
- Many algorithms are too complicated and hard to understand.
- Theoretical analysis focuses on upper limits; need for practical performance testing.
- Data-heavy applications call for efficient algorithms; need for collective benchmarks!

Purpose.

- Implement algorithms in OO paradigm.
- Visualize their functionality.
- Offer a collective benchmark focused on biological data.

Introduction: About the algorithms

- 35 string searching algorithms presented in C (Charras and Lecroq).
- Each has a preprocessing and a searching phase.
- All receive first the pattern (preprocessing) and then the text (searching).
- All utilize the ‘sliding window’ approach.

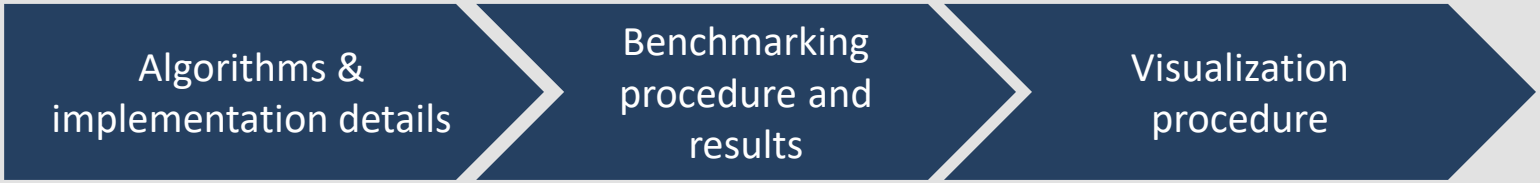


- Categorized in 4 groups: left to right, right to left, specific order, any order.

Introduction: Line of work Vs. Presentation order

Line of work.

Presentation order.



Implementation: Points of interest

Implemented in Java; Object-Oriented approach (Sedgewick).

Common interface.

- Common public methods: **constructor** + ***search*** + ***searchAll***
- Clean separation of preprocessing and searching, consistency.
- Efficient searching of a pattern in different texts

Optimization. Not the point of this thesis. Consistent port of C source code.

The '\0' issue. Termination character in C strings. Reason of most modifications.

Benchmarking: Decisions

Past work. Measured on # of character comparisons; only a handful of algorithms where compared.

Algorithms? All.

Data? Biological. Escherichia coli genome sequence ({A, C, G, T}) of 4.5m chars. https://www.ezbiocloud.net/genome/explore?puid=172783

Measure of performance? Execution times

Functions? ***search*** and ***searchAll***

Pattern size? 2 groups:

- small {2, 3, 4, 5, 6, 7, 8, 9, 10}
- large {10, 20, 40, 80, 160, 320, 640}

Results. Displayed in 3 sections:

- Individual
- Collective
- Collective (grouped)

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4 scenarios:

- search for small
- search for large
- searchAll for small
- searchAll for large

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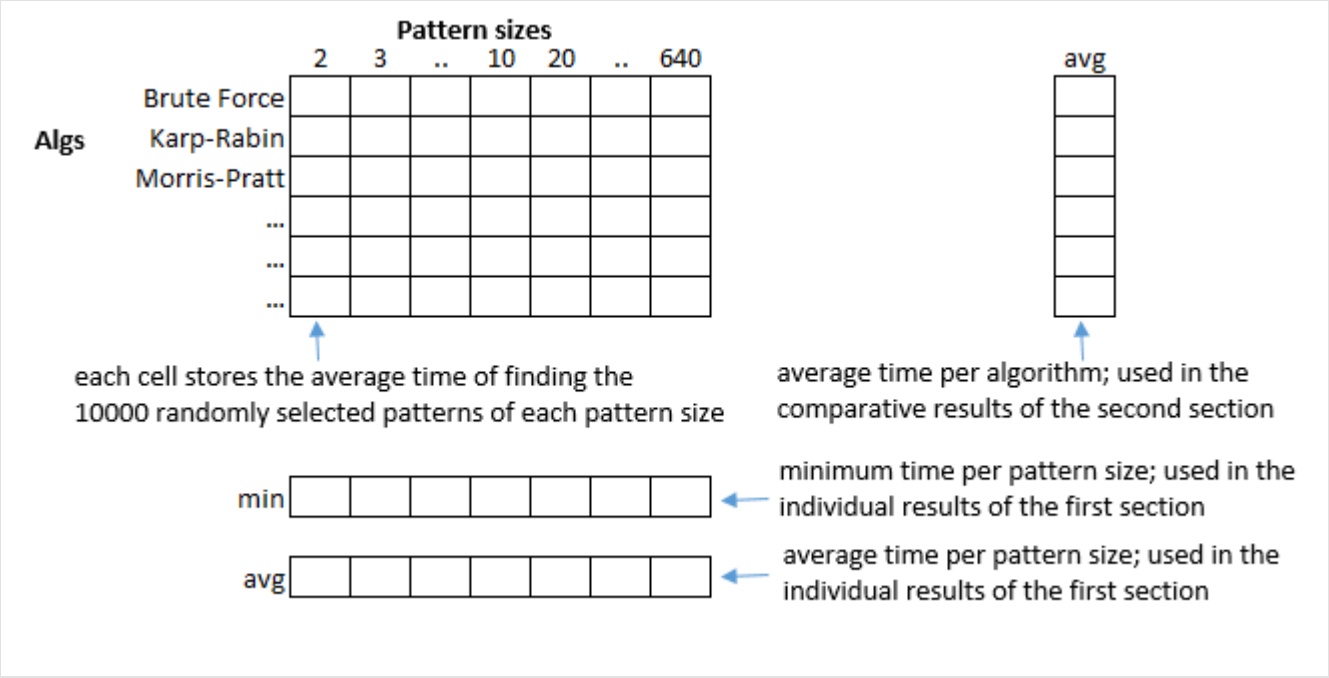
Benchmarking: Benchmark Suite

Implementation. Java. Exploits the Reflection API to automatically create and run the tests and auto-validate the correctness of the algorithms.

Scheme. Each algorithm is measured (average) in each of the pattern sizes by selecting randomly 10000 patterns; done for both ***search*** and ***searchAll.***



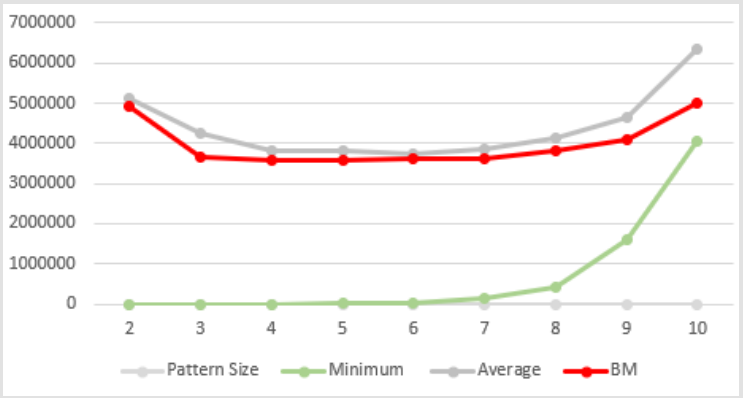
Benchmarking: Individual results

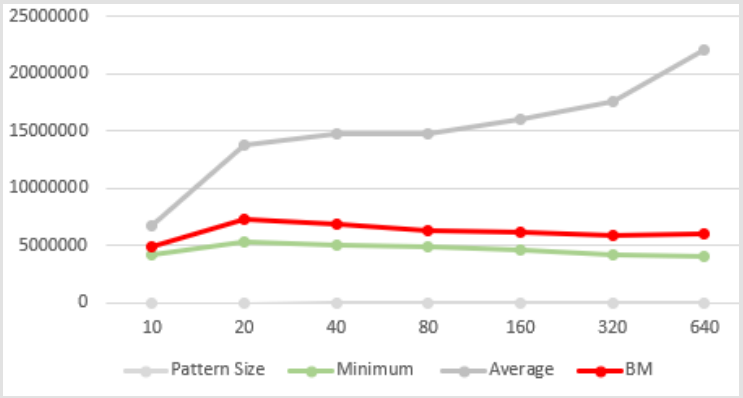
Results. For each algorithm four line charts; one for each scenario. Highlights the performance against the minimum and average times from all the algorithms.

Small patterns

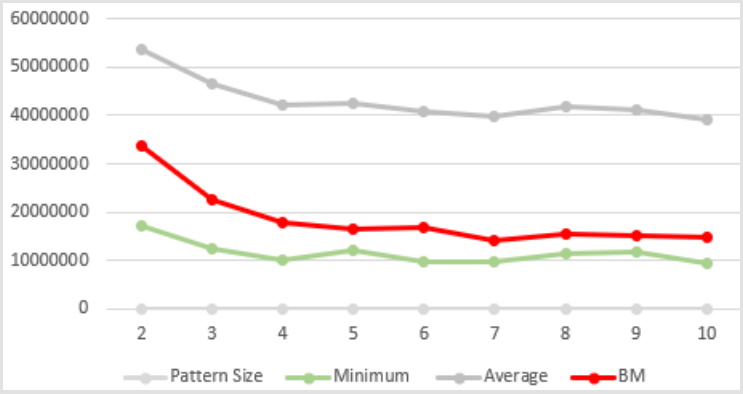
Large patterns

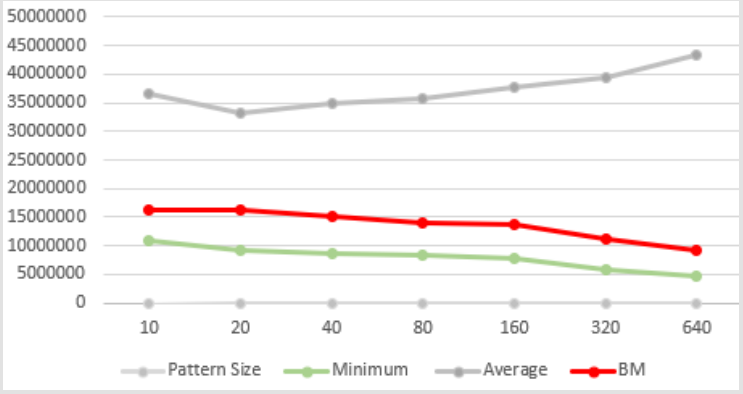
search



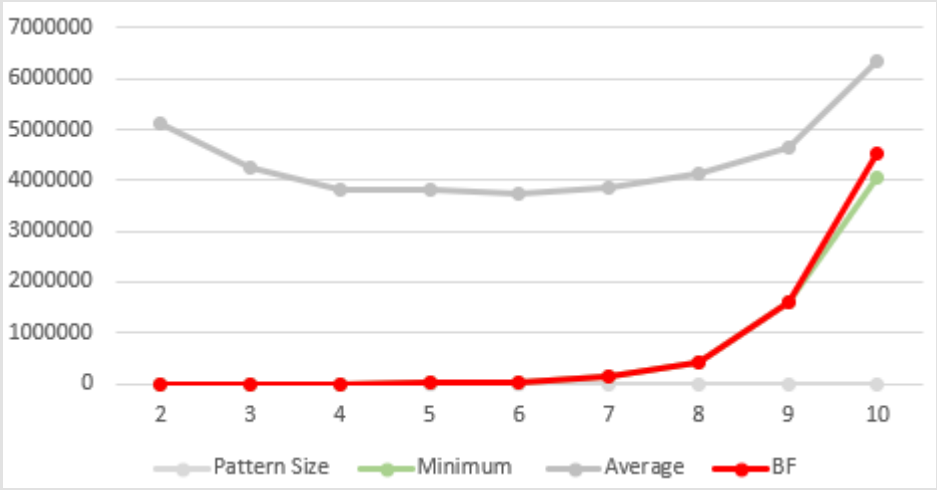


searchAll





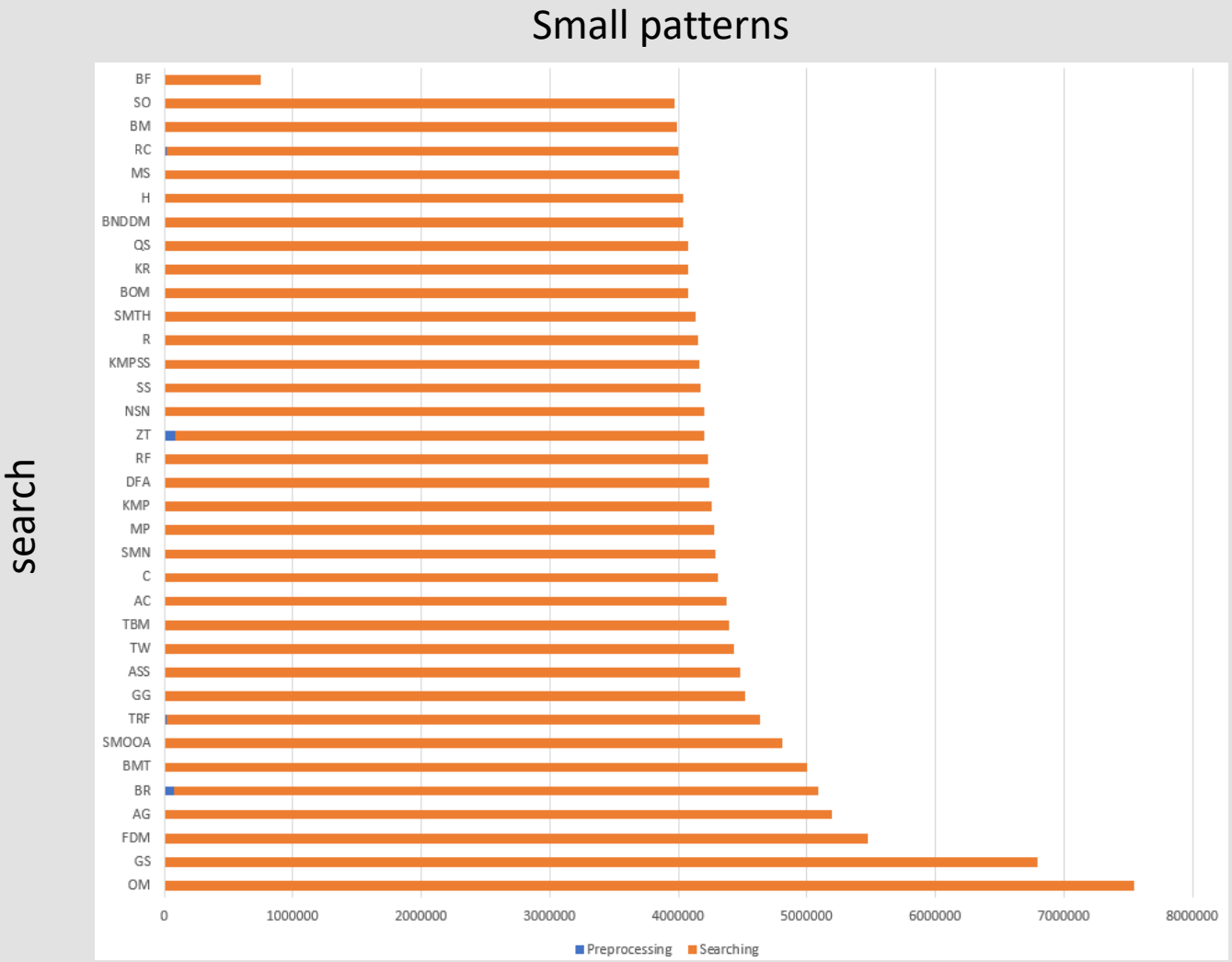
Benchmarking: Individual results, a surprising result!



Brute Force. For small alphabet and small patterns, lack of preprocessing phase thrives over shift tables and other preprocessing techniques.

Benchmarking: Collective results

Results. For each algorithm, the average time on all patterns are displayed for each of the four scenarios.



Benchmarking: Collective results - summary

Best performing algorithms on average of all tested pattern sizes

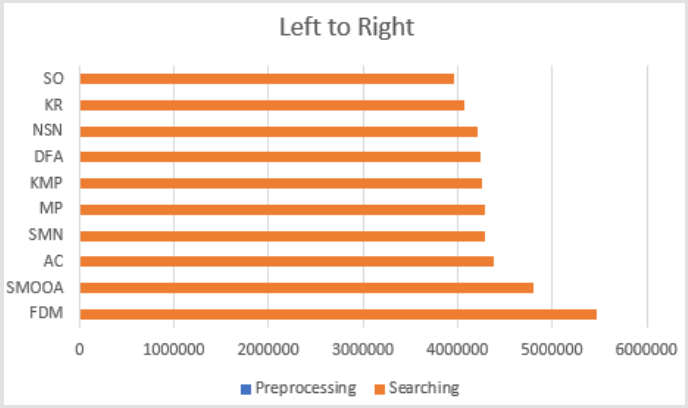
	Small patterns	Large patterns
search	Brute Force	Zhu-Takaoka
searchAll	Shift Or	Zhu-Takaoka

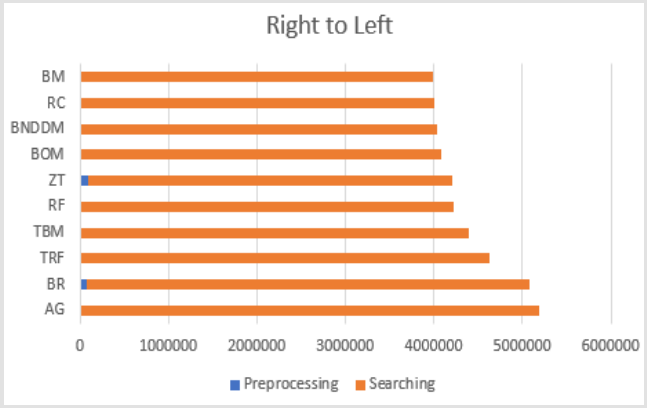
Remarks.

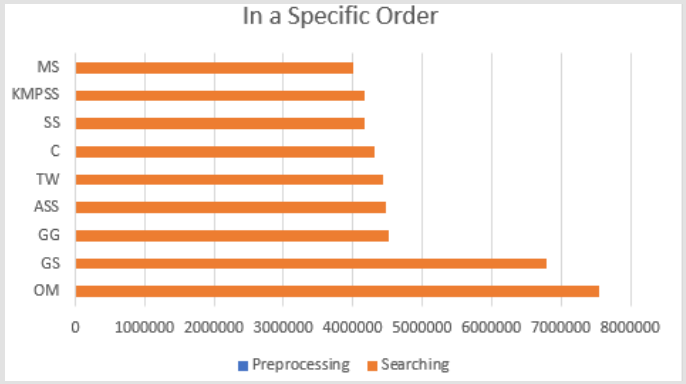
- In larger patterns, prevail algorithms that perform comparisons from right to left;
- Almost all algorithms of the Boyer-Moore family vastly outperform those of Knuth-Morris-Pratt family.

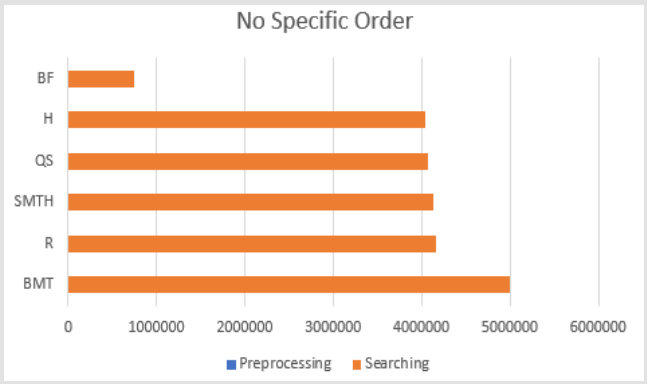
Benchmarking: Collective results (grouped)

Each scenario's collective result was grouped according to the character comparison order of each algorithm.









Search – small patterns

Visualization: Visualization Suite

Goal. Provide an animated glimpse of the functionality of a string search algorithm.

Implemented? HTML, CSS, JavaScript, jQuery

Advantages.

- Flexibility
- Adding a string search algorithm is simple.
- Easily and dynamically embeddable in web sites

Visualization: Visualization Suite

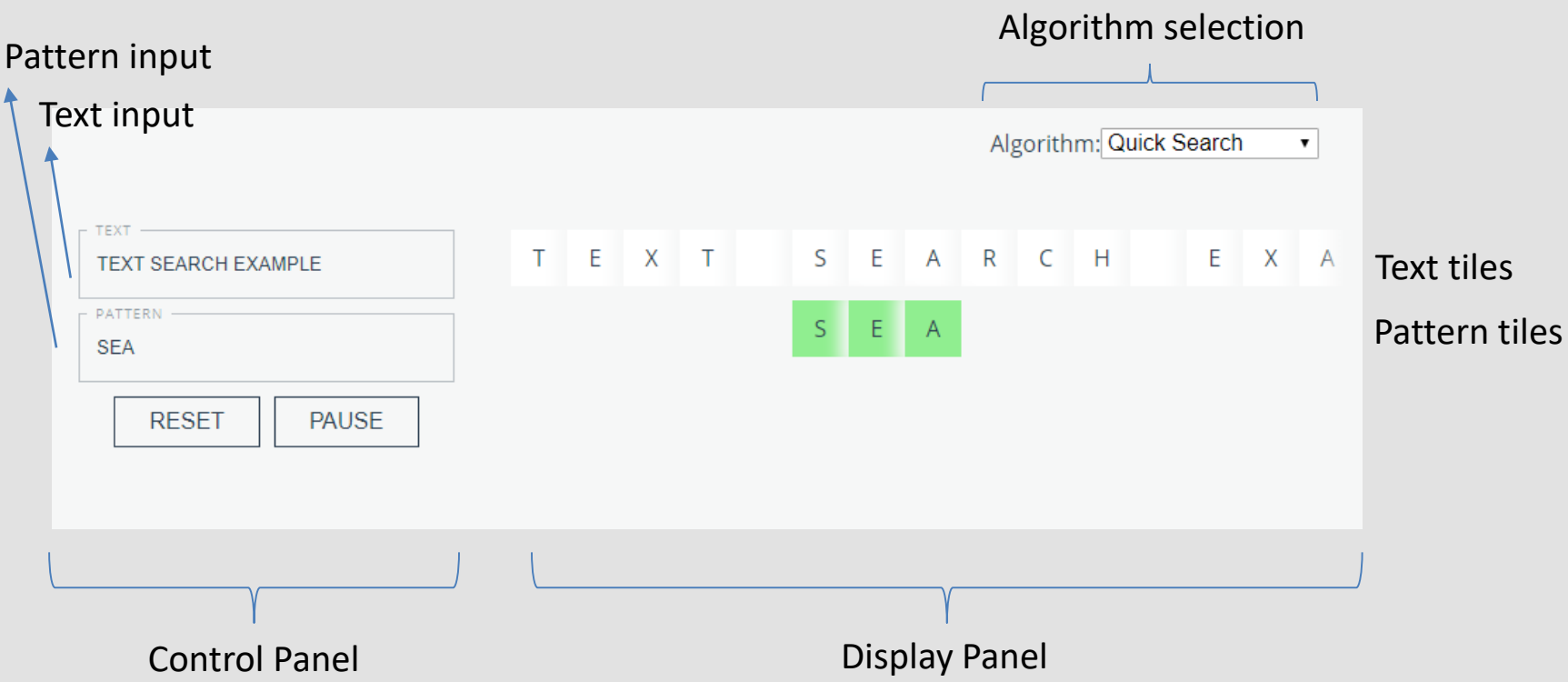
Basic Idea.

- All algorithms are ported to JavaScript.
- They can produce predefined queries describing the actions to be animated
- A JavaScript module acts as a hub that receives those queries; interprets them with respective animations.

Remarks.

- A resemblance of a controller-view model was implemented.
- A script adds dynamically functionality in all marked HTML elements.

Visualization: Visualization Suite Preview



Published with ***Surge*** tool as a static web site at esmaj.surge.sh

Conclusion

- 35 string search algorithms were ported/implemented in Java; the OO nature attempted to make the algorithms simpler to understand and reuse.
- We ranked their performance running benchmarks on huge biological sequence data
- Implemented a simple visualization suite to aid the visual understanding of their functionality.

Conclusion: Future Extensions

- Focus on optimizing some of the algorithms
- Use a bigger sample on the benchmarks (run all the possible substrings of a huge text-or several huge texts)
- Add more animations in the visualization suite

Thank you!

Any questions?