BLAST : Basic Local Alignment Search Tool

Projet court

Amory Antao
amoryantao@net-c.com

Université de Paris Cité
M2 Biologie Informatique

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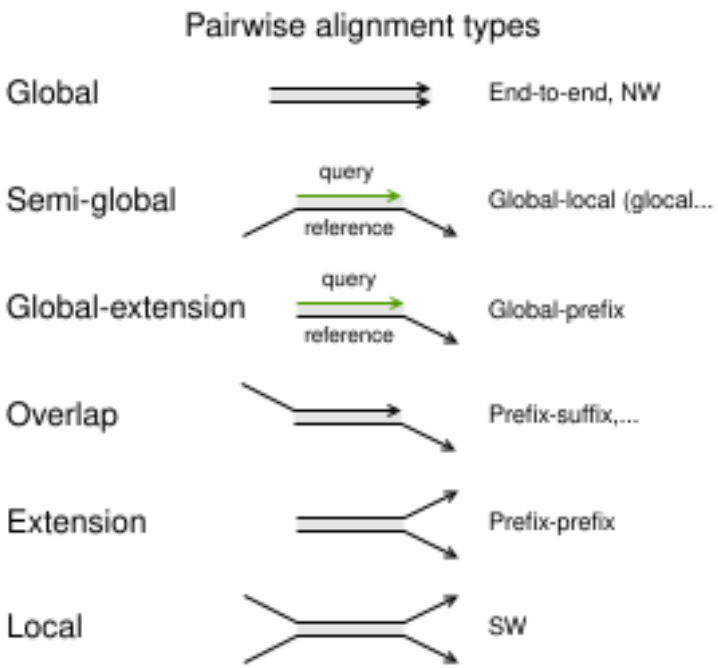
Introduction and Motivation

- Local alignments → function and evolution




```
Global  FTFTALILLAVAV
        F--TAL-LLA-AV

Local   FTFTALILL-AVAV
        --FTAL-LLAAV--
```

Introduction and Motivation

- Local alignments $\rightarrow$ function and evolution
- Explosion of biological data

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- Local alignments $\rightarrow$ function and evolution
- Explosion of biological data
- Limits of exact methods $\rightarrow$ need for heuristics

BLAST: General Principles

Three main steps:

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2. Search for hits
3. Extension of hits (X-drop)

BLAST I: Protein Example

Query:

M	A	T	G	L	A

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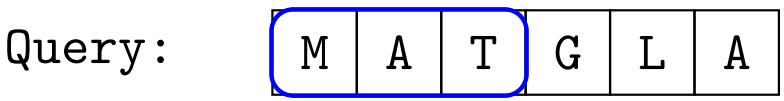

Words = MAT

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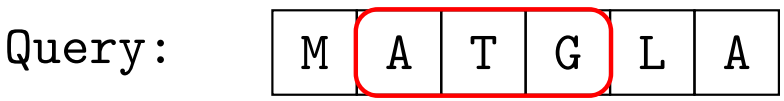

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Extract of BLOSUM62

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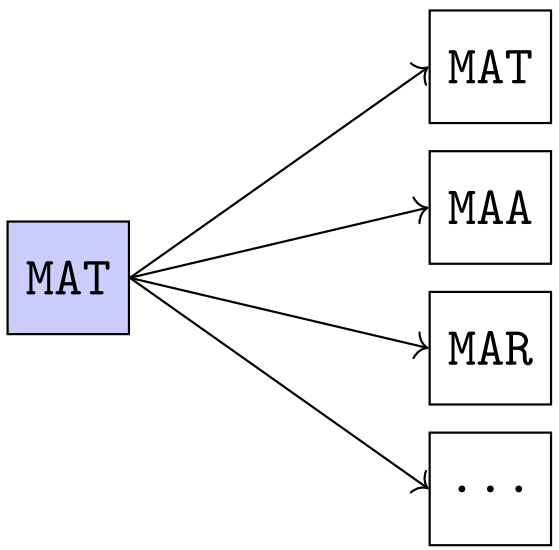

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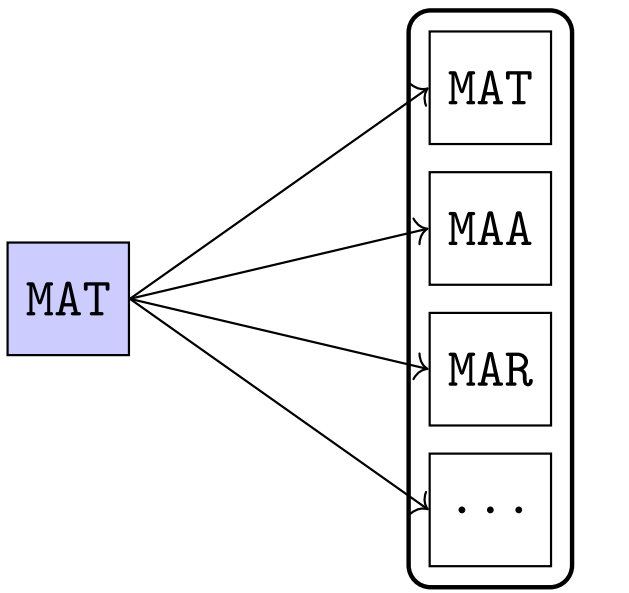

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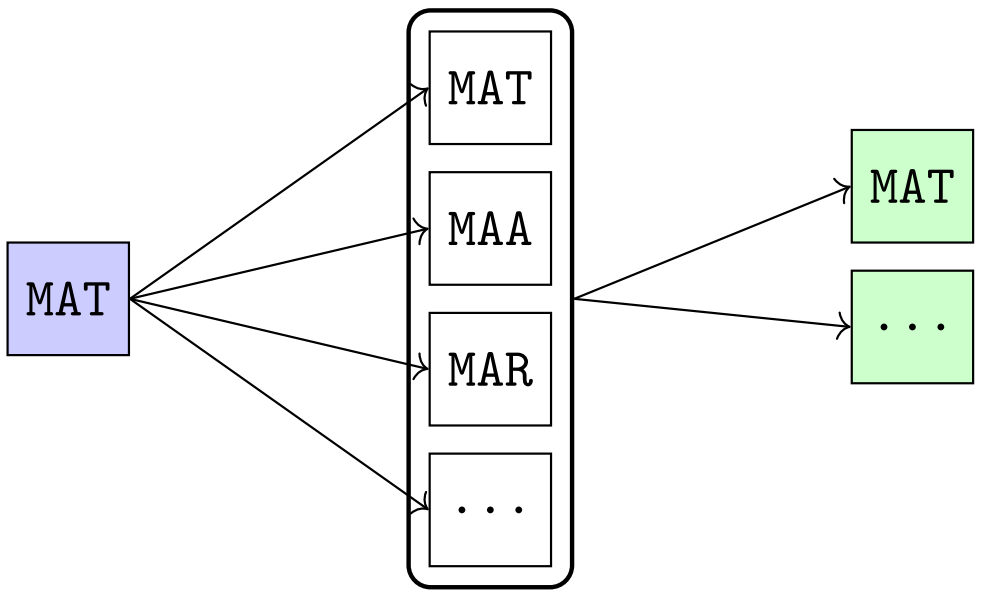

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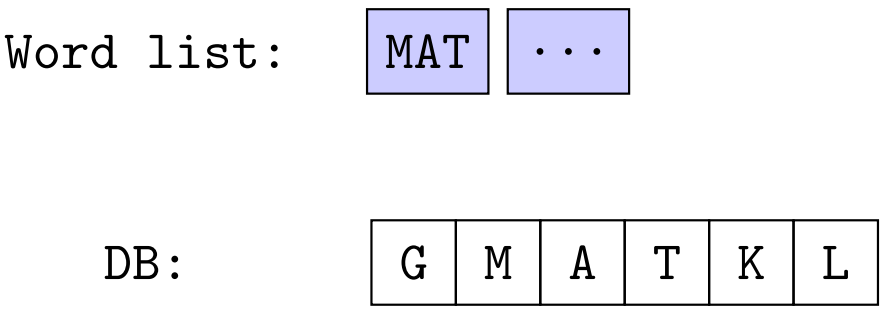

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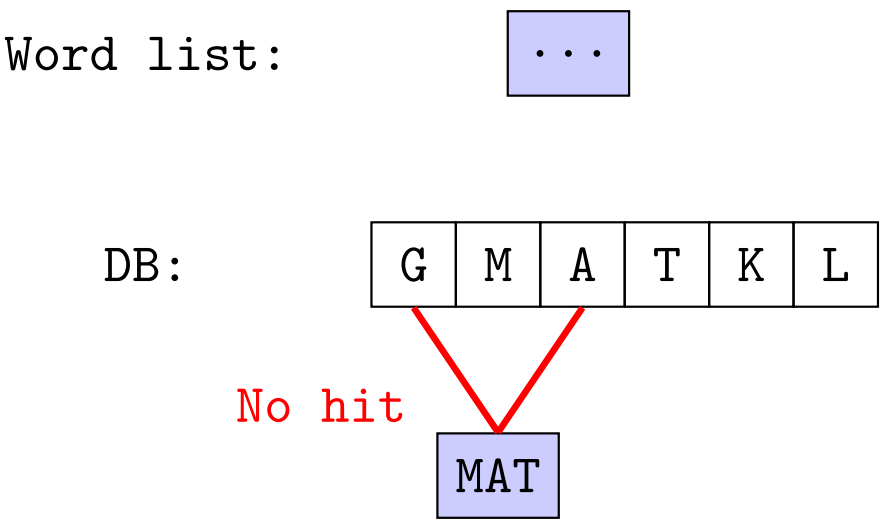

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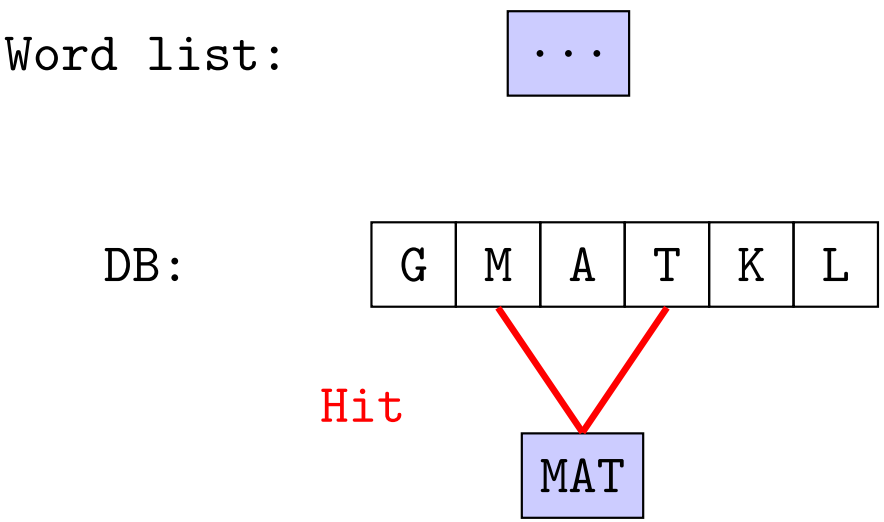

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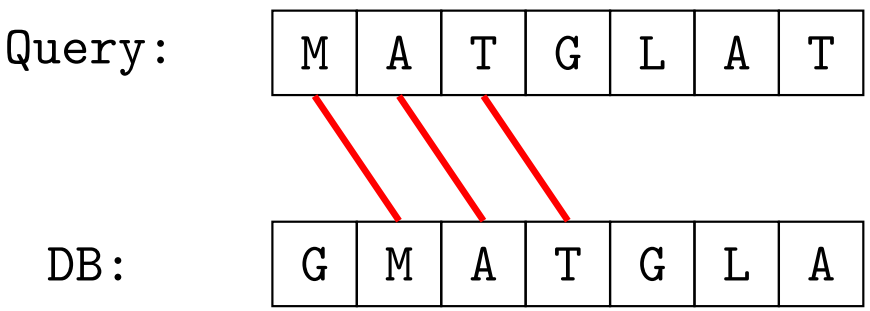

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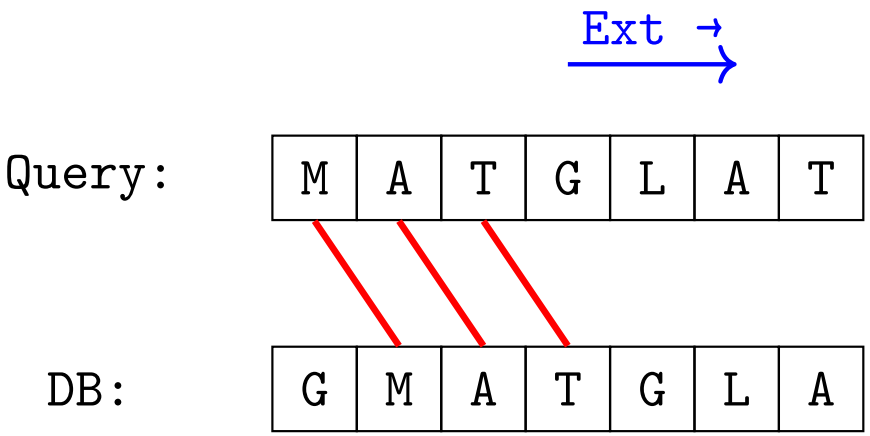

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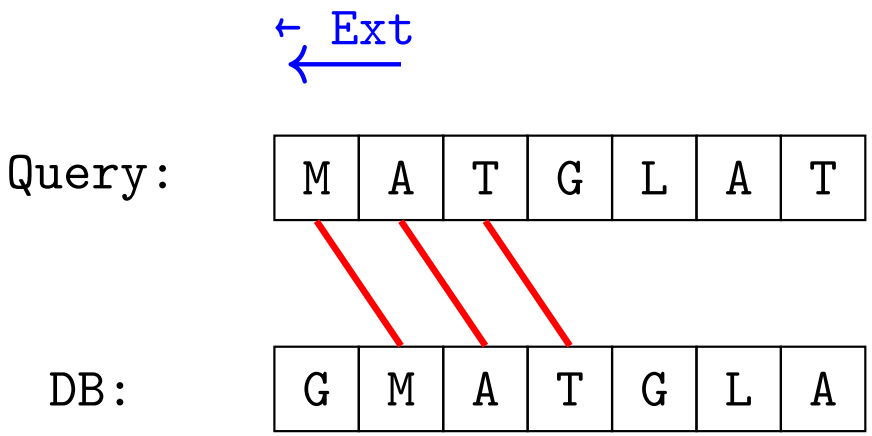

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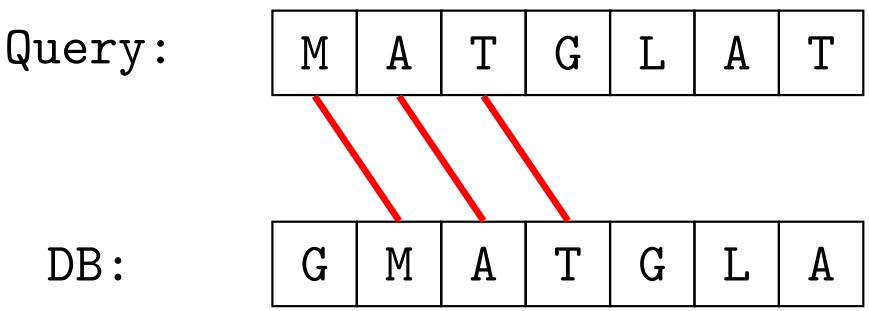

Final result: score_max right + score_max left

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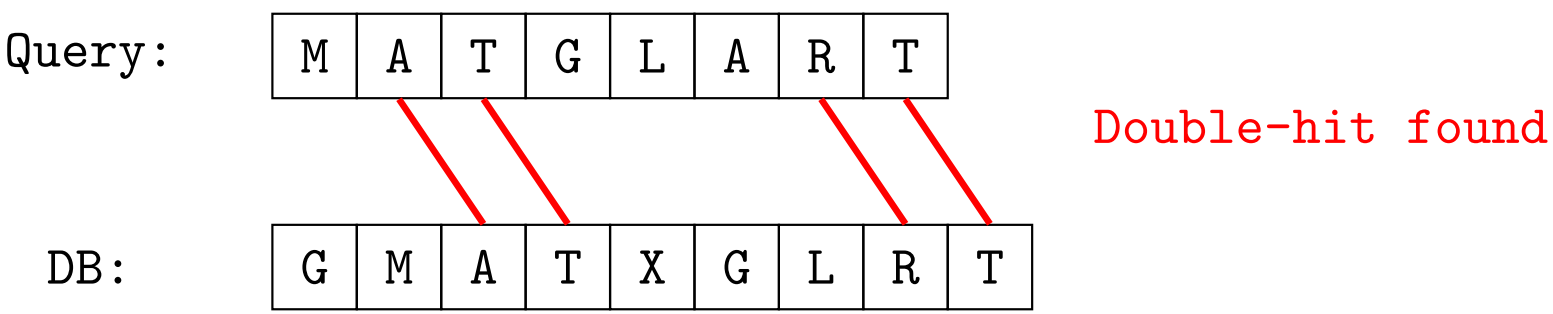

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Experimental Results

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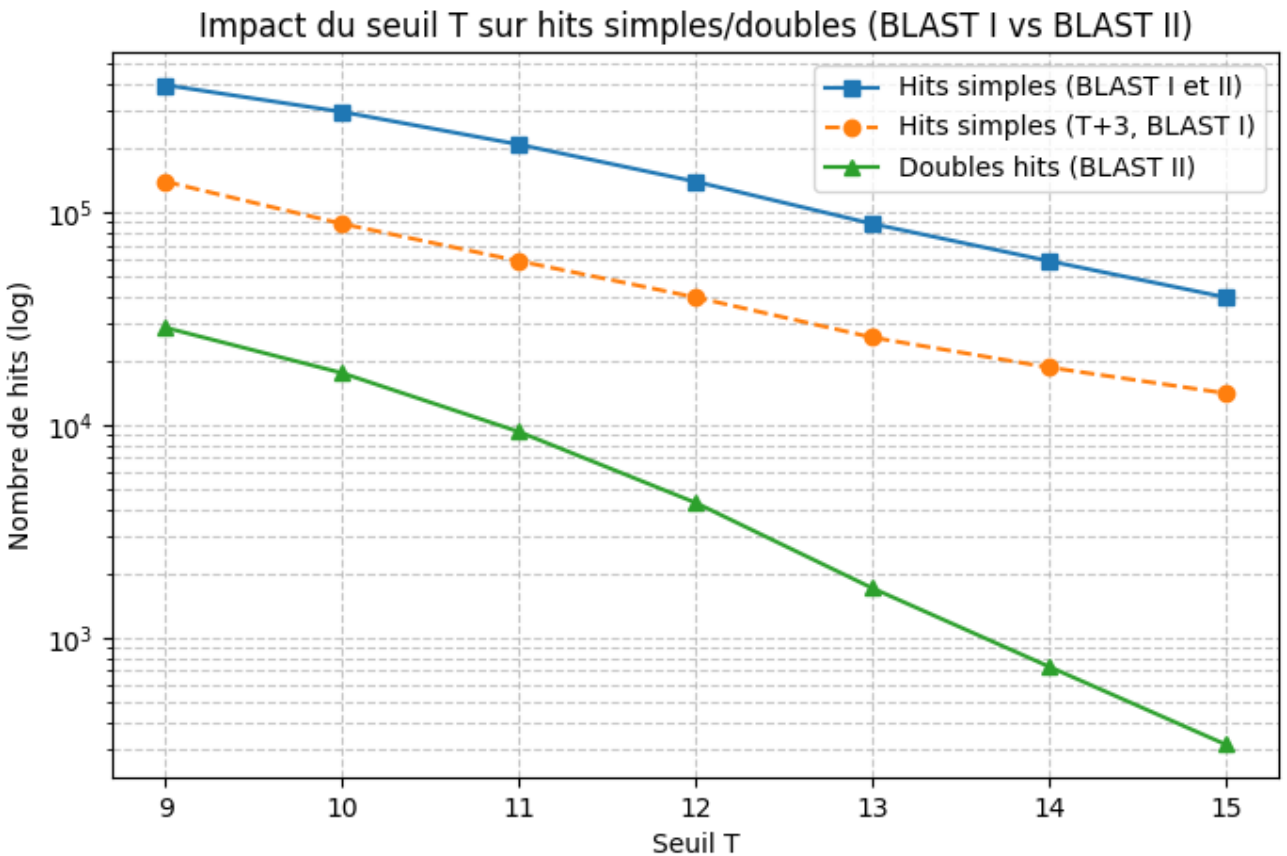

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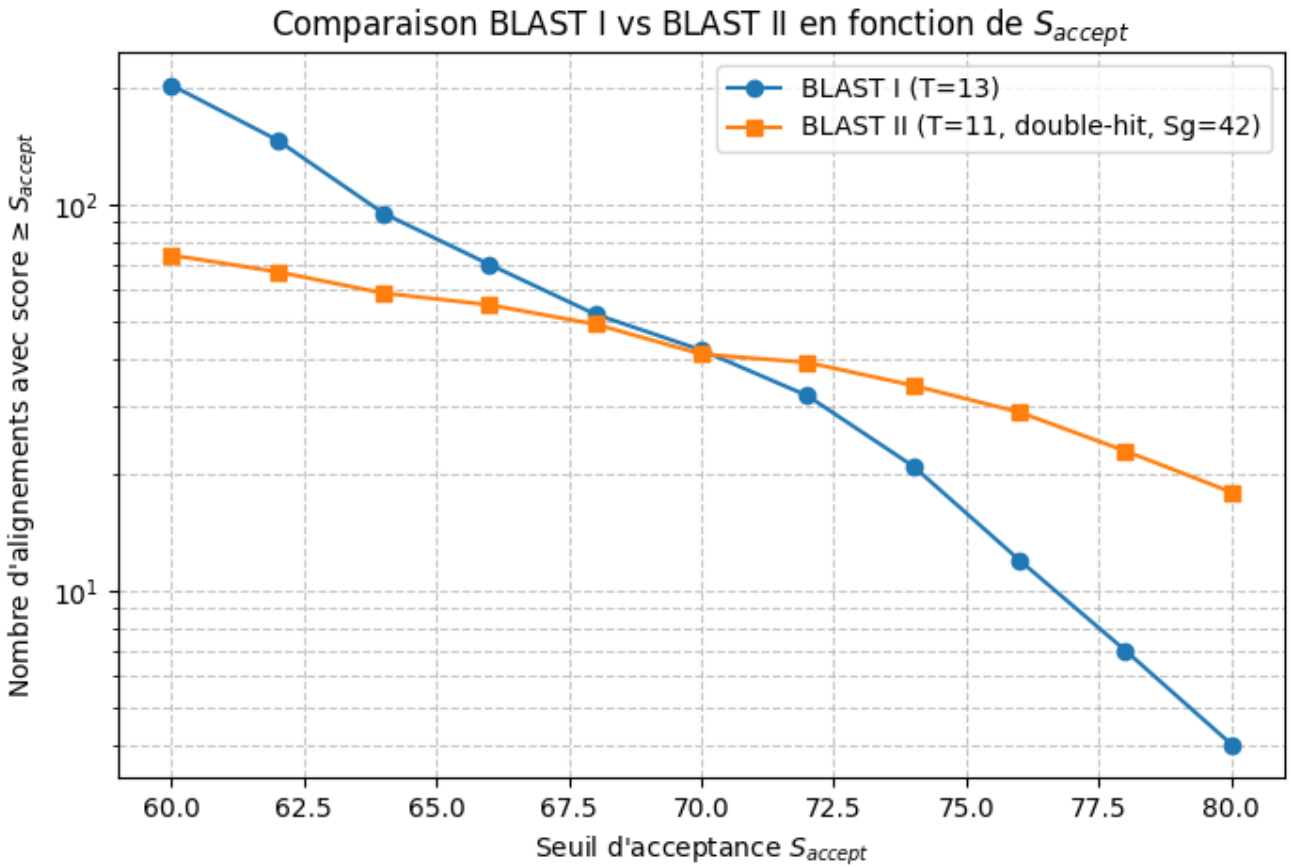

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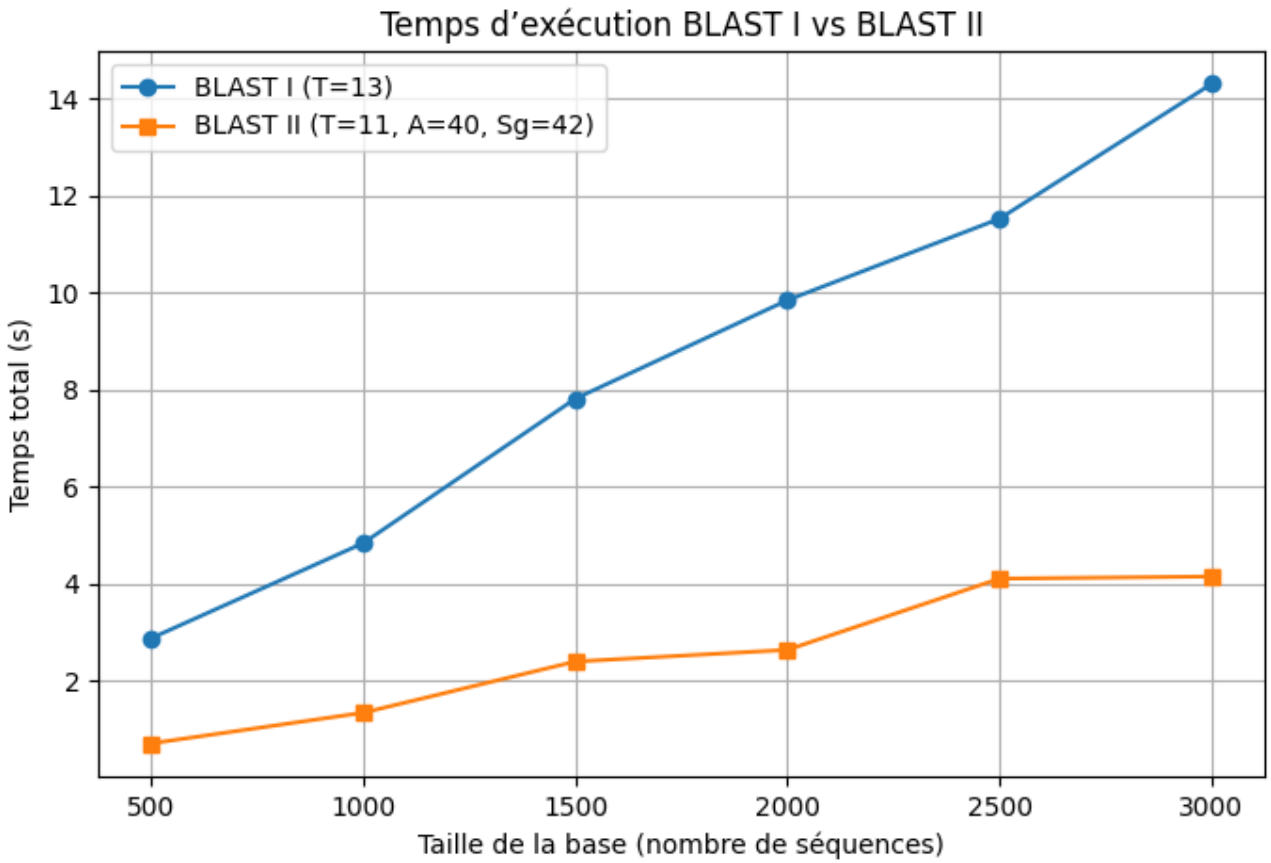
- Accepted alignments (BLAST I vs II).
- Runtime (BLAST II $\approx 3\times$ faster).



Discussion and Perspectives

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- Results consistent with the literature.

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- Evaluate on real datasets.
- Optimizations in the code.