Whole genome alignment in High Performance Computing environments

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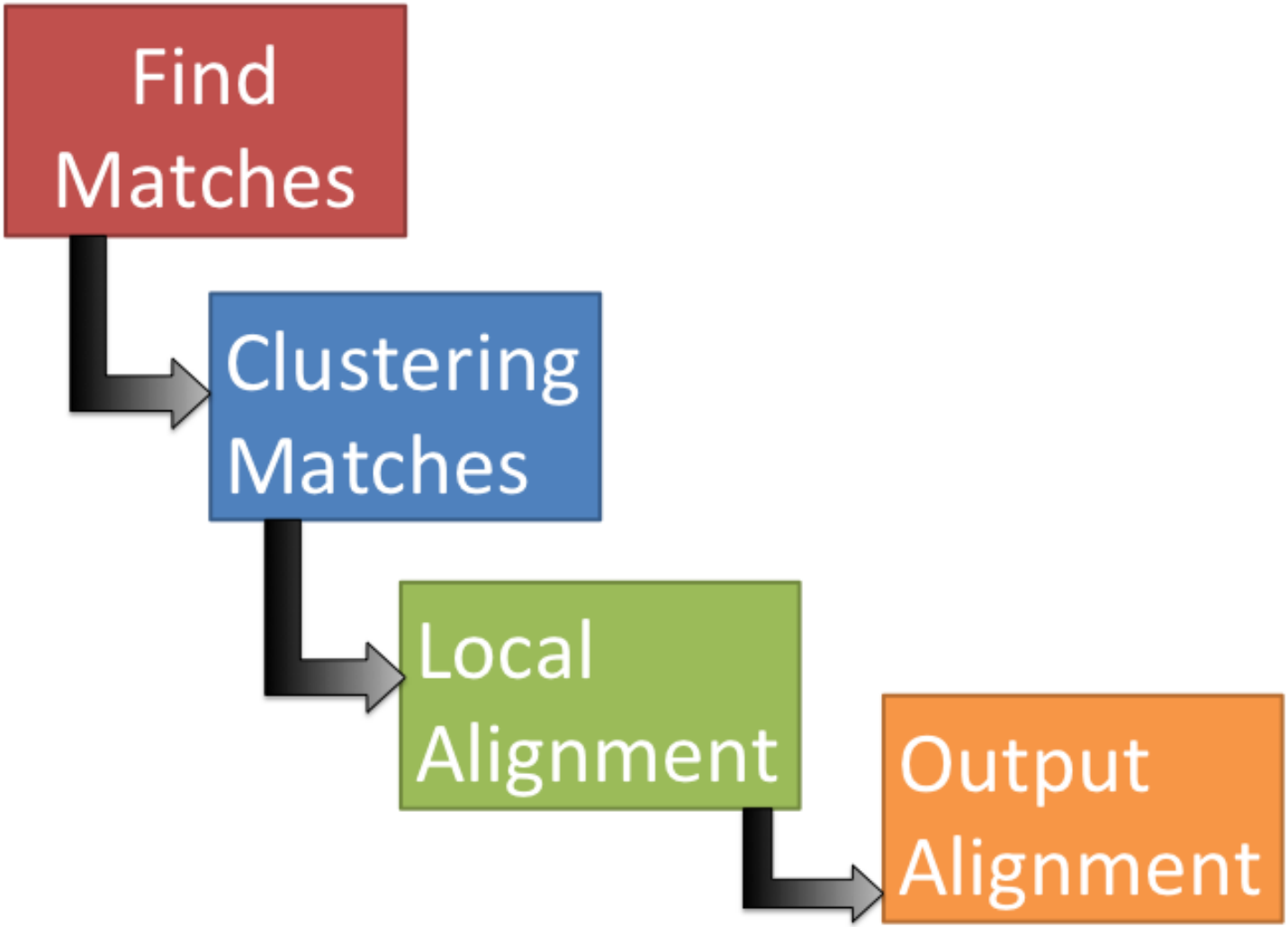
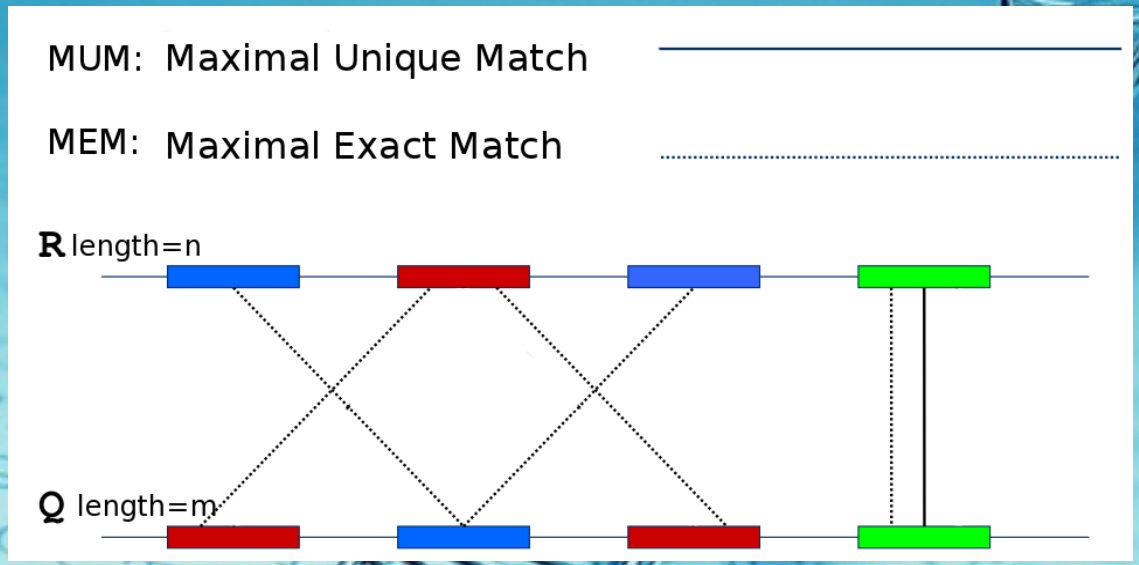
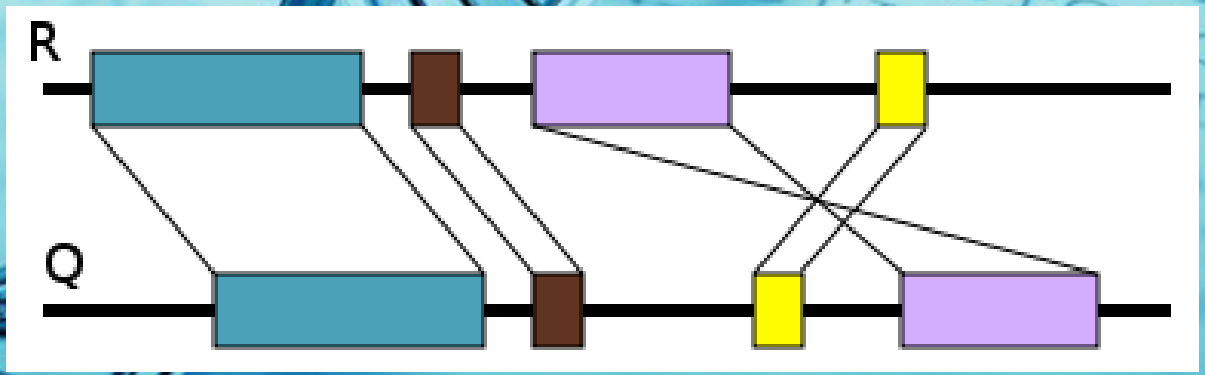
Whole Genome Alignment in MUMmer

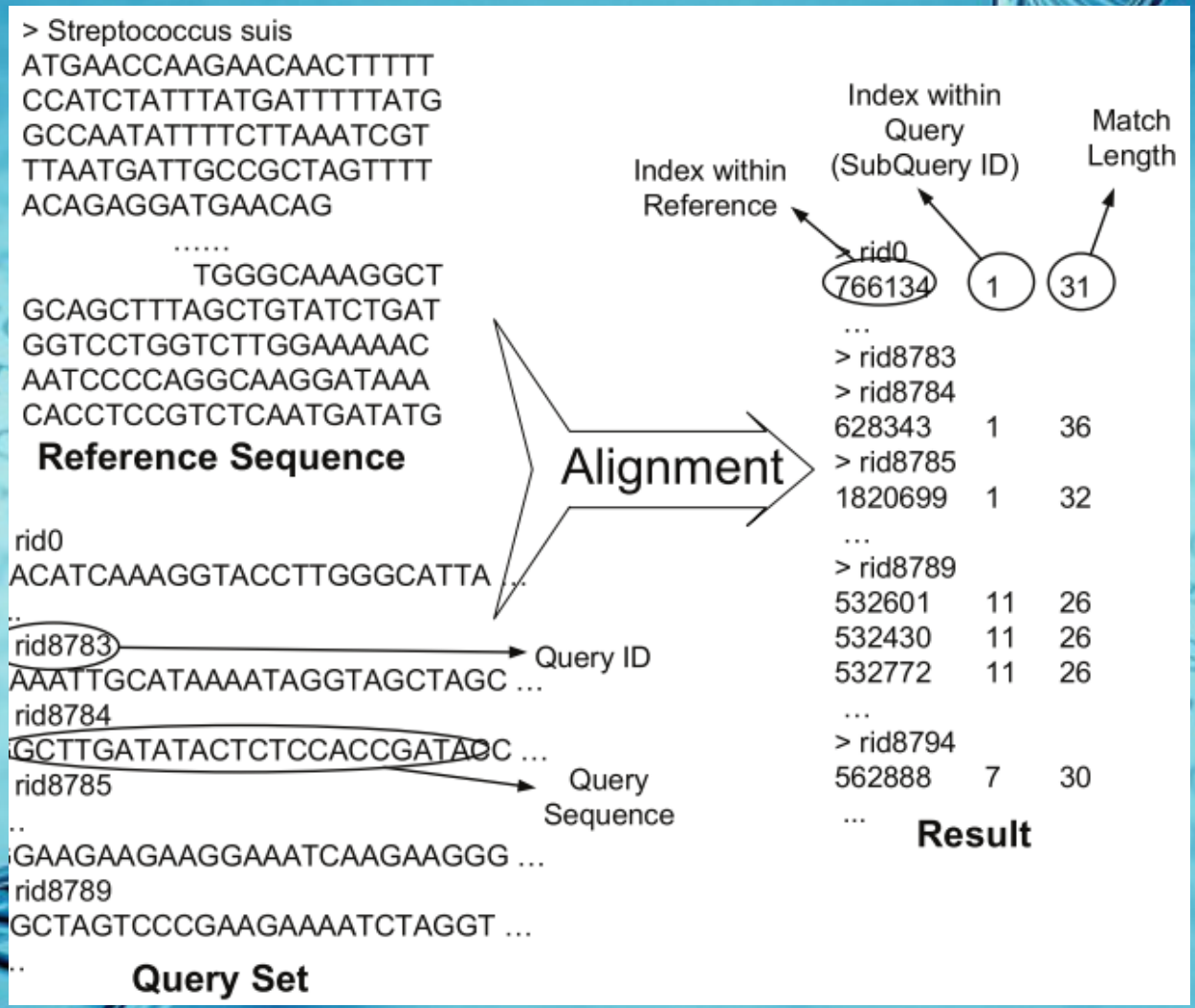


Search of Maximal Unique Matches





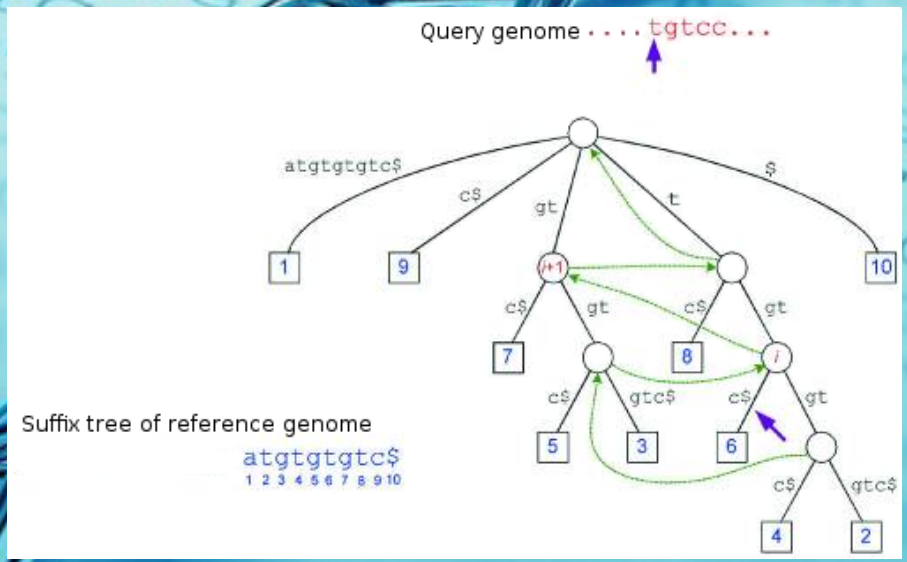
Genome alignment: search of Maximal Unique/Exact Matches



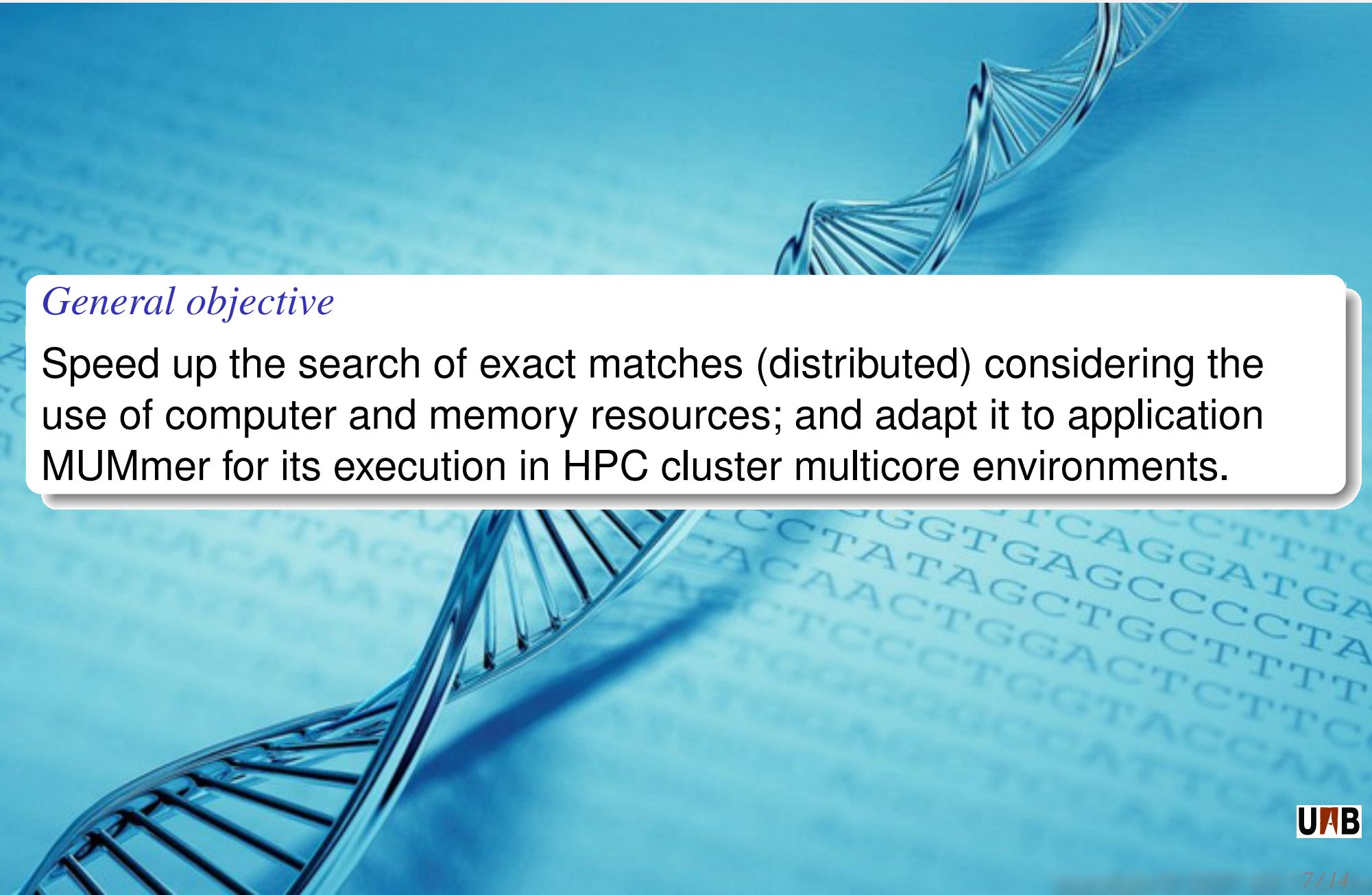
Traversal of suffix tree

Search of MUMs

1: **for each** Suffix in Q **do**
2: Compare suffix by traversing the suffix tree of R.
3: **if** $R[i-1] \neq Q[j-1]$ && node is a leaf **then**
4: The path of this traversal is a MUM-candidate.
5: **end if**
6: **end for**



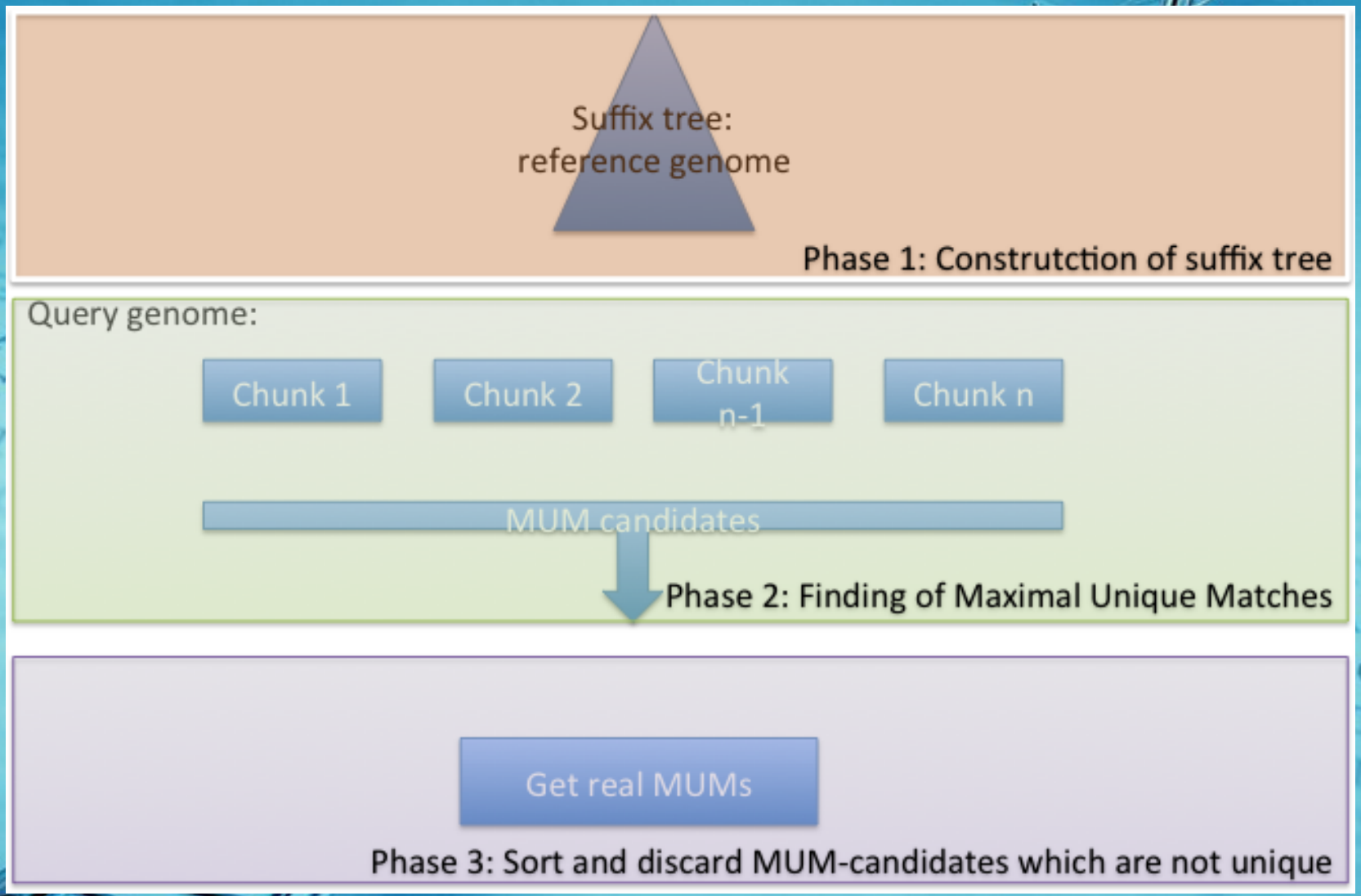
General objective



General objective

Speed up the search of exact matches (distributed) considering the use of computer and memory resources; and adapt it to application MUMmer for its execution in HPC cluster multicore environments.

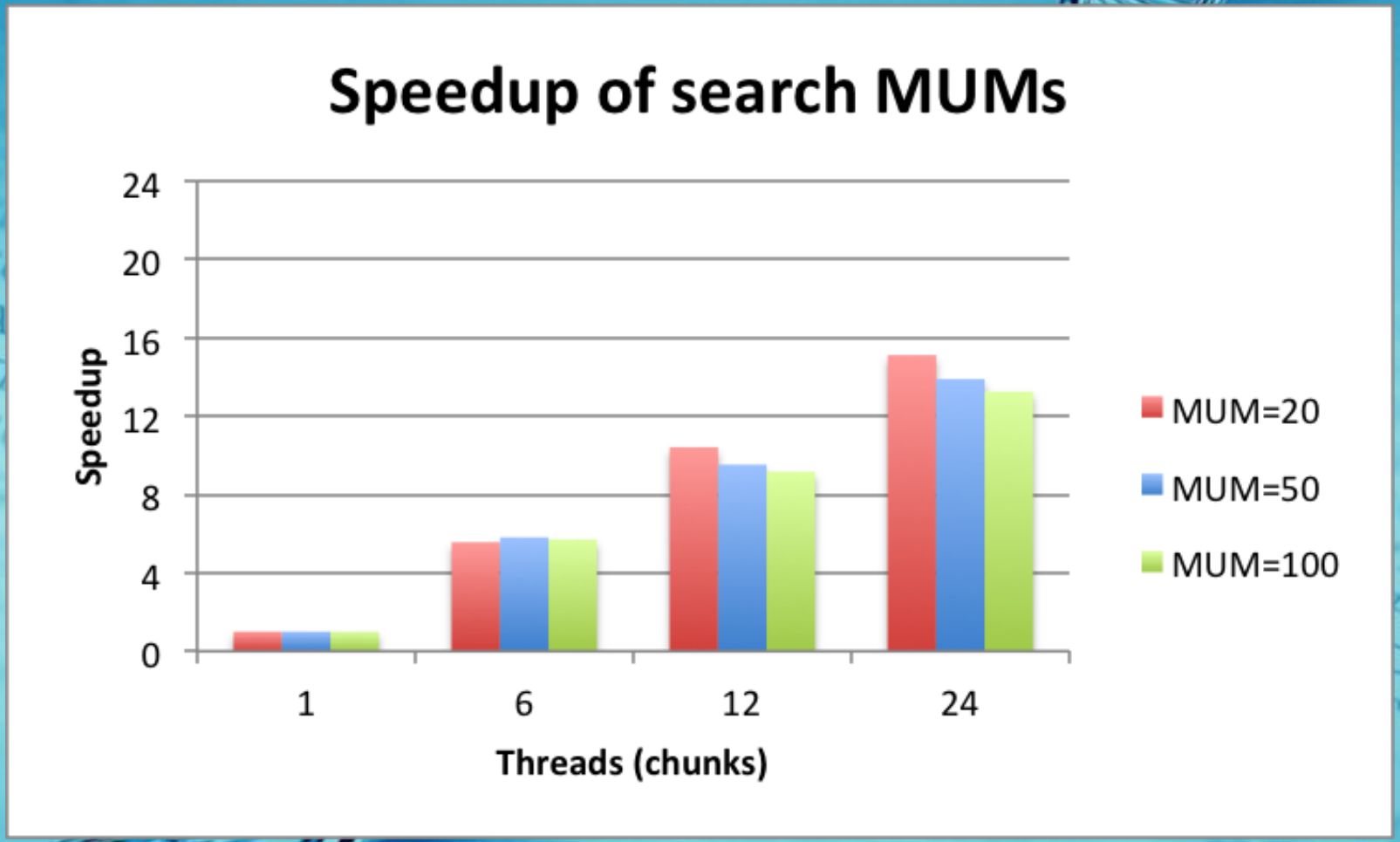
Search of MUMs in Multicore architectures



Parallel search of maximal unique matches

- Hardware:
  - 2 Processor Intel(R) Xeon(R) E5645 @ 2.4GHz of 6 cores each one, 32KB L1 cache, 256KB L2 and 12MB L3 shared cache per socket.
  - RAM: 96 GB
- Software:
  - Linux Kernel 2.6.32-220.el6.x86_64 #1 SMP
  - gcc 4.7.0 with OpenMP support
  - PAPI 5.0.1
- Genomes:
  - Reference: Human chromosome 21 single fasta file
  - Query: Mouse chromosome 16 single fasta file

Parallel search of maximal unique matches

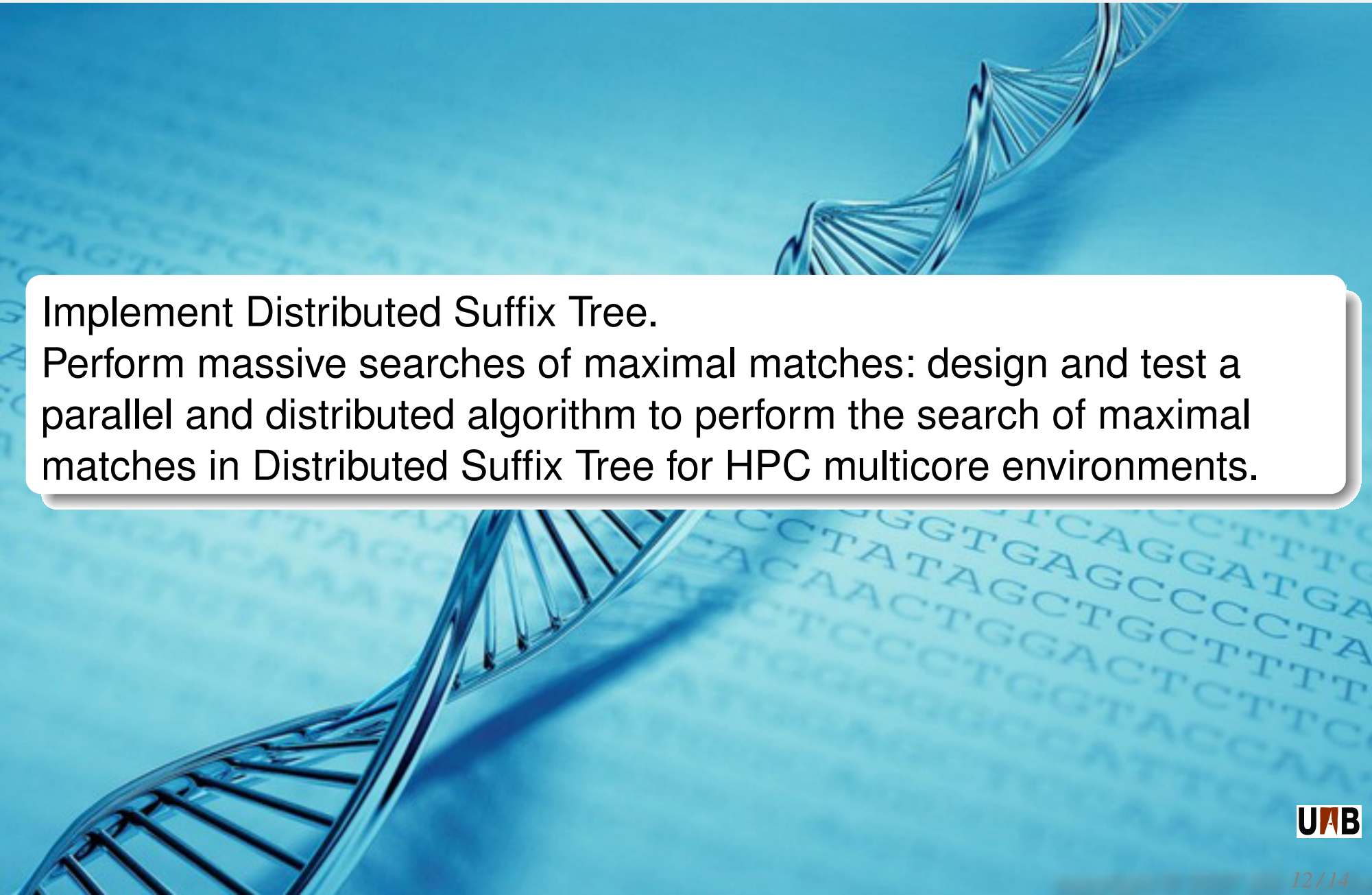


Conclusions

Current work

- Evaluation of performance to search MUMs of a query and reference genome in multi-core architectures with OpenMP.
- Results shows that the heaviest section of searching MUMs in a suffix tree is improved with the use of a multi-core architecture.
- Bottleneck is in suffix tree: traverse a suffix tree in multi-core architectures.

Future work



Implement Distributed Suffix Tree.
Perform massive searches of maximal matches: design and test a parallel and distributed algorithm to perform the search of maximal matches in Distributed Suffix Tree for HPC multicore environments.


Thanks!

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