# Alignment of whole genomes using MUMmer

## Presentation in Algorithms in Bioinformatics (TÖ111F autumn 2014)

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# Motivation

In 1999...

- the number of sequenced genomes was increasing rapidly
- when a new genome is sequenced, one could ask himself:
  - How does this genome align to the other genomes?

Problem:

- We have algorithms that were used for single gene sequences (up to 10,000 bp)
- But, they won't work well with whole genomes (millions of base pairs or more)
  - Take up way too much memory or
  - Have unacceptable computational time

# Introduction

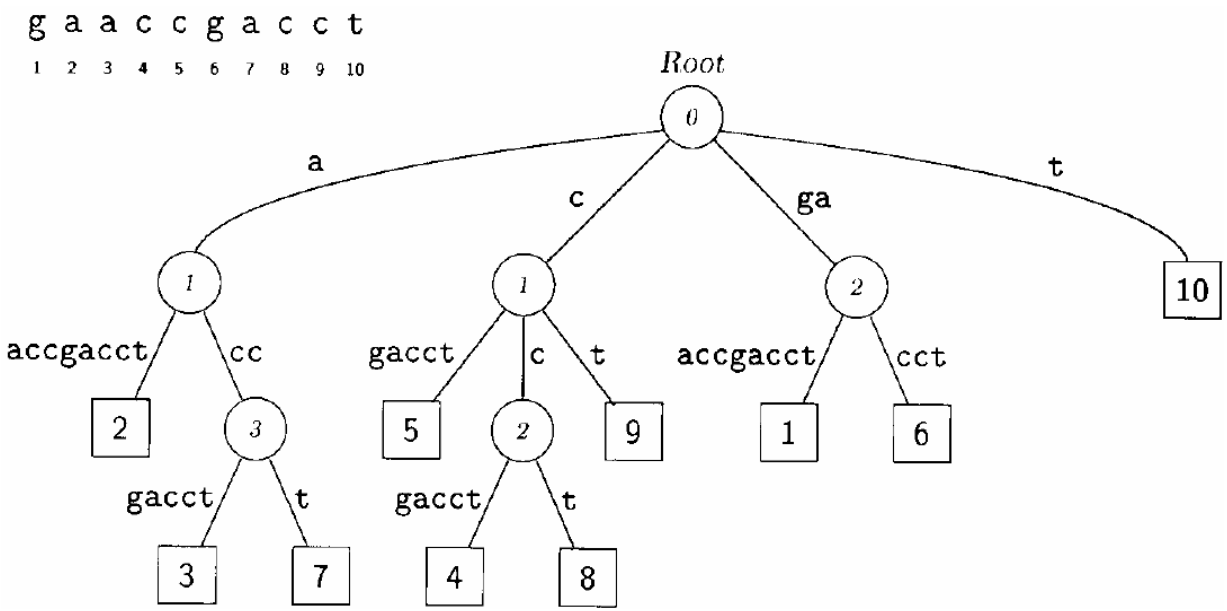
MUMmer:

- Is a system used to align whole genome sequences.
- Uses suffix trees as a data structure.
- Assumes that the two genomes are similar/related.
- The algorithm can be split into several steps that I'll talk about in detail

# Step 1: Creating a suffix tree

A suffix tree is a compact representation that stores all possible suffixes of an input sequence.

- Square nodes are leaves.
  - Store information about the starting position of the suffix.
- Circular nodes are internal nodes.
  - That means two or more sequences share the same prefix.
  - Store information about the length of the shared prefix.



# Step 1: Creating a suffix tree

(Animation sem býr til suffix tree)

# Step 2: MUM decomposition

# Step 3: Sorting the matches found in the MUM alignment

# Step 4: Closing the gaps

# MUMmer 3

# Conclusion