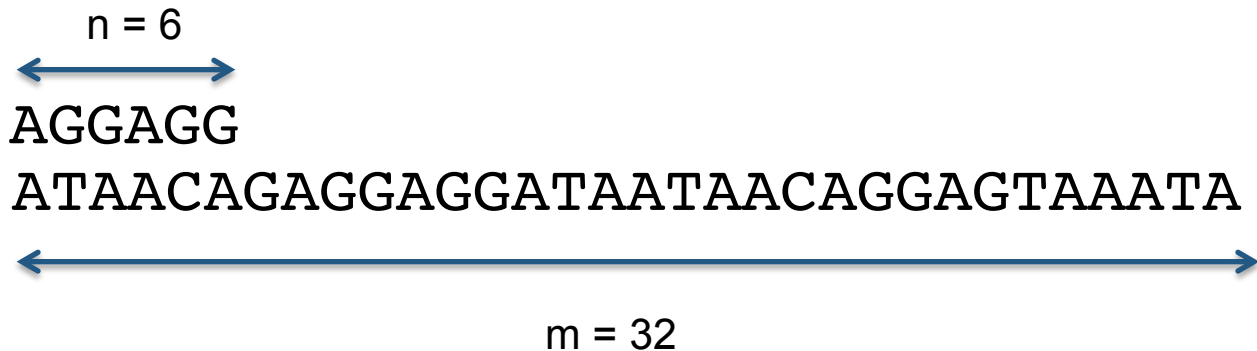


3. Gene prediction

- All genes end on a stop codon
- A simple algorithm for gene prediction
- Searching for start and stop codons
- Predicting all the genes in a sequence
- Making the predictions more reliable
- **Boyer-Moore algorithm**
- Index and suffix trees
- Probabilistic methods
- Benchmarking the prediction methods
- Gene prediction in eukaryotic genomes

String searching algorithms

- Naive algorithm
 - n : length of the string (or pattern)
 - m : length of the searchable text
 - number of comparisons in the worst case: $O(n * (m-n))$



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Improving the performance of string searching

- Preprocess the pattern
 - Boyer-Moore algorithm
- Preprocess the searchable text
 - Index
 - Prefix tree

The Boyer-Moore algorithm

- Start the comparisons from the end of the pattern
- Use information on the occurrences of characters within the pattern

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- A striking example
 - no A in the pattern
 - 6 positions (the length of the pattern) can be skipped at once

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- Start the comparisons from the end of the pattern
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- A striking example
 - another C occurs in the pattern
 - slide the pattern accordingly

CGGC^TC
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The Boyer-Moore algorithm

- Start the comparisons from the end of the pattern
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- A striking example
 - yet another C occurs in the pattern
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ATAACAGGAGTAAATAACGCTCGAGTAAATA

The Boyer-Moore algorithm

- Start the comparisons from the end of the pattern
- Use information on the occurrences of characters within the pattern
- A striking example
 - the pattern has been found !

CGGCTC
ATAACAGGAGTAAATA**CGGCTC**GAGTAAATA

The Boyer-Moore algorithm

- Start the comparisons from the end of the pattern
- Use information on the occurrences of characters within the pattern
- Tables of index have to be built from the pattern
- The longer the pattern, the greater is the gain