DAAD Deutscher Akademischer Austausch Dienst
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Robert Mercas
rgm@informatik.uni-kiel.de

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Algorithms and data structures on faulty sequences

Motivation:

Errors occur due to noise, corruption of data, or mishaps

- electronically transmitted information (bit stream)
- natural language (spoken or written text in some alphabet)
- in genetics (heredity transmission of DNA, mutated binding of nucleotides, protein synthesis of amino acids)

Problem:

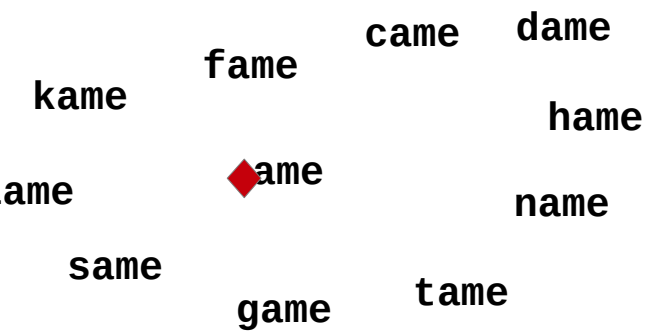
Given a big piece of text and some pattern, in the form of sequences of characters, identify efficiently within the given text all (approximate) occurrences of the pattern.

Solutions:

- avoid them
- assimilate and recognize them

Approximations:

- mismatches



- abelian equivalences

Directions:

- combinatorics on words
- data structures
- algorithms

Data structures:

- (new) suffix arrays
- (new) suffix trees
- *k*-encodings
- longest previous factor
- longest common prefix
- Rauzy graphs

Algorithms:

- classic pattern matching
- jumbled pattern matching
- histograms analysis

Combinatorics on words:

- weak and strong periodicity of words
- non-transitivity of the compatibility relation
- approximations of the "three-squares lemma"
- bounds on the number of repetitions

Applications:

- enrichment of the research area and connections with related fields
- improvement of already existing approximation algorithms regarding biological sequences alignment (global or local)
- better natural language processing tools
- improvement of the DNA sequencing algorithms by improving the time of the assembly of reads

Objectives:

- the investigation of the pattern matching problem in the setting of faulty sequences with bounded errors having as focus the improvement of the time and/or space complexity.
- the investigation of the indexing problem in the presence of bounded errors with focuse on the construction of data structures that reduce the preprocessing and/or query time.
- the investigation of the *k*-equivalence pattern matching problem in a dynamic settings with focus on the reduction of the running time of the online algorithm.