#### Sequence Bioinformatics

WS 2022/23

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Auckenthaler

#### Blatt 6

(Abgabe am 30.11.2022)

#### Task 1: Right-minimal unique substrings (2 points)

One right-minimal unique substring in barbara is "barb". "barb" only can be found one in barbara and all proper prefixes of u (i.e. bar, ba, b) occur at least twice in s. L is not given but |barb| = 4 > 0 Other possible substrings are "arb", "ara", "rb", "ra" and "bara". You can see the full suffix tree for "barbara" in Figure 1.

You can solve this task using the suffix tree by look at a leaf node and go back to the branching node. Then, you add the first letter of the terminal branch.

Example:  $(1 \Longrightarrow \text{barb}, 2 \Longrightarrow \text{bara}, 3 \Longrightarrow \text{arb}, 4 \Longrightarrow \text{ara}, 5 \Longrightarrow \text{a\$}, 6 \Longrightarrow \text{rb}, 7 \Longrightarrow \text{ra})$ The right-minimal unique substrings are highlighted in Figure 1

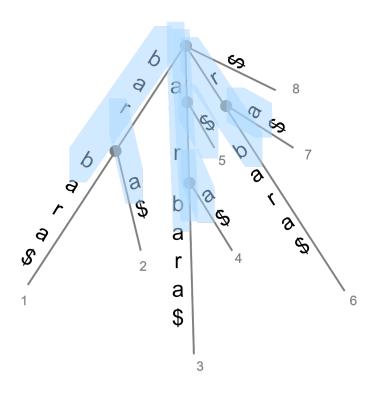


Figure 1: Suffix tree for "barbara".

## Task 2: Determine whether a query is present (2 points)

To run our script, navigate to the src folder and enter the following command: java assignment06/FindQueries\_Auckenthaler\_Dittschar.java "assignment06/data-06/text.fasta" "as signment06/data-06/queries.fasta"

# Task 3: Report all occurrences (3 points)

See code execution in Task 2.

## Task 4: Report all MUMS (3 points)

To run our script, navigate to the src folder and enter the following command: java assignment06/MUMS\_Auckenthaler\_Dittschar.java "assignment06/data-06/AGCT\_GGCC.fasta"