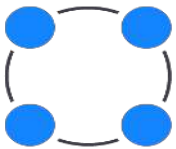
Автоматический анализ ошибок сборки SPAdes



ИНСТИТУТ БИОИНФОРМАТИКИ

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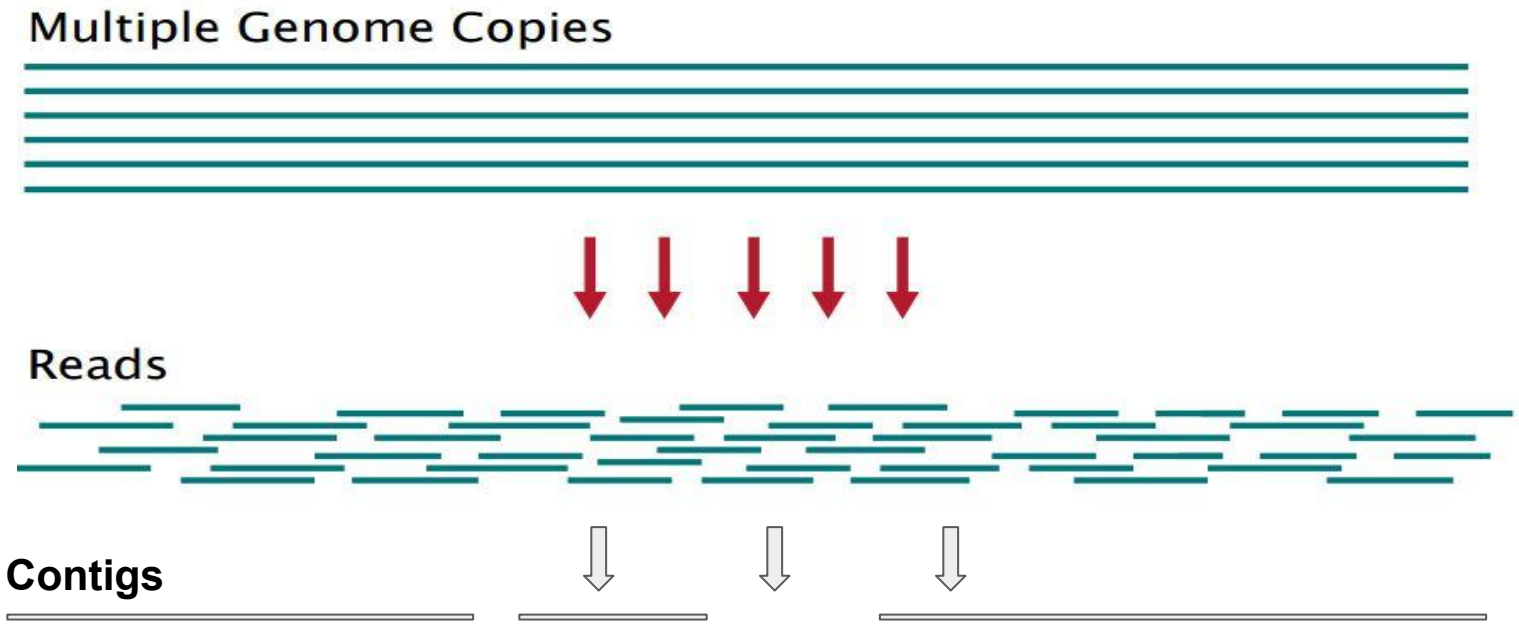
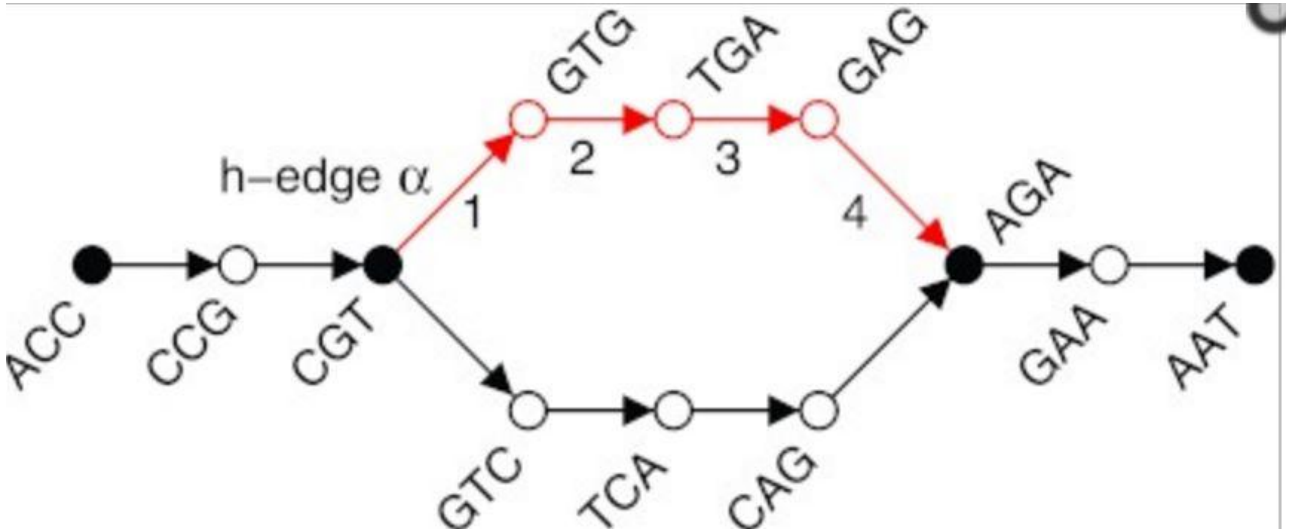


Issues:

- Dictionary contains only 4 letters
- Errors in reads
- Repeats
- Little context clues

SPAdes - genome assembler

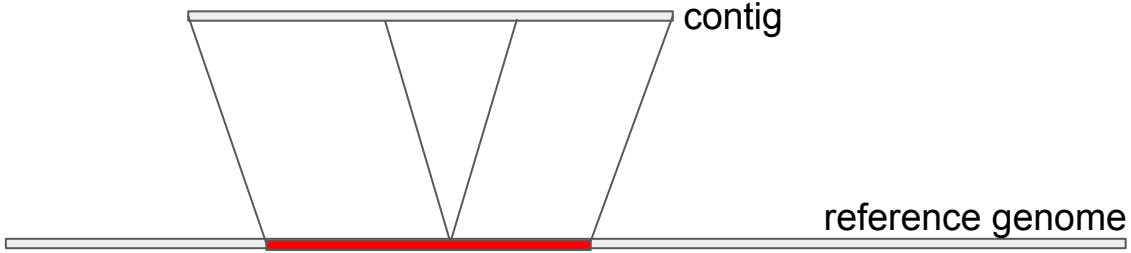
- One of the leading prokaryote assemblers.
- Uses De Bruijn graphs.



A de Bruijn graph on reads ACCGT***C***AGAAT and ACCGT***G***AGAAT

QUAST - assembly quality checker

- Can use a reference genome to check the assembly quality.
- Produces different metrics: quantitative, qualitative.
- Produces misassembly infos.



- Currently each misassembly case is investigated manually by looking at the assembly graph. That requires a lot of time.

Project objectives:

- Use alignment information provided by QUAST to draw misassembled parts of the graph.
- Auto-detect misassembly types of those parts:

• Bad or missing data	• Wrong simplifications	• Incorrect repeat resolving