Combining de Bruijn graph, overlaps graph and microassembly for *de novo* genome assembly

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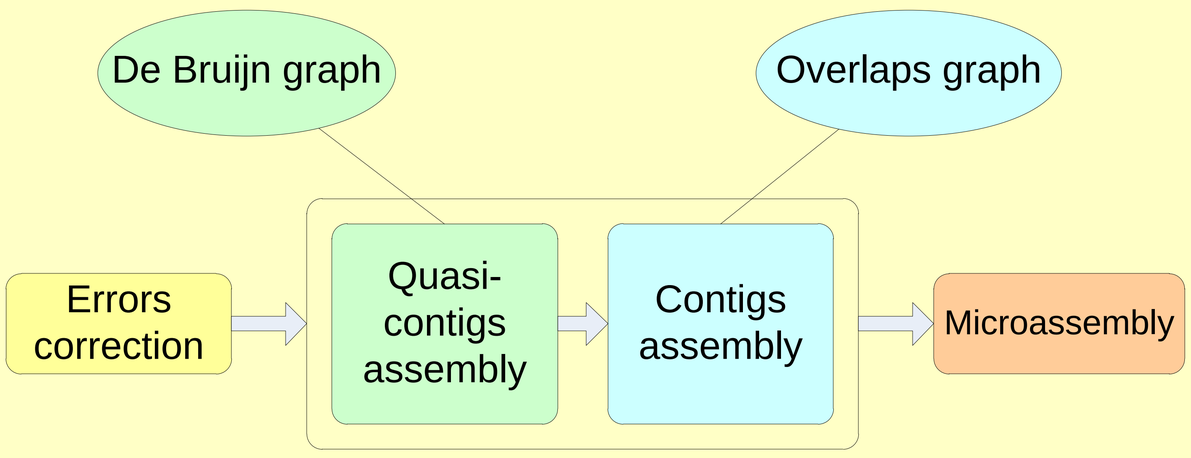
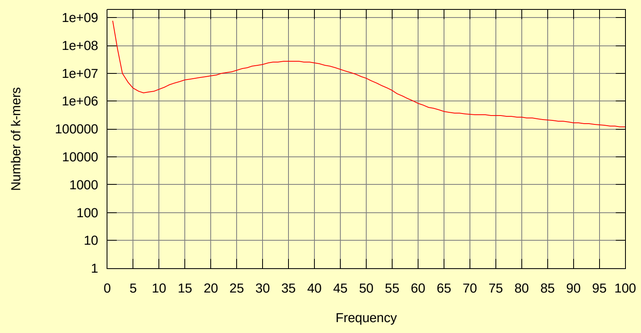
Assembler architecture

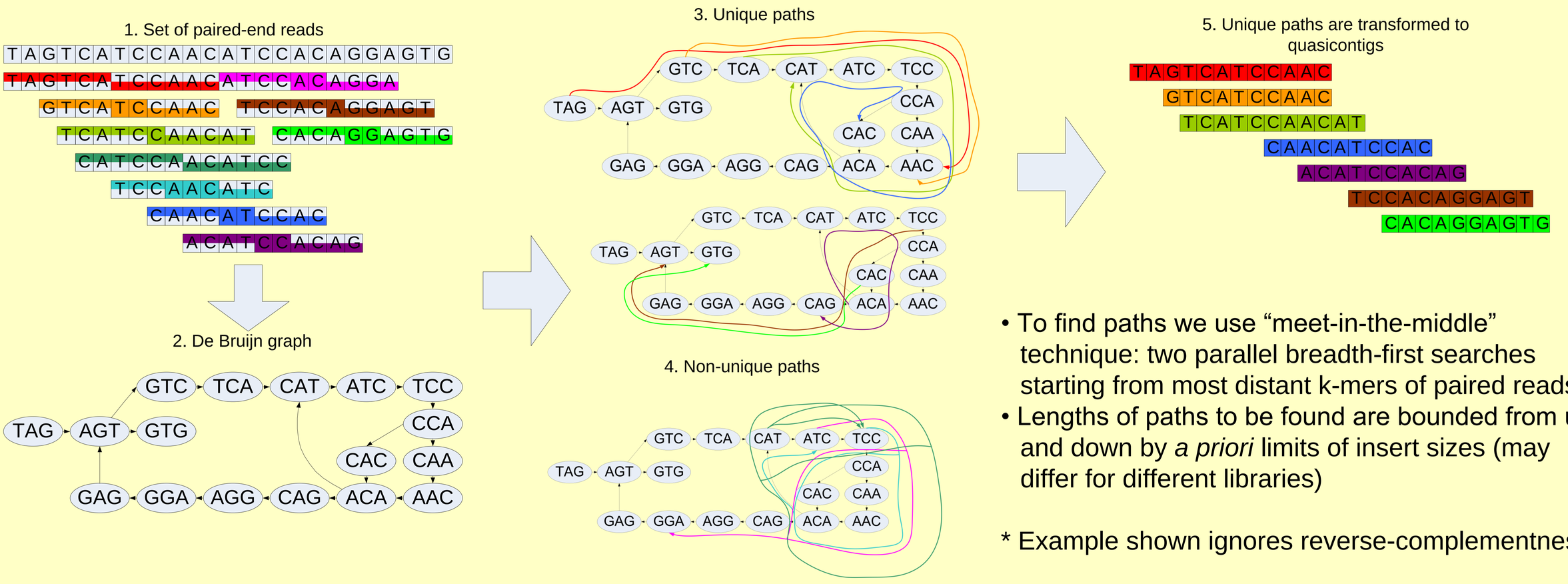


Errors correction

- Reads truncation
- K-mers frequency analysis
- Split k-mers into buckets according to their prefixes



Quasicontigs assembly



- To find paths we use “meet-in-the-middle” technique: two parallel breadth-first searches starting from most distant k-mers of paired reads
- Lengths of paths to be found are bounded from up and down by *a priori* limits of insert sizes (may differ for different libraries)

* Example shown ignores reverse-complementness

Contigs assembly

- Quasicontigs are given as input to “overlap-layout-consensus” module
- Short quasicontigs are thrown out to get to a reasonable size of an input data, e.g. 10-fold coverage

Microassembly

- All of the paired-end reads are aligned to the contigs with Bowtie (reads in a pair are aligned independently).
- If both reads in a pair are aligned to different contigs such reads are called *bridging* and the contigs are called *bridged* (see Figure).
- For every pair of bridged contigs we can infer their order from orientations of alignments of the bridging reads.
- All pairs of reads with at least one read aligned to one of these contigs are used to build a relatively small de Bruijn graph.
- In this graph we search for the path connecting two contigs in the same as quasicontigs are assembled

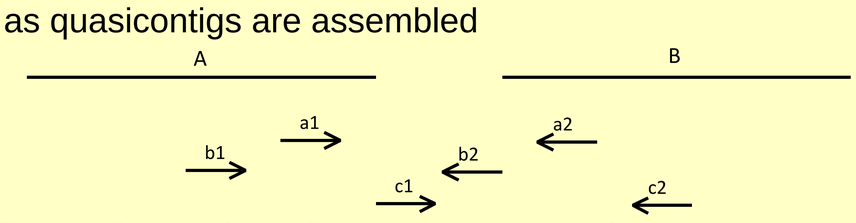


Figure. Contigs A and B are bridged, reads a1 and a2 are bridging, pairs (b1, b2) and (c1, c2) can be used for microassembly.

Experiments

• Dataset – *E. Coli* genome 160-fold coverage paired-end reads library SRR001665 with insert sizes of about 200 bp.

• We got about 10 million quasicontigs with a total size of two Gbp.

• This data was truncated to 175 Mbp.

• After contigs assembly there were 525 contigs with an N50 size of 17804 and a maximum size of 73908.

• After microassembly there were 247 contigs with an N50 size of 53720 and a maximum size of 167319. This contigs cover 98% of the reference genome.

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