DNAMAN Sequence Analysis Software

Sequence Assembly

BIOINFORMATICS PLATFORM

Sequence Assembly

De novo Assembly
 Re-Sequencing (Reference-Based)
 Assembly Parameters
 Assembly with Trace Files

De Novo Assembly

- No reference sequence available
- Assemble overlapping short reads into long contigs
- Each short reads is aligned with others to produce a score matrix
- Contigs are assembled based on scores
 - High score pairs aligned first
 - Low score pairs last Contigs are assembled based on scores
- Computation intensive

Re-Sequencing Assembly

- Reference sequence available
- Each short reads is aligned to Reference (No score matrix needed)
- Computation less intensive than De Novo Assembly

Assembly Parameters

- 1. Select sequences for assembly from File/Folder/Channel
- Quality of short sequences can be improved by filtering ambiguous regions
- 3. Choose type of assembly
- 4. Set overlap end qualification requirements
- 5. Set fast alignment parameters
- 6. Choose Final Assembly method
- 7. Press Assemble button to start

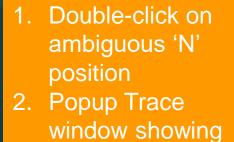
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Assembly with Trace Files

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Assembly with Trace Files

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