

Algorithms in Genome Research

Winter 2012/2013

Exercises

Number 2, Discussion: 02. November 2012

1. What are mate pairs? How do they simplify the assembly problem?
2. Discuss the main experimental problems that make sequence assembly difficult.
3. In the overlap phase of an assembly, prefix-suffix “local alignments” are sought.
 - (a) Work out the details of a dynamic programming algorithm.
 - (b) What are the time and space complexities of the seed-based algorithm mentioned in class?