

Algorithms in Genome Research

Winter 2005/2006

Exercises

Sheet 4, Discussion 08.12.2005

1. How does an interpolated Markov model differ from a hidden Markov model?
How does an interpolated context model differ from an interpolated Markov model?
2. What sort of information may be used in a prokaryotic gene finder?
3. What are the main issues why eukaryotic gene finding is much more difficult than prokaryotic gene finding?
What are the algorithmic/computational techniques that are used in order to account for this increased difficulty?