Things to know before the exam are

Perl:
- Basic data types and control structures (scalars, lists, for and while loops, if-else blocks)
- Basic string manipulation (functions used in the alignment program)

Global pairwise alignment (Needleman-Wunsch):
- Definition of a sequence alignment
- Running time and space requirement of optimal pairwise sequence alignment by dynamic programming
- Score of an alignment with and without affine gaps

Dynamic programming algorithm for pairwise alignment
- Computation of scoring matrix $V$
- Traceback

Alignment accuracy
- Comparison of computed alignment to “true” one

Cross-validation
- Selection of gap penalty

Scoring matrix
- Computing substitution scoring matrix from alignments

BLAST:
- Basic BLAST algorithm
  - Find kmers by hashing query and target
  - Find maximal local segment
- Speedup in running time

Local alignment (Smith-Waterman):
- Difference in recurrence and traceback between this and global alignment

Profiles:
- Score nucleotide against profile
- Profile vs profile

Multiple sequence alignment
- Basic iterative heuristic
- Progressive alignment