BNFO $601 - \frac{10}{16}/2017 - First$ exam review sheet

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