BNFO 601 - Second exam review sheet

Things to know before the exam:

## HMMs

- Compute probability of alignment
- Viterbi
- Maximum likelihood estimation of probabilities
- Forward and backward probabilities
- Expected maximization (Baum Welch)

Expected accuracy

- Expected accuracy score
- Posterior probability calculation from a set of alignments
- Calculating posterior probability from forward backward probabilities
- Calculating posterior probability from partition function matrices

Short read mapping

- Masked seeds
- BFAST approach
- Limitations of current methods
- Exact short read alignment

## Genome alignment

- General strategy
  - Longest increasing subsequence
  - Find high scoring segments
  - Do constrained alignment in between segments
- Limitations of current methods
- Exact genome alignment

## Applications:

• Metagenomics