Bioinformatics Exam 1 Review sheet

In-class portion will include:

- building dynamic programming matrix (manually), given 2 sequences & a scoring scheme
- finding global alignment using traceback given completed matrix
- Perl programming (code interpretation):
  - be able to identify/describe:
    - scalar variables
    - arrays
    - hash tables
    - control structures
    - input/output statements
    - assignment operations
  - be able to trace (show output) of programs containing:
    - simple loops (while and for)
    - if/elsif/else structures
    - string operations:
      - substring
      - concatenation
      - substitution (s)
      - transliteration (tr)
- interpretation of results from:
  - PubMed
  - GenBank
  - BLAST
- answering general questions about
  - database searching
    - uses of AND, OR, NOT, quotation marks, parentheses
    - which database(s) to search for what kind of information
    - first/second/third generations of databases
  - reading scientific literature
    - parts of papers
    - bibliographic information
  - vocabulary terms you should know:
    - central dogma of molecular biology
    - transcription / translation
    - primary/secondary/tertiary structures of proteins
    - homology & its implications
    - algorithms
    - alignment
      - global
      - semiglobal
      - local

For the in-class portion, you may bring a one-page (two-sided) “cheat sheet” of your own design for your own use during the exam. The in-class portion will comprise 65% of your exam grade.