BIOINFORMATICS C
Southern California Trial Event

1. **DESCRIPTION:** Teams will complete a written exam on the theory behind bioinformatic methods and their applications in solving biological problems.
   A TEAM OF UP TO: 2 **EVENT TIME:** 50 minutes
2. **EVENT PARAMETERS:**
   a. Each team may bring up to two 8.5" x 11" sheets of paper, which may be in a sheet protector sealed by tape or laminated, that may contain information on both sides in any form and from any source without any annotations or labels affixed.
   b. Each team may also bring writing utensils and two stand-alone non-programmable, non-graphing calculators. Teams will not have access to the internet during the event.
3. **THE COMPETITION:**
   Teams will be given 50 minutes to complete a written test on the topics below, with questions including but not limited to: writing pseudocode, describing common algorithms, explaining concepts, performing calculations, and applying bioinformatics concepts and algorithms to real-world problems.
   a. Biological prerequisites
      i. Central dogma of life
      ii. Nucleic acids and proteins: chemical properties of building blocks; structure and function of common forms; methods for sequence determination
   b. Types of bioinformatics databases
   c. Sequence alignment
      i. Biological motivation
      ii. Scoring matrices (PAM, BLOSUM, PSSM); gap penalties
      iii. Pairwise sequence alignment: Needleman-Wunsch; Smith-Waterman; Gotoh
      iv. Multiple sequence alignment: ClustalW; BLAST software; FASTA; Hidden Markov Models and the Viterbi algorithm
      v. Assessing sequence alignments: E-value; P-value
   d. Protein structure analysis
      i. Structural alignment methods
      ii. Methods for secondary structure prediction
         (1) From sequence: Chou and Fasman, PHD, PSIPRED
         (2) From structure: DSSP
      iii. Methods for three-dimensional structure prediction
         (1) Molecular dynamics simulations: CHARMM, AMBER
         (2) Homology modeling
         (3) Threading and fold recognition
         (4) Deep learning: energy minimization methods; end-to-end models
   e. Computational protein design
      i. Docking algorithms to design protein interactions
      ii. Rosetta for *de novo* protein design
4. **SCORING:**
   a. High score on the test wins.
   b. Ties will be broken by selected questions from the test.

RECOMMENDED RESOURCES:

1. rosalind.info