BB 497/597 Basic Nucleic Acid and Protein Sequence Analysis, Fall 2014 (1 credit)

Instructor

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Aims of the course

BB 497/597 is a practical course that focuses on extracting information from nucleic acid and protein sequences using a variety of online tools. The course aims to make students familiar with and proficient in the use of a range of sequence analysis programs and other resources available on the Web. Students will learn the application of sequence analysis tools by using them to answer questions about a particular DNA sequence from the databases and the protein it encodes. In this way, they will learn not merely how to use the sequence analysis tools, but also how these methods are used to obtain and integrate information about genes and proteins, starting with sequence files.

Learning Outcomes

After completing this course, students should have a familiarity with the use of various online tools available for nucleic acid and protein sequence analysis and be able to integrate the information to obtain a unified picture of the genes and proteins they are analyzing.

Students will use online tools and resources to analyze unknown sequences as detailed below:
• Determine whether the sequence encodes a protein(s) by using an online ORF Finder.
• Determine the identity of putative proteins encoded by the sequence.
• Carry out a BLAST search on protein sequences to infer functional and evolutionary relationships among genes and to identify members of gene families.
• Find the chromosomal locus for the gene and its inheritance pattern from the OMIM database.
• Find gene length, number of exons and mRNA sequences, including splice variants from the NCBI Reference Sequence Database
• Determine the molecular function of the encoded protein, post-translational modifications, if any, signal sequences, subunit structure, whether it is a membrane protein, variant forms and their relationship to disease conditions, if applicable, using databases such as UniProtKB/Swiss-Prot.
• Find structure information on the protein and any mutant forms, if available, at the PDB or other sites.
• Determine if there are known protein-protein interaction partners for the protein of interest using the STRING database and identify the functions, if known, of the interacting proteins.
• Determine the expression profile of the gene of interest as well as orthologous genes in other species using databases like BGee.
Students will use the information extracted from these and other online resources, such as PubMed and GeneReviews, to construct an integrated, current and coherent description of the structure and function of the gene(s) and the encoded protein(s) and indentify important unanswered questions about the gene/protein.

Evaluation

Your grade will be based on a paper that you write describing the characteristics of the gene sequence and its encoded protein, using the analyses you carried out with the online tools available to you. Detailed instructions for this assignment will be posted at the class website. Your report will be graded based on the thoroughness of your analyses as well as on your synthesis of the information you obtain into a coherent and thoughtful overview. Your writing will be expected to conform to the standards expected of a professional in this field.

General OSU and Departmental Policies

Disabilities/ Special Accommodations

 "Students with documented disabilities who may need accommodations, who have any emergency medical information the instructor should know, or who need special arrangements in the event of evacuation, should make an appointment with the instructor as early as possible, no later that the first week of the term. In order to arrange alternative testing, the student should make the request at least one week in advance of the test. Students seeking accommodations should be registered with the Office of Services for Students with Disabilities."

Student Conduct

The Department of Biochemistry/Biophysics and the Biology Program follow the university policies on student conduct. These can be found at http://oregonstate.edu/admin/stucon/regs.htm.

Cheating or plagiarism by students is subject to the disciplinary process outlined in the Student Conduct Regulations. Students are expected to be honest and ethical in their academic work. Academic dishonesty is defined as an intentional act of deception in one of the following areas:
* cheating- use or attempted use of unauthorized materials, information or study aids
* fabrication- falsification or invention of any information
* assisting- helping another commit an act of academic dishonesty
* tampering- altering or interfering with evaluation instruments and documents
* plagiarism- representing the words or ideas of another person as one's own

Behaviors disruptive to the learning environment will not be tolerated and will be referred to the Office of Student Conduct for disciplinary action.

"The goal of Oregon State University is to provide students with the knowledge, skill and wisdom they need to contribute to society. Our rules are formulated to guarantee each student's freedom to learn and to protect the fundamental rights of others. People must treat each other with dignity and respect in order for scholarship to thrive. Behaviors that are disruptive to teaching and learning will not be tolerated, and will be referred to the Student Conduct Program for disciplinary action. Behaviors that create a hostile, offensive or intimidating environment based on gender, race, ethnicity, color, religion, age, disability, marital status or sexual orientation will be referred to the Affirmative Action Office.