
An Advanced Undergraduate Course in Microbial Bioinformatics and Biotechnology Documentation

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Introduction

This is a companion website for the online bioinformatics course offered to undergraduate students at Can Tho University.

Sequence Alignment with BLAST

The goals of these problem sets are to acquaint you with sequence databases and analysis tools and provide problems to solve so that you become adapt at working with sequence and using the available online tools.

We have organized the course so that we provide you with a set of problems each week that can be solved through one or several of the online databases.

2.1 Problem 1

The first problem set focuses on rather simple sequence searches. Searching for a string of As, Gs, Ts, & Cs is made possible through the use of an algorithm that searches for strings of nucleic acid bases or amino acids (or simply letters). The one algorithm that most of us use is called BLAST, which stands for Basic Local Alignment Search Tool. Using this tool one can determine if the sequence that you have is similar to any sequence in biological databases. There are three possible results from a BLAST search of sequence databases.

Indices and tables

- *genindex*
- *modindex*
- *search*