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DELAWARE
BIOTECHNOLOGY
INSTITUTE
Room 102**

bioinformatics.udel.edu

BIOINFORMATICS SEMINAR

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miRADOR: A NOVEL PLANT miRNA PREDICTION TOOL

Small RNAs (sRNAs) in plants (20-24 nt) are a highly abundant class of noncoding RNAs that regulate silencing processes, mostly on the basis of sequence complementarity. There are several classes of small RNA that differ in both their biogenesis as well as their mode of silencing. With the advent of next generation sequencing technologies, sRNAs can be sequenced at a low cost in a short amount of time. However, because of complexity of the various sRNA classes and their sheer volume, it is difficult to accurately classify the small RNAs within these datasets. It is for this reason that I have developed several tools to assist in the classification of these sRNAs. Today, we will focus on the development of a micro RNA (miRNA) prediction tool that I have developed. *miRador* is a novel miRNA prediction tool designed to quickly predict miRNAs utilizing a set of sRNA libraries and a genome sequence. By combining these results with *sPARTA*, a target prediction and validation tool, we can accurately classify miRNAs in a variety of plant species.

PRISCILLA HEMPEL

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GENOMIC AND TRANSCRIPTOMIC ANALYSIS OF HETEROTROPHIC ACTINOBACTERIA WITH LIGHT-ENHANCED GROWTH

Light is an environmental cue and source of energy in surface water environments. Conversion of light energy to chemical energy by phototrophs has been well characterized in prokaryotes. However, the conversion of light to information and the cellular response to this environmental cue has not been widely characterized. Recent work demonstrates that 3 strains of Actinobacteria lacking functional photosystems grow faster in light than in dark. We hypothesize that Actinobacteria convert light to information that increases their organic carbon uptake. My aim is to identify shared genes among these species and characterize the transcriptional response of freshwater Actinobacteria caused by light so that I can identify biological pathways involved in actinobacterial cellular response to light. Transcriptomic analysis shows that Actinobacteria have coordinated immediate and delayed responses to light availability, particularly in transcription factors. Because Actinobacteria are ubiquitous in surface freshwater environments, understanding how light affects their carbon metabolism will contribute to our broader understanding of carbon cycling in freshwater environments.

IMAM CARTEALY

PhD Student, UNIVERSITY OF DELAWARE

GENES PREDICTION IN METABOLIC PATHWAY BY USING GO TERM SEMANTIC SIMILARITY

Various similarity measures have been developed to quantify the semantic similarity of GO terms and applied it in quantitative comparison of functional similarity of gene products. Those measures are basically can be classified into 3 methods: edge-based, node-based, and hybrid method. Edge-based methods rely on the structure of GO graph, while node-based methods rely on information that is contain by the node. The hybrid methods combine both edge and node-based method. In this project, we develop a semantic similarity measures that include both the information content and the graph. We consider the GO terms as a feature of genes and build gene vector based on it. We use the semantic similarity to quantify the similarity between genes and predict the gene membership in the metabolic pathway.



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