

<b>Research Theme: Computational Biology; Functional Genomics</b>
<b>Research Project Title: LEO – Life Expression Omnibus</b>
<b>Principal Investigator/Supervisor: Asst. Prof. Marek Mutwil</b>
<b>Co-supervisor/ Collaborator(s) (if any):</b>
<b>Project Description</b>
<p><b>a) Background:</b> The identification of gene function is needed to understand how a living cell works, and how we can rationally develop new medicines and improved crops. However, our knowledge of gene function is still far from complete. For example, Escherichia coli is the most studied bacteria, but ~2,000 of the 4,225 (47%) protein-coding sequences lack experimentally verified function. To remedy this paucity of functional information, researchers typically predict the function of uncharacterized genes with sequence similarity approaches. However, sequence similarity alone often cannot reveal when and in which biological process a gene is active. To this end, gene co-function networks based on gene expression patterns have been used with great success to assign genes to biological pathways. However, this valuable method has only been applied to a small number of model organisms, which limits our knowledge of gene function.</p> <p><b>b) Proposed work:</b> This proposal aims to analyze gene function through gene expression networks in the whole kingdom of life, comprising Animalia, Plantae, Fungi, Protista, Archaea/Archaeobacteria, and Bacteria/Eubacteria. We will process millions of gene expression samples from hundreds of species and use genomic, transcriptomic, and machine learning analyses to construct gene co-function networks and predict gene function. The broader impact of a better understanding of gene function is vast. For example, in bacteria, we will be able to link uncharacterized genes in pathogenic bacteria to protein synthesis and consequently provide novel targets for antibiotic research. In animals, we will reveal which gene families are expressed in neurons of vertebrates but are absent in invertebrates, thus allowing the study of the evolution of the central nervous system. These are just a few examples</p> <p><b>c) Preferred skills:</b> Python programming or other programming language, strong interest in computational biology</p>
<b>Supervisor contact:</b>
<b>If you have questions regarding this project, please email the Principal Investigator:</b> mutwil@ntu.edu.sg
<b>SBS contact and how to apply:</b>
Associate Chair-Biological Sciences (Graduate Studies) : <a href="mailto:AC-SBS-GS@ntu.edu.sg">AC-SBS-GS@ntu.edu.sg</a> Please apply at the following:



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