

7<sup>th</sup> International Conference on

# Proteomics & Bioinformatics

October 24-26, 2016 Rome, Italy

## Mathematical modelling of evolution of tetranucleotide usage patterns of whole bacterial genomes to improve phylogenetic inferences

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Nowadays, complete genome sequences of multiple bacteria became readily available for analysis. Current work which uses whole genome based alignment (WGS) approach for phylogenetic and phylogenomic research believe to resolve contradiction between gene based trees, but this approach multiplies the problem in terms of gene annotation, orthology prediction and inadequate alignment of sequences. Therefore one of the most prospective ways for genome comparison and phylogenomic inferences is then based on annotation and alignment free genome linguistic approaches, i.e. comparison of oligonucleotide usage patterns (OUP) of genome-scale DNA fragments. Until now, this approach still lacks a reliable evolutionary model to explain the mechanisms and dynamics of changes in OUP which hinders the application of this approach to systematically compare to other well-known methods such as marker genes and/or whole genome sequence based alignment. The aim of the current work is divided into three important topics: i) Comparative analysis of multiple complete genome sequences representing different phylogenetic branches at different taxonomic levels to identify the driving forces of OUP evolution; ii) Analysis of topological incongruences between phylogenetic trees based on orthologous gene alignments, whole genome alignments and alignment free OUP patterns; iii) Improving phylogenetic inference by reconciliation of sequence based and pattern based evolutionary models. The major output of this research is an innovative evolutionary model implemented in a form of a computer program for phylogenetic inferences based on combination of alignment based and alignment free approaches.

### Biography

Xiaoyu Yu has completed his MSc in Bioinformatics and is currently doing a PhD (2<sup>nd</sup> year) in Bioinformatics at the University of Pretoria. He has currently no publication with one in working progress and has attended and presented posters in many conferences in Europe such as ECCB 2014, ECCB 2015 and VAAM 2016.

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