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12<sup>th</sup> International Conference and Expo on

## Proteomics and Molecular Medicine &

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

### Advancements in Bioinformatics and Drug Discovery

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#### miRmapper: A tool for interpretation of miRNA-mRNA interaction networks

Gary Hardiman<sup>1,2</sup>, da Silveira W A<sup>1</sup>, Renaud L<sup>1,2</sup>, Simpson J<sup>1</sup>, Glen W B Jr<sup>1</sup>, Hazard E S<sup>1</sup> and Chung D<sup>1,2</sup> <sup>1</sup>Medical University of South Carolina, USA <sup>2</sup>Hollings Marine Laboratory, USA

Current estimates predict that miRNAs potentially regulate up to 30% of the protein-coding genes in the human genome. Differentially expressed (DE) miRNAs that modulate a large number of mRNA transcripts ultimately have a greater influence in determining biological outcomes, a concept we term 'miRNA network centrality'. Here we describe the development of a tool, 'miRmapper' which identifies the most dominant miRNAs and modulated mRNAs in a miRNA-mRNA network and recognizes similarities between miRNAs based on commonly regulated mRNAs. Using a list of miRNA-Target gene interactions and a list of DE transcripts, miRmapper provides several outputs: 1) an adjacency matrix that is used to calculate miRNA similarity utilizing the Jaccard distance 2) a dendrogram 3) an identity heatmap displaying miRNA clusters based on their effect on mRNA expression 4) a microRNA impact table and 5) a barplot that prssovides a visual illustration of this impact. We tested this tool using non-metastatic and metastatic bladder cancer cell lines and demonstrated that the most relevant miRNAs in a cellular context are not necessarily those with the greatest fold change. Additionally, by exploiting the Jaccard distance, we unraveled novel cooperative interactions between miRNAs from independent families in regulating common target mRNAs: i.e. 5 of the top 10 most influential miRNAs regulate the same biological pathway. The utility of 'miRmapper' was further examined using adult zebrafish as a systems toxicology model, where exposure to the endocrine disruptor (ED) bisphenol A (BPA), impacted the miRNOme and established an epigenome more susceptible to cancer development.

#### Biography

Gary Hardiman is currently the Scientific Director at the Center for Genomics Medicine Bioinformatics of MUSC (Medical University of South Carolina, USA) He is also the Head of Hollings Marine Laboratory, USA. He is an Adjunct Professor and Visiting Scholar, Grice Marine Laboratory, College of Charleston, SC, USA. He is an Editorial Board Member for the journals *Pharmacogenomics, Expert Review of Molecular Diagnostics, Genes* and *High-Throughput*. His research encompasses three areas: gene environment interactions, cystic fibrosis trans-membrane (CFTR) gene modifiers and systems biology tool development for big data analysis.

ghardimanwork@gmail.com

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