SPACE LIFE SCIENCES SYMPOSIUM (A1)
Fundamental Gravitational Biology (7)

Author: Prof. Alena Shmygelska
National Aeronautics and Space Administration (NASA), Ames Research Center, United States,
alenas@andrew.cmu.edu

COMPUTATIONAL META-ANALYSIS OF DIFFERENTIAL GENE EXPRESSION IN SPACEFLIGHT AND SIMULATED MICROGRAVITY CONDITIONS.

Abstract

To understand the essential features of biological regulatory pathways acting under the conditions of spaceflight and simulated microgravity, we designed and implemented computational framework for systematic meta-analysis of microarray datasets pooled from a number of related studies. Analysis was performed across multiple organisms and tissues including human, mouse, yeast, and worm.

The power of meta-analysis profiling using cDNA or DNA microarrays has been demonstrated by several group in the literature for a number of biological conditions including diseases and aging. To improve understanding of differentially expressed and co-expressed genes in microgravity conditions, we developed a computational method, comparative meta-profiling relying on Bayesian Networks reconstruction, which identifies and assesses the intersection of multiple gene expression signatures from a diverse collection of microarray data sets.

We collected and analyzed 8 published microgravity data sets, comprising skeletal muscle and bone tissues of a mouse and T cells of a human, independently whole genome profiling of yeast and worm was assessed. From this, we characterized common transcriptional profiles that are universally activated in multiple biological organisms and/or tissue samples under the microgravity relative to the control conditions, our results revealed common apoptosis and other cell-regulatory pathways. The significance of the detection was assessed by a non-parametric permutation test, including calculation of P-values and false discovery rates. Multiple visualization plots are provided to view common regulatory modules in microgravity conditions.