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CORRELATION ANALYSIS AS PART OF A NOVEL BIOMARKER ANALYSIS SYSTEM FOR
ASTRONAUT HEALTH IN SPACE**Abstract**

Spaceflight is known to have severe effects on almost every single system of the human body. Issues arising in every system, from the skeletomuscular system, to the circulatory system, to stress factors, can play huge roles in disrupting astronaut health and are a danger to establishing long-term human presence in space for the foreseeable future. Although the monitoring and treatment methods currently implemented are partially effective, there is currently no comprehensive method of diagnosing, monitoring, and treating spaceflight-based illnesses. This study uses a novel method we have developed, known as gene-pair correlation analysis, to analyze data from multiple studies in the NASA GeneLab open science repository. We explore the viability of combining multiple gene expression datasets, including DNA- and RNA-level expression analyses to provide an overarching view of genome correlation alterations in astronauts. Combining data from multiple astronauts, from multiple studies and multiple time points allows us to identify specific fundamental features of spaceflight that are common to all these different studies instead of mischaracterizing biomarkers and features that are only specific to individual studies. This study also integrates correlation analysis into a genome-level data analytics pipeline in conjunction with modern methods like differential gene expression, network interconnectivity analysis, and functional pathway analysis, to identify a shortlist of genes that we believe are likely to play controlling roles in the physiological effects experienced by astronauts in spaceflight. The importance of gene-pair correlation breakdown in many important biological pathways is discussed, in addition to their clinical importance in space medicine. We also explore the viability of using these genes as biomarkers to monitor astronaut health, as well as the possible drug interactions and treatment methods that could be utilized when using these drugs as a basis for gene therapies. This study proposes a novel, scalable method that uses multiple fundamental analyses to classify and identify priority targets for astronaut health monitoring and as candidates for gene therapy.