Microbial Optical Data Processing: A Key Step in the Metabolic Assessment of Lunar Explorer Instrument for space biology Applications (LEIA) and BioSentinel's Payload Data

Chinmayee Govinda Raj[1,3], Natalie Ball[2,3], Jessica Chau[2,3], Diana Gentry[3], Rachel Gilbert[2,3], Lauren Liddell[3,4] Mark Settles[3], Sergio R. Santa Maria[3]

[1]Blue Marble Space Institute for Science, [2]KBR Inc., [3]NASA Ames Research Center, [4]Logyx LLC

The BioSensor payload platform on BioSentinel and LEIA autonomously collects optical data from microbial model organisms in liquid culture [1]. The BioSensor is designed to monitor metabolic activity using absorbance measurements of cell density and alamarBlue [2], a readily available colorimetric redox indicator dye.

BioSentinel, a pioneering NASA CubeSat, uses yeast to study deep space radiation [3]. LEIA investigates radiation and lunar gravity response. The experimental setup includes 16 wells equipped with three LEDs (570, 630, and 850 nm) and their corresponding photodetectors. One well is a calibration control without biology while the rest have desiccated cultures. Autonomous rehydration initiates the experiment. Data from the BioSensor are received from the flight and ground units, enabling comparison to uncover location-based metabolic rate variations.

This study presents a Python Jupyter notebook developed for efficient data processing of multiple CSV files containing date and time columns, temperature, and well illumination data. It offers a user-friendly interface while maintaining computational power, automatically recognizing and iteratively processing data files in a user-input path. A Hampel filter with a short window eliminates outlier artifacts from sensor dropout. Because absorbance is a relative measurement, conversion from raw illumination requires defining a "blank" value, so the first data points are averaged to provide the necessary denominator. A cube-root function correction mitigates undesired drift caused by air pockets during the fluidic card filling phase, maintaining optical path length consistency. Beer-Lambert's law is applied to further convert absorbance values to cell and dye form concentrations, the desired science parameters. The processed data are saved and visualized as SVG plots.

Future plans include extracting specific science parameters from the processed data like growth rate and metabolic rate, and identification of features corresponding to metabolic and phenotypic shifts such as starvation, shifts from aerobic to anaerobic growth, and osmotic stresses.

References:

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