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AN INSTRUMENT BASED SOLUTION FOR FORWARD CONTAMINATION

Abstract

As increasingly complex space instruments are designed and developed for measuring biological and chemical processes, forward contamination will continue to grow as a concern for planetary science. High value results, such as a positive detection of extant life, will face intense scrutiny and debate as to whether the detection was a false positive, even with extensively cleaned instruments. Data from previous rover and lander assemblies have shown that completely ridding a system of all organics is not feasible, and will become more difficult as instruments use biochemical reagents components that cannot withstand a bake-out procedure. As such, in addition to preventing forward contamination, we propose detecting contamination through instrumentation. The Search for Extra-Terrestrial Genomes (SETG) project is currently developing an instrument to search for life on other worlds through nucleic acids. A benefit to nucleic acids as a biomarker is that they allow for the detection of life and for comparison to known Earth organisms. By mapping DNA from a potential extant organism onto a phylogenetic tree, it is possible to measure how different the detected lifeform is from other life, and thus estimate the likelihood that the detection was due to contamination. Initial data indicates that modern low-mass, low-power sequencing technology such as the Oxford Nanopore MinION can differentiate between closely genetically related organisms. Such technology can be adapted to a spacecraft instrument, as shown through a proposed architecture for a Mars life detection mission. Further work is being done to refine the accuracy of the MinION, as well as gauge the value of the proposed SETG instrument in relation to other instruments that search for other biomarkers. Irrespective of choice of biosignature, forward contamination will play a large role in the planning of a mission, the design of an instrument, and the scrutiny that any potential results will face; selecting and developing systems that can account for it will be a key factor in future astrobiology endeavors.