

The microbial Antarctic Resource System: integrating discoverability and preservation of environmental annotated microbial -omics data.

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Microbial organisms, including Archaea, Bacteria and unicellular Eukaryota, collectively dominate the Earth in terms of bio- and functional diversity. Their study, often constrained by technology, has strongly benefited from the recent advancements in high throughput DNA sequencing techniques. The vast amounts of microbial data generated in the wake of these developments, however, remains severely underrepresented on open access biodiversity data repositories (e.g. GBIF). Moreover, when sequencing data has been made publicly available, is often poorly annotated with metadata and environmental variables, making it difficult to find or query. Therefore, the microbial Antarctic Resource System (mARS) aims to fill this lacuna by documenting and geo-referencing (Antarctic) microbial datasets, and linking the sequence data on INSDC repositories with associated environmental measurements. This way, mARS helps to preserve data, connect researchers to the existing wealth of molecular information, and allow these datasets to be more effectively mined. Given the general complexity of microbial ecological datasets, mARS needs to operate between different data archiving standards, such as MIXS, which is oriented towards DNA sequence data, and the biodiversity based DarwinCore standard. Integrating microbial data with these existing systems, as well as connecting with communities behind them has been a major challenge in the continued development of mARS.

Oral preference