

# Extreme metagenomics using nanopore sequencing: a field report from Svalbard, 78° N.

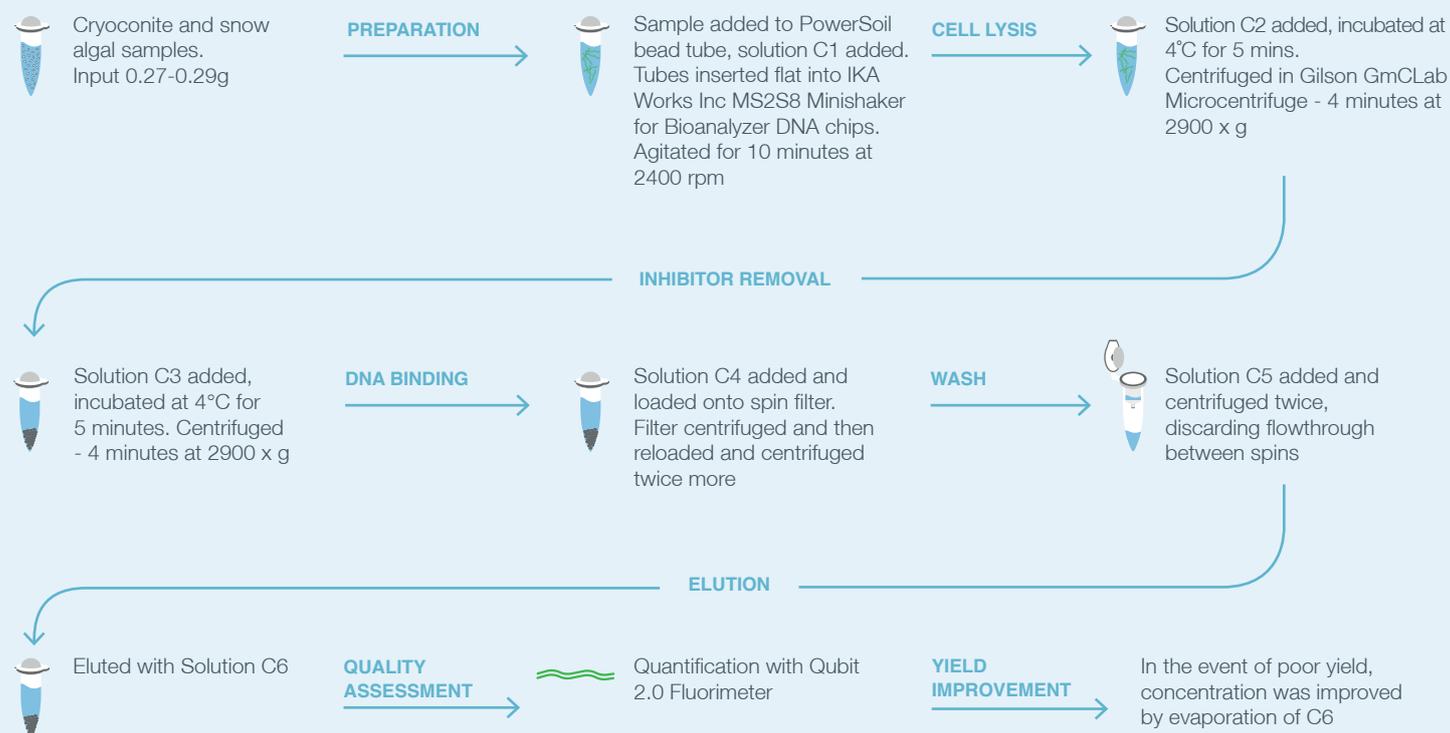
Logistical arrangements in extreme environments present a considerable challenge to field investigations. Edwards *et. al* explored the feasibility of offline analyses of metagenome profiles in order to characterise the microbiota of a High Arctic glacier.

A highly portable field lab was successfully used to provide insights into microbial community composition using suboptimal datasets without access to cloud-based bioinformatics resources. This would ultimately allow more in-depth examination of these communities to better understand their role in sensing and amplifying environmental change impacts in the Arctic.

## Sample preparation

Extraction performed as PowerSoil DNA Isolation Kit protocol, with some amendments.

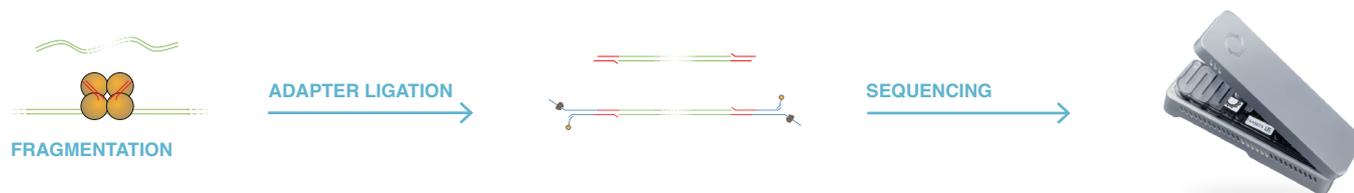
Sample preparation  
~ 75 minutes



## Library preparation

As per Rapid Sequencing of genomic DNA for the MinION device using SQK-RAD001

Library preparation  
~ 10 minutes



200 ng high molecular weight DNA in 7.5 µl transposase fragmentation. PowerSoil routinely produces DNA fragments of 20-25 kb.

Edwards *et. al*, 2016, Extreme metagenomics using nanopore sequencing: a field report from Svalbard, 78°N, BioRxiv, <https://doi.org/10.1101/073965>

ANALYSIS