

School of Biotechnology and Biomolecular Sciences

Phylogenomics of a radioactive legacy site reveals new Archaea phyla of unknown function

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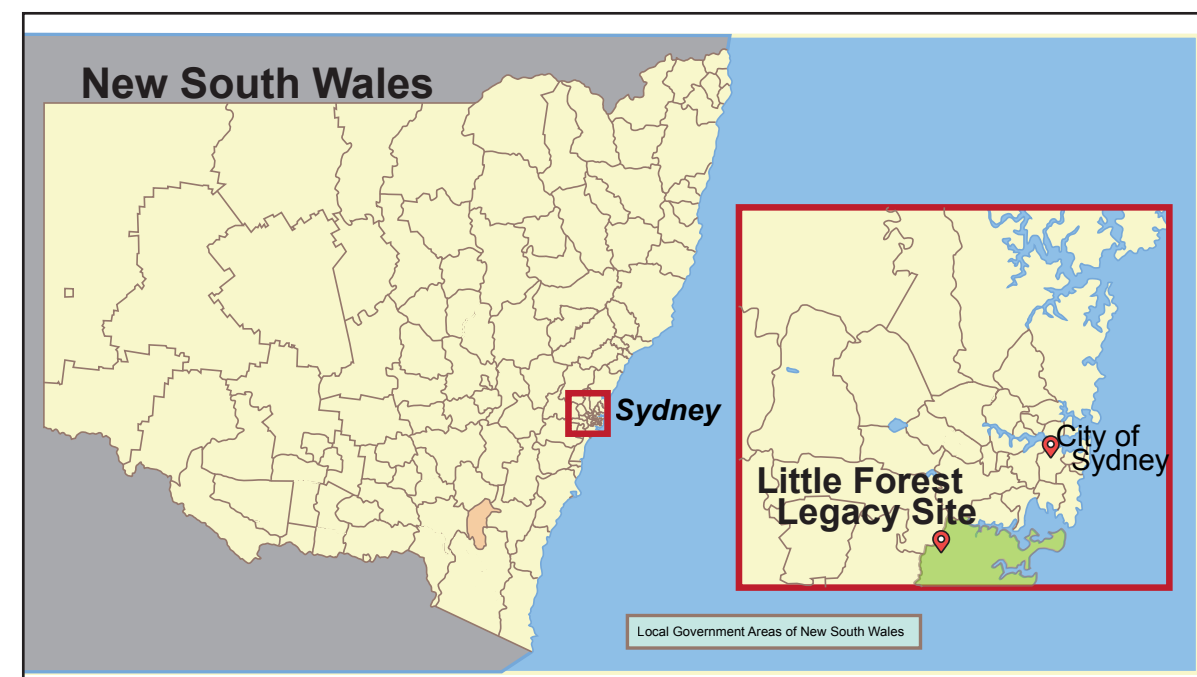
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Introduction

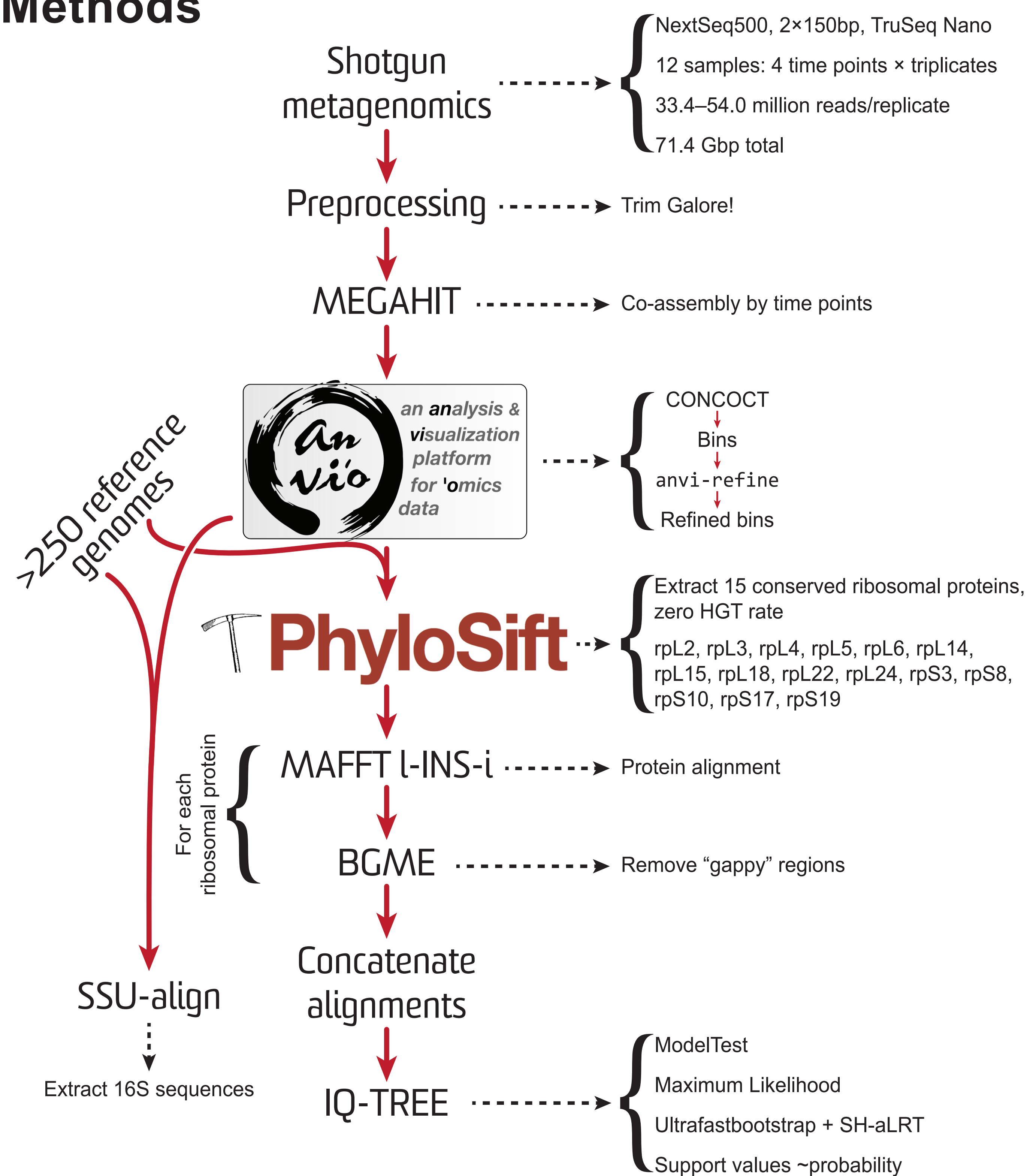
- Mixed radiochemical (inc. ²³⁹⁺²⁴⁰Pu and ²⁴¹Am) and organic/contaminated waste (steel drums, lab equipment, paper, etc.) was disposed of in shallow (3 m deep) trenches from 1960–1968
- Previous research investigate functional and population dynamics during a rainfall event using shotgun metagenomics. This revealed a broad abundance of candidate and potentially undescribed taxa [1].



Objectives

Explore potential new high-rank taxa with genome-based metagenomics focusing in Archaea.

Methods



References

[1] Vázquez-Campos X, Kinsela AS, Bligh MW, Harrison JJ, Payne TE, Waite TD. (2017). Response of microbial community function to fluctuating geochemical conditions within a legacy radioactive waste trench environment. *Appl Env Microbiol* [Accepted]. Preprint at bioRxiv 121376.

Results

318 genomes total with ≥50% completeness / ≤10% redundancy

