Improving access to ancient metagenomic data with the community-curated Ancient

metadata repository

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Finding relevant sequencing data is not trivial

Public data is useful for:

- comparative data generation
- meta-analysis variables
- public data reanalysis
- field development tracking

But can be hard to find

incomplete metadata (missing fields)

Metagenome

- inconsistently reported metadata (lat:lon vs. site name; cal vs uncal 14C)
- data in different archives (ENA; Institute FTP)
- stored in papers, not with data itself

Simplify with community curated sample lists

AncientMetagenomeDir is: Release v20.09 stats: Ancient metagenomic sample lists (TSV file) of Publications: 87 basic but essential and consistent metadata Total Samples: 1024 Citation Ancient host microbiomes: 443 Geographic location: Ancient microbial genomes: 269 information: DOIs Controlled country list, Ancient sediment metagenome: 312 Lat:Lon Sample ages: Links to data: Sample type: rounded to archives, term ontologies last 100y accession IDs

Benefits for your research



Metadata easy to access and to update (simple spreadsheet format)



Standardised fields: rapid filtering to samples that you actually want



Takes you to the raw data (or back to original publication) Comprehensive: includes most of published samples of field



Regularly updated: quarterly releases

Ensuring quality metadata: template for other fields

Community

Field-wide consensus of definitions

Suggestions for other fields - use:

- Peer-review to check for accuracy Wider 'net' for literature screening



Collaboration

- Use collaborative tools (github, slack) Online platforms allows communication
- across time-zones (inclusivity)



Automation

- Metadata field specification checks Long-term release archiving



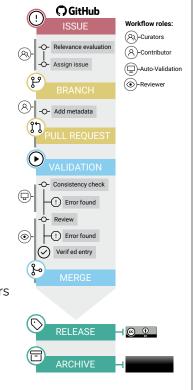
Accessibility

- Write documentation for new contributors Offer training workshops for new
- concepts and skills (e.g. github)



Integration Utilise existing resources for linked

data (term ontologies, data archives)





aDNA metadata reporting needs improving **Future directions**

Expand to library-level



metadata Make project infrastructure



Develop standardised aDNA-wide metadata reporting sheet?

Want to get involved? Join the SPAAM community!

https://spaam-community.github.io/



template for use by other fields

Avaliable at: https://github.com/SPAAM-community/AncientMetagenomeDir

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