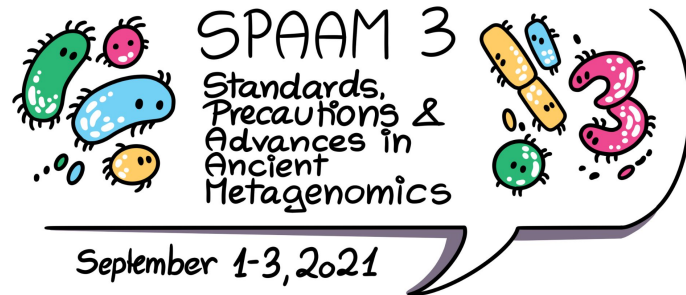


Standards,  
Precautions &  
Advances in  
Ancient  
Metagenomics



September 1-3, 2021

## Session 4: Tool up or die - gaps and solutions in ancient metagenomics analysis

Aida Andrades Valtueña | 3rd September, 2021 | SPAAM3



# Session 4 Agenda



## 4 Speakers

**Irina Velsko**

MPI EVA

**Maxime Borry**

MPI EVA

**James Fellows Yates**

MPI EVA

**Frederic Lemoine**

Institut Pasteur

## Discussion

A joint discussion with the presenters. All attendees can ask questions and participate in this discussion of key topics presented in this session.



## Break

Session 4 will begin at:

7:10 Pacific Time

16:10 Central European Summer  
Time



# Objectives for this Session

01

Hear about tools  
developed by SPAAM3  
members

02

Discuss which tools we  
will like to have to work  
in ancient  
metagenomics

03

Create a trusting  
environment where we  
can discuss new tools  
ideas (maybe establish  
collaborations??!)



# Potential topics to discuss

- Do certain taxonomic identifiers work best with certain substrates/sample types, i.e. dental calculus vs coprolites vs sediments?
- When characterizing an ancient oral microbiome with shotgun data is it good practice to use more than one taxonomic identifier tool? How do you synthesize or reconcile those results?
- Is it safe to say with metagenomic screening that more is not always better concerning reference genomes in the database? Or would it be ideal to have as many genomes as possible but we are adapting databases to computational resources?
- With AMPHY is there any option for calculating SNV site coverage and selecting for the optimal partial deletion of the SNV Alignment to remove ambiguous sites in genomes included in the alignment?
- How is everyone making snp alignments these days?

