

SPAAMTisch meetings topics rota:

1. Add a topic if you have an idea (can be anything from very little details to a paper to a discussion on a paper on in SPAAM)
2. Cross out already discussed topics

- ☒ ~~What SPAAMTisch should be for you~~
- ☒ ~~Taxonomic classifiers: e.g. KrakenUniq (can be others too)~~
- ☒ ~~How to deal with taxonomic tables~~
- ☒ ~~How to deal with taxonomic tables and ASVs tables, comparing between each other~~
- ☐ Adapter Removal for metagenomic classification
- ☒ ~~mSourceTracker and other metagenomic composition and QC tools~~
- ☒ ~~Decontamination/ authentication of aDNA~~
- ☒ ~~SNP evaluation~~
- ☐ Ethics of our work
- ☐ Dealing with challenges associated with this work (e.g. lots of things don't lead to enough data to draw conclusions, prioritisation of funds/energy?) aka PhD vent time
- ☐ Non-scientific topics just regular socializing
- ☒ ~~Phylogenetic trees~~
- ☐ molecular clocks
- ☐ BEAST
- ☒ ~~Functional analyses on pathogens or microbial communities~~
- ☒ ~~metagenomics assembly~~
- ☐ filtering out contaminants and keeping real species in the OTU tables
- ☐ statistical tests to validate your results on biological questions
- ☐ Kmer matching vs Mapping methods: who wins?
- ☐ databases!
- ☐ This paper specifically: [Reynoso-García et al.](#) (maybe we can contact the author to present?)