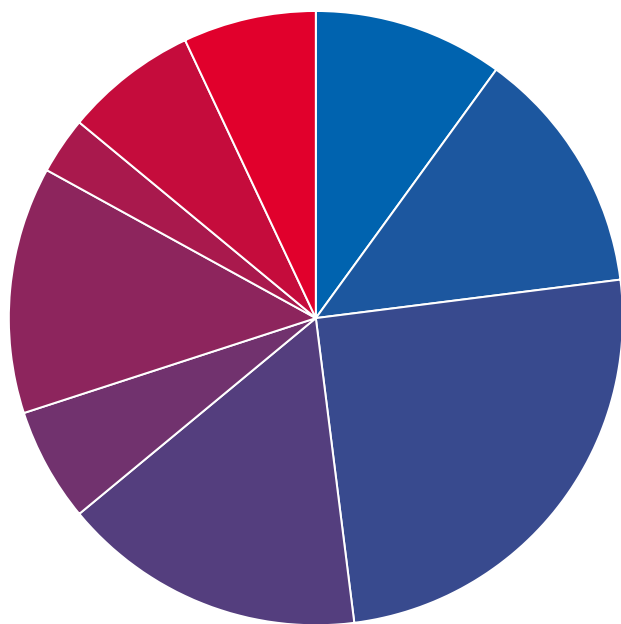


Which of the following do you consider the biggest gap in the toolset of MGM?



- Scalable phylogenetic analysis (large phylogenetic trees): **10%**
- Comparative phylogenetics (tree comparisons): **13%**
- Comparative (functional) metagenomics - analyze your sample in the context of many other samples and finding publications with similar profiles: **25%**
- Tools to infer phenotypes from genomic samples (e.g. predicting AMR, best growth medium for the given genotype or similar): **16%**
- Tools to infer observables from (functional) metagenomic samples (e.g. predicting the host health state, growth conditions of plants ...): **6%**
- Tools for building custom databases from private or public data: **13%**
- More elaborate visualizations, please specify: **3%**
- More dedicated reference databases, e.g. habitat specific taxonomic profiling databases or functional analysis databases: **7%**
- Other: **7%**

Source: TechValidate survey of 69 users of QIAGEN Digital Insights



TechValidate
by SurveyMonkey

✓ Validated

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