

Microbiome data science workflow in application to appendicitis

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"Our second genome" or "our last organ"

- Microbiome consists of microbes living on human
- Is associated with many diseases or disorders...
 - Inflammatory bowel disease and cancer
 - ADHD, autism, schizophrenia...
- ...and with health...
 - Health of gut and metabolism
 - Regulation of immune system...
- Research has been increased in recent years
- Interactions between human and microbiome are complex and they are not well-known

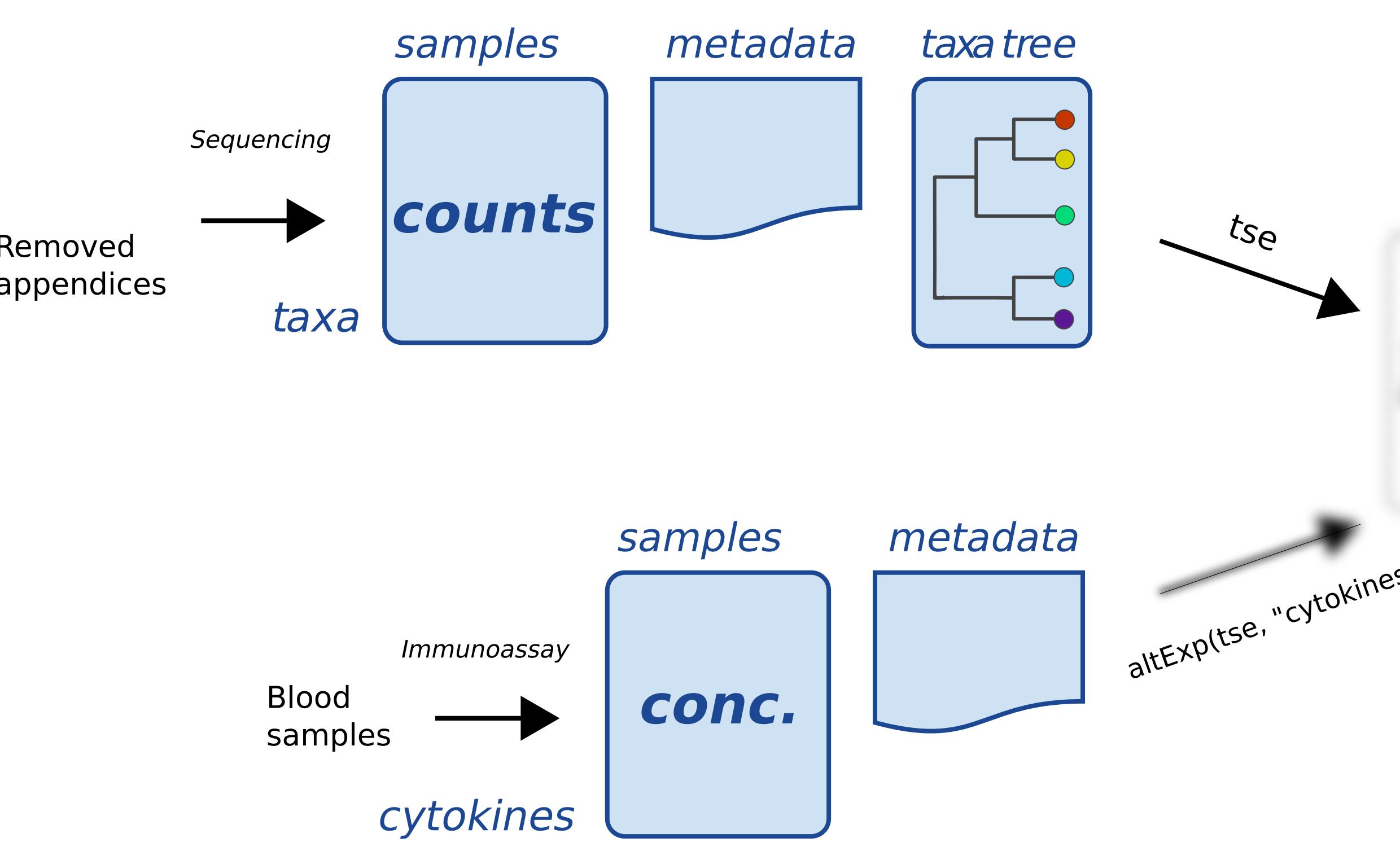
*Unpublished data

Workflow: TreeSummarizedExperiment & miaverse*

Import data

This workflow starts by importing bacterial abundance data and cytokine concentration data into the TreeSE data container.

RAW DATA



New microscope

- Microbiome research has been technology-driven
- The field is rapidly evolving as new methods become available
- **Sequencing and computational methods have an essential role**

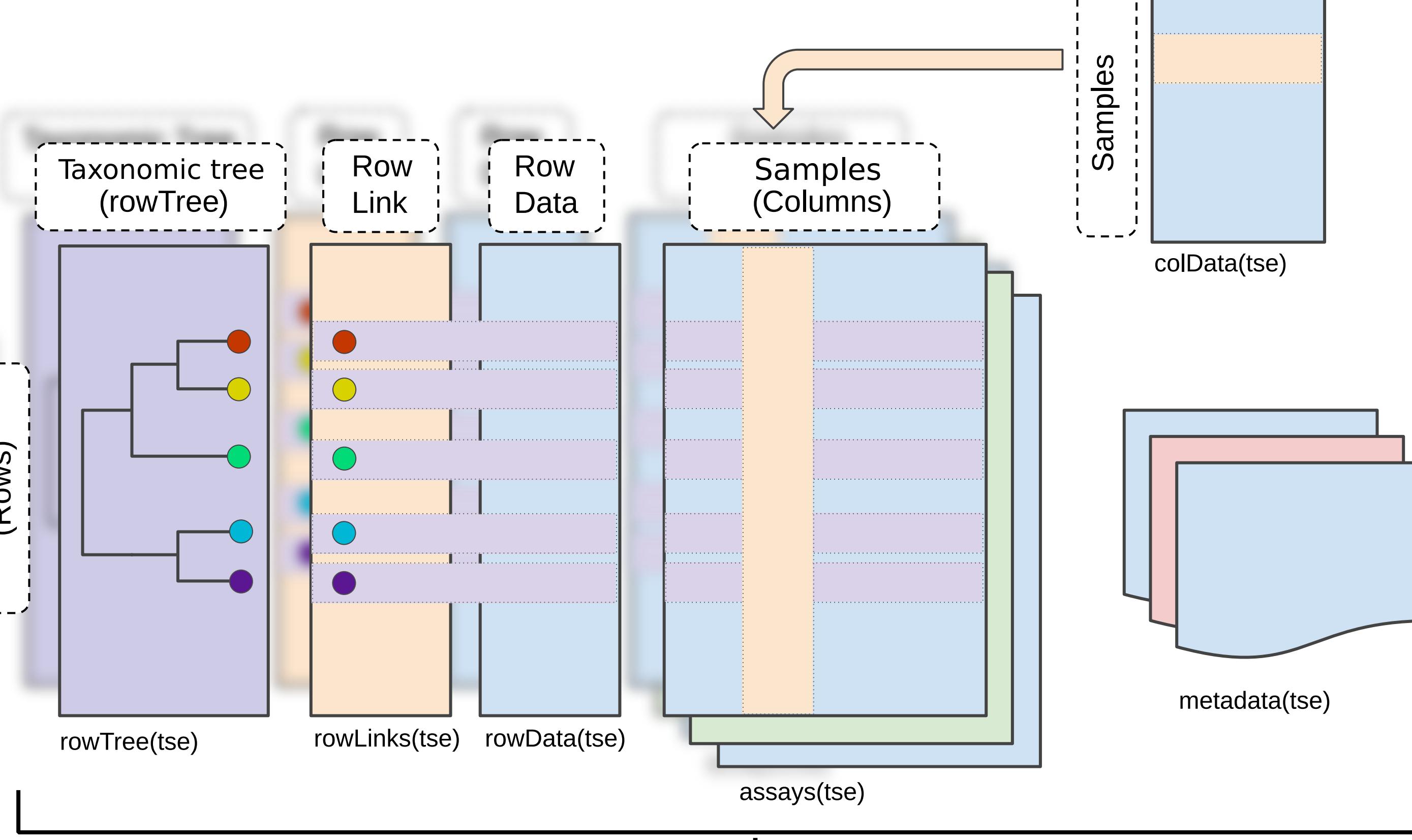
The purpose of this work

1. To develop efficient, reproducible and scalable workflow
2. To answer, if microbiome explains the severity of appendicitis

This work is part of the Microbiology APPAC (MAPPAC) trial
Vanhatalo S, Munukka E, Sippola S, Jalkanen S, Grönroos J, Marttila H, Eerola E, Hurme S, Hakaniemi AJ, Salminen P; APPAC collaborative study group. (2019) Prospective multicentre cohort trial on acute appendicitis and microbiota, aetiology and effects of antimicrobial treatment: study protocol for the MAPPAC (Microbiology APPendicitis ACute) *BMC Open Res* 9:e031137. doi: 10.1186/bmopen-2019-031137

The TreeSummarizedExperiment object

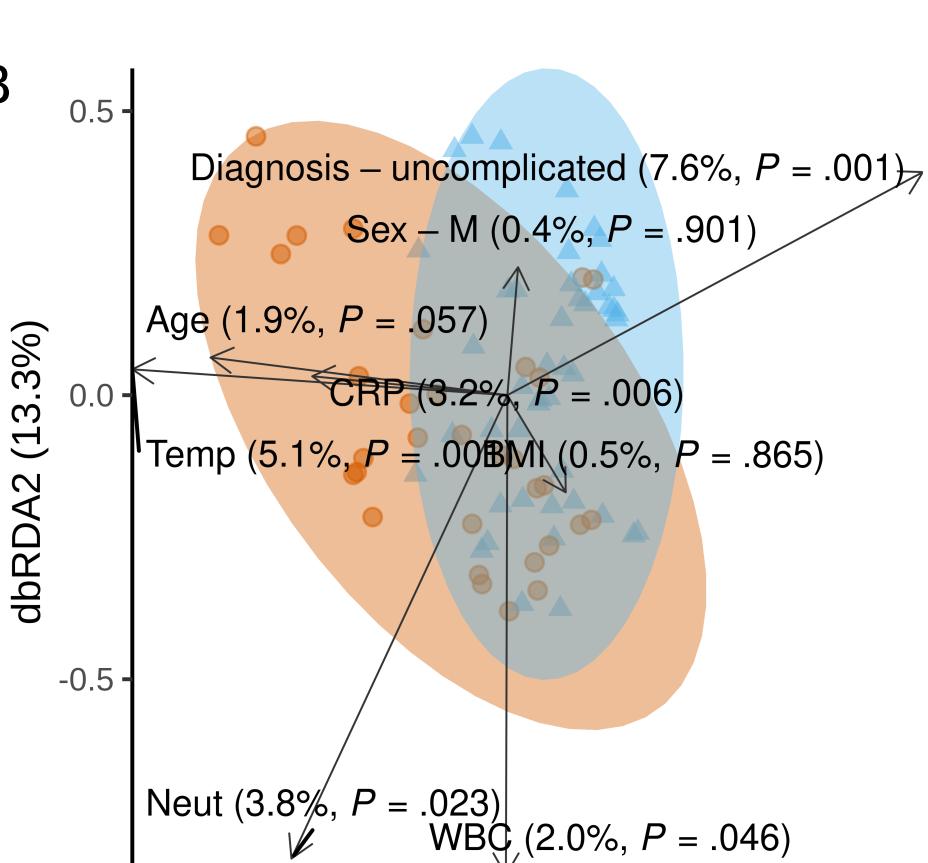
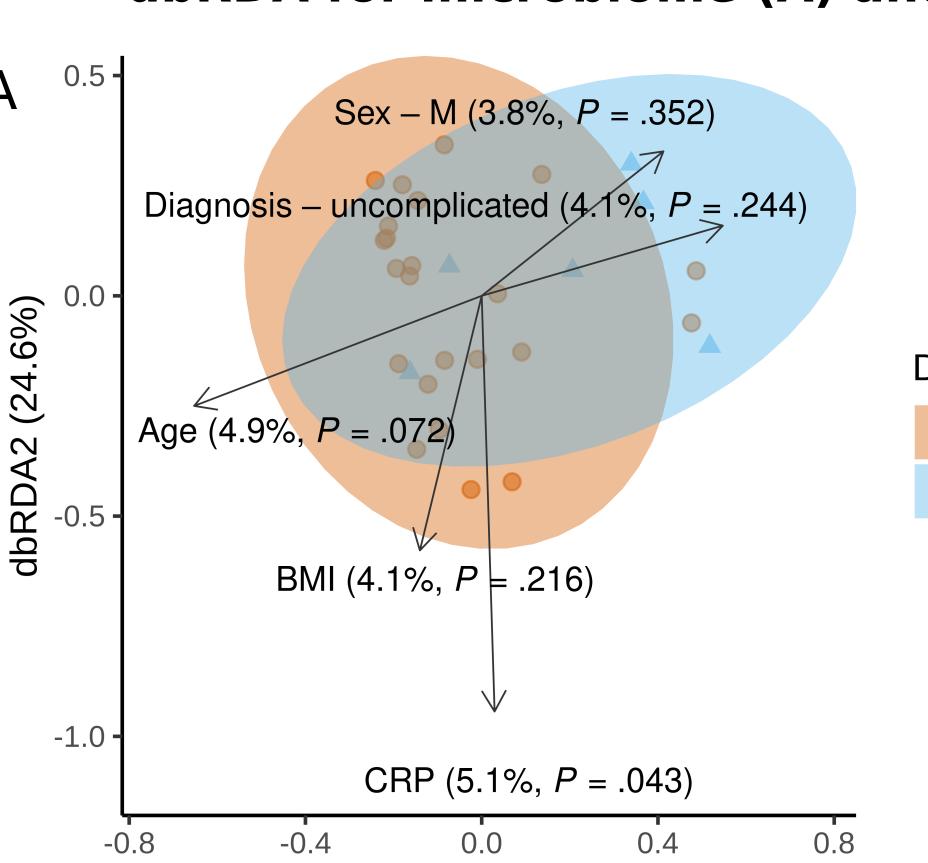
The TreeSE object is uniquely positioned to support optimized multi-assay data access, manipulation, and visualization.



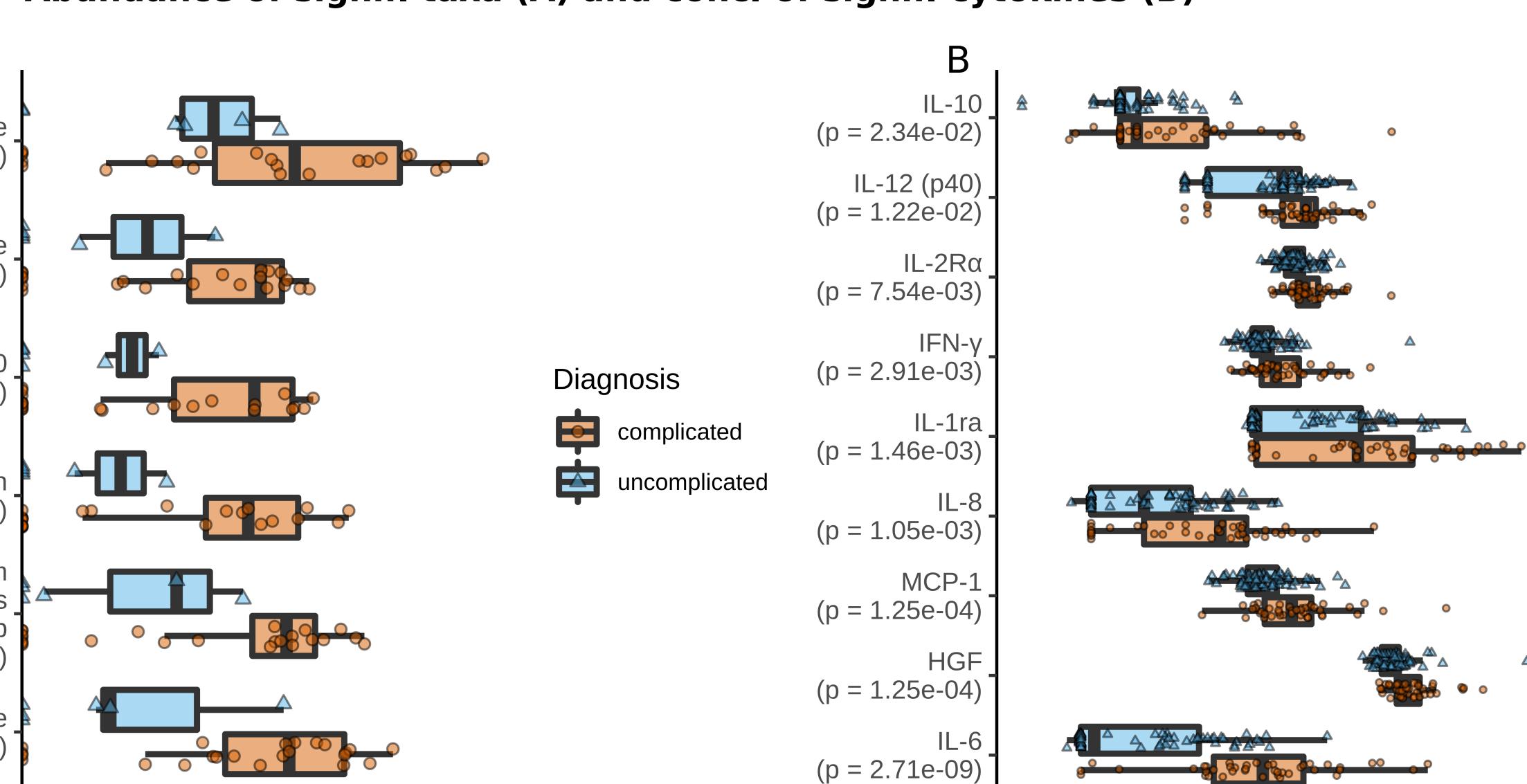
The miaverse pipeline

The miaverse framework contains tools designed for microbiome data analysis. It requires data in the TreeSE format.

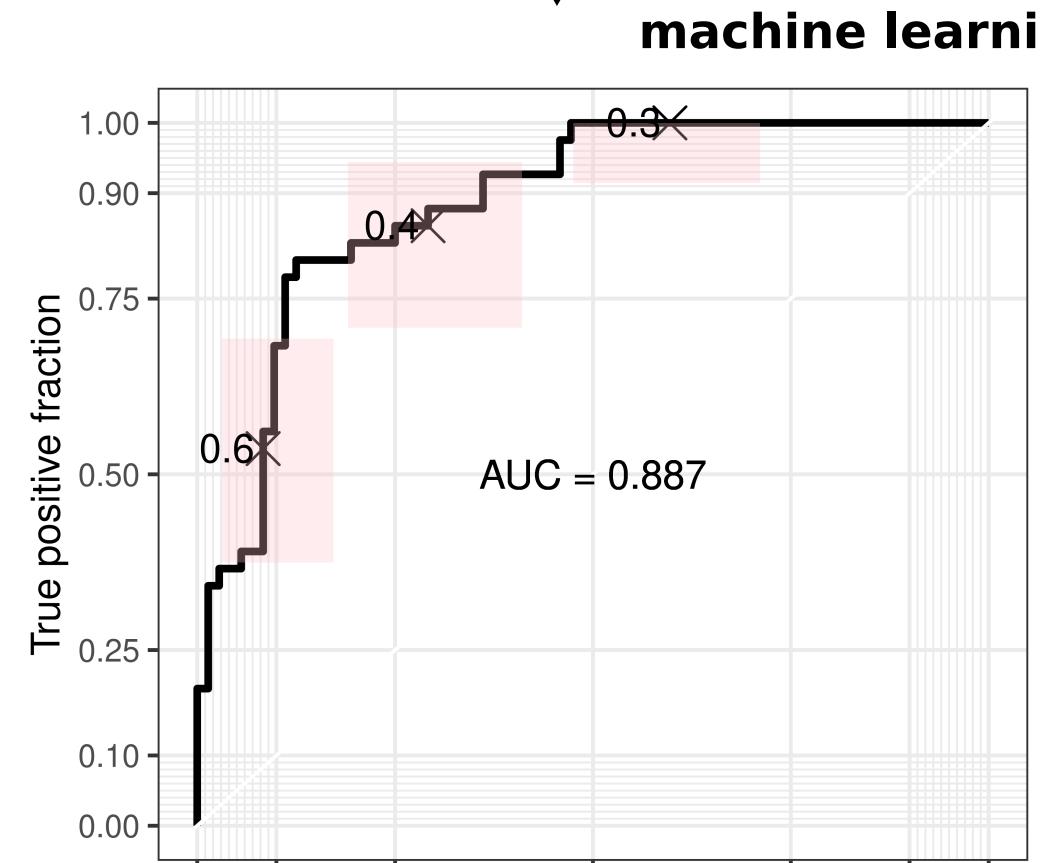
dbRDA for microbiome (A) and cytokine (B)^[1]



Abundance of signif. taxa (A) and conc. of signif. cytokines (B)^[2]



Prediction of appendicitis form based on cytokine profile using XGBoost machine learning algorithm^[4]



```
[1] mia::transformSamples(tse, ...)  
mia::runRDA(tse, ...)  
ggord::ggord(x, ...)  
[2] ancombc::ancombc(tse, ...)  
wilcox.test(x, ...)  
ggplot2::ggplot(x, ...) + geom_boxplot()  
[3] mia::agglomerateByRank(tse, rank = "family")  
mia::getExperimentCrossAssociation(tse, ...)  
complexHeatmap::Heatmap(x, ...)  
[4] caret::train(x, y, "xgbtree", ...)  
ggplot2::ggplot(x, ...) + geom_roc()
```

Conclusions

- Microbiome seems to affect to the severity of inflammation
- The form of appendicitis can be predicted based on cytokine profile
- More samples needed
- **Created workflow is reproducible and scalable**

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22.01.2020 NEWS

Pioneering Finnish Research Chosen in Top Ten of the Decade – Changes Treatment of Acute Appendicitis Worldwide

f chevron-down

Journal of the American Medical Association (JAMA) has chosen research from Finland as one of the ten articles that are most important to clinical medicine and public health published in the 2010s. The research shows that for most patients, antibiotics could replace surgical treatment when it comes to uncomplicated acute appendicitis. The research article is the only surgical treatment article from Finland to be chosen by the American Medical Association, has the world's widest circulation when it comes to weekly published peer-reviewed high-quality medical publications.

The APPendicitis ACuta (APPAC) trial
Salminen P, Paajanen H, Rautio T, et al. (2015) Antibiotic Therapy vs Appendectomy for Treatment of Uncomplicated Acute Appendicitis: The APPAC Randomized Clinical Trial. *JAMA*. 313:2340–2348. doi:10.1001/jama.2015.6154

More information on microbiome data science



<https://microbiome.github.io/>

Acknowledgements

Vanhatalo S, Munukka E, Sippola S, Jalkanen S, Grönroos J, Marttila H, Eerola E, Hurme S, Hakaniemi AJ, Salminen P; APPAC collaborative study group