MICROB-PREDICT

MICROBiome-based biomarkers to PREDICT decompensation of liver cirrhosis and treatment response

D4.9. Multi-omic data analysis software public release

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1. Executive Summary

MICROB-PREDICT aims to develop integration tools and machine learning approaches to investigate the role of microbiome in late-stage liver disease. Here, we have packaged the association and biomarker analysis workflows developed in WP4 into a software called **Multi-Omics for Relationships in Phenotypes and Health (MORPH)**, which is publicly available at https://github.com/arumugamlab/MORPH-multi-omics.

2. Deliverable report

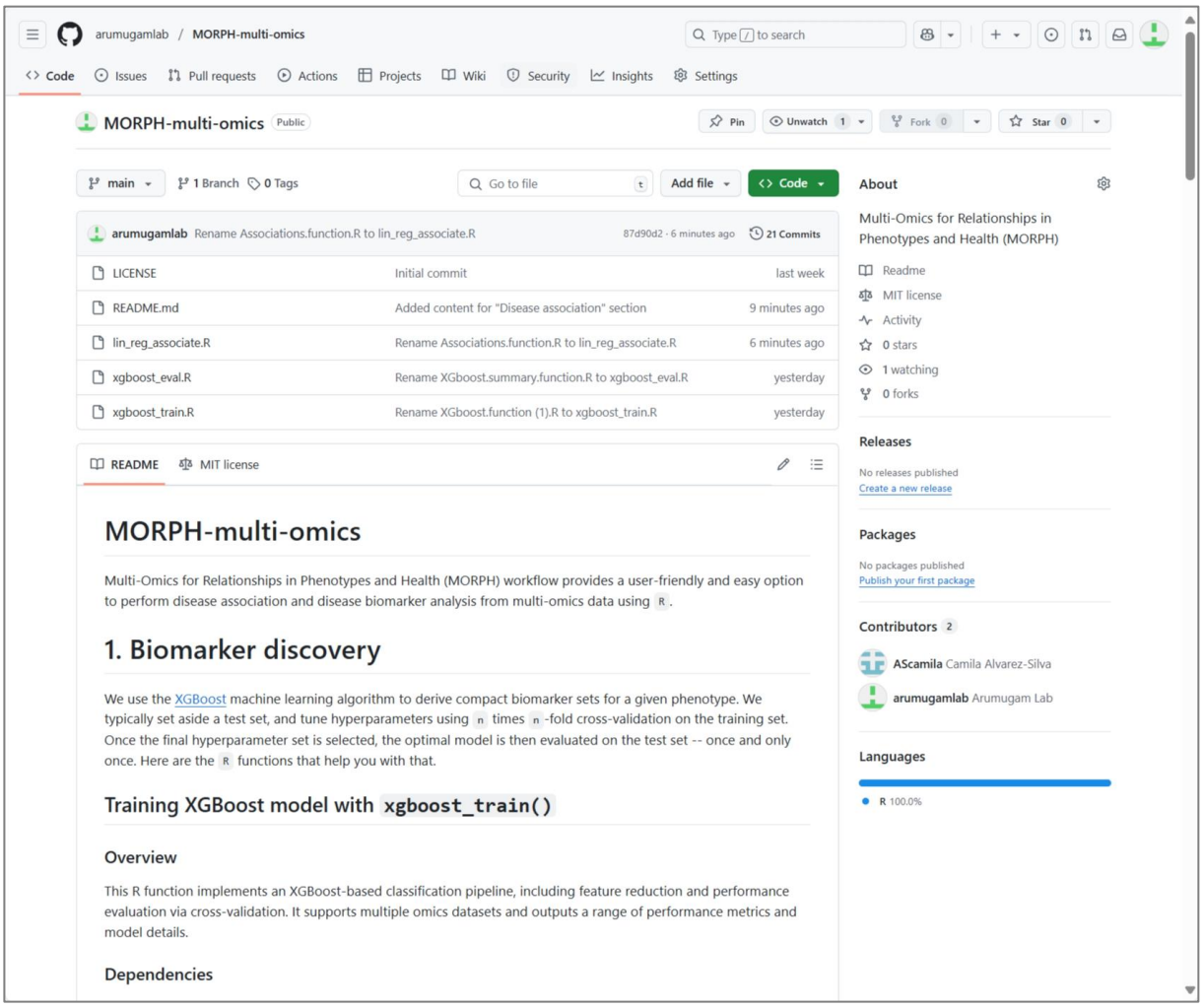


Figure 1. Screenshot of the GitHub repository website for MORPH.

A major objective of WP4 is the development of novel algorithms for multi-omics analysis and biomarker discovery ("**Objective 2: To develop novel algorithms for integrated host-microbial multi-omics analysis and biomarker discovery using systems medicine approaches**" and "**Task 2: Develop novel methods for integrating multi-organismal microbiome data**"). We have developed these algorithms during the last 6 years and implemented into a workflow. They have been and are being used to perform disease association analysis and biomarker discovery analysis in three objectives ("**Objective 4: To predict the development of decompensation and progression to ACLF and validate in silico**", "**Objective 5: To predict the response to Rifaximin treatment and validate them in silico**", and "**Objective 6: To predict the response to albumin treatment and validate them in**

silico") as well as two tasks ("**Task 5: Develop novel methods for integrating gut metatranscriptomic, host genetic, host-microbial metabolomic and proteomic data**" and "**Task 6: Discover, prioritize and validate novel biomarkers**").

After improvements during several iterations of using this workflow, we have bundled it into a GitHub repository as a software package that we named **Multi-Omics for Relationships in Phenotypes and Health (MORPH)**. This is available at https://github.com/arumugamlab/MORPH-multi-omics. We have added user instructions on how to apply this workflow on their own multi-omics datasets generated from the host-derived and microbiome-derived omics (see **Figure 1**).

3. Conclusion

With the fully functional software publicly released on GitHub with documentation, this deliverable is now complete.

4. Acknowledgement and Disclaimer

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