Predicting microbial growth to understand biological resilience

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Project Objectives

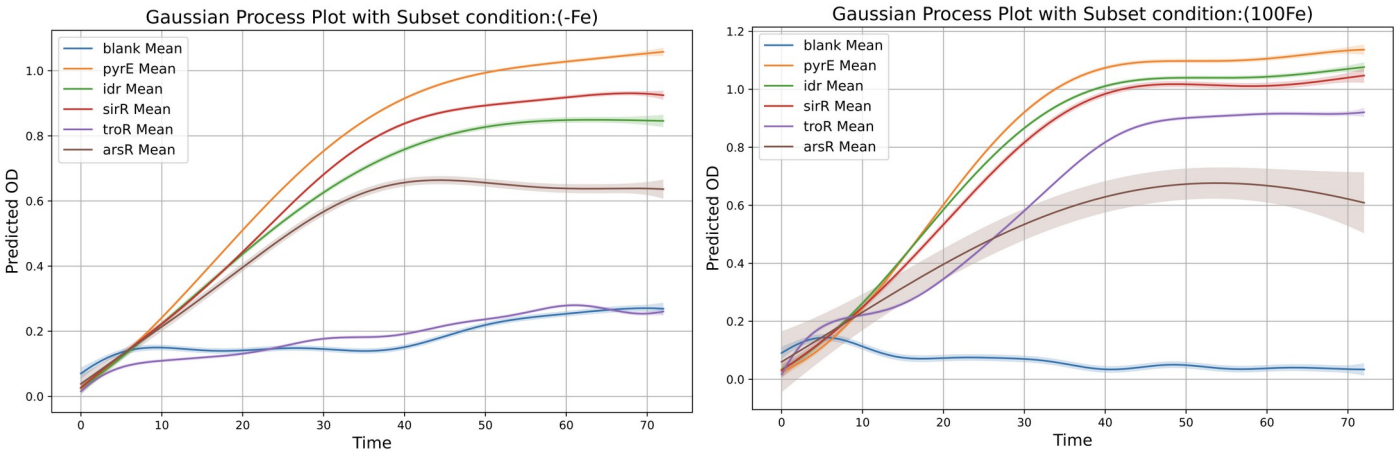
Our goal was to fix and improve MicroNet into a web application that makes advanced microbial growth analysis accessible. We leveraged Gaussian Process (GP) regression from the AMiGA Python package to provide a dynamic, non-parametric alternative to traditional rigid Sigmoid models. The platform allows researchers to easily upload data, fit growth curves, perform statistical comparisons, and generate publication-ready visualizations without needing coding expertise.

Current Progress

We have developed a stable version of MicroNet ready for deployment. Key achievements include implementing core features for plotting raw data, generating GP models and heatmaps, and comparing parameters. We have also successfully resolved critical challenges related to data handling and file processing.

Preliminary Results

A case study on Haloferax volcanii iron metabolism demonstrated MicroNet's effectiveness. The analysis confirmed that a TroR knockout strain performs poorly in low-iron conditions, validating the application's ability to detect significant growth differences and handle complex experimental designs.



Challenges

Development involved overcoming several technical obstacles, including migrating packages, resolving Docker issues, and ensuring robust handling of various data file formats and user uploads.

Next Steps

Deployment to Duke servers and public hosting. Further testing and refine the user interface. Future development will focus on expanding user configuration options, adding new analytical methods, and incorporating future users feedbacks.

Tools Used

MicroNet is built with a Ruby on Rails backend and integrates the AMiGA (Python) framework.

References

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