MicroNet: A Web App for Analyzing Microbial Growth with Gaussian Processes

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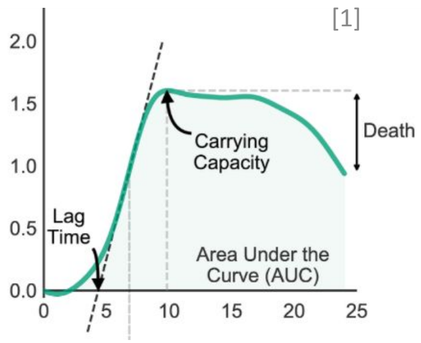
Background

Microbial growth is measured with optical density (OD): the more microbes present, the more light will be absorbed. These OD values are plotted across time to make **growth curves**, a representation of how microbial populations change over time. Traditionally, these curves have been modelled parametrically.

[1]



Traditional Models vs Gaussian Processes

Traditional sigmoidal functions rely on underlying assumptions about microbial growth that may not hold under stressed conditions [2].

Enter **Gaussian Process regression** (GP), a dynamic, nonparametric model that can fit complex patterns

[1]

$$\ln OD(t) \sim N(\mu(t), \Sigma) \qquad \sigma_{ij} = k(t_i, t_j)$$

$$k(t_i, t_j) = \sigma_{RBF}^2 exp\left(-\frac{(t_i - t_j)^2}{2l^2}\right) + \sigma_{noise}^2 \cdot \delta_{i=j}$$

Advantages	Limitations
No underlying assumptions	Computational complexity
Uncertainty estimates	Kernel selection

AMiGA and MicroNet

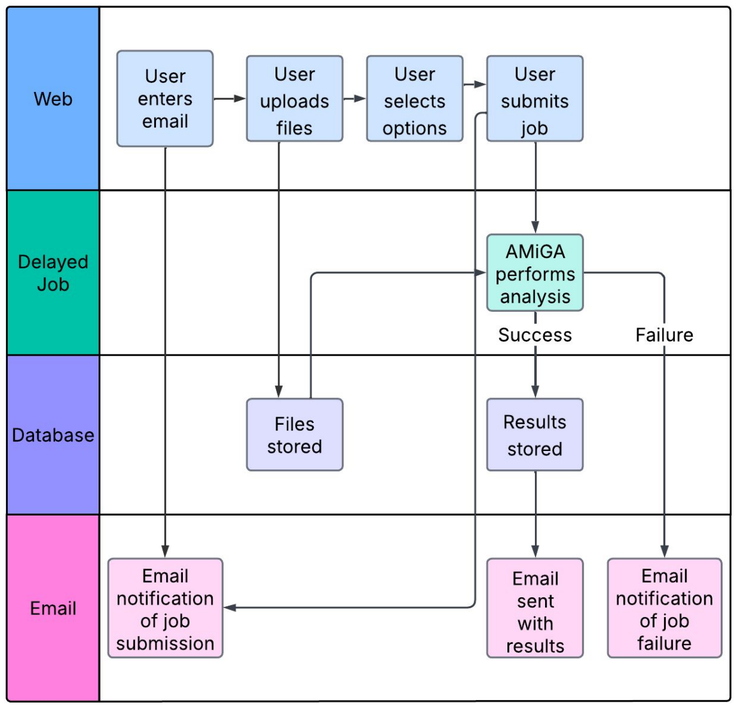
- **AMiGA:** Python package developed by Midani et al.
  - Models microbial growth data using GP methods.
- **MicroNet:** Web App built on top of AMiGA
  - More accessible to researchers w/o coding knowledge and experience

Further Studies

- Additional testing and debugging of features and interface
- Giving users additional configuration options
- Deploying application to Duke servers and online hosting

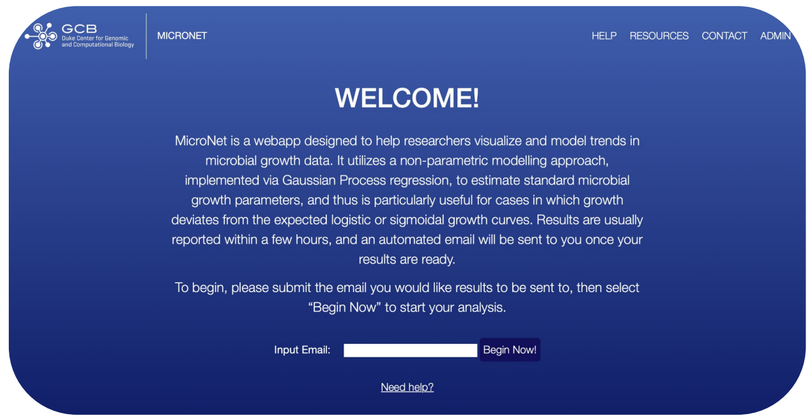
Methods, Results, and Discussion

How does MicroNet Work?

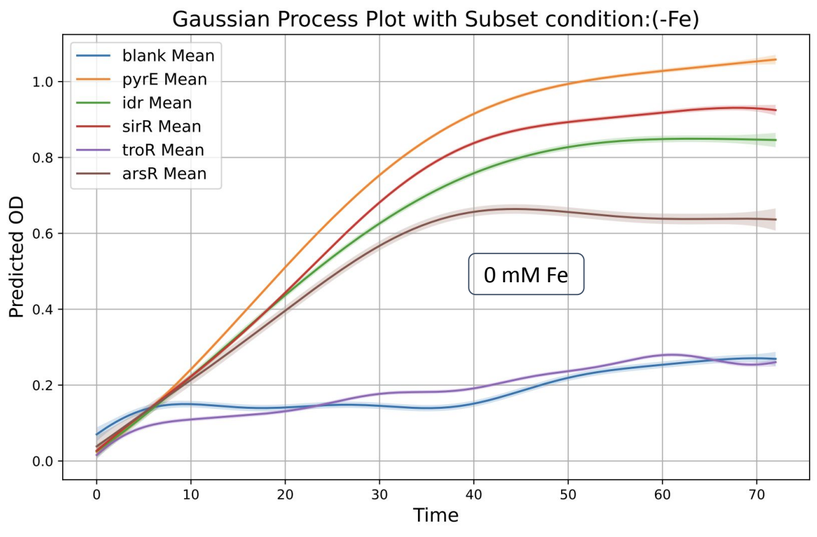


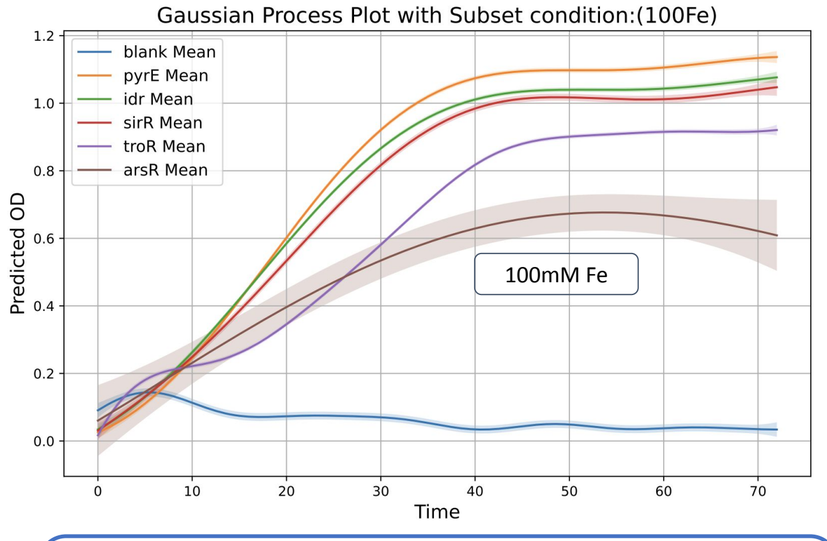
MicroNet features:

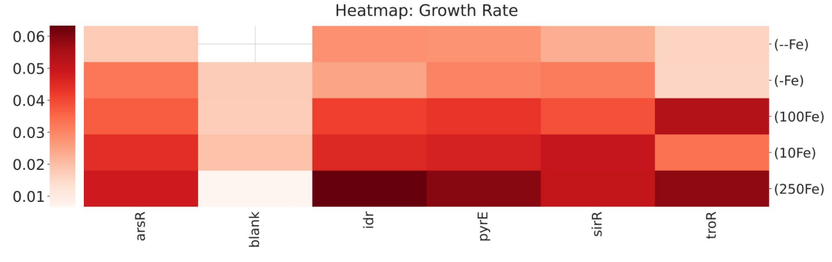
- Plot raw growth data by well
- Fit growth curves as GP models and generate growth parameters
- Test for significant differences between curves and parameters
- Generate visualizations for analysis



A Case Study into the Iron Metabolism of Archaea *H. volcanii*







- Evaluation of *H. volcanii* wild-type (WT) and KO mutant strains growth in different iron levels [3]
- **Our analysis with MicroNet shows that the TroR knockout strain performs poorly in low iron,** indicating the importance of the TroR gene as a homeostatic regulator of iron metabolism

References

1. Midani, F. S., Collins, J., & Britton, R. A. (2021). AMiGA: Software for Automated Analysis of Microbial Growth Assays. mSystems, 6(4), e0050821. https://doi.org/10.1128/mSystems.00508-21
2. Tonner, P. D., Darnell, C. L., Engelhardt, B. E., & Schmid, A. K. (2017). Detecting differential growth of microbial populations with Gaussian process regression. Genome research, 27(2), 320–333. https://doi.org/10.1101/gr.210286.116
3. Martinez Pastor, M., Sakrikar, S., Hwang, S., Hackley, R. K., Soborowski, A. L., Maupin-Furlow, J. A., & Schmid, A. K. (2024). TroR is the primary regulator of the iron homeostasis transcription network in the halophilic archaeon Haloferax volcanii. Nucleic acids research, 52(1), 125–140. https://doi.org/10.1093/nar/gkad997

Acknowledgements

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