

# Bayesian optimization techniques to discover the optimal microbiome signatures for reducing Salmonella multi-drug resistance

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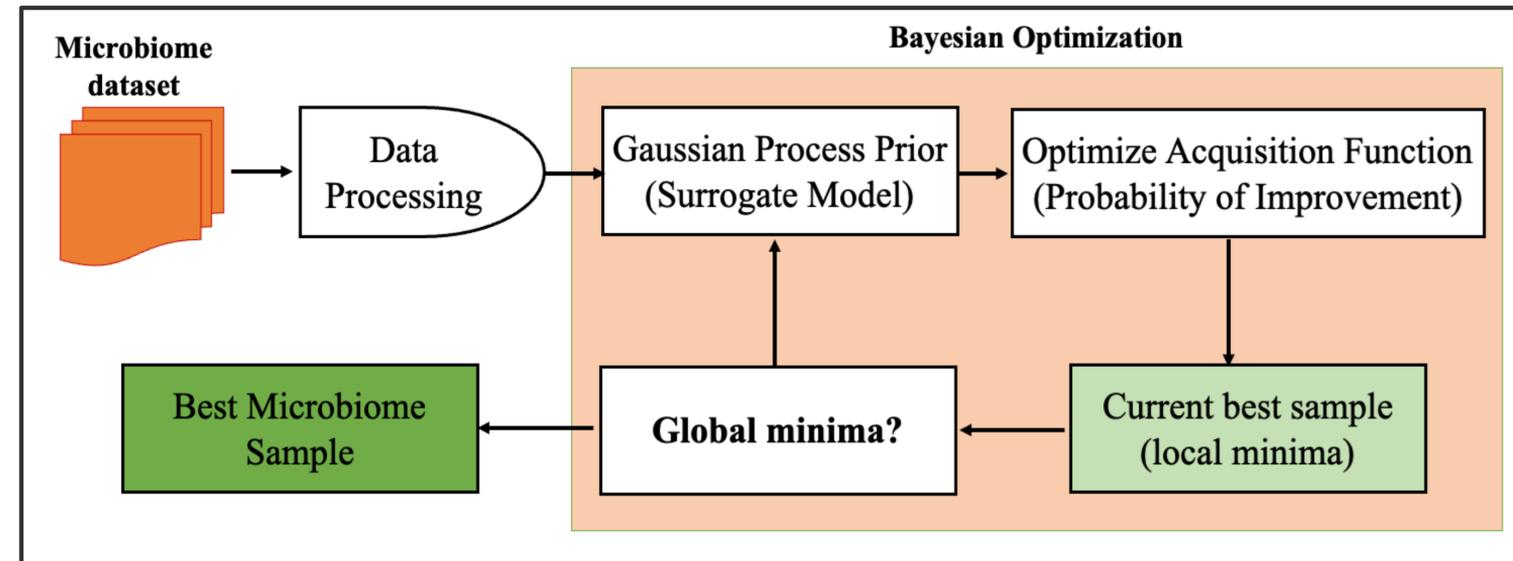
## Research Objective

- Animal sourced foods including contaminated poultry meat and eggs contribute to human non-typhoidal **Salmonellosis**, a foodborne zoonosis.
- Salmonella contamination in poultry is a global public health concern due to its widespread consumption as a primary nutritional source.
- Identifying optimal microbiome signatures that can reduce Salmonella prevalence and increase food safety

## Learning Steps

- Predictive analysis
- Explanatory analysis
- Time complexity
- Not good for combinatorial expression

## Approach



## Best Microbiome Signature

g__Lactobacillus	0.4298
g__Rummeliibacillus	0.1395
f__Planococcaceae--Other	0.0880
g__Acinetobacter	0.0543
f__Clostridiaceae	0.0388
g__Streptococcus	0.0306
g__Enterococcus	0.0272
g__Corynebacterium	0.0252
f__Enterobacteriaceae	0.0244

## Why Gaussian Process?

- Retrieves a region with high probability
- Closed form means and variance
- Excellent for exploration exploitation trade-off

## Data Corpus

- 11 farms over 4 years
- Pre-harvest and post-harvest samples
- Multi-drug resistance score

## Acquisition Function

Probability of Improvement

$$P(f(x_*) < y_{best}) = \Phi\left(\frac{y_{best} - \mu(x_*)}{\sigma(x_*)}\right)$$

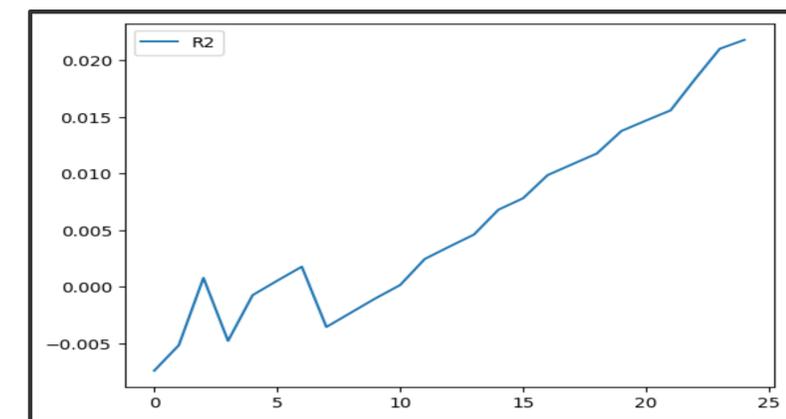
## Training

50 initial samples

25 optimal selections

**Tools:** Python, scikit-learn

## R2 coefficient of determination



## References

Towards Optimal Microbiome to Inhibit Multidrug Resistance, Nisha Pillai, Bindu Nanduri, Michael J Rothrock Jr., Zhiqian Chen and Mahalingam Ramkumar, IEEE CIBCB 2023