**Introduction**

Current bacterial models are built from gene annotations, where gene function is deduced through homology-based algorithms and tools, such as RAST (RAPid Annotation using Subsystem Technology). Novel functional roles are often undiscovered when these annotations cannot be extrapolated from current annotation software.

Using flux-balance analysis (FBA) software, metabolic models can be used for *in silico* prediction of growth rates and biomass yield upon a variety of growth conditions.

Recent developments using multi-phenotype assay plates (MAPs) provide a high-throughput technique for profiling bacterial phenotypes upon a variety of growth conditions. Recent developments using multi-phenotype assay plates (MAPs) provide a high-throughput technique for profiling bacterial phenotypes upon a variety of growth conditions.

Coupling PM experiments with FBA software, metabolic models can be reconciled and optimized to best predict bacteria response and yield.

**Experimental Design**

**Genomics**

*RAST Gene Annotations*

Membrane Transport; K, P, H; Metabolism Polypeptide Synthesis and Degradation; Respiration

**Phenomics**

![Growth curve model](image)

\[ \frac{\dot{y}}{y} = \frac{A - y}{1 + \exp\left(\frac{C}{y} - \lambda\right)} + 2 \]

**Results**

![Growth curves](image)

**Table 1. A comparison between experimental results and FBA prediction.**

<table>
<thead>
<tr>
<th>Phenotypic Result</th>
<th>FBA Prediction</th>
</tr>
</thead>
<tbody>
<tr>
<td>G</td>
<td>48</td>
</tr>
<tr>
<td>NG</td>
<td>0</td>
</tr>
</tbody>
</table>

**Questions**

Why were these reactions missing from model?

Continue to model, sequence, and assay a broad and diverse set of bacteria – can we improve annotations?

**Additional Information**

https://vdm.sdsu.edu/pmanalyzer

https://edwards.sdsu.edu/dbbp

Funding by NSF: (DEB-1046413) (CNS-1305112) (MCB-1303800) (DUE-1259951)

Contact presenter at dcuevas08@gmail.com