Objective
The main objective of this project is to create a mathematical model for species *Pseudomonas aeruginosa* by using its known reactions and metabolites.

Background
This project concerns the metabolism of a pathogen, i.e. *P. aeruginosa*, and its interactions with other organisms. *P. aeruginosa* has the ability to maintain decades-long infections in the lungs of humans, due to the metabolic adaptability of its environment (Bartell et al., 2017). This project serves in collaboration with UC San Diego hospitals regarding microbial interactions between *P. aeruginosa*, a pathogen found in the lungs of cystic fibrosis patients, and the bacterium *Bacillus subtilis*, which has been observed to kill *Pseudomonas* biofilms in hospitals. By creating models for these species, their microbial interactions can be predicted.

Methodology
Built a dictionary for *P. aeruginosa* using BiGG, a UCSD database containing information about "genome-scale metabolic network reconstructions."

Curated and organized the dictionary to build a model for *P. aeruginosa* using COBRA Toolbox and MATLAB.

Perform simulations on the model through Fluid Balance Analysis (FBA), a process used to analyze constraint-based models.

FBA helps determine how an organism utilizes its metabolites and reactions that take place within it or in the extracellular matrix.

Results
Created dictionaries for *P. aeruginosa* containing 1495 reactions and 1284 metabolites.

Table 1. Four reactions from the dictionary.

<table>
<thead>
<tr>
<th>Reaction ID</th>
<th>Reaction Name</th>
<th>Reaction Net rate</th>
<th>Reactions per 1000</th>
<th>Reactions per 1000</th>
</tr>
</thead>
<tbody>
<tr>
<td>u020402</td>
<td>Glu. oxaloacetate</td>
<td>0.6</td>
<td>145.0</td>
<td>145.0</td>
</tr>
<tr>
<td>s020402</td>
<td>Glu. oxalacetate</td>
<td>0.6</td>
<td>145.0</td>
<td>145.0</td>
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</tr>
</tbody>
</table>

Table 2. Four metabolites from the dictionary.

Simulating Gene Knockouts
- By changing the reaction bounds and knocking out genes in pairs, its resulting relative growth rates can be plotted.

Model Properties
- Identifies the position of a certain pathway in a subsystem and sorts them.

Topographical Features
- Shows the stoichiometry of the entire network (reaction by metabolites), where the nonzero entries are shown by dots.

Conclusions
*P. aeruginosa* PAO1 has been explored, its metabolism and reactions were used to determine its interaction with *B. subtilis*. The model *P. aeruginosa* PAO1 is now in BiGG nomenclature and ready to be part of a community model that includes *B. subtilis*. The reformatted model can accurately stimulate growth and robustness on various culture media compositions.

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