Table of Contents

1 Introduction 1

2 Background 3

2.1 Microbiomes 3

2.1.1 The Rhizosphere and Phycosphere 4

2.2 Metagenomics & 16S rRNA Profiling 4

2.2.1 Metagenomics Costs & Possible Solution 5

2.3 Bridging the Microbiomes 6

2.3.1 Chlamydomonas and the ICL 6

2.4 Spectroscopy 7

2.4.1 Spectrophotometry & the Beer-Lambert Law 8

2.4.2 Fluorescence Spectroscopy 9

3 Methodology 10

3.1 Growing Chlamydomonas & Strains 10

3.1.1 Media 11

3.2 Experiments & Data 11

3.2.1 Tecan & Photobioreactor 11

3.2.2 Screening Experiments 12

3.2.3 PBR Experiments 13

3.2.4 PBR Correlating Data Usage 13

3.3 Modeling I 14

3.3.1 Extension of the Beer-Lambert Law 15

3.3.2 Forced Constraints on Modeling 16

3.3.3 Exclusion of Fluorescence Measurements & Models 16

3.3.4 Calibration Samples Preparation for Modeling 17

3.4 Data Processing 19

3.5 Modeling II 19

3.5.1 Obtaining the Extinction Coefficients 20

3.5.2 General Form of Predictive Models....21
3.5.3 Model Application to PBR Data....22
3.6 K-Space & Model Optimization....22
3.6.1 K-Space Calculation....23
3.6.2 Theory of Model Optimization....23
3.7 Absorbances to Cell-Counts....24
4 Results & Analysis....26
4.1 Modeling III....26
4.1.1 Single-Strain Calibration Contributions....27
4.1.2 SynCom Calibration....28
4.1.3 Analysis of General Model Behavior....31
4.1.4 Models 4 & 5....31
4.2 Pivoting the Thesis Scope....34
4.3 Modeling IV: Engineering Solutions....35
4.3.1 Special K....35
4.3.2 Optimization of Model S....38
4.4 Pivoting back to Analysis....41
4.4.1 Analysis of Screen 4....42
4.4.2 Model Transferability to Photobioreactor (PBR)....44
4.4.3 PBR Data Modeling....46
5 Discussion....54
5.1 Summary of Results....54
5.1 Implications....55
5.1 Limitations....56
5.1 Recommendations....56
6 Conclusion....57
References....58
Appendix....61

Declaration of Authorship

ABSTRACT

A high-throughput method for studying host-microbiota interactions is being development at the Max Planck Institute for Plant Breeding Research. This high-throughput system models phycospheres—the aquatic analogue of a rhizosphere—by leveraging an absorbance measuring photobioreactor and rationally composed combinations of microorganisms or synthetic communities (SynComs). The SynComs are comprised of harvested and indexed soil bacteria and the ubiquitous freshwater microalgae, *Chlamydomonas reinhardtii* (CC-1690) that serves as host. The aqueous nature of the system makes it a good candidate to be measured using absorbance spectrophotometry, and the Beer-Lambert law is applied to determine the fractions of bacteria and host in the system. Multiple Beer-Lambert models are created and deployed on existing and continuously generated data. The complexity of the system, however, does not allow for the trivial application of these models. The analysis of the calibration data used to create the models suggest the existence of an optimal model and is subsequently found. The existence of this model facilitates the determination of correction factors that allow the initially created model's predictions to be optimized and are subsequently applied to the data under study.