Table of Contents

**1 Introduction1**

**2 Background3**

2.1 Microbiomes3

2.1.1 The Rhizosphere and Phycosphere4

2.2 Metagenomics & 16S rRNA Profiling4

2.2.1 Metagenomics Costs & Possible Solution5

2.3 Bridging the Microbiomes6

2.3.1 Chlamydomonas and the ICL6

2.4 Spectroscopy7

2.4.1 Spectrophotometry & the Beer-Lambert Law8

2.4.2 Fluorescence Spectroscopy9

**3 Methodology10**

3.1 Growing Chlamydomonas & Strains10

3.1.1 Media11

3.2 Experiments & Data11

3.2.1 Tecan & Photobioreactor11

3.2.2 Screening Experiments12

3.2.3 PBR Experiments13

3.2.4 PBR Correlating Data Usage13

3.3 Modeling I14

3.3.1 Extension of the Beer-Lambert Law15

3.3.2 Forced Constraints on Modeling16

3.3.3 Exclusion of Fluorescence Measurements & Models16

3.3.4 Calibration Samples Preparation for Modeling17

3.4 Data Processing19

3.5 Modeling II19

3.5.1 Obtaining the Extinction Coefficients20

3.5.2 General Form of Predictive Models21

3.5.3 Model Application to PBR Data22

3.6 K-Space & Model Optimization22

3.6.1 K-Space Calculation23

3.6.2 Theory of Model Optimization23

3.7 Absorbances to Cell-Counts24

**4 Results & Analysis**26

4.1 Modeling III26

4.1.1 Single-Strain Calibration Contributions27

4.1.2 SynCom Calibration28

4.1.3 Analysis of General Model Behavior31

4.1.4 Models 4 & 531

4.2 Pivoting the Thesis Scope34

4.3 Modeling IV: Engineering Solutions35

4.3.1 Special K35

4.3.2 Optimization of Model S38

4.4 Pivoting back to Analysis41

4.4.1 Analysis of Screen 442

4.4.2 Model Transferability to Photobioreactor (PBR)44

4.4.3 PBR Data Modeling46

**5 Discussion54**

5.1 Summary of Results54

5.1 Implications55

5.1 Limitations56

5.1 Recommendations56

**6 Conclusion57**

**References58**

**Appendix61**

**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.