

Development of an R Toolbox for Near-Infrared Spectroscopy Data Processing and Analysis of Plant Metabolic Phenotypes

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Chapter 1

Introduction

The advancement and widespread use of high-throughput experimental technologies in the field of plant biology have introduced significant challenges in managing and analysing the vast datasets effectively. Addressing these challenges require innovative methods that maximize the data utility while minimizing computational inefficiencies and resource consumption, ensuring robust insights into complex biological systems (<https://www.frontiersin.org/research-topics/6856/machine-learning-in-plant-science/articles>).

The understanding of interplay between plant physiology and its hidden biochemical process is crucial for the improvement of basic plant science and addressing global challenges such as food security, crop resilience and combating climate change [1]. In recent years, advanced High-Throughput analytical techniques such as Near-Infrared Spectroscopy (NIRS) and Liquid Chromatography-Mass Spectrometry (LC-MS) has instigated a paradigm shift in plant biology [2][3].

Chapter 2

Background

The background of this study include

2.1 Related Work

2.2 Near Infrared Spectroscopy (NIRS)

2.3 R Programming

2.4 Machine Learning

2.4.1 Partial Least Square Regression (PLSR)

2.4.2 Random Forest (RF)

2.4.3 Convolutional Neural Network (CNN)

2.5 Mass Spectrometry and Liquid Chromatography

Chapter 3

Implementation

3.1 Packages

Github, testing, actions

3.2 Contributions elsewhere

3.3 HPC runs

Chapter 4

Results and Discussion

4.1 Data charecterestics

histogram, spectra

4.2 Baseline Machine Learning Models Pablo

PLS, RF, CNN

4.2.1 Variable importance

4.3 Variations in Baseline systems

4.3.1 modifying the Test and Training split

4.3.2 input data length

4.4 Sues

Chapter 5

Reference

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2. Pulok K. Mukherjee, Quality control and evaluation of herbal drugs, Evaluating natural products and traditional medicine. 2019, doi:10.1016/C2016-0-042328, ISBN:978-0-12-813374-3
3. Nizamani, M. M., Zhang, Q., Muhae-Ud-Din, G., Wang, Y. (2023). High-throughput sequencing in plant disease management: A comprehensive review of benefits, challenges, and future perspectives. *Phytopathology Research*, 5(44). <https://doi.org/10.1186/s42483-023-00215-7>
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