

Configuration Manual

MSc Research Project Programme Name

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MSc Project Submission Sheet

School of Computing

Student Name: Vikas Khatri

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Programme: MSc in Data Analytics **Year:** 2023

Module: Research Project

Lecturer: Sasirekha Palaniswamy

Submission Due

Date: 14 Dec 2023

Project Title: Machine Learning to forecast Cell growth in Bioreactor using

Raman spectroscopy

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Date: 14 Dec 2023

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Configuration Manual

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1 Introduction

The configuration manual is the procedure, outlining the key aspects of the research implementation. Hardware/Software requirements, dataset collection and data import, data pre-processing, implementation and evaluation are part of this configuration manual. The configuration manual helps to outline the key steps taken to carry out the research and build the model.

2 Hardware Requirement

Organisation's infrastructure is used to carry out this study. SIMCA (Soft independent modelling by class analogy) workstation in the lab is used to configure the task. The lab workstation with the hardware configuration of 64-bit Windows 10 OS, Intel(R) Core (TM) i5-10500 CPU @ 3.10GHz Processor and 32GB of RAM are used.

3 Software Requirement

SIMCA software is used to build the model and SIMCA version 17.0.2.34594 is used.



Figure 1: SIMCA software

4 Dataset selection

This study makes use of company data. The bioreactors in the laboratory, which are controlled by a DCU (digital control unit), produce the data. The Modular Fermentation and Culture System (MFCS), which is connected to DCU, analyses and processes bioreactor data, permits trending, and creates recipes that are often used in laboratories. To store and distribute data to various systems, MFCS is linked to a site historian/PI (Process Intelligence) server. Firewalls divide the networks where the MFCS and PI systems are located: the lab network and the company network. Bioreactor data is made available on the enterprise network by the PI system, which is utilised by SIMCA online. The parameters of the bioreactor's batch data are gathered by SIMCA online and made available to the SIMCA client located in the laboratory.

Raman spectroscopy is a stand-alone piece of equipment in the lab; to measure the VCD, the Raman probes are directly attached to the bioreactor. VCD is measured on a regular basis for every batch. The Raman system exports the VCD data as a comma-separated values (CSV) file, which is then entered into SIMCA in the laboratory.

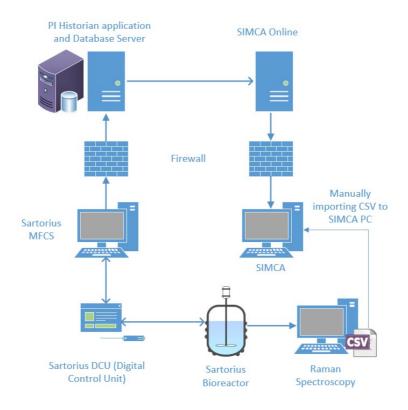


Figure 2: System Architecture

5 Importing required dataset

Dataset from above systems then imported to SIMCA.

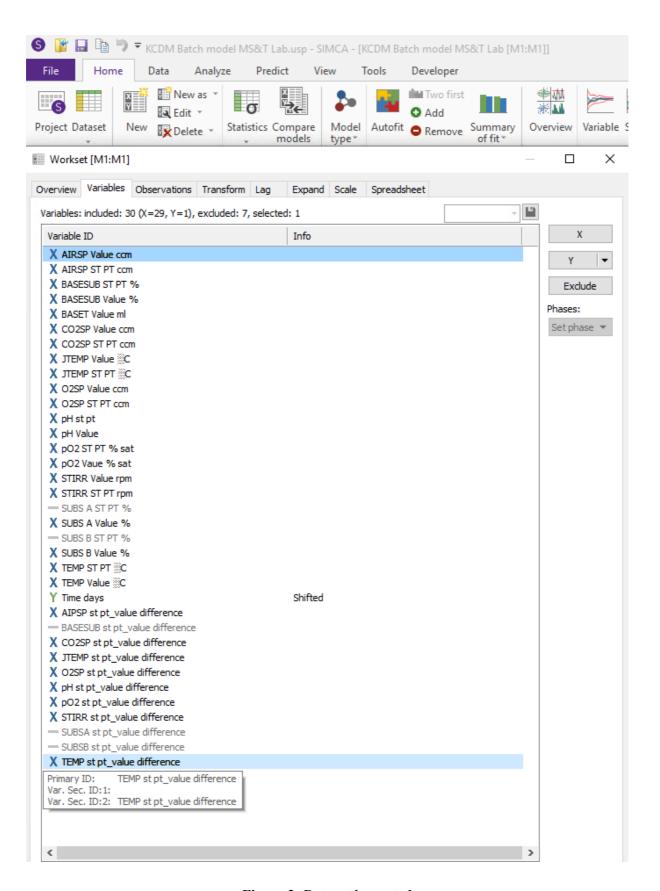


Figure 3: Dataset imported

6 Pre-processing

The batches were produced throughout a range of dates and months, thus SIMCA generated a new parameter called "Time days" that allows all the batches to be compared. Time days reflect the stage of the batch within a day, such as the first, fourth, etc., rather than on a single time or day. To process the input and create the model, SIMCA performed this step. Every batch's "Time days" parameter is displayed in the figure below. Every colour on the trend indicates a batch, while the y axis displays the number of days the batch ran for, and the x axis represents the primary id (there is a unique primary id for each timestamp).

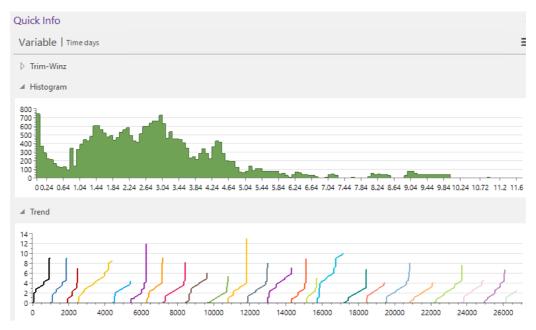


Figure 4: Time days parameter representing each batch's timeline

Outlier value can be selected and removed from the variable window.

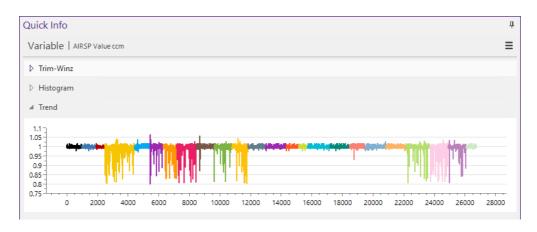


Figure 5: AIRSP Value for each batch

Additionally, looking at each variable's trend, co-related variables which don't add any value to models are dropped from model building.

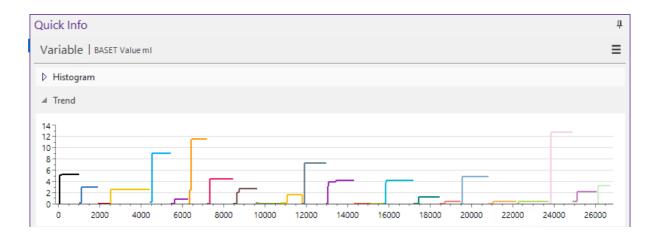


Figure 6: BASET Value for each batch

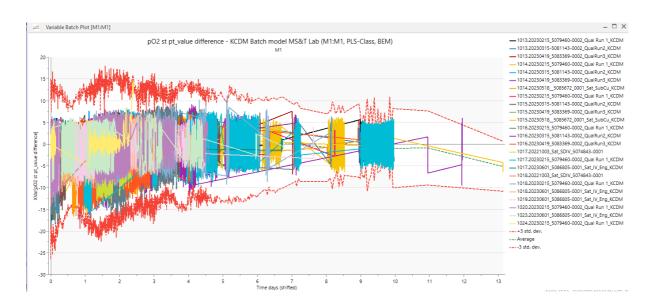


Figure 7: pO2 set point value difference for each batch

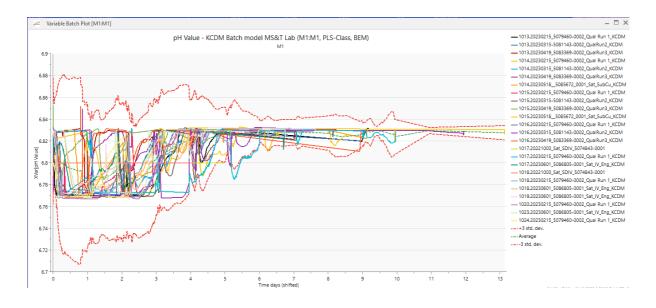


Figure 8: pH value for each batch

7 Model building

Offline data from Raman spectroscopy was added to batch evolution model to make the batch level model.

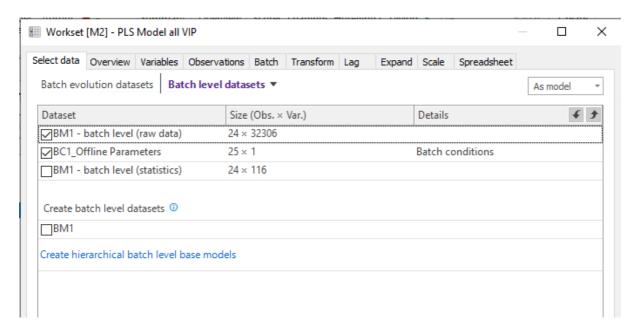


Figure 9: Batch level models

Summary of fit can be shown by selecting the model and clicking at "Summary of fit" icon on the menu bar highlighted in yellow.

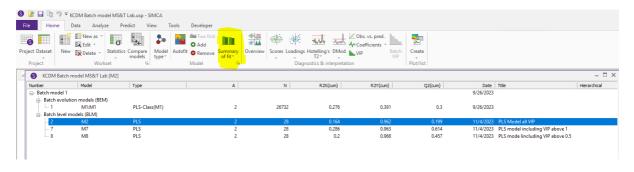


Figure 10: Summary of fit

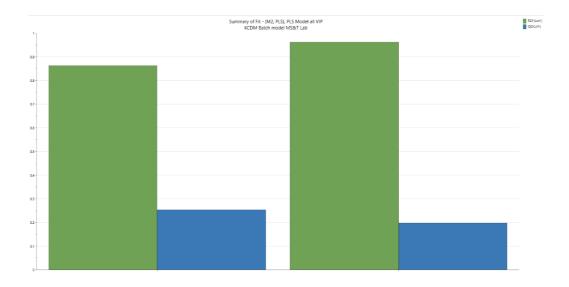


Figure 11: Summary of fit plot – all VIP value

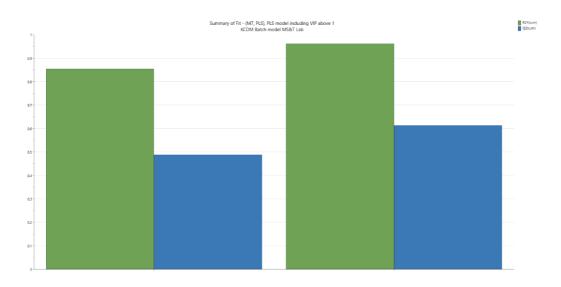


Figure 12: Summary of fit plot – VIP above 1

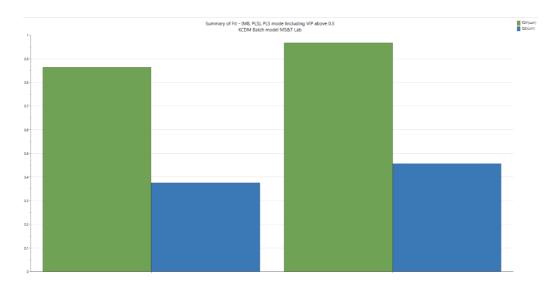


Figure 13: Summary of fit plot – VIP above 0.5

VIP plot can be shown by selecting the model and clicking at "VIP" icon on the menu bar highlighted in yellow.

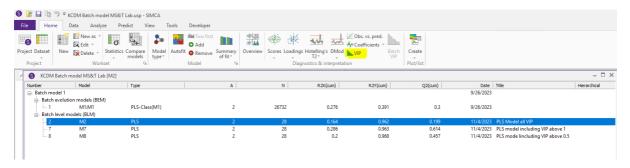


Figure 14: VIP plot for models

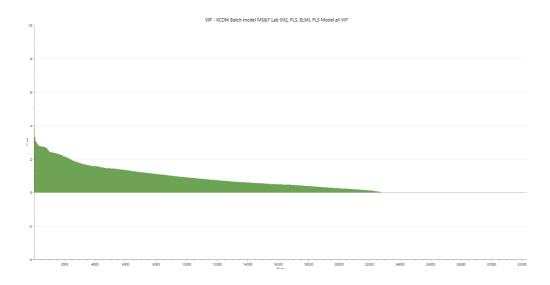


Figure 15: VIP plot (all values)

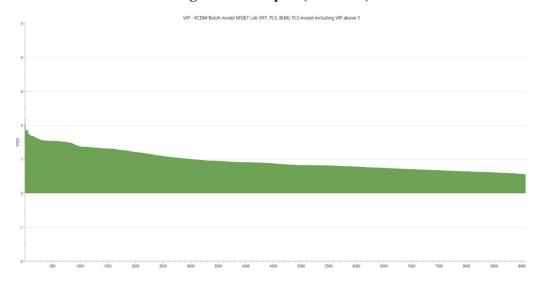


Figure 16: VIP plot – VIP above 1

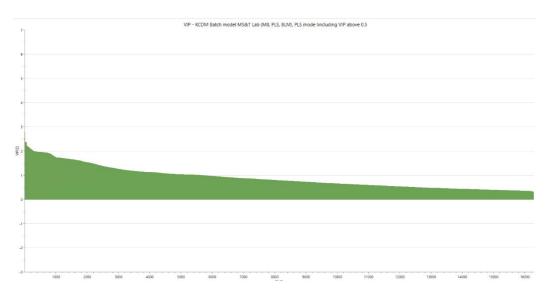


Figure 17: VIP plot – VIP above 0.5

8 Evaluation of models

For each of the three studies, the PLS algorithm was employed to assess the model. The observed and projected values of VCD for each batch are displayed below. The model predicted (X axis) the VCD, while the observed value (Y axis) is the one imported from Raman spectroscopy. With a good model all the points will fall close to the 45-degree line. The fit of the observations to the model is indicated by the RMSEE in the footer. The similar metric, the RMSECV, is calculated through the cross-validation process and indicates how predictable the model is.

Observed vs predicted plot can be shown by selecting the model and clicking at "Obs. Vs. pred." icon on the menu bar highlighted in yellow.

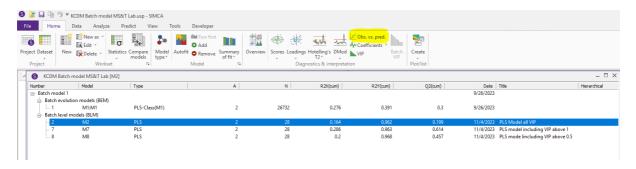


Figure 18: Obs. vs pred. plot

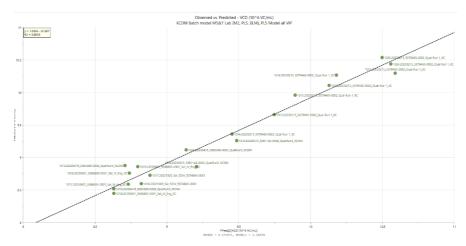


Figure 19: Observed vs predicted plot – all VIP model

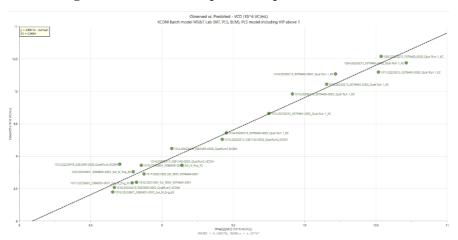


Figure 20: Observed vs predicted plot -VIP above 1 model

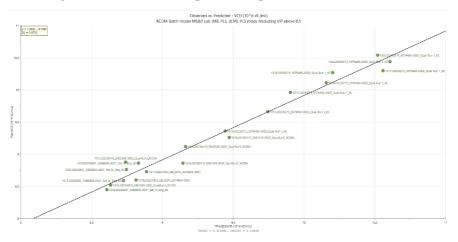


Figure 21: Observed vs predicted plot -VIP above 0.5 model

One batch is used as a "test" batch and predicted using predict functionality within SIMCA. Batch is specified as the training batch and result can be seen in below figure.

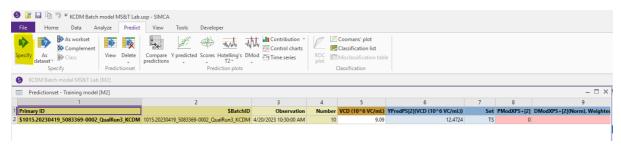


Figure 22: Test model prediction