

Intelligent Radiological Imaging Systems

IRIS-MRS-AI

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Introduction

Intelligent Radiological Imaging Systems (IRIS) is the main name for all tools that are generated by our Computational Imaging Lab (CIL) located at the Biomedical Institute of Bogazici University. For further information please visit www.iris.com.tr. IRIS Magnetic Resonance Spectroscopy (MRS)- Artificial Intelligent (AI) is a standalone tool that complied on MATLAB 2020a for Windows, MATLAB 2020b for Linux and Mac distributions. The source code of this tool is publicly available on <https://github.com/Computational-Imaging-LAB/IRIS-MRS-AI>. This project was supported by TUBITAK 1003 grant 216S432. This manual is created for v0.1.

Besides manually entering the data, IRIS-MRS-AI supports the data formats listed below;

- Excel files (.xls,.xlsx)
- CSV files
- LCModel outputs (.coord)

Download and Installation

IRIS-MRS-AI standalone packages can be downloaded from www.iris.com.tr. For installing standalone version execute downloaded iris file. After installation depending on your choices at installing the IRIS-MRS-AI setup will create a shortcut on the desktop. For running on MATLAB, clone the GitHub repository and add all the files in the current directory. To start the tool please execute the “*iris.m*” script located in the cloned repository.

IRIS-MRS-AI Overview

Intelligent Radiological Imaging Systems (IRIS) magnetic resonance spectroscopy (MRS) artificial intelligence (AI) (IRIS-MRS-AI) is a MATLAB-based tool powered by AI. IRIS-MRS-AI consists of 2 main modules which are Normal User and Advanced User. IRIS-MRS-AI is a standalone tool and complied in Mac, Linux, and Windows operating systems.

All the source code for each operating system (OS) is the same but in the Github repository, there are branches for each OS to prevent any complications.

3 modules of IRIS-MRS-AI were indicated using blue, green, and orange colors. Using IRIS-MRS-AI IDH and TERTp mutations in gliomas can be classified with MRS and MS data. As shown in [Figure 1](#).

The Normal User (green) module consists of 2 parts. These 2 modules are systematically similar for providing consistency and enhancing user experience (UX). These modules are explained in detail in the following sections. Briefly, in this module, users can input their MRS and MS data to classify IDH and TERTp mutations using built-in models.

The Advanced User (orange) module consists of 2 parts. The trainer part is for training a custom model using any structured dataset. The classifier part is for using trained models to classify input data. Users

can use their custom models on the classifier part. Briefly, this module offers users to create and manipulate their models using IRIS-MRS-AI.

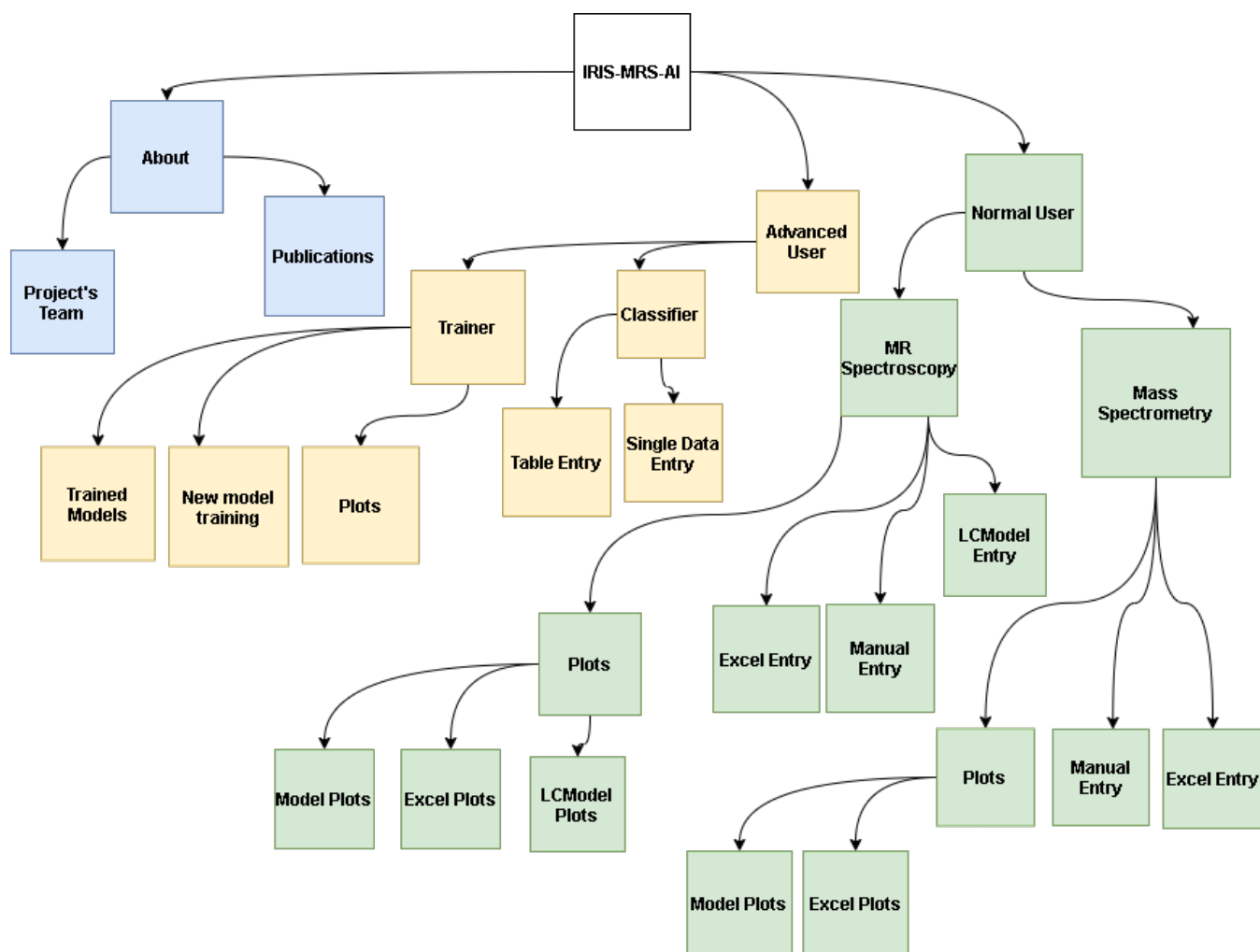


Figure 1: Overview diagram of IRIS-MRS-AI

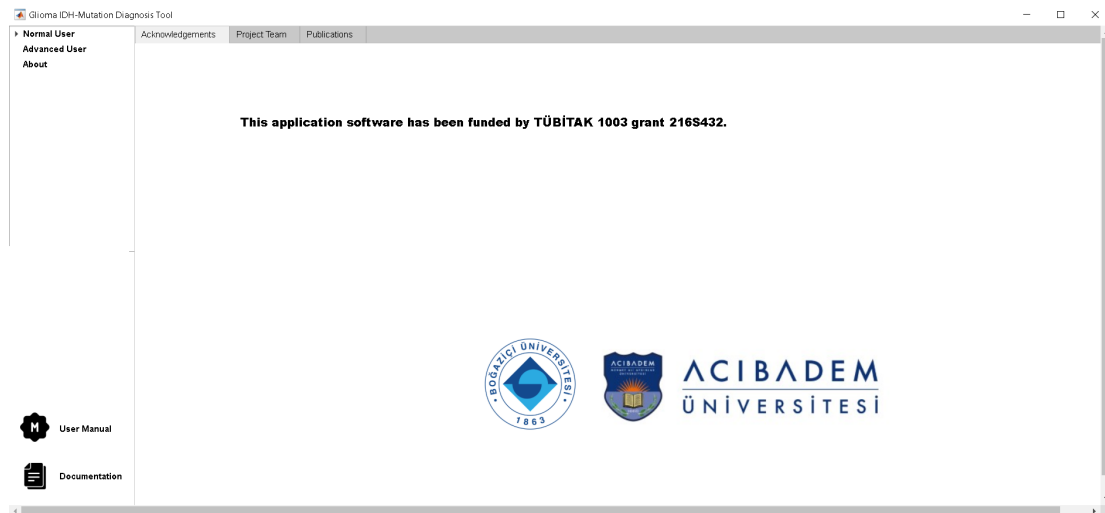


Figure 2: Landing page of IRIS-MRS-AI

IRIS-MRS-AI Modules

Normal User Module

In this module, users can input their Magnetic Resonance Spectroscopy (MRS) data or Mass Spectrometry (MS) data to classify Isocitrate dehydrogenase (IDH) and telomerase reverse transcriptase promoter (TERTp) mutations in gliomas.

Normal User Module (NUM) consists of 2 parts that are MRS and MS.

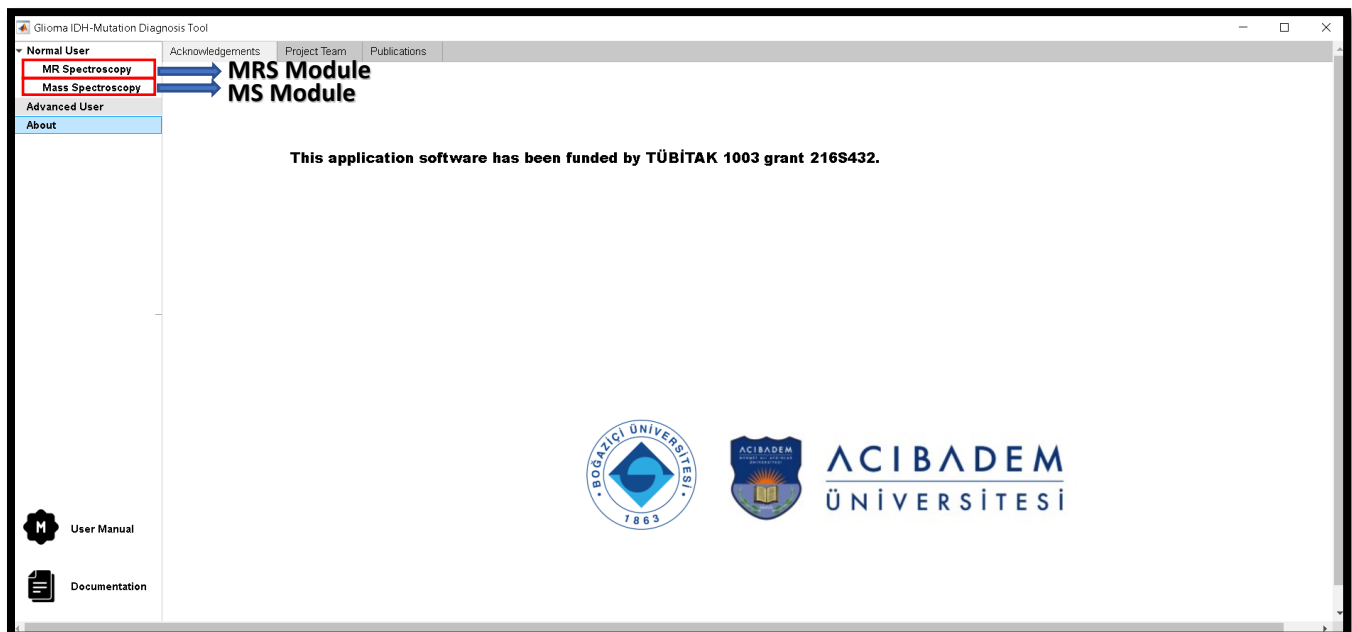


Figure 3: Menus of Normal User Module

MRS Module

In the MRS module, users can classify their MRS data in terms of IDH and TERTp mutations. MRS module involves Manual Entry, Table Entry, and Plots sections. In the following figure overview of the MRS module, is shown.

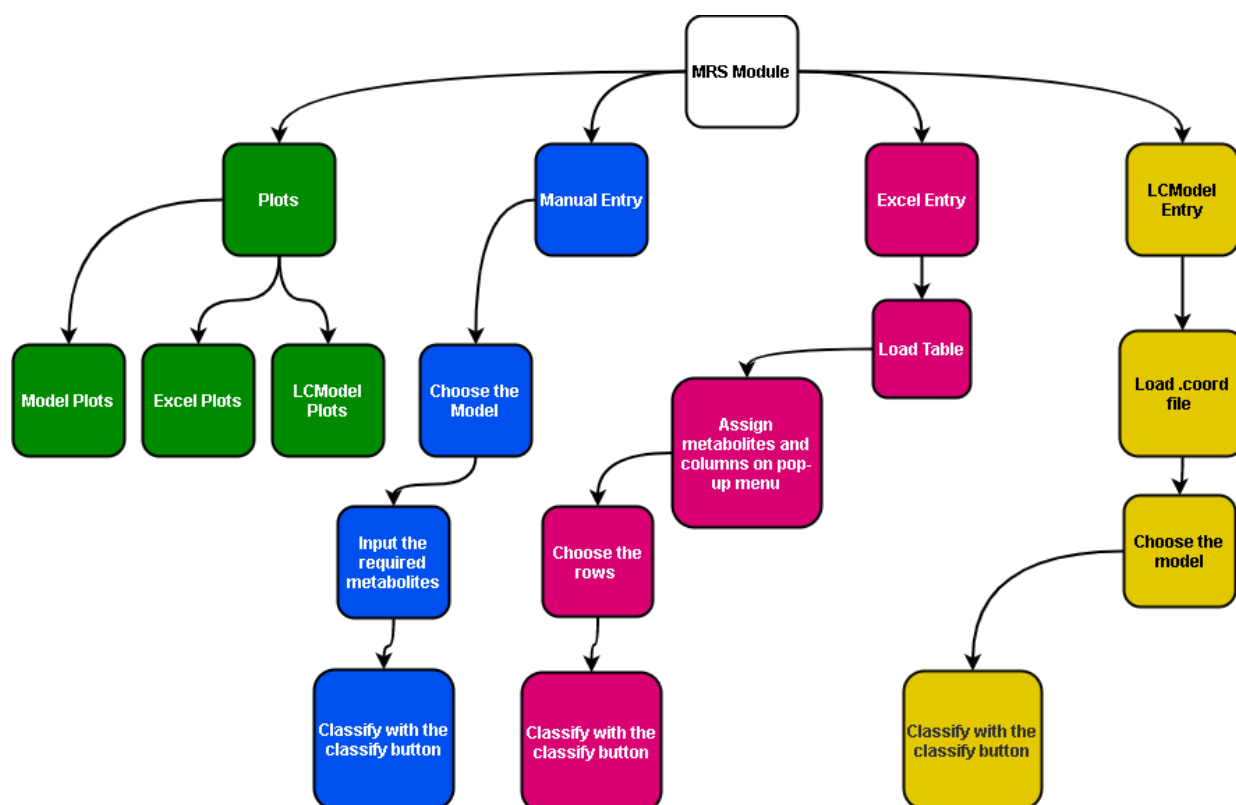


Figure 4: Block scheme of MRS Module

In this module, we offer 5 different binary models to classify subgroups of IDH and TERTp mutations. In the following figure metrics of these models and data sizes are shown.

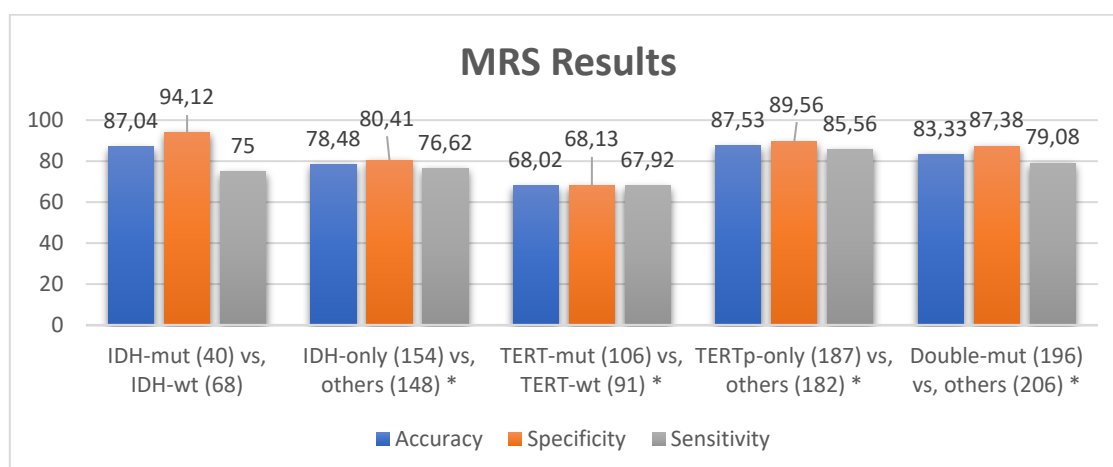


Figure 5: MRS Module built-in models' metrics

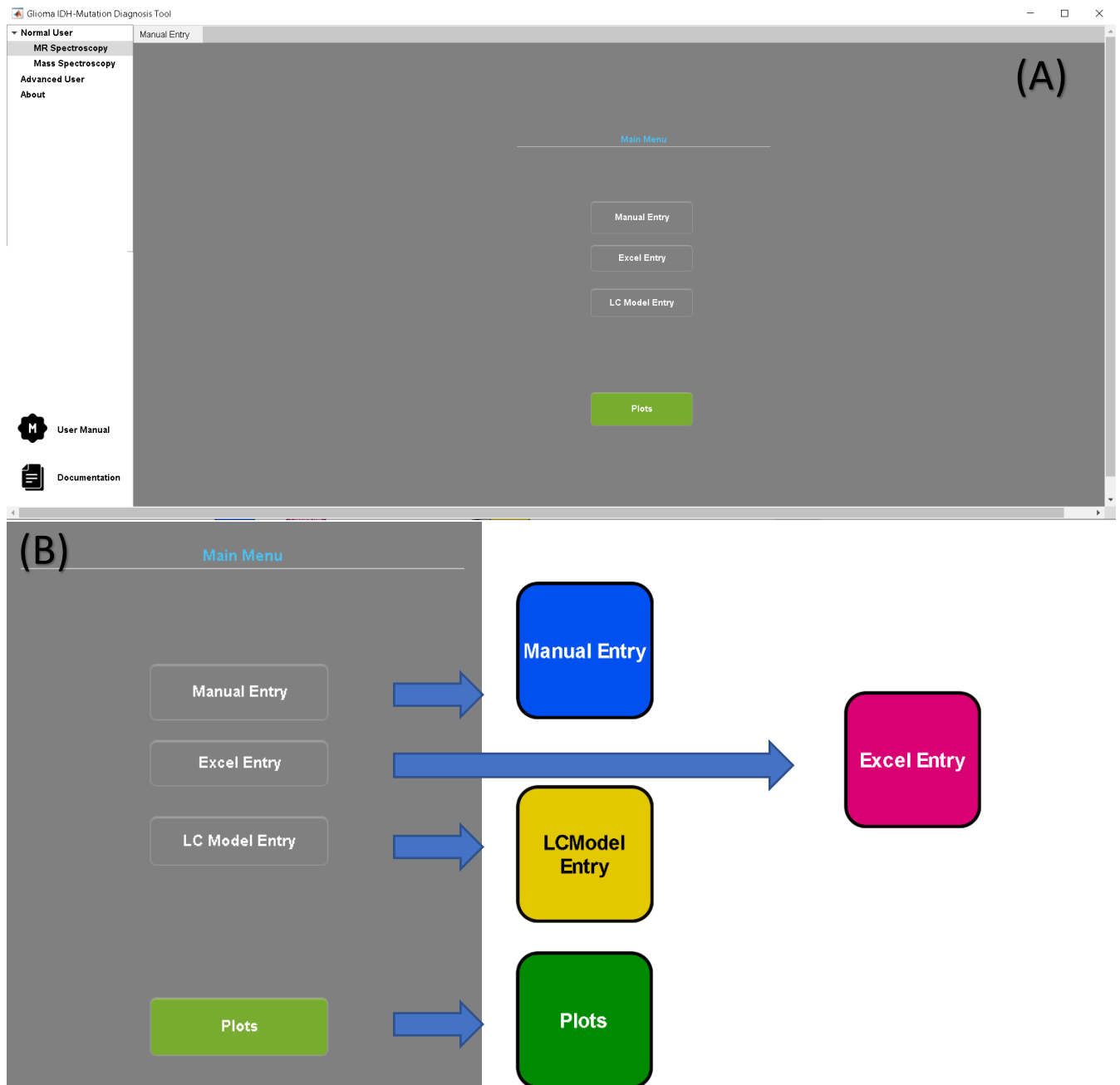


Figure 6: (A) UI of MRS Module, (B) Zoomed image of UI and corresponding blocks from Figure 4

Manual Entry



In this part, users can use built-in models. There are 5 different models for IDH mutation, TERTp mutation, IDH wildtype TERTp mutation (TERTp-only), IDH mutation TERTp wildtype (IDH-only), and IDH mutation TERTp mutation (Double-mutant) classification. In the Figure 7 UI of Manual Entry, part is shown.

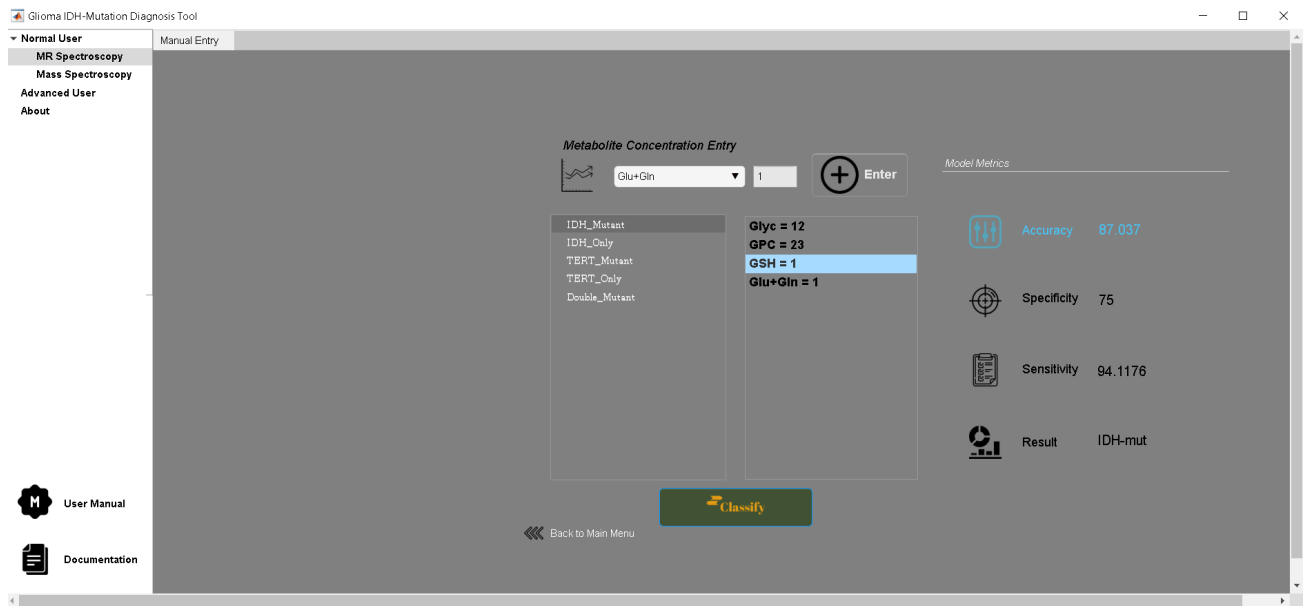


Figure 7: UI of Manual Entry part

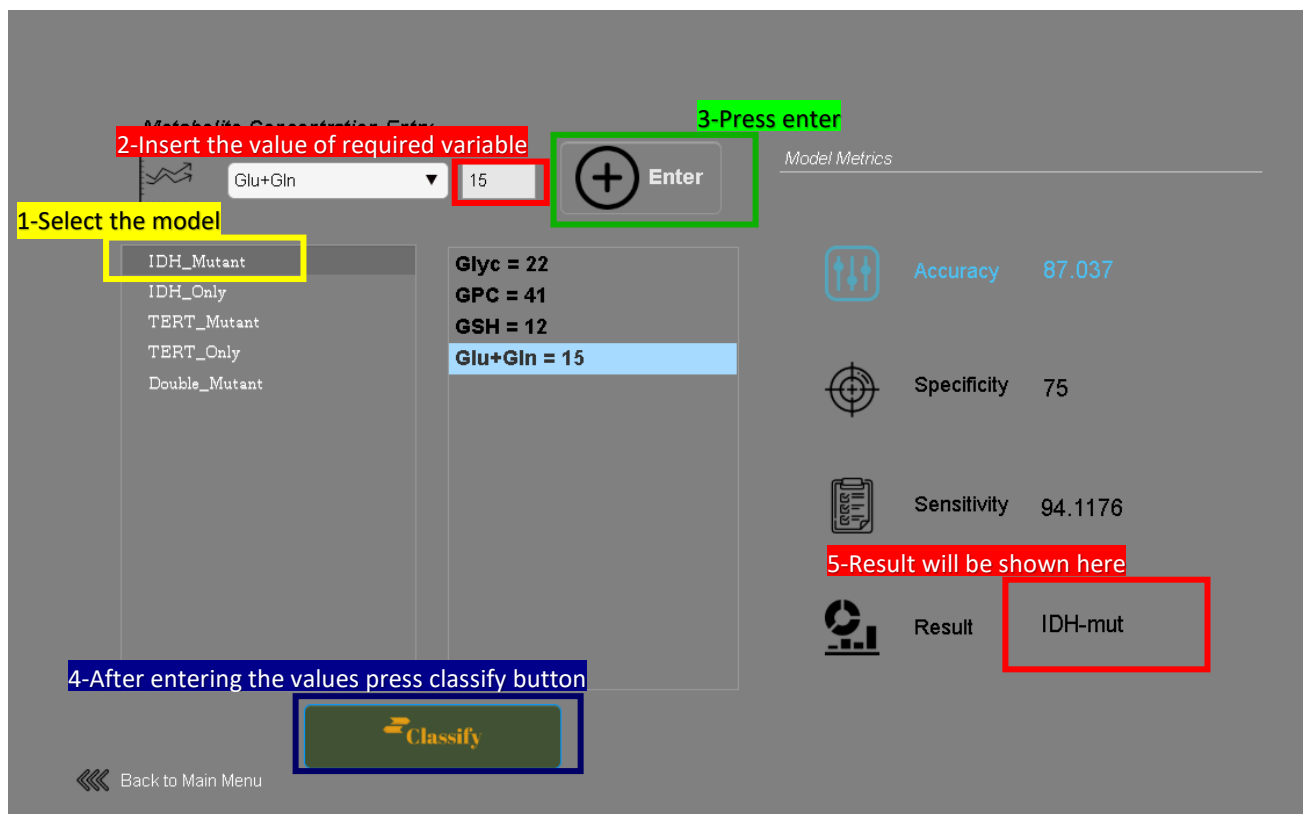
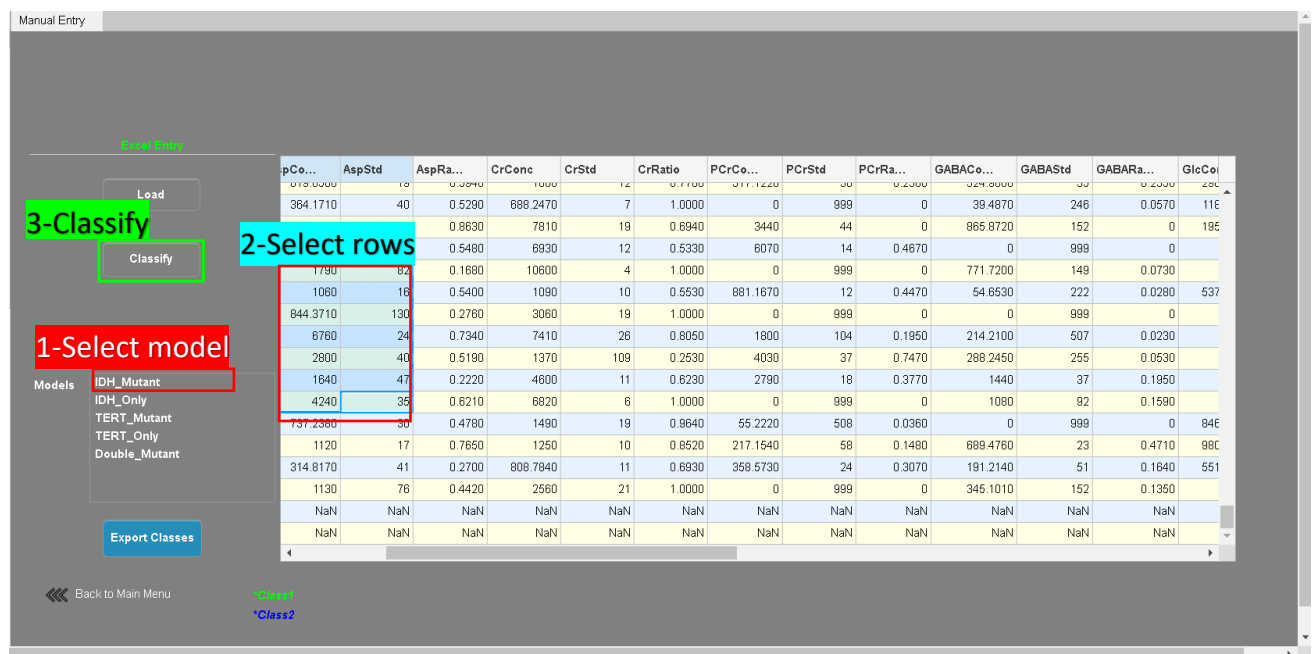
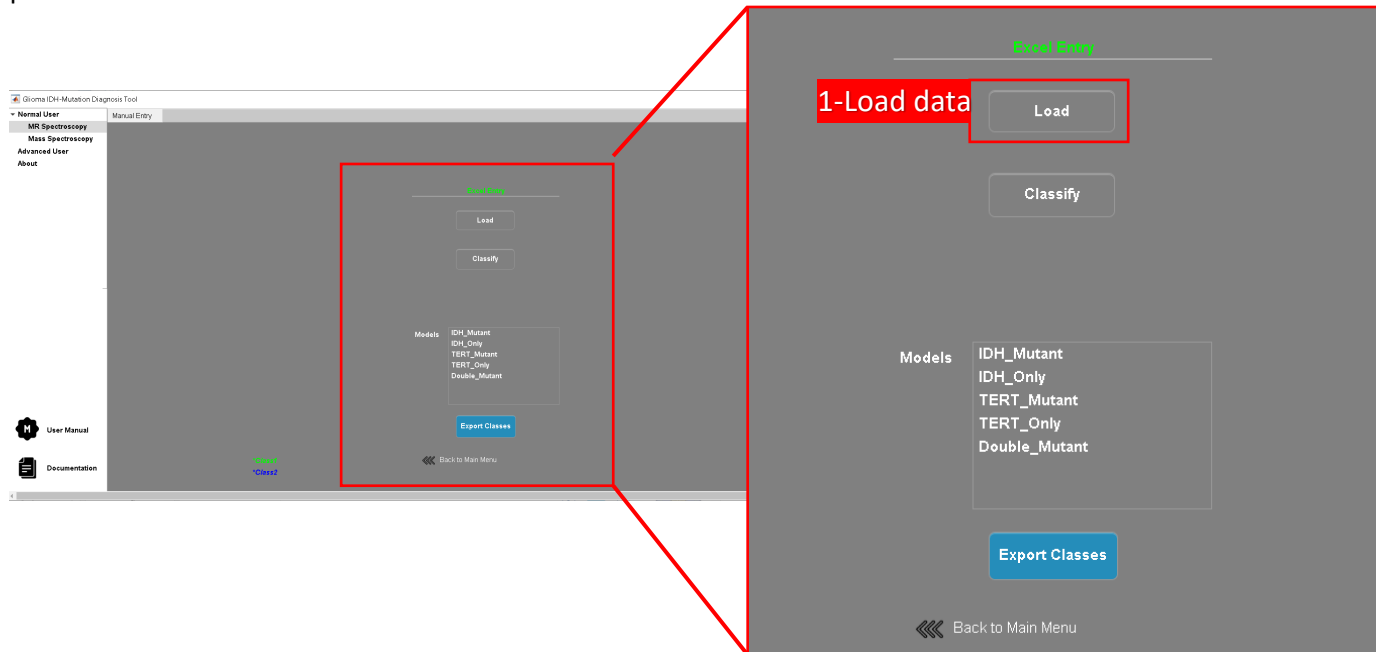


Figure 8: Zoomed Manual Entry part

Excel Entry

Excel Entry In this part, users can input their structured MRS metabolite data in the IRIS-MRS-AI to classify them in terms of mutations. This part has the same default models as the manual entry part has. In the UI of the Excel Entry part is shown. In the flow of use of Excel Entry part is shown.



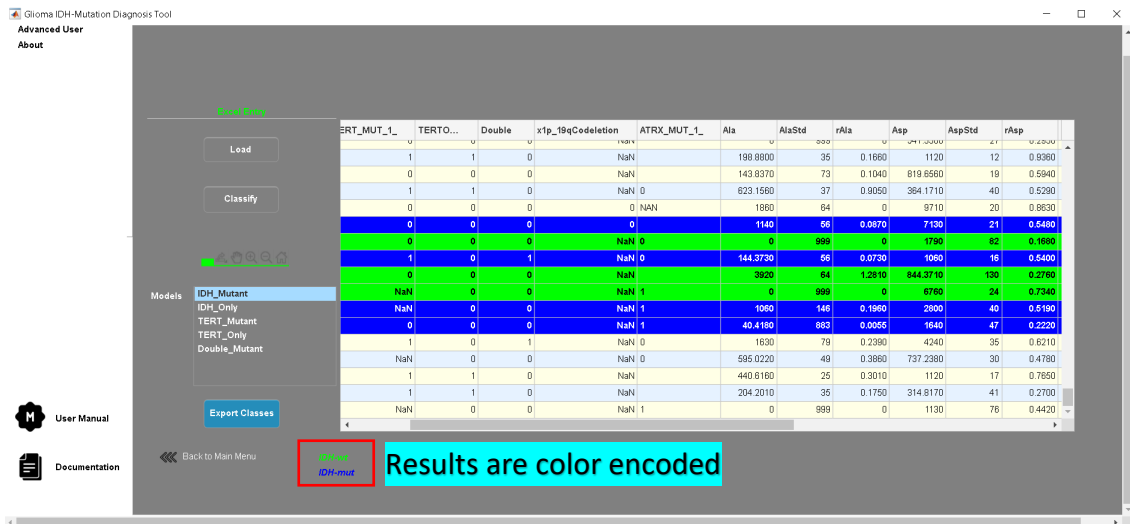


Figure 11: Excel Entry Results

LCModel Entry



LCModel Entry part is planned for commonly used software LCModel in the MRS community. Users can use their outputs that come from data quantification. LCModel Entry needs .coord and .table files to be present in the current directory that users work on.

Basically with the LCModel part users can ;

- Plot the spectrum of their metabolites,
- Manipulate components of figures,
- Export figures with paper quality,
- Directly classify from .coord and .table files,
- Perform multi-data classification.



Figure 12: LCModel Entry Landing Page

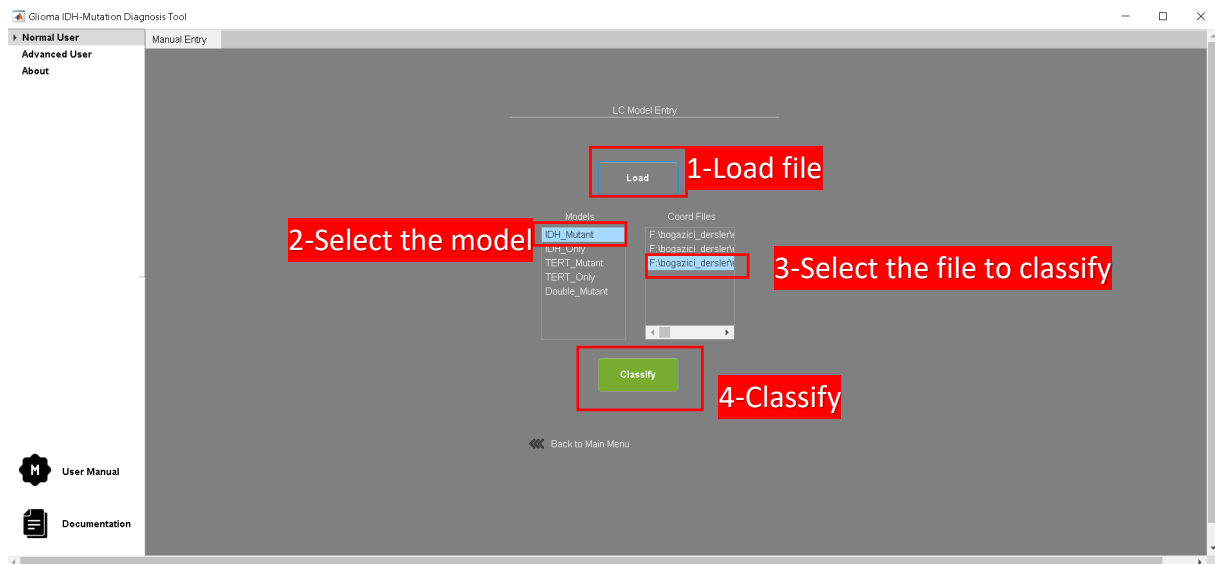


Figure 13: Landing page of LCModel Entry

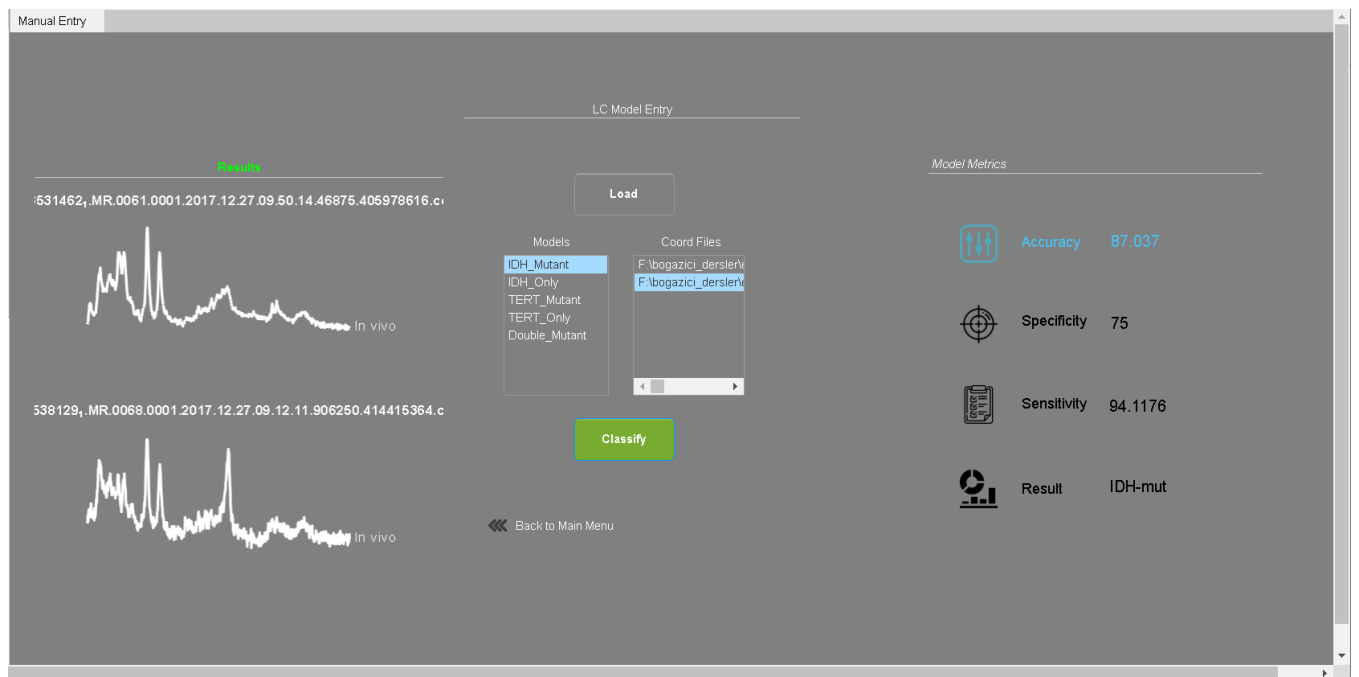


Figure 14: Results of classification

Plots

Plots

In the plots menu, users can explore details of the models, data, and spectrums. In the model plot, details of the models are visualized. In this plot menu (Figure 16) we provide insights into the built-in models. IRIS-MRS-AI has many plotting options such as line, box, bar, radar, etc. After loading the data table users can visualize their data to investigate it in a better way.

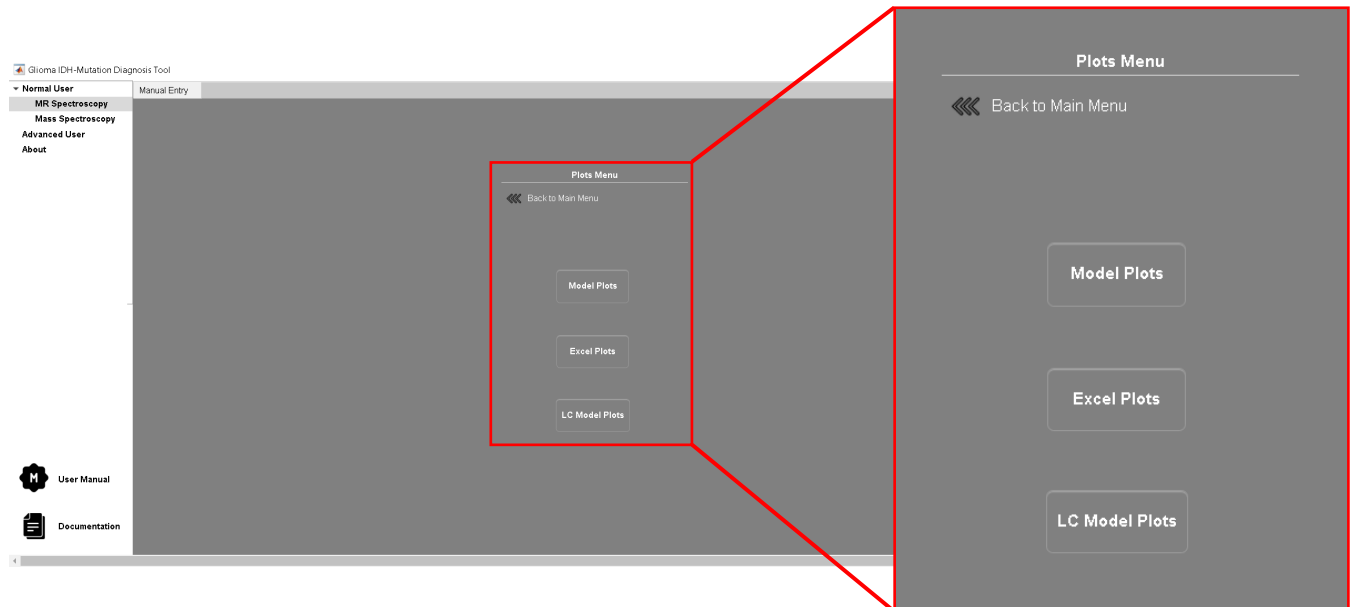


Figure 15: Plots Menu

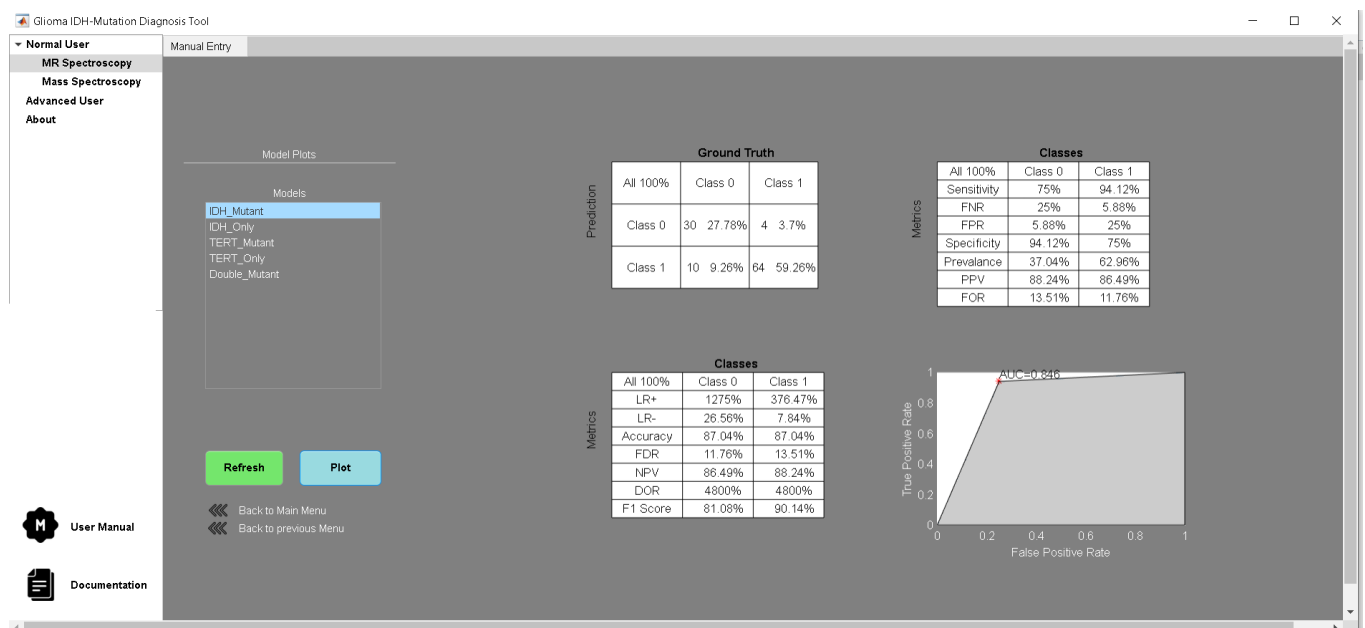


Figure 16: Model Plot

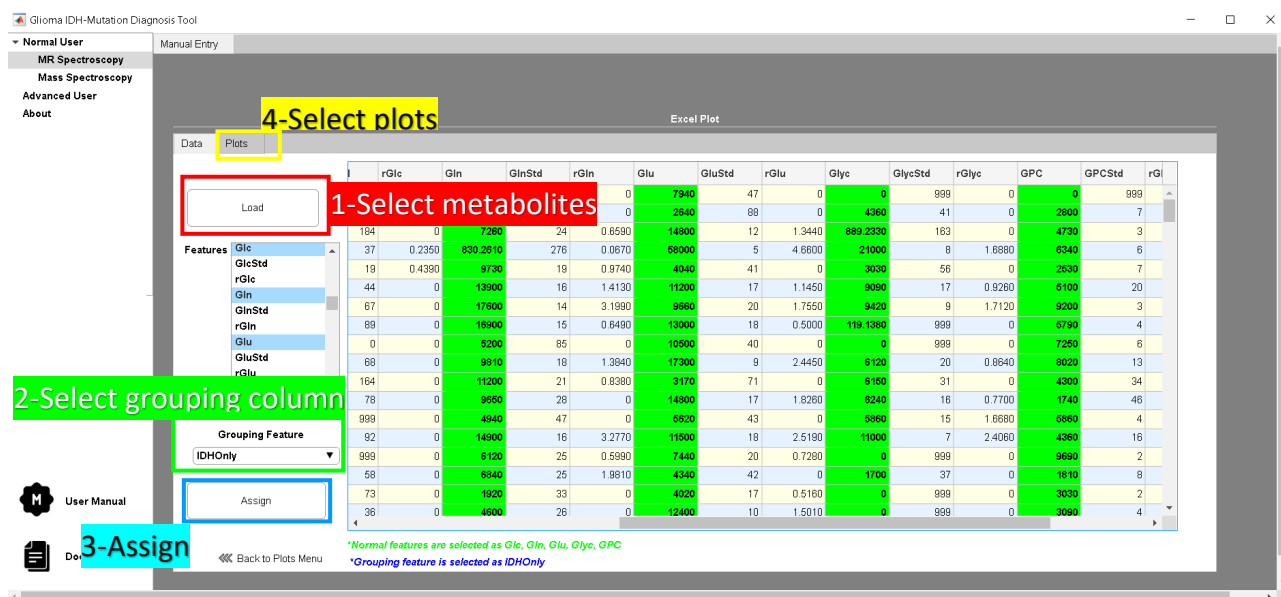


Figure 17: Landing page of Excel Plot

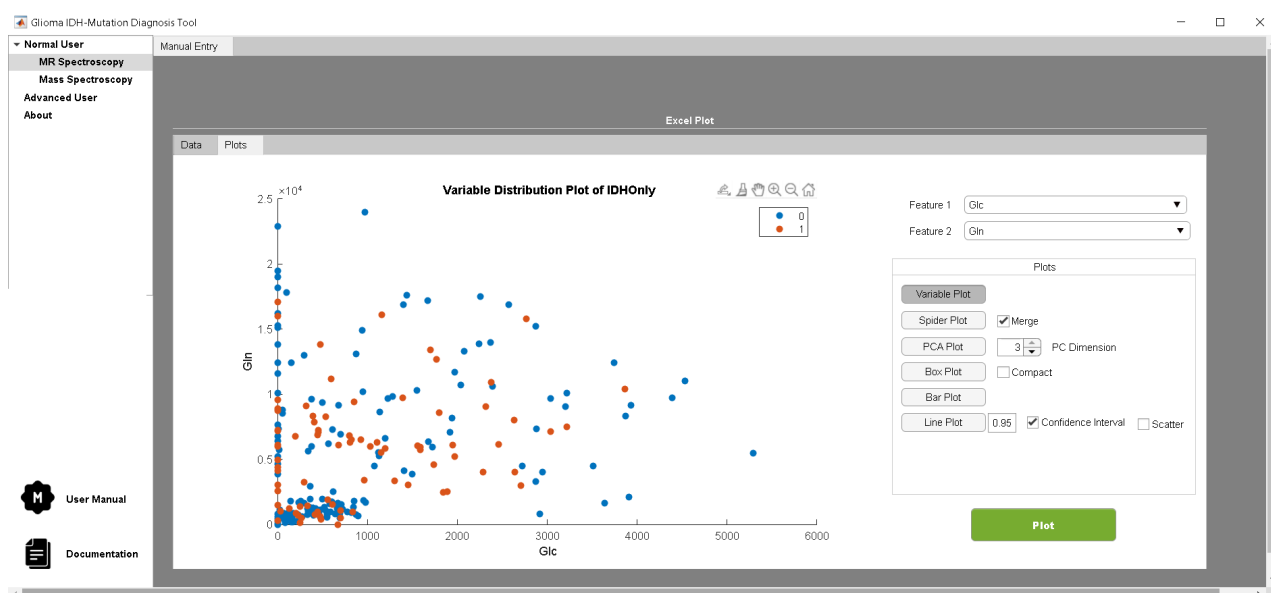
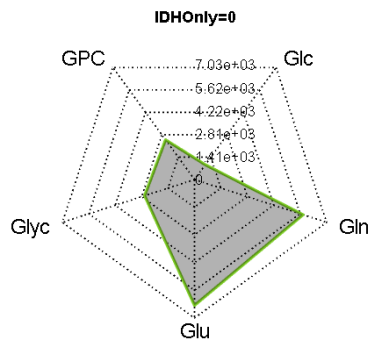


Figure 18: Plot Menu of Excel Plot

A



B

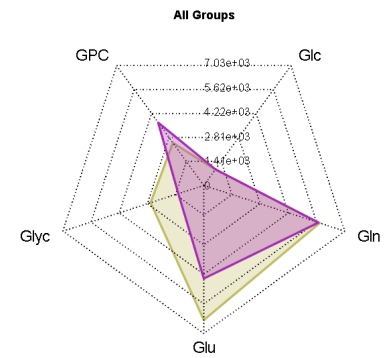
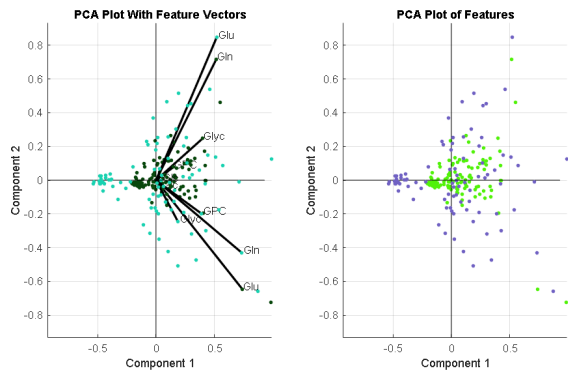


Figure 19: Spider Plots (A) Separate plots for each group, (B) Merged Plot

A



B

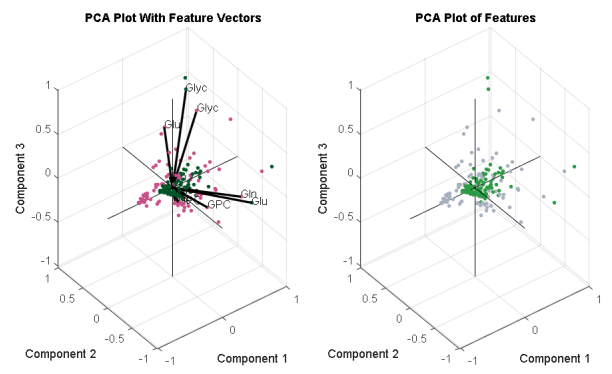


Figure 20: PCA Plot (A) 2D-PCA Plot, (B) 3D-PCA Plot

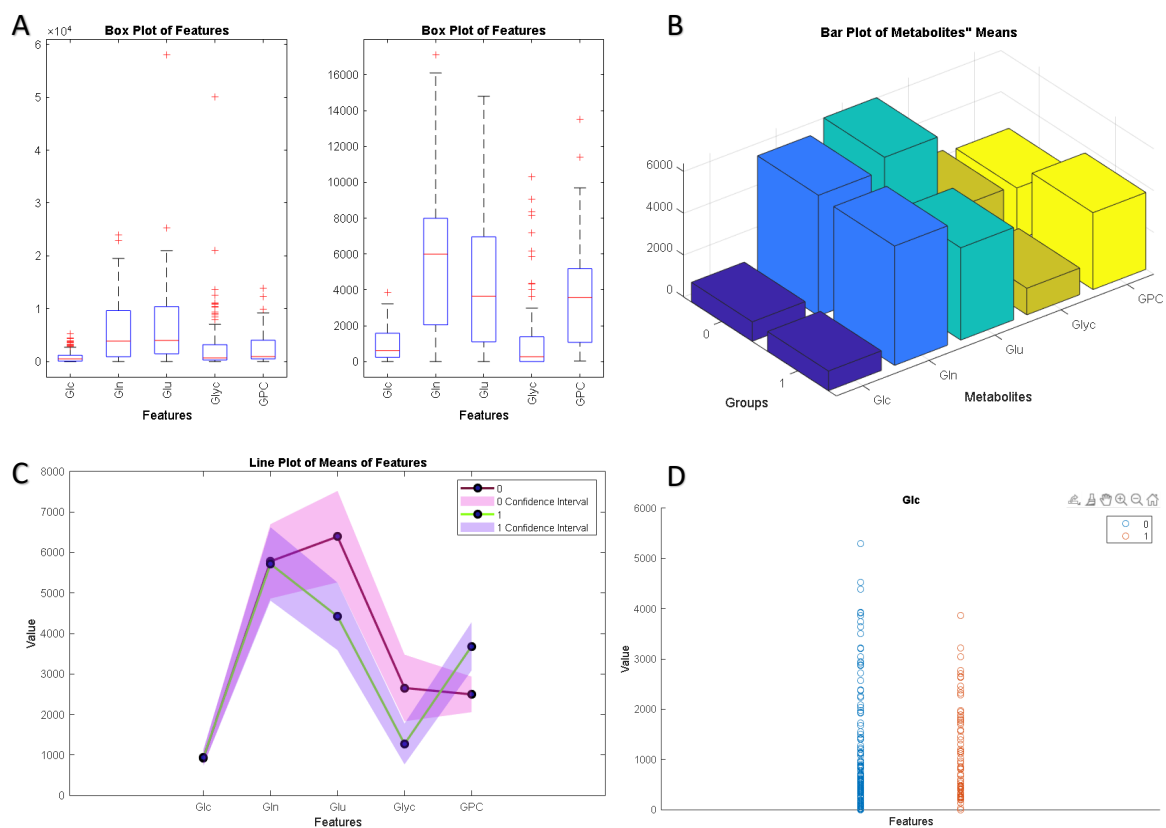


Figure 21: Plots. (A) Box plots of each group, (B) Bar plot of each metabolite, (C) Line plot of metabolites, (D) Scatter plot of metabolites

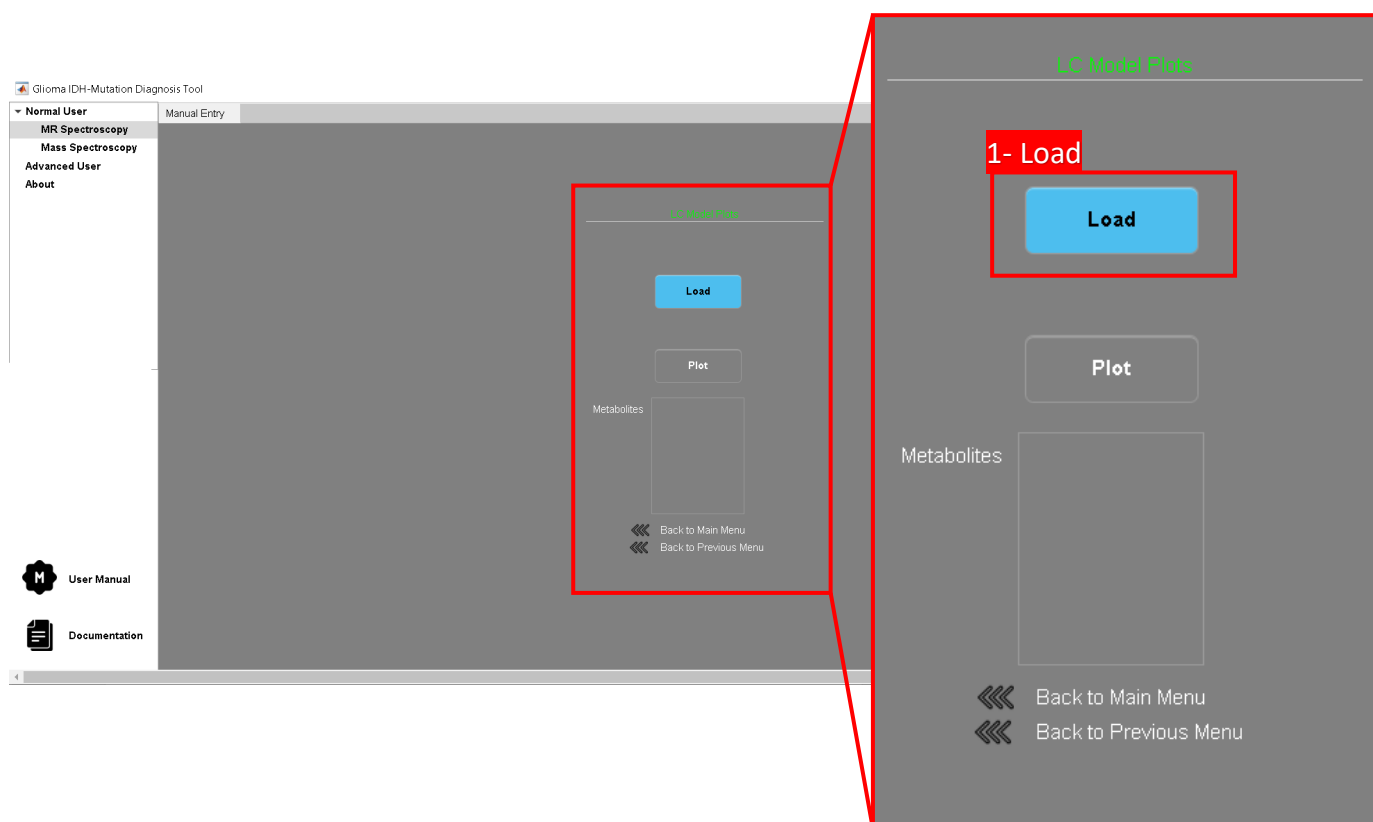


Figure 22: LCModel Plot

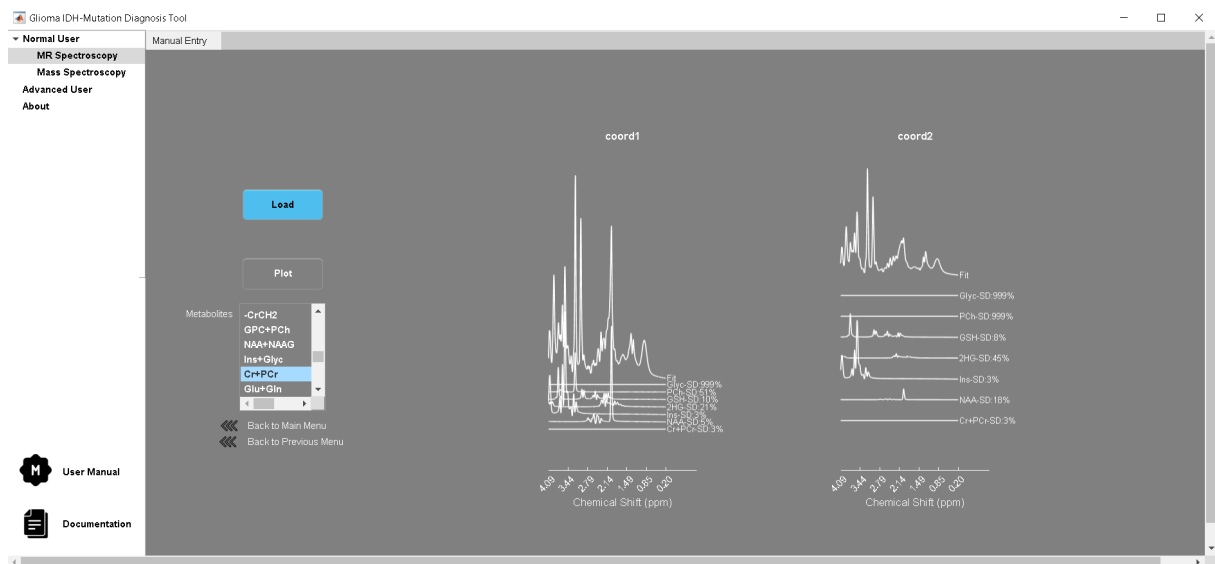


Figure 23: Plots of coord files

MS Module

In the MS module, users can classify their MS data in terms of IDH and TERTp mutations. MS module involves Manual Entry, Table Entry, and Plots sections. In the following figure overview of the MS module, is shown. The flow of this module is the same as the MRS module. This module has its own models trained using Mass Spectrometry data which is the difference between the MRS module.

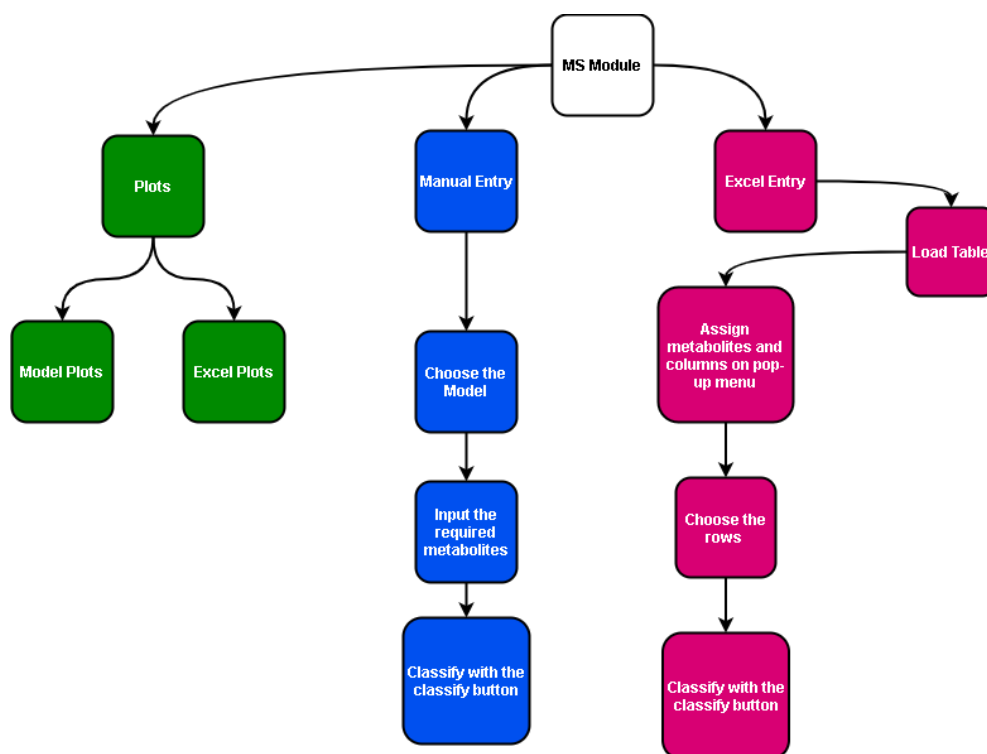


Figure 24: Overview of MS Module

In this module, we offered 4 different models to classify subgroups of IDH and TERTp mutations in gliomas. In the following performance of these models is shown.

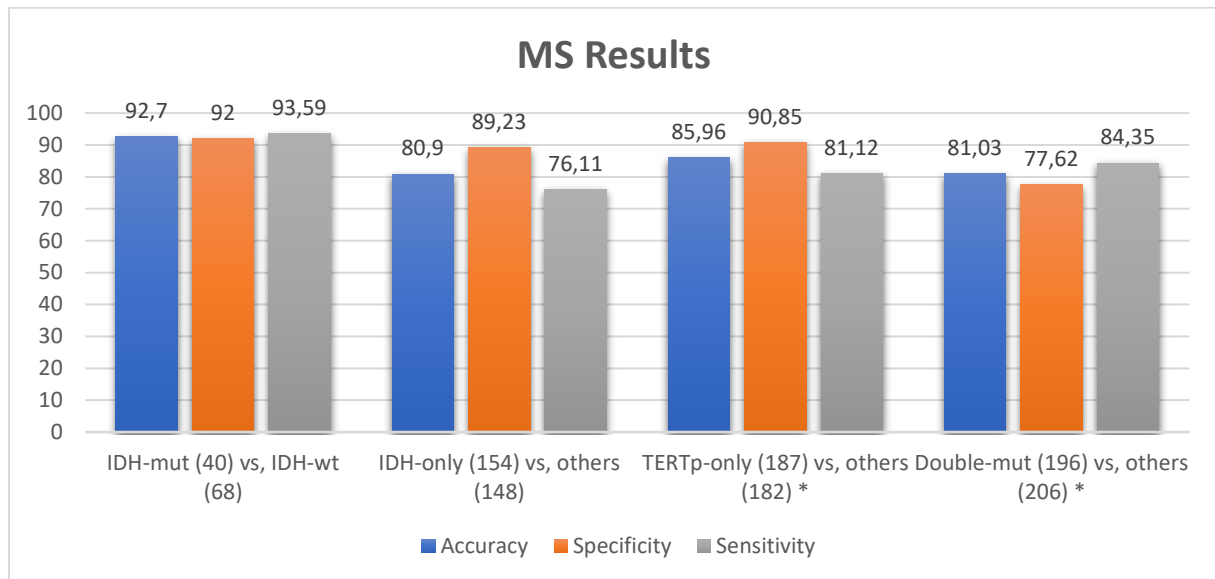


Figure 25: MS Module built-in models' metrics

Advanced User Module

The Advanced User Module (AUM) is planned for customization. Users can train their own models and use them on the tool to classify their input data. Our tool provides visualization as in the Normal User module, synthetic data generator, feature selection methods, validation methods, and summary reports of experiments.

AUM has trainer and classifier parts. In this version, users can update only xlsx files as inputs to train their models.

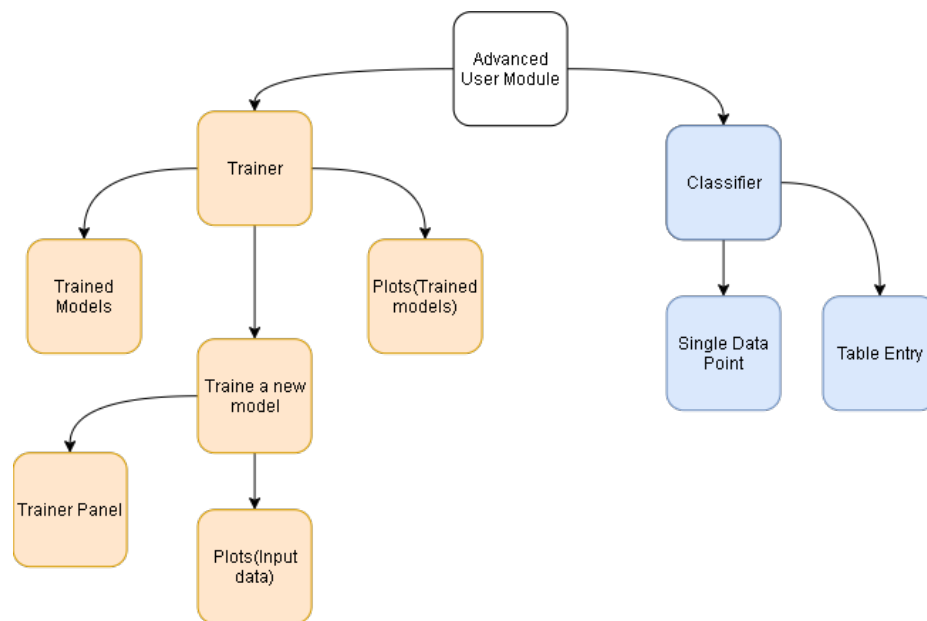


Figure 26: High-level overview of AUM

Trainer

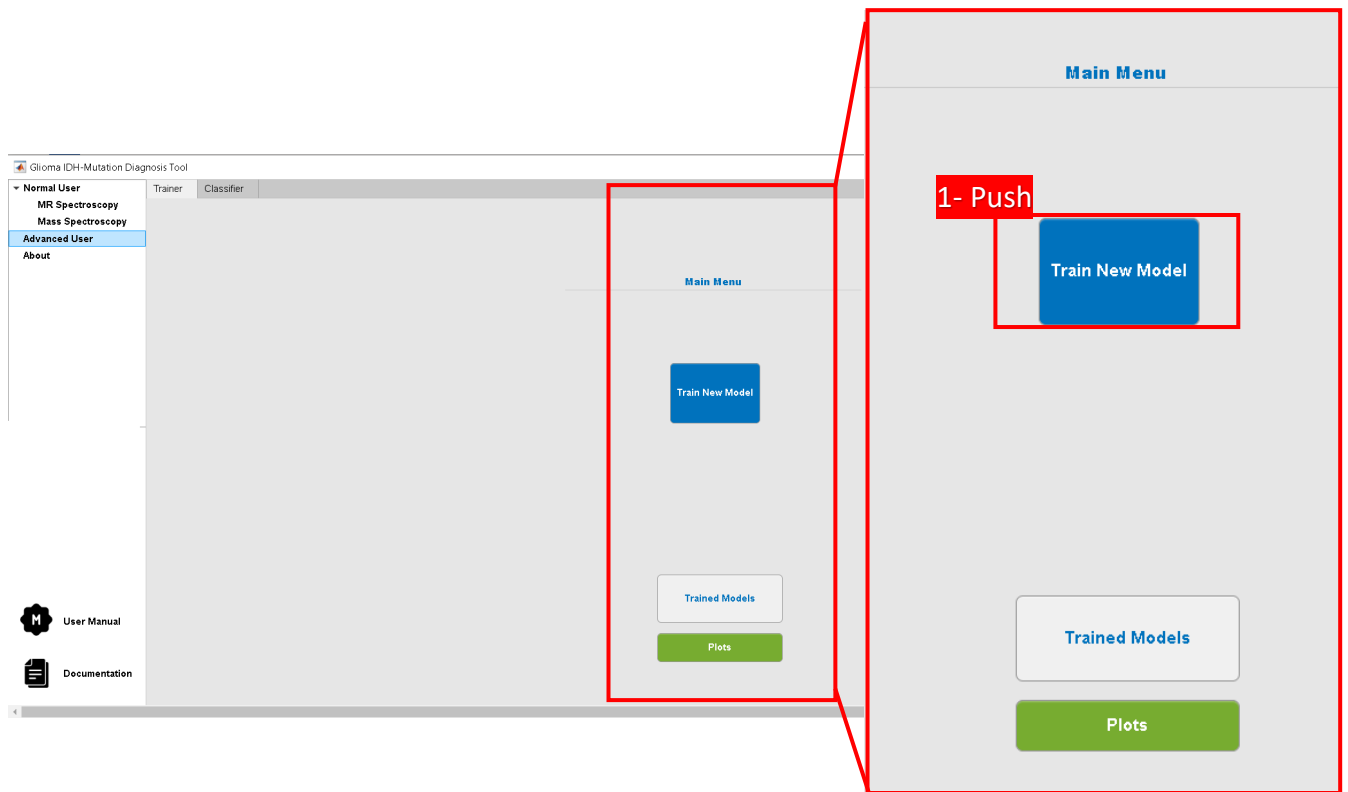


Figure 27: Advanced User Module landing page

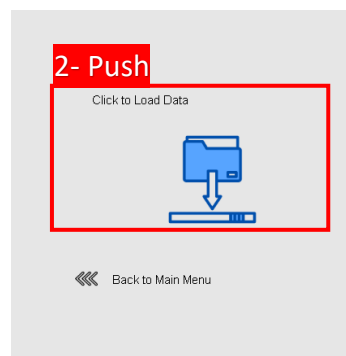


Figure 28: Loading page of AUM

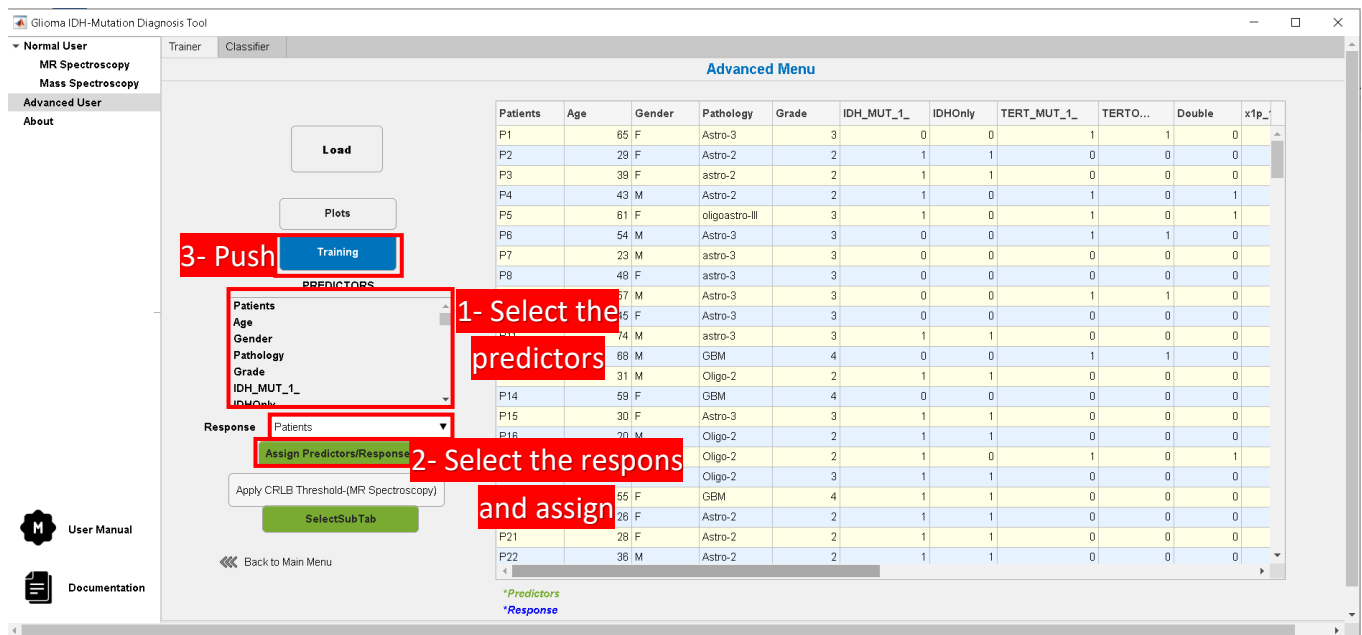


Figure 29: UI of Trainer

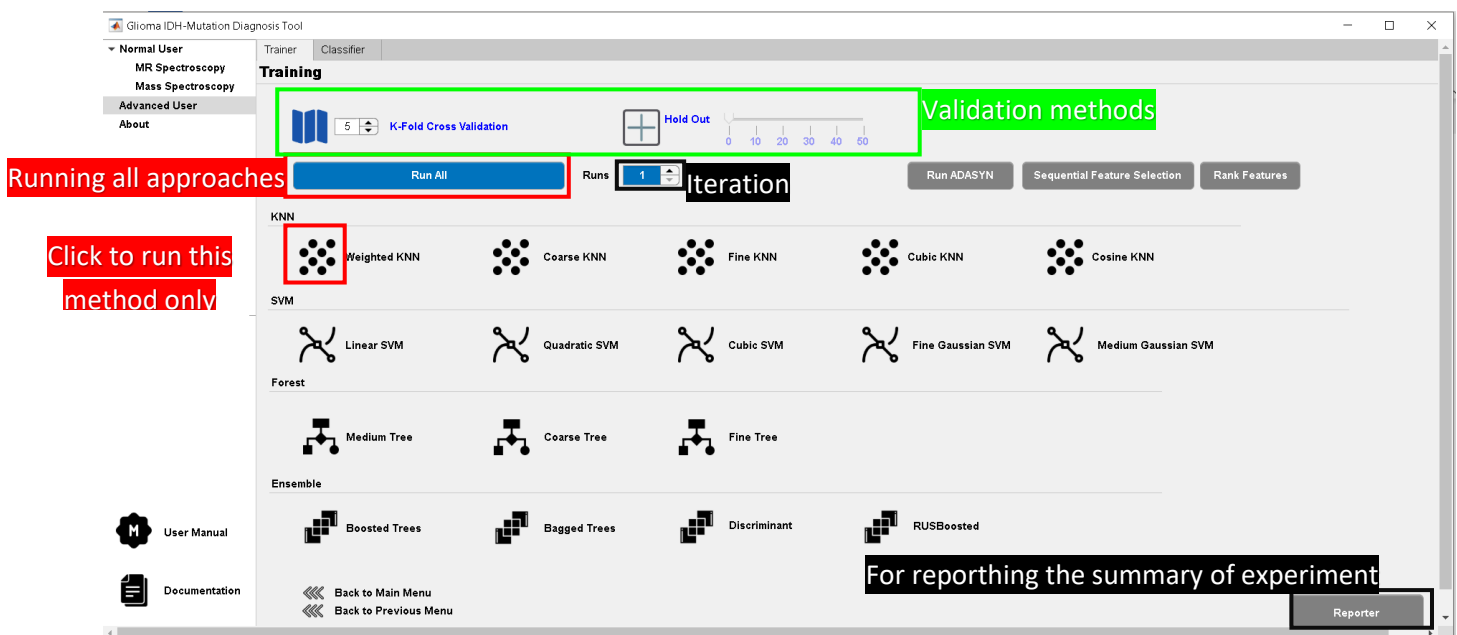


Figure 30: Menu of trainer panel

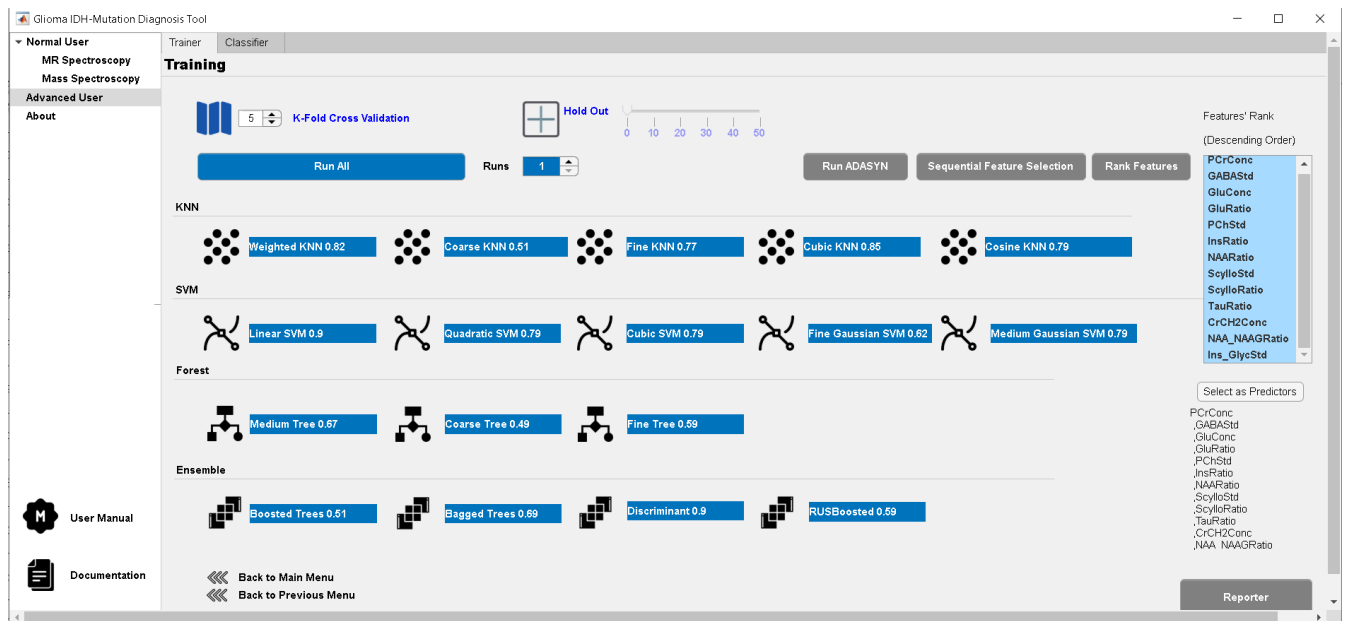


Figure 31: Results after executing 'Run All'

For saving the models that we trained users should press icons next to the models that they want to save. After clicking the icon a new pop-up will open as shown in the following figure.

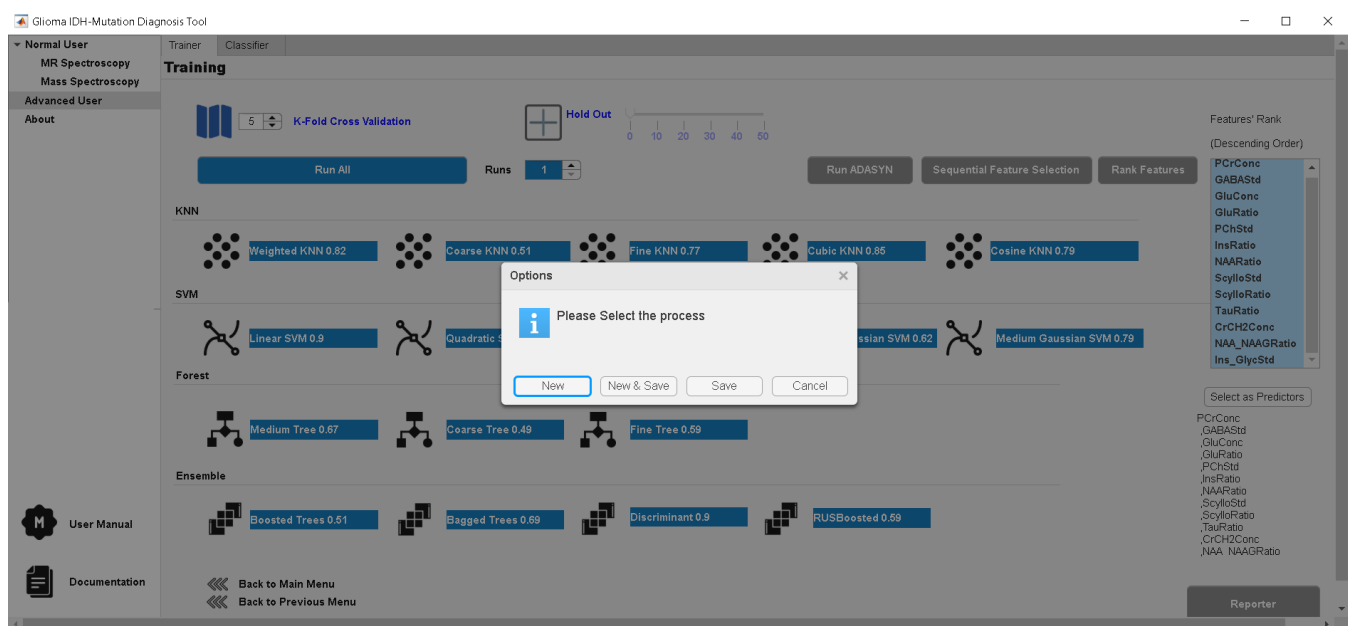


Figure 32: Saving UI

For training new model please press new button. This button will train the model but will not save it anywhere. It is planned for fast investigating. If you want to create a new model and save it please press the New&Save button. If you want to save the trained model please press the save button.

Classifier

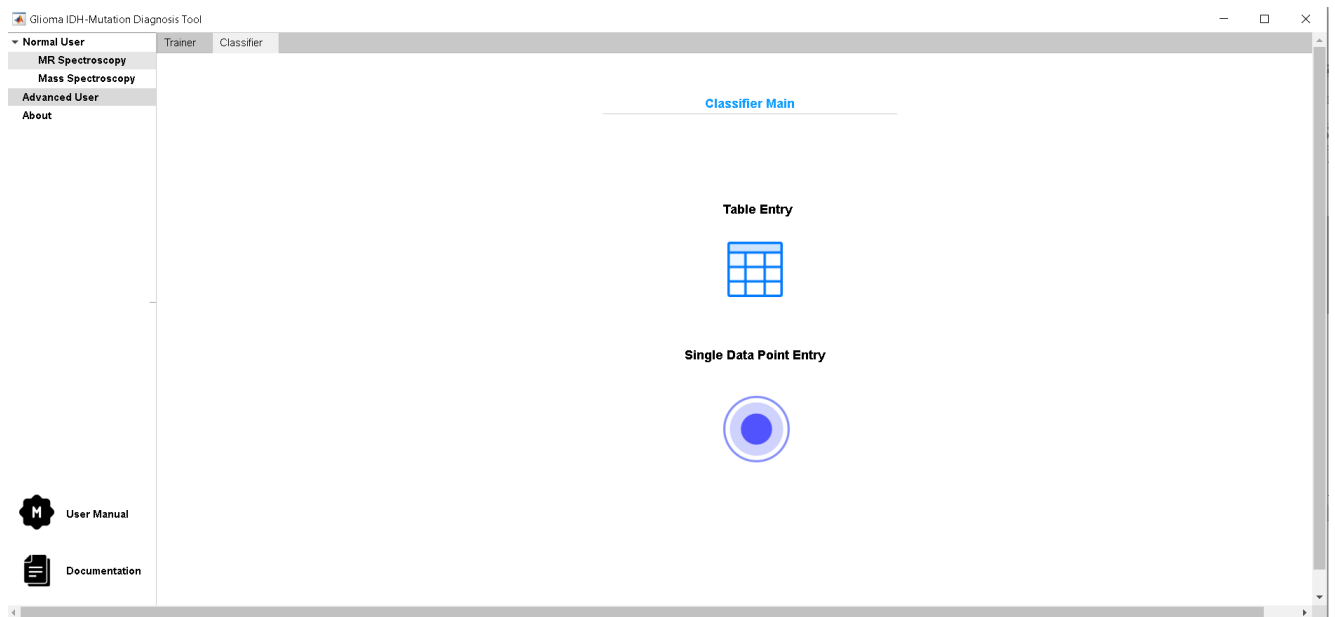


Figure 33: Landing page of classifier

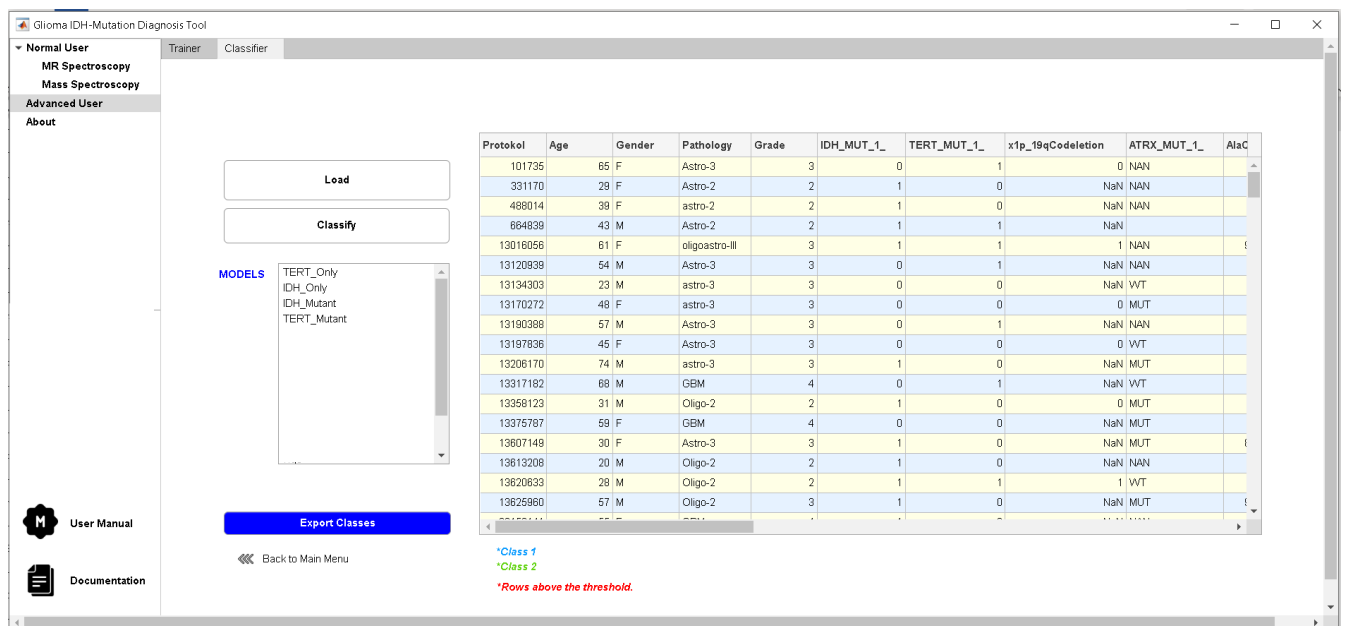


Figure 34: UI of classifier

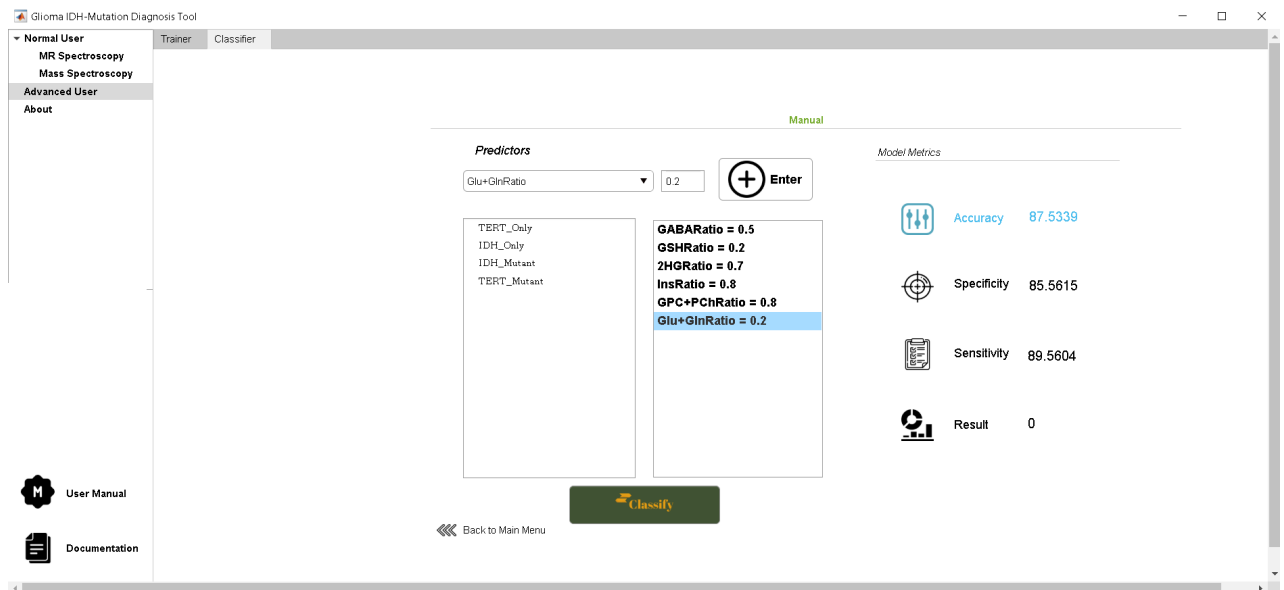


Figure 35: UI of Single Data Point Entry

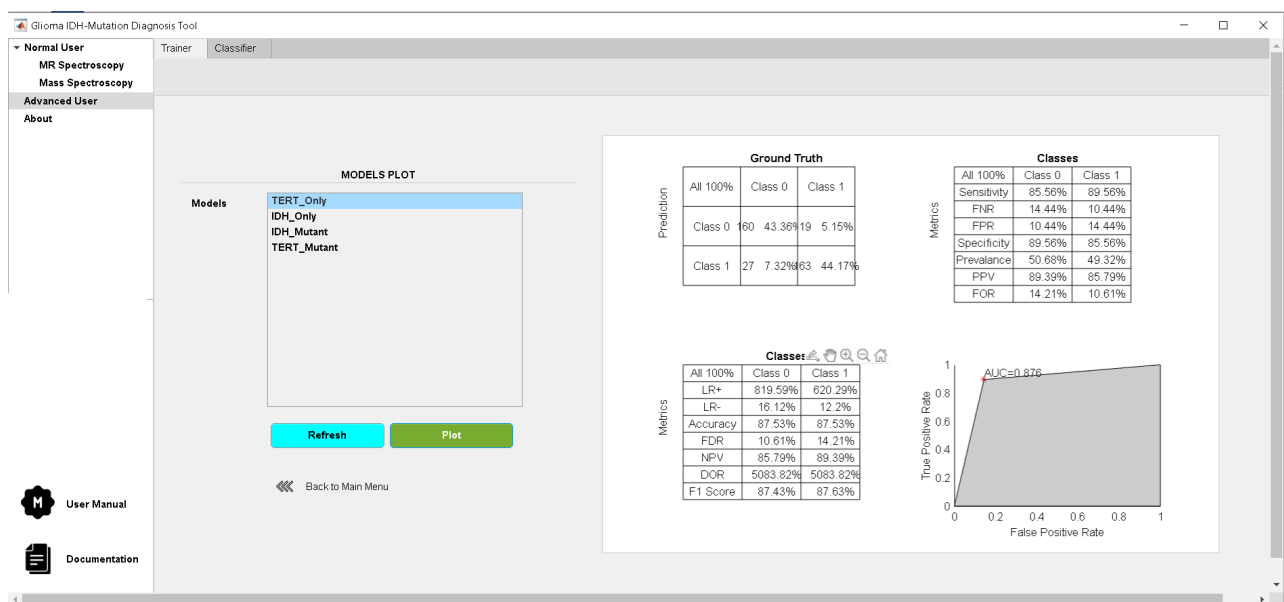


Figure 36: Model plot menu

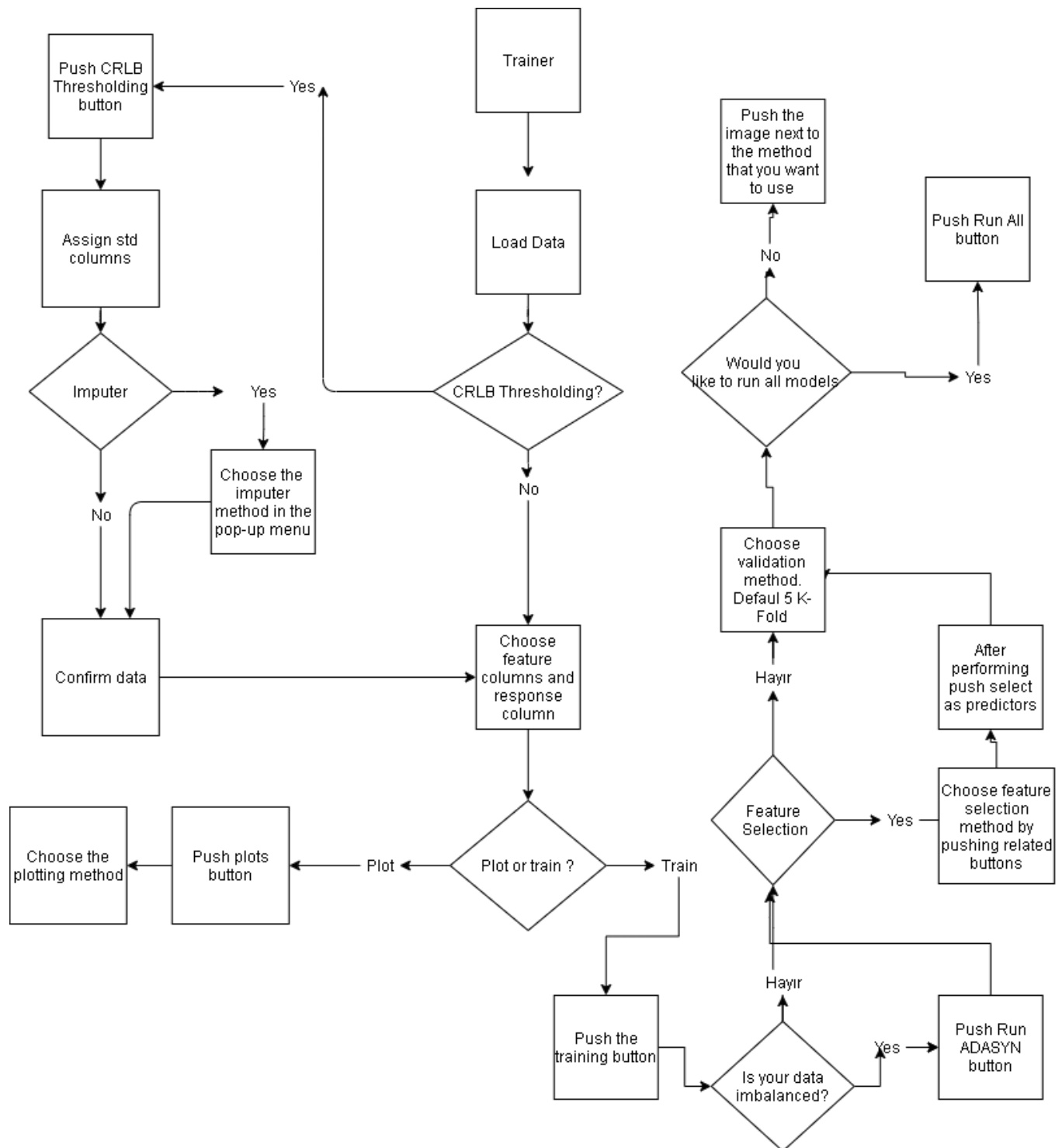


Figure 37: Flowchart of Trainer Module

About

This project has been funded by TÜBİTAK 1003 grant 216S432. Computational Imaging Lab (CIL) which is located in the Biomedical Institute of Boğaziçi University will maintain this application software. This software is publicly available on GitHub (<https://github.com/Computational-Imaging-LAB/IRIS-MRS-AI>). This project has been accepted to ISMRM 2021.

For citation : Bas A, Sacli-Bilmez B, Hatay GH, Ozcan A, Levi C, Danyeli AE, Can O, Yakicier C, Pamir MN, Ozduman K, Dincer A, Ozturk-Isik E. Glioma Genetic Diagnosis Software for Detection of IDH and TERTp Mutations based on 1H MR Spectroscopy and Mass Spectrometry. International Society for Magnetic Resonance in Medicine. Vancouver, Canada May 15-20, 2021. (digital poster)



Figure 38: Landing page of About