

Jaqpot5 tutorials

Jaqpot 5: How to simulate
biodistribution scenarios using
custom PBPK models

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| USE: | How to simulate biodistribution scenarios using custom PBPK models |
| VERSION: | V.1.0 |
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INTRODUCTION

Jaqpote 5 is a user-friendly web-based e-infrastructure that allows model developers to deploy their predictive models and share them through the web. The Jaqpote 5 GUI directs the model developers to further document their models in a way that can be easily understood and used by end-users with little or no experience on machine learning and statistical analysis. The GUI also allows the end-users to apply the models on their own data for validation and/or prediction purposes and the results are collected and visualised in automatically generated tables, graphs and reports. All major machine learning and statistical data-driven algorithms are supported in Jaqpote 5, by integrating popular libraries such as the Python Scikit-learn and the R Caret libraries. Jaqpote 5 has been designed as a generic modelling and machine learning web platform, but particular emphasis is given on serving the needs of the chemo/bio/nano/pharma/ communities by integrating QSAR, biokinetics, dose-response and read-across models. Jaqpote 5 has been developed by the [Unit of Process Control and Informatics](#) in the School of Chemical Engineering at the National Technical University of Athens.

This document provides a tutorial for simulating biodistribution scenarios using custom PBPK models that have been deployed on Jaqpote5. The resource has been made available at <https://app.jaqpote.org/>.

HOW TO ACCESS A CUSTOM PBPK MODEL

An important module introduced in Jaqpot 5 is custom PBPK models that have been deployed through a developed R client. A Jaqpot user can run simulations using these models, e.g. generate forward and reverse dosimetry scenarios, provided that he has access to a model through the organization she/he is part of.

After logging into Jaqpot, the user is directed to Jaqpot's Home page, from where he can go to the models section by clicking the 'Models' tab on the left banner of the screen (Figure 1).

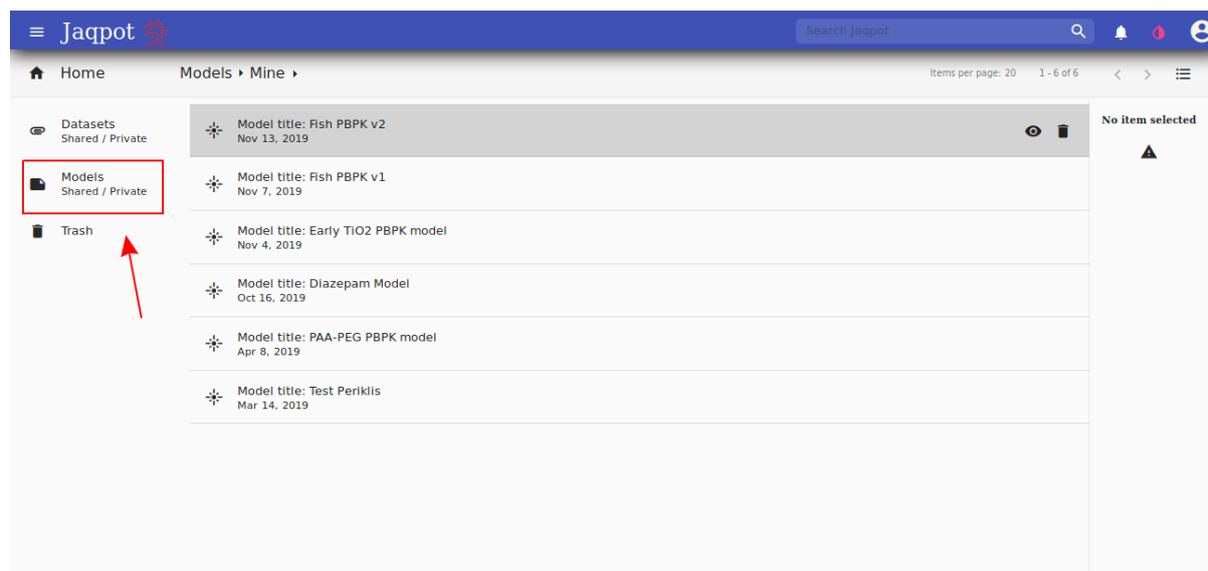


Figure 1. 'Models' Tab

The initial screen includes models deployed by the user, private and shared ones. In order to access models that have been shared to the user via organisations, the user should click on the arrow right next to the 'Mine' tab on the top of the screen and then click the 'Shared' button (Figure 2).

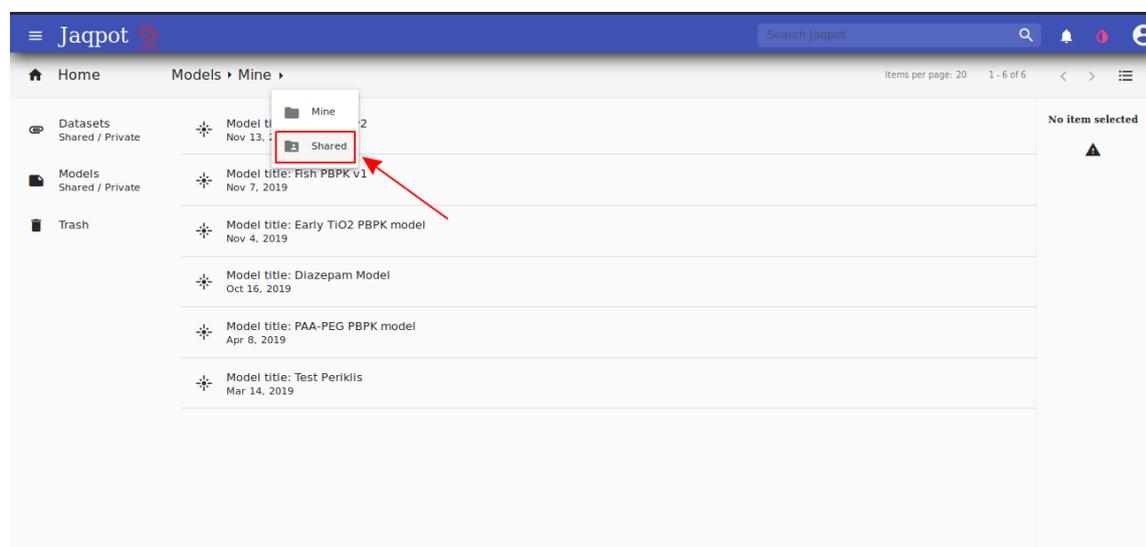


Figure 2. Selecting Share models

Following that, the user can access a specific model by clicking on the 'View' button, which is located on the far right end of the model's row (Figure 3).

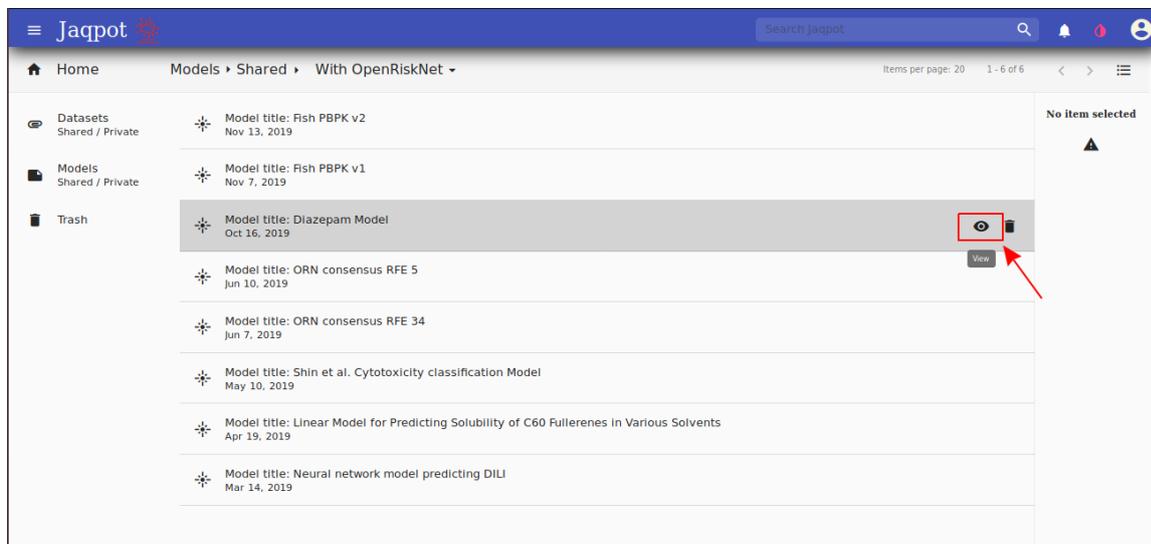


Figure 3. Clicking on the 'View' tab

MODEL ENVIRONMENT

The model environment comprises 4 tabs: 'Overview', 'Features', 'Predict/Validate' and 'Discussion'. The 'Overview' tab provides a coarse description of the PBPK model, as well as specific directions which refer to the model, e.g. how to fill in the input section (Figure 4).

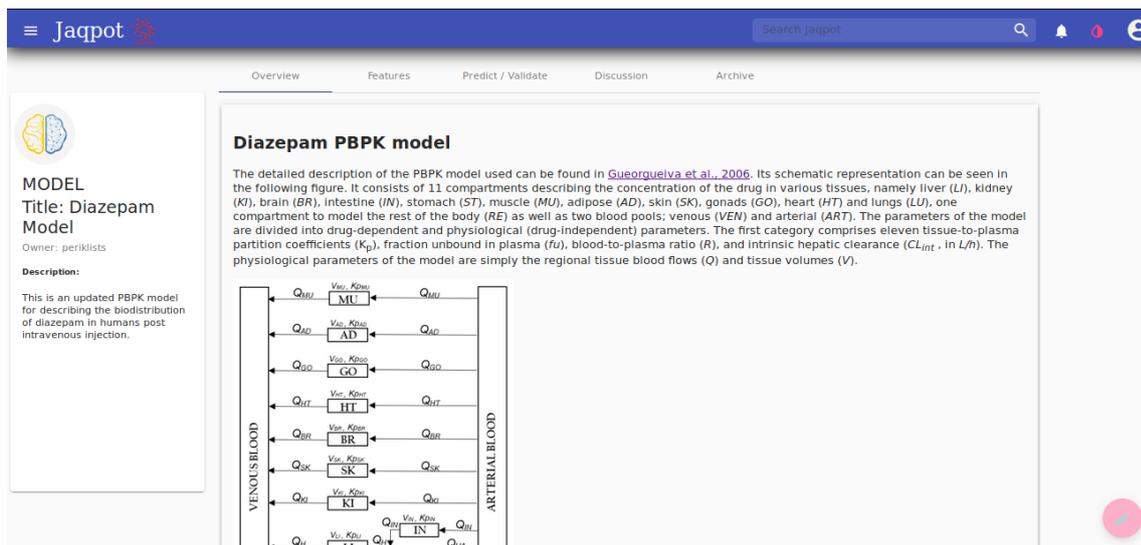


Figure 4. 'Overview' tab of the Diazepam model

The 'Features' tab informs the users about the dependent and independent features; each feature comes with description and units (Figure 5).

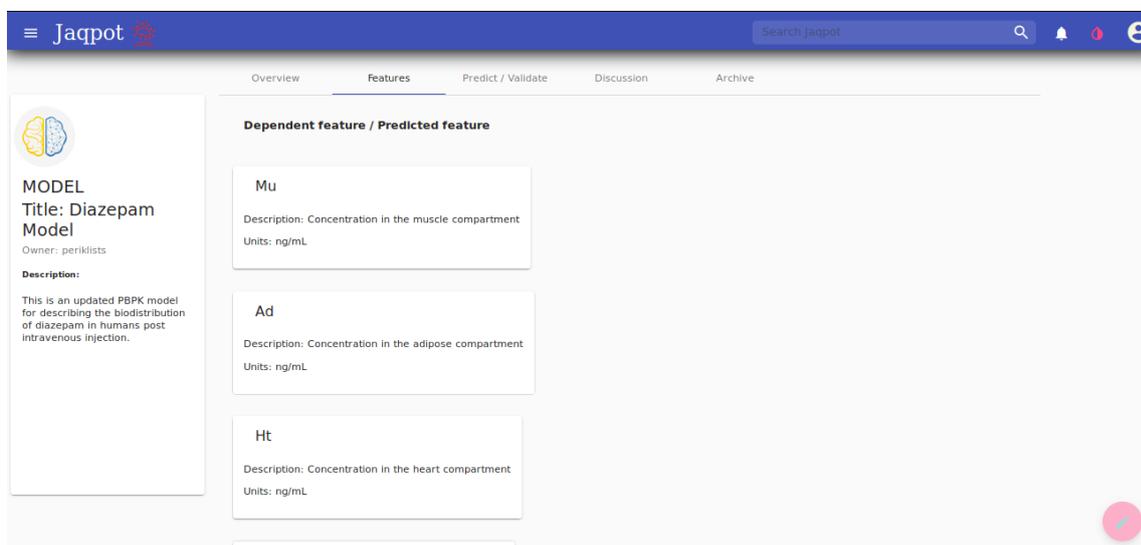


Figure 5. 'Features' tab of the Diazepam model

The 'Predict/Validate' tab is the core of the model environment. Here, the user can provide an instance of the independent features and acquire the model predictions, which, in the case of PBPK models consist mainly of concentration or mass- time profiles. The user can provide the input in two ways: the first one is through uploading a csv file containing the respective information and the second one is through filling in the input directly in Jaqpot's Graphical User Interface (GUI). In case the input consists of many features, it is strongly recommended that the user follows the first method, i.e. download the csv template (Figure 6), fill in the values (Figure 7), upload the complete csv (Figure 8), select 'None' in the pop up window asking for a dataset ID (Figure 9) and then start the prediction process (Figure 10).

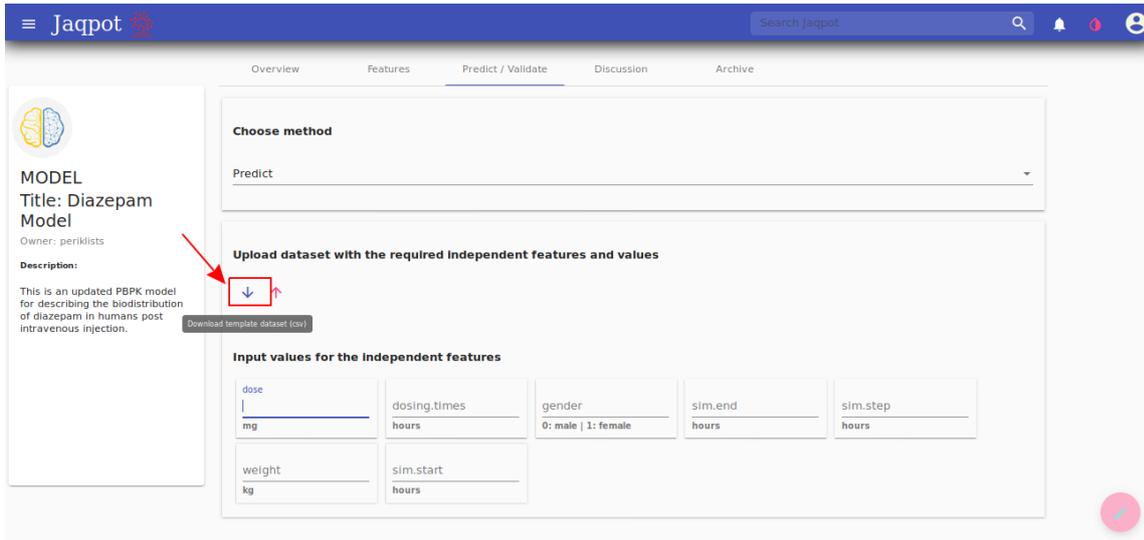


Figure 6. How to download a dataset template in csv format

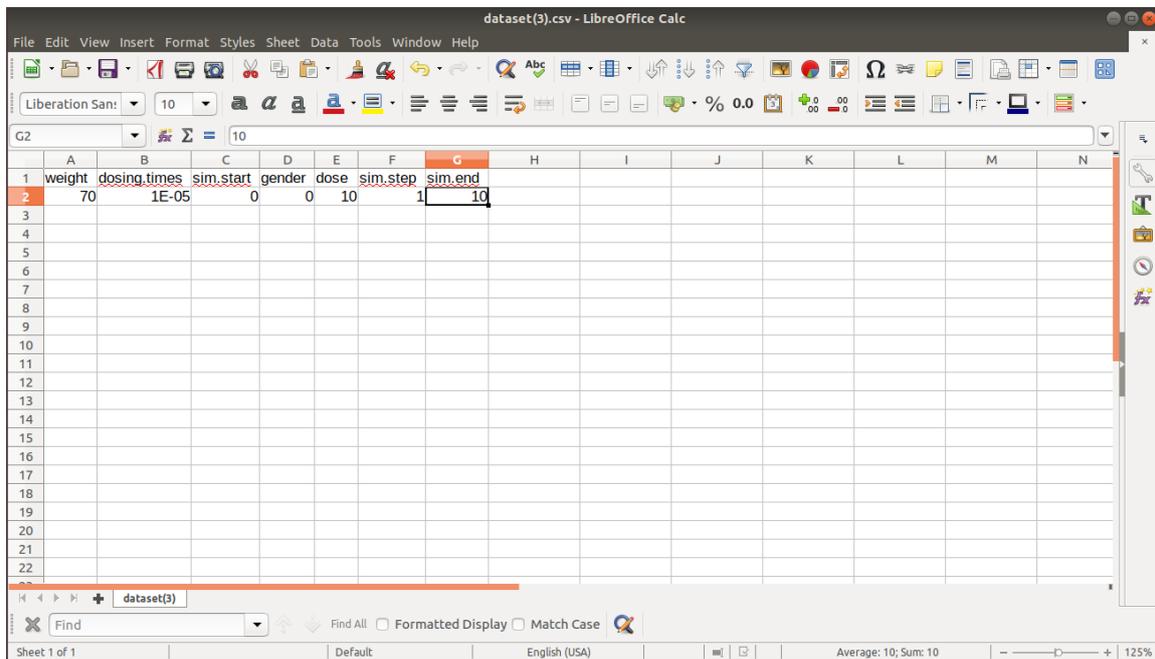


Figure 7. Complete the csv with appropriate values

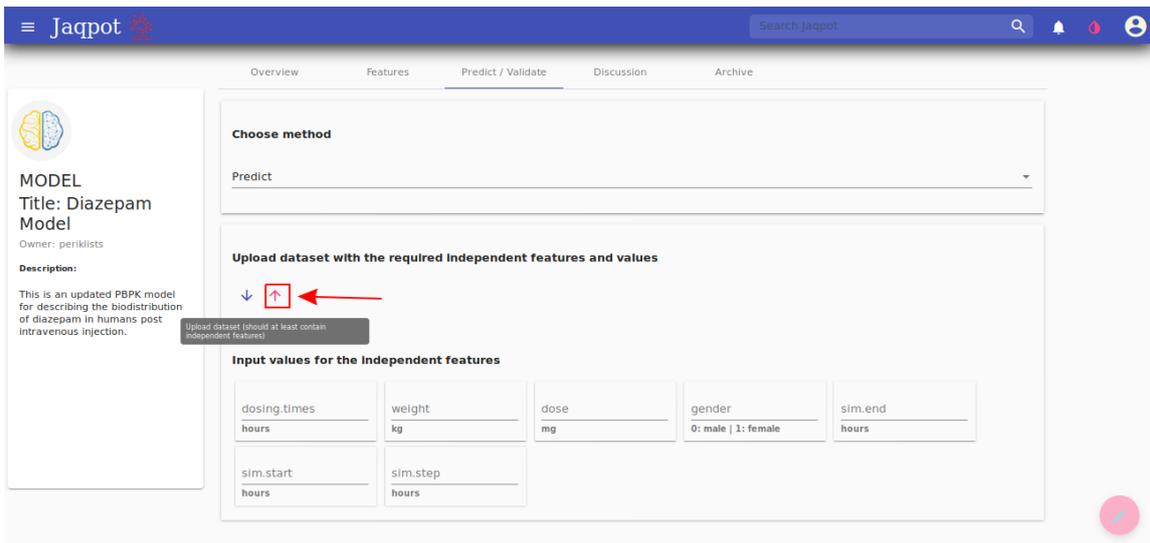


Figure 8. Upload the complete dataset

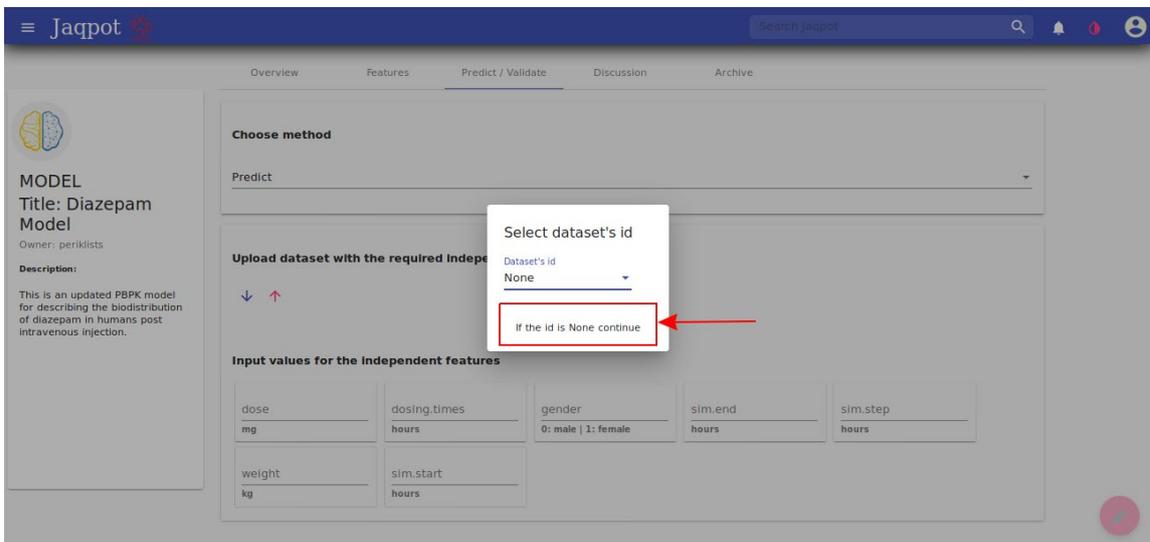


Figure 9. Select 'None' in the dataset id and then click on 'continue'

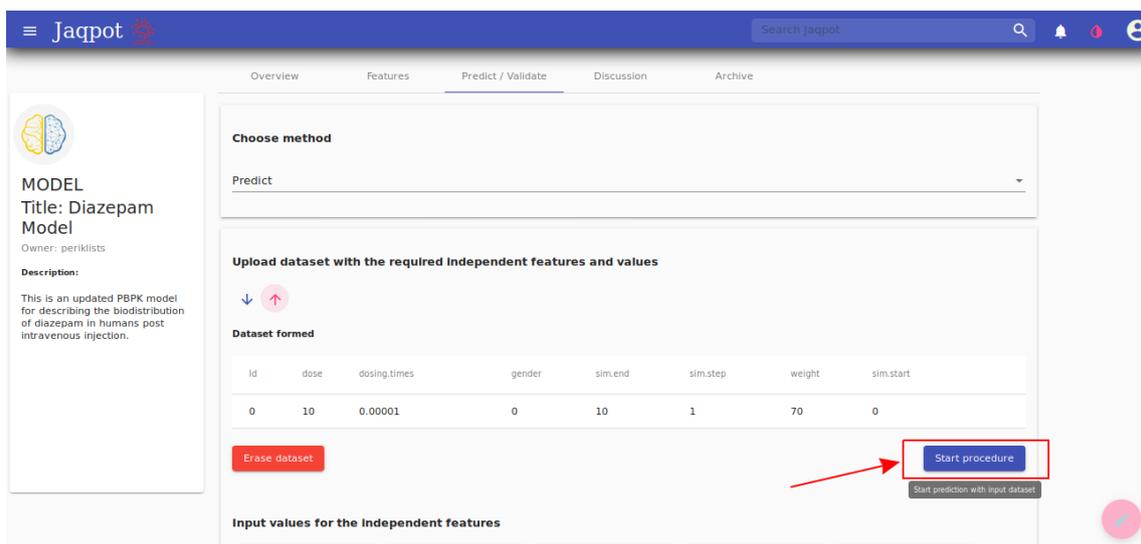


Figure 10. The upload process unlocks the 'start procedure' button

As it is clear in Figure 10, once the csv is uploaded the user can review the filled values and then press the 'start procedure' button to initiate the prediction, or click on 'Erase dataset' if a mistake is spotted.

It has to be noted that if a model supports vectorized input (e.g. a vector of multiple doses), the user can only provide this kind of input only through the GUI in the following format: [value1, value2, ...] (Figure 11). In this case, the 'Start' button on the bottom right end of the screen appears only after all values have been filled in, so NULL values are not feasible.

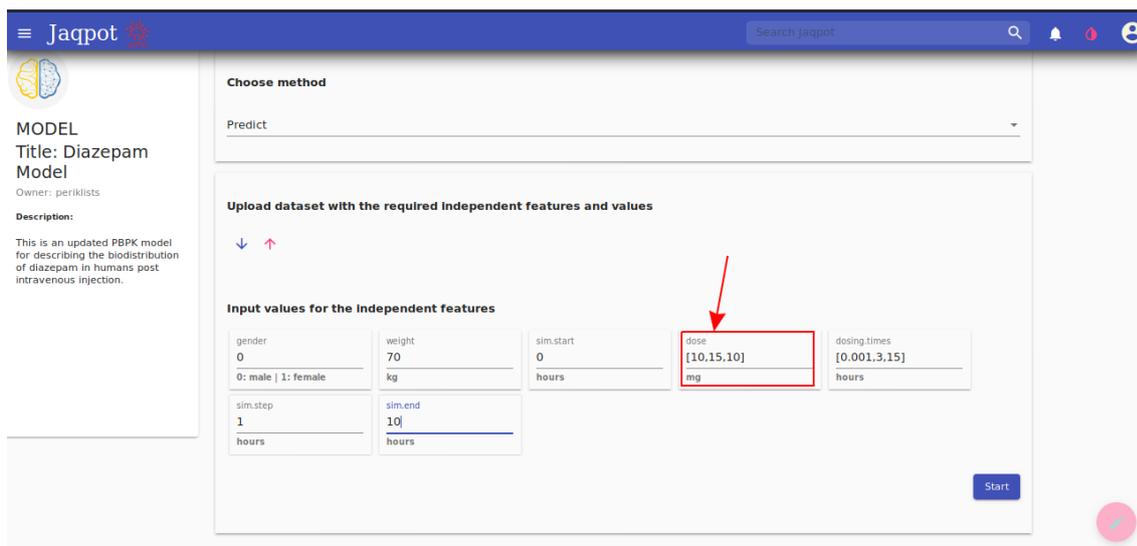


Figure 11. Example of a vector input on the GUI

When the prediction process is initiated, a small log is generated on the screen and, if no error occurs, the user can proceed to the results by clicking on the double arrow icon on the bottom of the screen (Figure 12).

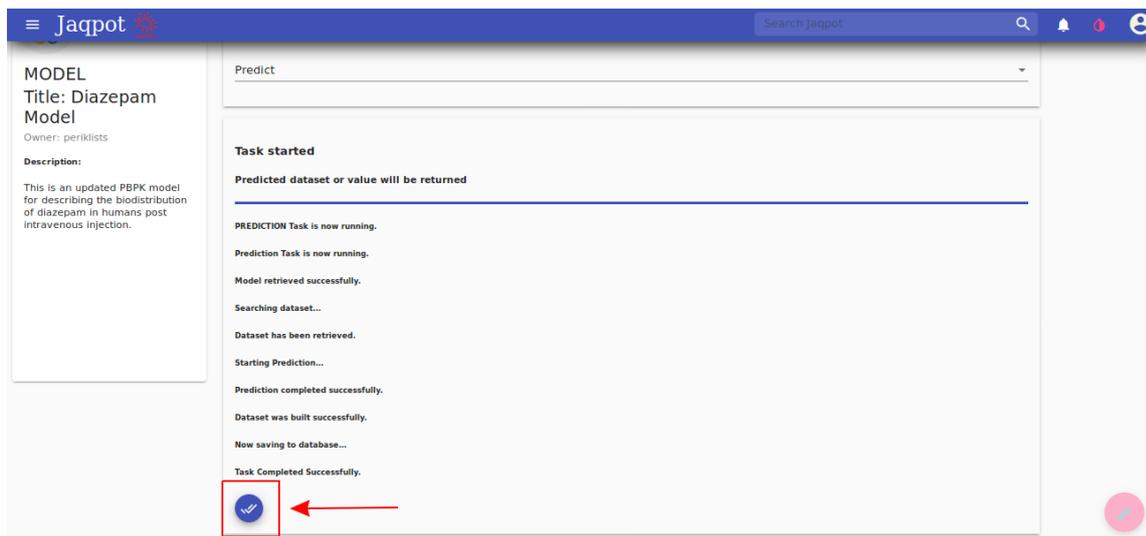


Figure 12. Click on the 'View prediction' icon to obtain the predictions

The results are given on a tabular format on the GUI and can be downloaded for further processing by clicking on the download button (Figure 13).

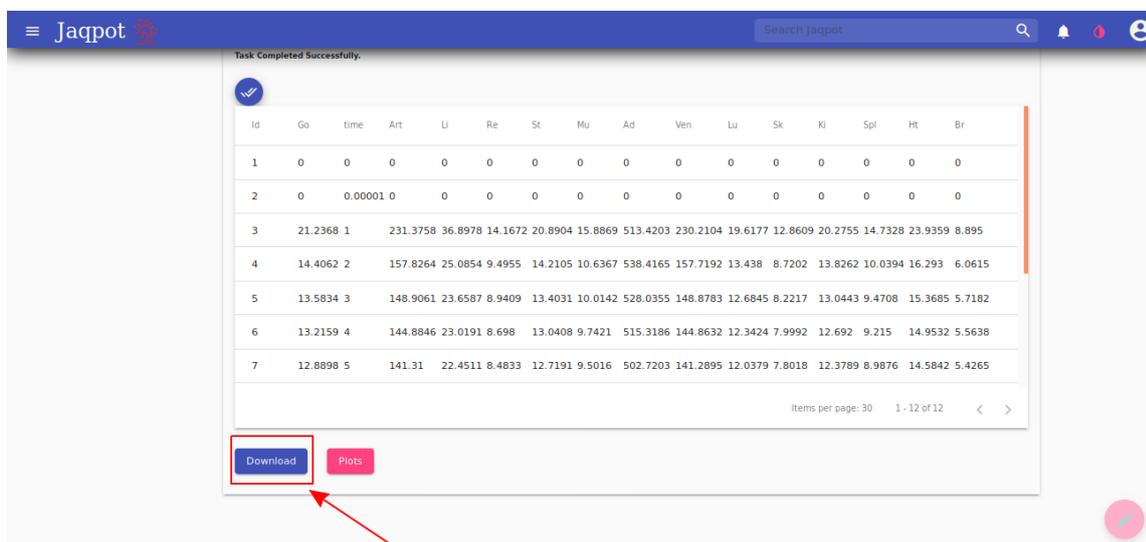


Figure 13. The 'Download' button allows downloading the results in a csv format

The 'Plots' button which is positioned right next to the 'Download' button allows the user to produce plots by selecting the desired dependent features using the drag-and-drop technique (Figure 14). The desired plot then appears under the predictions (Figure 15).

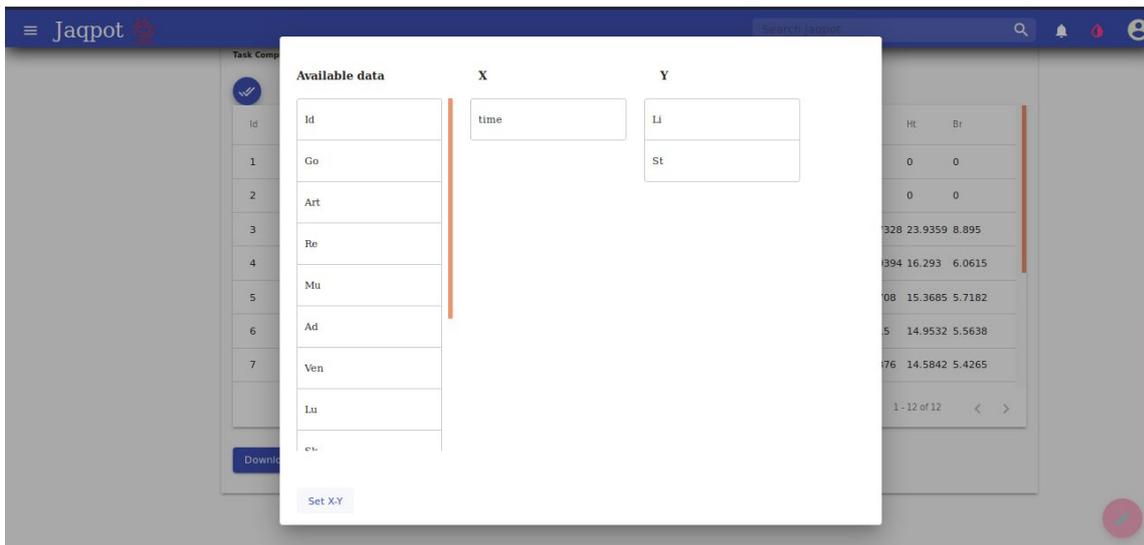


Figure 14. A plot can be generated by dragging and dropping the desired dependent features on the x and y-axis respectively

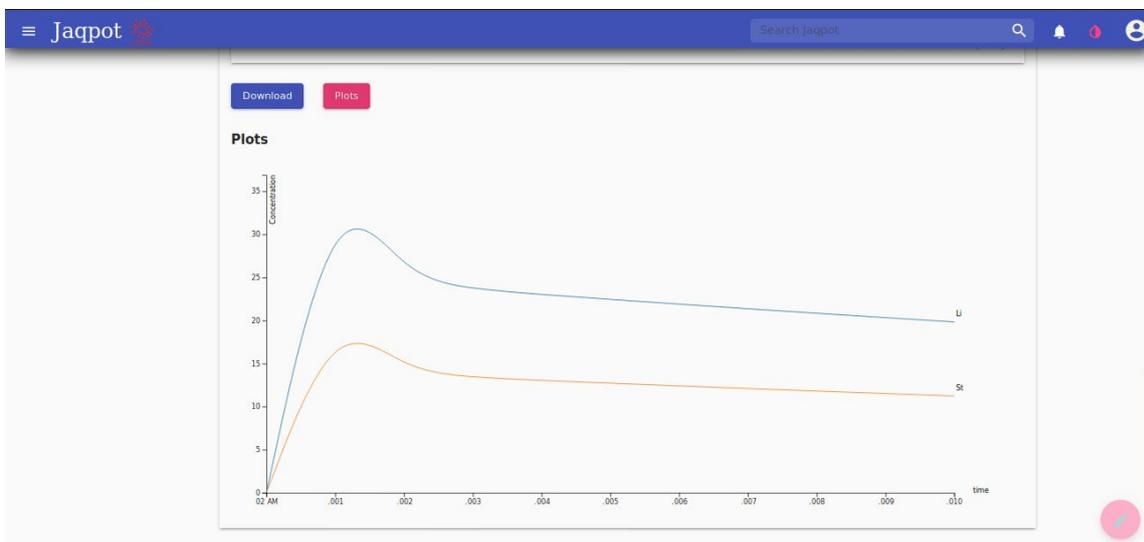


Figure 15. Plot that shows the concentration of diazepam in the liver and stomach compartment

Finally, the user can add comments and remarks or ask a question regarding the model under the 'Discussion' tab (Figure 16).

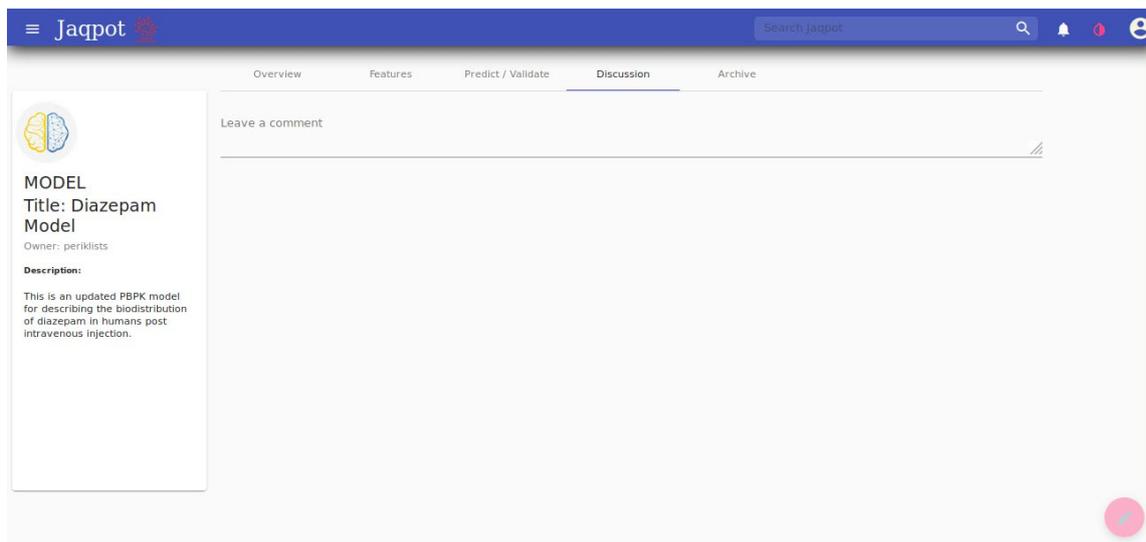


Figure 16. 'Discussion' tab of the Diazepam model

Support

