

JADBio

AutoML Platform

OVERVIEW

A state-of-the-art automated Machine Learning Platform, designed for Life Scientists, enabling them to effortlessly make new discoveries and extract knowledge from publicly available or own-study data, without the need for coding



How Does it Work?

You start by generating all your study data. That could either be data that has been processed and normalized by a Bioinformatician, or public data available in the known data repositories. You JUST upload that curated dataset to the JADBio app in a .csv or other delimited file format, select the desired predictive outcome, and watch the tool perform the analysis. Most analyses complete in a couple of hours.

Will it Work with My Data?

JADBio can work with any of the following data types:

- DNA
- RNA
- Protein
- Metabolites
- Single cell (any type)
- Sequence Data (SNP, methylation, etc.)
- Clinical
- Signals (EEGs, etc.)
- Images

And any combination of the above...

What Can I Predict with JADBio?

- Disease Status (Diagnosis)
- Disease Subtype
- Response to Treatment
- Phenotypic Trait
- Time to Event (Death, Metastasis, Relapse)
- Other discrete or continuous quantities

What Do I Get as a Result?

Our Auto-ML analysis provides you with:

01 Predictive models that could also be applied on new data	02 A set of most-relevant to your question predictive biomarkers (biosignatures)
03 Many visualizations to interpret results	04 Decision support information to apply model

JADBio identifies accurate predictive models that use as few biomarkers as possible.

JADBio Benefits

01 Achieves an unprecedented level of automation in performing AI-based analysis	02 Focuses on knowledge discovery applying novel feature selection algorithms		03 Keeps getting better with usage employing meta-level learning, i.e., ML on the ML results
04 Can also handle molecular data (low sample, high dimensional)	05 Simultaneously handles different data types (multi-omics, genetic, medical images, medical signals, etc.)		06 Correct and unbiased methodology
07 Bio-specific functionalities, featuring Survival analysis, bio-specific data preprocessing		08 Deep tech, Novel tech. Not just connecting existing black-box algorithms; developing new algorithms to solve open problems	

AUTOMated Machine Learning in 5 steps

Prepare the Data for Analysis

- 01 Create your JADBio project
- 02 Upload your curated, own-research or a publicly available dataset



Perform Predictive Analysis

- 01 Select the outcome to predict by
JADBio will perform a

Classification if the outcome to predict is binary
e.g. case-control, categorical or different cancer types

Regression if the outcome is continuous
e.g. the viral load

Survival Analysis if the outcome is the time to an event
e.g. death, relapse, etc.

- 02 What predictive performance metric would you want to optimize for?

AUC, Accuracy, F1 Score

R2, Mean Squared Error

Concordance Index

Discover Knowledge

- 01 Automatically get the biomarkers that collectively lead to optimal predictions.
- 02 Examine their role in predictions and added-value within analysis results.



Interpret the Results

The analysis of your data produces a wealth of visuals, plots, and graphs for interpretation of the model

- ROC and Precision-Recall curves for optimizing classification thresholds
- ICE graphs visualizing the prediction dependency on specific feature values
- PCA / UMAP plots on the signature markers showcasing sample distribution as per the predictive model
- Kaplan-Meier curve for stratifying to low/medium/high risk groups
- Predicted Probabilities Distribution plot for each class (categorical outcomes)
- Other graphs/plots

Apply the Trained Model

How do you intend to apply the trained model?

- Validate model against labeled samples
- Predict outcomes for unlabeled samples
- Explore what-if scenarios (manually entered predictor values)
- Download the model to make predictions off-line



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<https://jadbio.com>

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Or contact us at social@jadbio.com for a demo