H2O.ai and Snowflake Partner in Health





Automated Machine Learning for

DNA Analysis

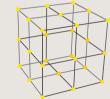
The Data

DNA information is distributed across more than 20,000 genes and half a million clinically relevant mutations. There are nearly 22,000 columns of data in the gene sequences of each patient which H2O.ai and Snowflake can process in mere seconds.

			_

Autogenerated Code

Convert VCF files to a dataset that is suitable for machine learning. The SQL is dynamically generated and predictions are automatically created for every single patient in the table in a matter of seconds.



Machine Learning

Evaluate patient risk of disease and understand how common this risk has been among past patients. The pretrained model that best fits the data is automatically selected from all available models.

The Solution

Model Interpretability

Automated drift detection identifies any variance between the training data and the specific table being used for model scoring. Model transparency reveals which specific cellular pathways have played a role for the diagnosis.



H2O Gene Mutation AI is a machine learning-powered patient risk assessment application that uses the Snowflake Data Cloud to bring intelligent clinical decision support directly to clinicians and provide advanced analytics for pharmacogenomics and pharmacovigilance pipelines.





Explainable Insights

Shapley reason codes provide insights at the local gene level and at the global level for the entire population represented in a given table. Different distributions show how an individual's results compare to those of similar patients.

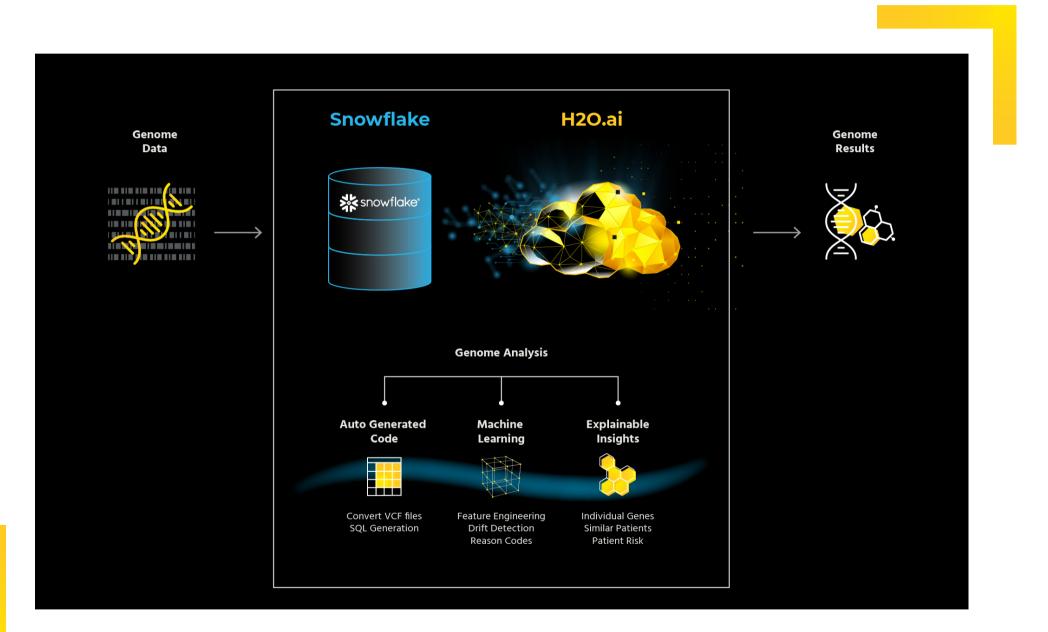


How it Works

H2O Gene Mutation AI combines the Snowflake database and the H2O AI Cloud to bring intelligent clinical decision support directly to clinicians and provide advanced analytics for pharmacogenomics and pharmacovigilance pipelines.

DNA data can be massive, which makes the Snowflake Data Cloud an ideal place to store, cleanse and prepare the data for analysis.

H2O.ai's advanced machine learning pipeline processes massive datasets and extracts valuable information based on a patient's mutation profile.





Core Capabilities



State-of-the-Art Clinical Decision Support

Make AI part of the triage process, leveraging ML and patient data tables to evaluate disease risk.



Identification of Similar Patients

Look up tables of historical patients whose outcomes are known, find the most similar ones to the specific patient and understand the similarities. 00

Discover the Drivers for Individual Risk

Visualize and explore drivers automatically extracted from ML algorithms to estimate patient risk and store that output in table format.



Evaluation of Demographic Biases

Use historical patient tables to evaluate any unintended biases in the model due to lack of demographic diversity in the patient population.



H2O.a



Explore Avenues for Therapeutic Interventions

Understand how patient risk is affected by various factors, in a dose-response type what-if analysis, and store the results in tables.



Integration of Multiple Data Types

Leverage a variety of data types, tables with different molecular results, clinical measurements, or medical notes for the same patients to further refine the disease model.

Local and Global Insights

01

Information Gauge and Shapley Graph

The Gauge offers visually the patient's risk to the disease. The same information is presented within the relevant text at the top of the panel. The text also offers the classification of this patient as having HIGH or LOW RISK based on the risk score.

The Shapley plot to the right of the panel shows the patient's genetic contribution to the reported risk (grey bars, label local), in comparison to the average contributions across the cohort (yellow bars, label global).

Each bar is one gene of the top ten most contributing genes for this patient and indicate a contribution towards high or low risk, respectively.

Information: Gauge & Shapley Graph

Gauge

The Gauge is color-coded to indicate high or low-risk patient.

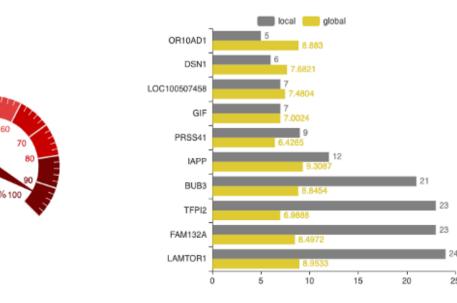
Shapley Plo

he Shapley plot shows the contribution of each feature towards the estimated risk. Consider the following when inspecting the Shapley graph

- Only the top 10 contributing features for the current patient are shown.

has been predicted to be predisposed for HIGH RISK with a prediction value of 94.23%. The determinant factor for moving the prediction towards High Risk is the mutation burden of gene Patient HG02481 LAMTOR

Patient: HG02481 Prediction: 94.23%



snowflake[®]

Shapley series (gray) corresponds to the current patient. Global Shapley (vellow) refers to the cohort and is the average of all shapley values for each patient in the dataset

Negative shapley values indicate that the feature is driving the prediction towards 0 (low-risk). Positive values are driving the prediction towards 1 (high-risk)

Similar Patient Comparisons

02

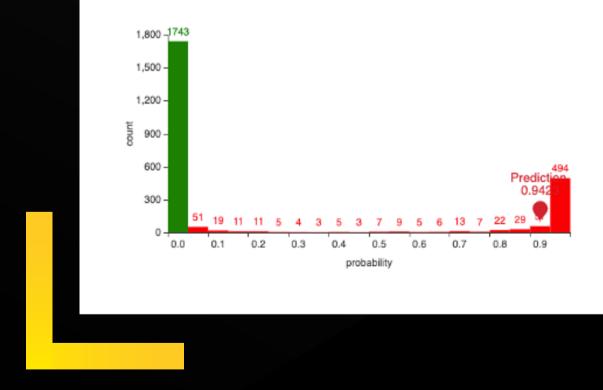
Histogram

This panel helps evaluate how confident we should be in declaring a patient with this specific risk score (Gauge) as HIGH or LOW RISK.

The histogram shows how risk is distributed across the entire patient cohort. LOW RISK is marked with green color and HIGH RISK with red. The selected patient's risk is highlighted with a pin in the right position.

The further right a HIGH RISK patient is the better confidence in the evaluation. On the other side, the further left a LOW RISK patient is the better.

specific probability in the cohort.



snowflake[®]

H2O.ai

The following histogram shows the distribution of predicted risk in the train dataset. Comparing this distribution with the estimated risk for the selected patient, offers intuition on how common it is to find this

Individual Patient Risk

03

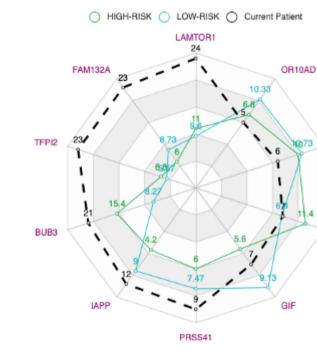
Radar Plot

A radar plot shows the individual patient's risk and identifies the specific factors behind those predictions.

he radar plot offers an explanation of the gene-level similarities and differences between the selected patient and the twenty most similar other patients in the cohort. The results are presented comparatively for the different risk groups. A group can be selected or deselected by clicking on the corresponding label at the plot's legend. Information: Radar Plot

The Radar plot visualizes and compares the mutation frequencies between the selected patient and the identified most simimilar patients, according to their estimated risk groupping. The user can easily compare each attribute in its own axis, as well as in aggregate, as differences in the size and shape of the depicted polygons.

The below Radar plot can help explain why some similar patients fall in different prediction categories.





1





Key Users

Data Scientists



Genomic data is complex to handle at scale. Gene Mutation Al leverages H2O.ai models and Snowflake Data Cloud for speed and scalability, so that each of the technologies work cooperatively.

Pharmacologists



Easily understand geneticallydriven, patient-specific drug efficacy and adverse effects.



H2O.ai

Physicians



With an easy-to-navigate interface that is easily accessible from a tablet or smartphone, physicians can examine a patient's genetic profile and gain insights ondemand.



Benefits



Accuracy

Additional data like other molecular results, clinical measurements, medical notes, images and more can be used to augment the initial model, gain more comprehensive insights and ultimately improve the quality of the patient's care plan.



Trust

Doctors can visually discover the genetic factors that impact individual risk and explore personalized avenues for therapeutic intervention. Model transparency allows doctors to see which specific cellular pathways have played a role for the diagnosis.



Speed

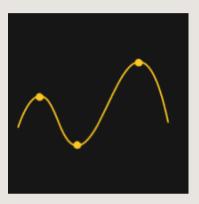
The pretrained model that best fits the data is automatically selected from all available models based on metadata within Snowflake data tables and metadata within the H2O machine learning models. Thousands of rows of DNA data are analyzed in seconds.





Scale

H2O.ai's gene mutation solution is flexible enough to analyze different types of disease outcomes without any additional coding requirements. The application supports multiple pretrained models, so the same patient can easily be examined for their risk of multiple diseases.



Flexibility

The power of Gene Mutation AI is accessible on any computer, tablet or smartphone, allowing physicians to explore the results while making rounds and discussing results at patient bedsides.





H2O.ai



Try For Free