



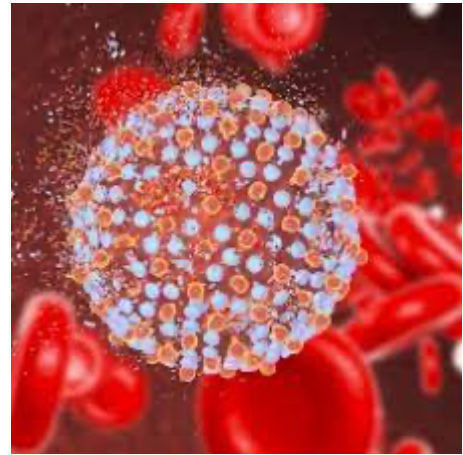
Case Study: Hepatitis C Classification

Hepatitis C Classification

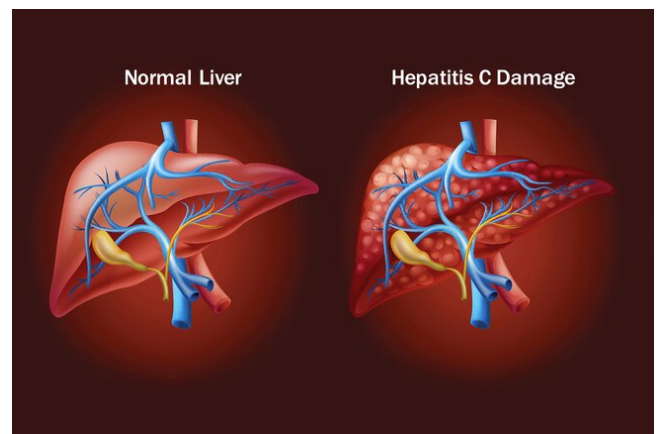


Hepatitis C is a disease caused by the Hepatitis C virus which cause an inflammation of the liver. The virus can cause serious illnesses including liver cirrhosis and cancer. Hepatitis C is a bloodborne virus and transmitted from person to person through unsafe injection, unsafe blood transfusions, injection of drugs and unsafe sexual practices. According to World Health Organization estimated 58 million people worldwide have hepatitis C virus infection and 1.5 new infections occur every year.

WHO estimated that 290000 people died in 2017 due to cirrhosis and liver cancer caused by hepatitis C virus. The effective vaccine for hepatitis C virus has not been available yet. However, the proper use of antiviral medicine can cure almost all patients with hepatitis C. Machine learning approaches can be used to diagnose the hepatitis C virus. The data derived from laboratory reports of blood donor and Hepatitis C patients are used as inputs to the machine learning algorithms which can classify each sample as blood donor, suspect blood donor, hepatitis, fibrosis or cirrhosis.



Source: <https://medlineplus.gov>



Source: <https://www.gandhimedicos.in>

Model Details

Model developer information and all details needed for governance

eethosai

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No.	Component	Values
1	Current Model Risk Rating	Green
2	Area	
3	Usecase	bishow
4	Model Category	Classification
5	Model Dependencies	
6	Model Usage	
7	Model Adjustment	
8	Model Owner	72
9	Model Developer	
10	Model Approver	
11	Model User	<p>[1]Lichtinghagen R et al. J Hepatol 2013; 59: 236-42. Hoffmann G et al. Using machine learning techniques to generate laboratory diagnostic pathways &C" a case study. J Lab Precis Med 2018; 3: 68-67. </p><p>[2]Creators:Ralf Lichtinghagen, Frank Kliswonn, Georg Hoffmann. </p>
12	Model Maintenance	
13	Documentation and Code	
14	Current Model Status	None
15	Implementation Platform	
16	Current Date	Aug 30, 2021

Model Visualization

Details of the Models

eethosai

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input

InputLayer

Dense

kernel (12x128)

bias (128)

ReLU

Dense

kernel (128x5)

bias (5)

Softmax

NODE PROPERTIES

typeDense?

moduletensorflow.keras.layers

namedense

ATTRIBUTES

activationrelu

batch_input_shape null, 12

bias_initializerZeros()

dtypefloat32

kernel_initializerGlorotUniform("GlorotUniform")

trainabletrue+

units128

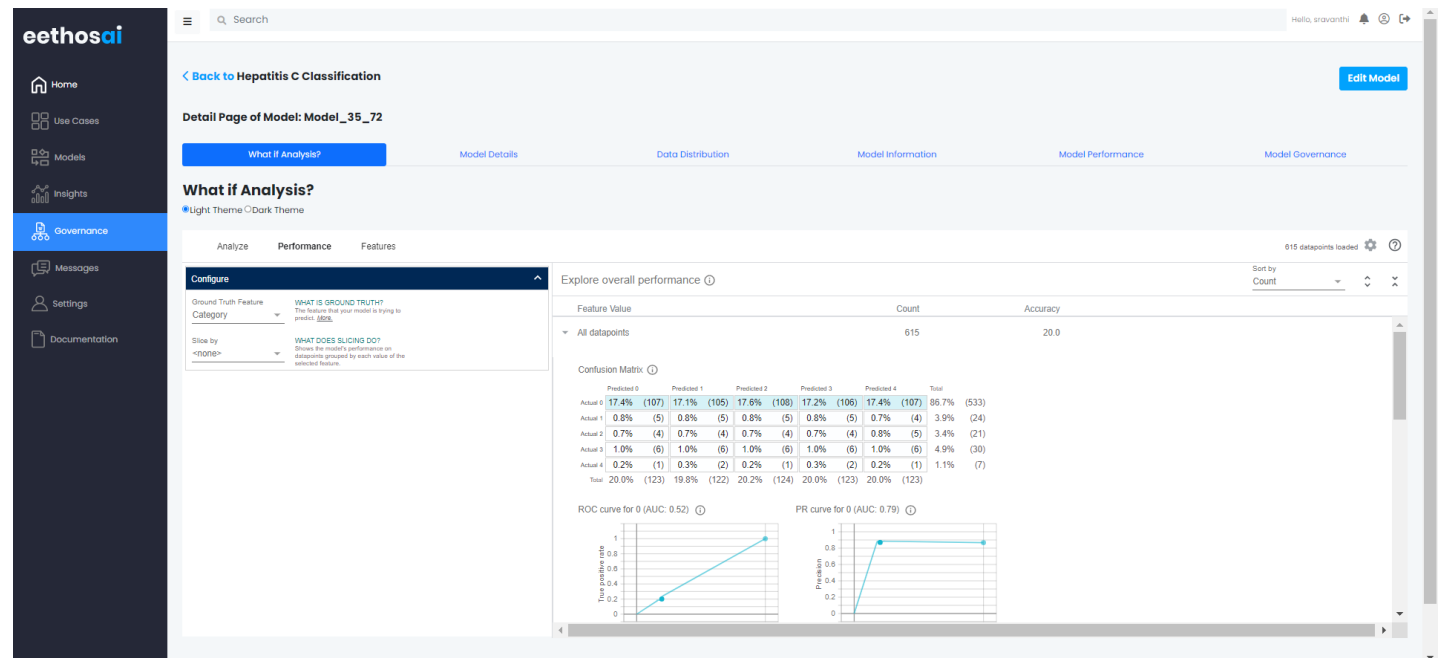
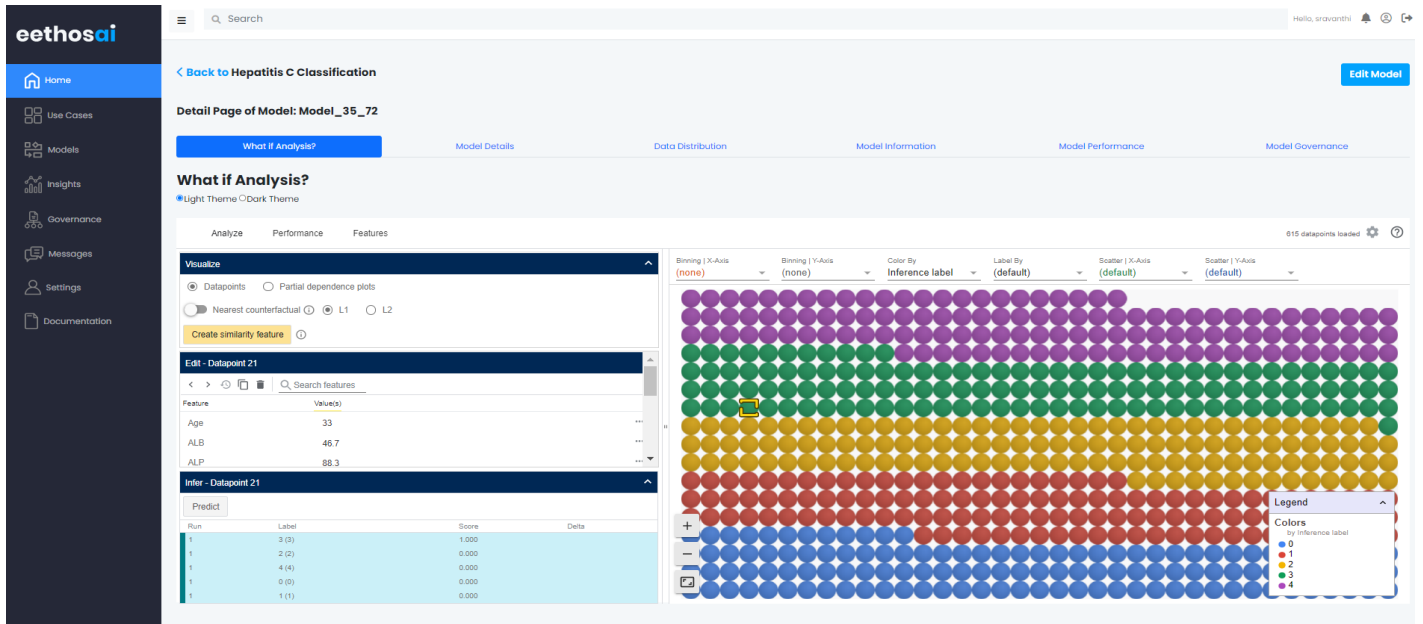
use_biasttrue+

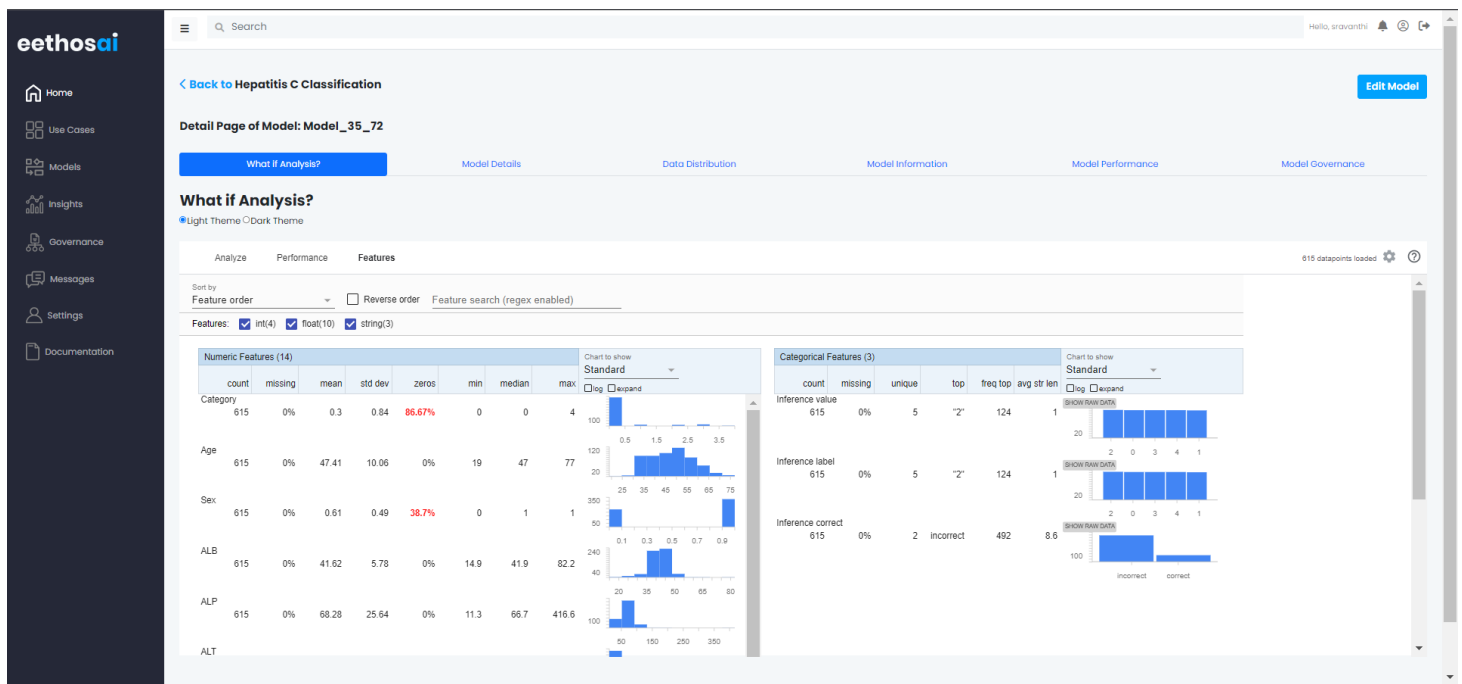
INPUTS

inputname: dense_input

kernelname: dense/kernel:0+

Analyzing Predictions





References

[1] Lichtinghagen R et al. J Hepatol 2013; 59: 236–42, Hoffmann G et al. Using machine learning techniques to generate laboratory diagnostic pathways – a case study. J Lab Precis Med 2018; 3: 58–67,

[2] <https://www.gandhimedicos.in>

[3] <https://medlineplus.gov>