

A

SVM模型推断马尔尼菲蓝状菌感染

输入特征值以获得模型的推理结果

白蛋白 (g/L)	30
淋巴细胞绝对值($\times 10^9/L$)	1.2
血红蛋白 (g/L)	100
谷草转氨酶/谷丙转氨酶	1
C-反应蛋白(mg/L)	35
谷丙转氨酶(U/L)	35
白细胞计数($\times 10^9/L$)	12
血小板计数 ($\times 10^9/L$)	90
浅表或胸腔淋巴结肿大, 0: 无; 1: 有	1
CD4+T细胞绝对计数(个/ μL)	50
谷草转氨酶(U/L)	35
年龄/年	50

清除数据 提交数据

通过 API 使用 使用 Gradio 构建 Settings

感染风险预测
预测结果: 有
可信度: 64.0%

B

SVM Model Inference

ALB	25
ALC	0.25
Hb	80
AST/ALT	2
CRP	80
ALT	30
WBC	12
PLT	75
POAL	1
CD4	50
AST	60
Age (years)	45

清除 Submit

通过 API 使用 使用 Gradio 构建 Settings

Result
Prediction: 1
Confidence: 88.0%

Figure S11. A web-based SVM model was developed for the prediction of talaromycosis

By entering a participant's clinical variables into the online tool available at <https://modelscope.cn/studios/LRYHJG/rf/summary> for users in China and <https://huggingface.co/spaces/HuJiaGuang/LRYHJG-TM> for international users, the corresponding probability of developing talaromycosis can be calculated. As demonstrated in Figures A and B, the probabilities of talaromycosis development for the two patients in our study were determined to be 0.64 and 0.84, respectively.