

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断结果

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/ $\mu L$ )	50
谷草转氨酶(U/L)	35
年龄/岁	50

**感染风险预测**

预测结果: 有  
可信度: 64.0%

**清除数据** **提交数据**

通过 API 使用 · 使用 Gradio 构建 · Settings

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

**Result**

Prediction: 1  
Confidence: 86.0%

**Clear** **Submit**

通过 API 使用 · 使用 Gradio 构建 · Settings

**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.