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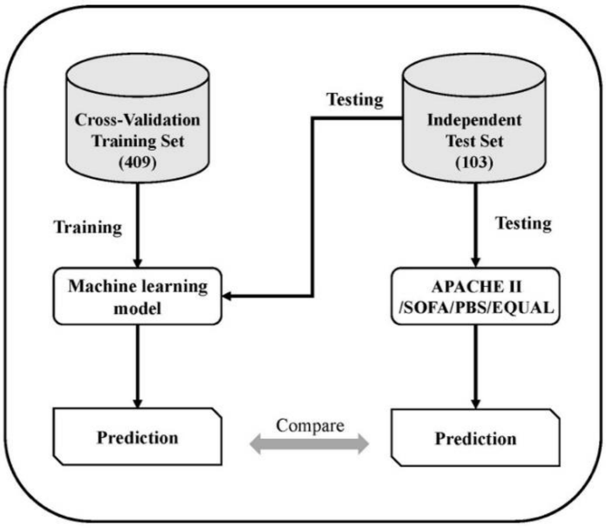
- 研究以跨校與跨域合作為基礎，成功結合醫學與人工智慧技術，開發一款機器學習模型，提升了念珠菌菌血症患者死亡率的預測準確性。

臨床上常用的病人感染嚴重程度之評估方式，如 Acute Physiology and Chronic Health Evaluation（APACHE II）、Sequential Organ Failure Assessment（SOFA）、Pitt Bacteremia Score（PBS），以及專用於黴菌感染之 European Confederation of Medical Mycology Quality（EQUAL）量表等，由於在臨床上進行評分需要費時與需要特定檢驗結果而有限制，較無法即時有效的預測念珠菌菌血症的預後。本研究旨在開發並驗證一款機器學習模型，讓模型可以評估患者的相關數據，提高預測的靈活性與精確性。

本研究使用 2014 年 1 月至 2019 年 7 月間 409 名念珠菌菌血症的患者數據進行堆疊模型（Stacked Generalisation Model, SGM）的建置，並使用同期間另外的 103 名患者數據來進行堆疊模型及傳統評估分數（APCHE II、SOFA、PBS、EQUAL）在 14 天死亡率預測中的表現進行驗證。交叉驗證結果顯示堆疊模型 SGM 在統計學上顯著優於 APCHE II、SOFA、PBS、EQUAL 的預測，在正確度上也達到 87%。

本研究結果顯示，機器學習模型在預測念珠菌菌血症患者死亡率上，與傳統臨床評分系統相比，擁有更好的表現，若結合於醫療資訊系統，可具有自動資訊化評分預測預後的優點，可為臨床決策提供輔助及建議，減少臨床的人力負擔，提升醫療品質。



【具體成果】

研究以跨校與跨域合作為基礎，成功結合醫學與人工智慧技術，開發一款機器學習模型，提升了念珠菌菌血症患者死亡率的預測準確性。透過整合高雄醫學大學、高醫體系醫院以及國立陽明交通大學的專業知識與資源，研究團隊從 2014 年至 2019 年間 409 名念珠菌菌血症患者的臨床數據建立堆疊模型，並另外使用 103 名患者數據，進行 APCHE II、SOFA、PBS、EQUAL 評分與堆疊模型的驗證。結果顯示模型在 14 天死亡率的預測表現，在統計學上優於傳統評分系統。

特別是在跨校合作中，陽明交通大學資訊工程專家提供專業的模型設計，高醫體系醫院則以醫學檢驗專業促進臨床資料的準確解讀，與高雄醫學大學團隊共同完成了跨域創新的研究成果。此模型已被驗證具備適用性，可作為臨床決策的重要輔助工具，不僅提升醫療品質，亦減輕了臨床工作者的負擔，為未來的臨床應用提供了新的方向。

【研究團隊】

1. 曾嵩斌：
   https://mlsb.kmu.edu.tw/index.php/zh-TW/%E5%B8%AB%E8%B3%87%E9%99%A3%E5%AE%B9/%E5%B0%88%E4%BB%BB%E6%95%99%E5%B8%AB/449

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3. 楊宗穎：https://lab-reg-med.mmc.edu.tw/Teacher_Detail.asp?hidPeopleID=6

4. 林尚儀：https://www.kmuh.org.tw/Web/WebRegistration/DocIntro/DocDetail?lang=tw&doctorID=960017

5. 胡毓志：https://www.cs.nycu.edu.tw/members/detail/yhu

團隊簡介：

本研究團隊結合醫學與人工智慧技術，開發精確的臨床決策輔助工具。由高雄醫學大學醫學檢驗生物技術學系曾嵩斌教授、醫學院院長盧柏樑教授、高醫附設醫院檢驗部微生物室林尚儀主任及馬偕醫學院醫學檢驗暨再生醫學系楊宗穎助理教授組成，並與國立陽明交通大學資訊工程學系胡毓志教授團隊進行跨領域合作。

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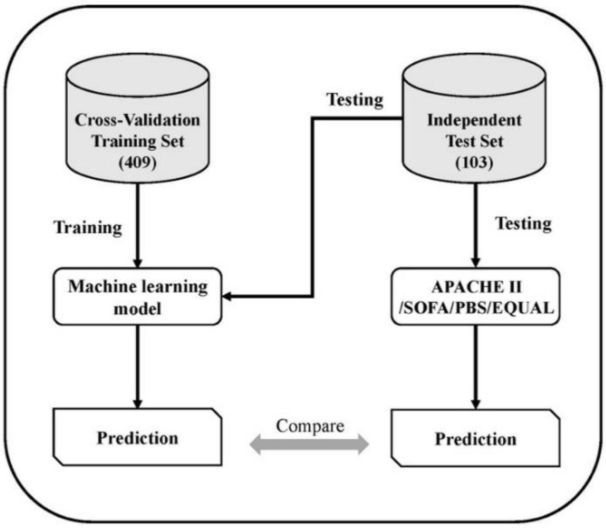
Clinical severity scores, such as the Acute Physiology and Chronic Health Evaluation (APACHE II), Sequential Organ Failure Assessment (SOFA), Pitt Bacteremia Score (PBS), and European Confederation of Medical Mycology Quality (EQUAL) score, face limitations due to their prespecified scorings standards, making them ineffective in reliably predicting the prognosis of candidemia. This study aims to develop and validate a machine learning (ML) model capable of evaluating patient data to enhance predictive flexibility and accuracy.

This study utilized data from 409 patients with candidemia, collected between January 2014 and July 2019, to develop a Stacked Generalization Model (SGM). An additional dataset of 103 patients from the same period was used to validate the performance of the SGM compared to traditional scoring systems (APACHE II, SOFA, PBS, and EQUAL) in predicting 14-day mortality. Cross-validation results demonstrated that the SGM significantly outperformed APACHE II, SOFA, PBS, and EQUAL in statistical accuracy, achieving an overall prediction accuracy of 87%.

The findings highlight that ML models show potential for improving mortality prediction amongst patients with candidemia compared to clinical severity scores. It provides valuable support for clinical decision-making, reducing the workload of healthcare professionals and improving the quality of care.



Concrete Results:

Through cross-institutional and interdisciplinary collaboration, the study successfully integrated medical expertise and artificial intelligence technologies to develop a machine learning model that significantly improves the accuracy of mortality predictions for patients with candidemia. With the expertise and resources of Kaohsiung Medical University, the affiliated hospitals of Kaohsiung Medical University, and the National Yang-Ming Chiao Tung University, the research team developed a Stacked Generalization Model using clinical data from 409 patients with candidemia collected between 2014 and 2019. An additional dataset of 103 patients was used to validate the model's performance against traditional scoring systems, including APACHE II, SOFA, PBS, and EQUAL. The results indicated that the model outperformed traditional scoring systems in predicting 14-day mortality.

The collaboration particularly benefited from the expertise of Yang Ming Chiao Tung University's specialists in model design and the affiliated hospitals of Kaohsiung Medical University's input in clinical data interpretation, complementing the efforts of the Kaohsiung Medical University team. The interdisciplinary innovation has produced a validated model with high applicability, serving as an essential tool for clinical decision-making. This model not only improves the quality of healthcare but also reduces the workload of clinical practitioners, paving the way for new directions in future clinical applications.

【Research Team】

Team Members:

1. Sung-Pin Tseng：

   https://mlsb.kmu.edu.tw/index.php/zh-TW/%E5%B8%AB%E8%B3%87%E9%99%A3%E5%AE%B9/%E5%B0%88%E4%BB%BB%E6%95%99%E5%B8%AB/449

2. Po-Liang Lu：

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3. Tsung-Ying Yang：

   https://lab-reg-med.mmc.edu.tw/Teacher_Detail.asp?hidPeopleID=6

4. Shang-Yi Lin：

   https://www.kmuh.org.tw/Web/WebRegistration/DocIntro/DocDetail?lang=tw&doctorID=960017

5. Yuh-Jyh Hu：https://www.cs.nycu.edu.tw/members/detail/yhu

Research Team Introduction: The research team incorporates medical expertise with artificial intelligence technology to develop precise clinical decision-support tools. The team includes Professor Sung-Pin Tseng from the Department of Medical Laboratory Science and Biotechnology at Kaohsiung Medical University, Professor Po-Liang Lu, Dean of the College of Medicine, Dr. Shang-Yi Lin, Director of the Microbiology Laboratory at Kaohsiung Medical University Hospital, and Assistant Professor Tsung-Ying Yang from the Department of Medical Laboratory Science and Biotechnology at Mackay Medical College. In addition, the team collaborates with the computer science expert, Prof. Yuh-Jyh Hu from National Yang Ming Chiao Tung University, driving interdisciplinary innovation.

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