

Deep learning model for rapid outbreak detection in a rapid phenotypic AST system

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Introduction

Clonal outbreaks threaten hospital patients and increase costs through infection prevention and control measures. These outbreaks are often caused by multidrug-resistant strains. QuickMIC is a rapid phenotypic AST system that provides MIC results directly from positive blood cultures within 2-4 hours. In addition to MICs, QuickMIC generates high-resolution phenotypic growth data that may contain strain-specific information. This study investigated whether such phenotypic fingerprints can be used to detect clonal strains.

Methods

Growth data from 3045 QuickMIC runs, representing 345 strain across 20 species were analyzed. A PyTorch-based machine learning pipeline was developed to learn run-level representations from high-resolution phenotypic images. Chamber-level features were extracted using a convolutional neural network and aggregated with a bidirectional LSTM to generate L2-normalized embeddings. Run similarity was measured using cosine distance, and strain grouping was evaluated with DBSCAN clustering. Performance was assessed by embedding separability between intra- and inter-strain pairs, strain level grouping accuracy and a streaming evaluation simulating real-time deployment.

Results

On an independent test set, the mean difference in cosine similarity between intra- and inter-strain pairs was 0.72, indicating strong separation of strain-specific embeddings. The ROC analysis resulted in an AUC of 0.960 (85% CI: 0.94-0.98), confirming strong discriminatory performance. At the optimal threshold ($\tau^* \approx 0.43$), the false-match rate was 0.10 and the miss rate was 0.06. In the simulated outbreak stream, the model consistently detected outbreak-related runs, achieving a mean F1-score of 0.8-0.9 across stream lengths while maintaining cluster purity of 0.78-1.

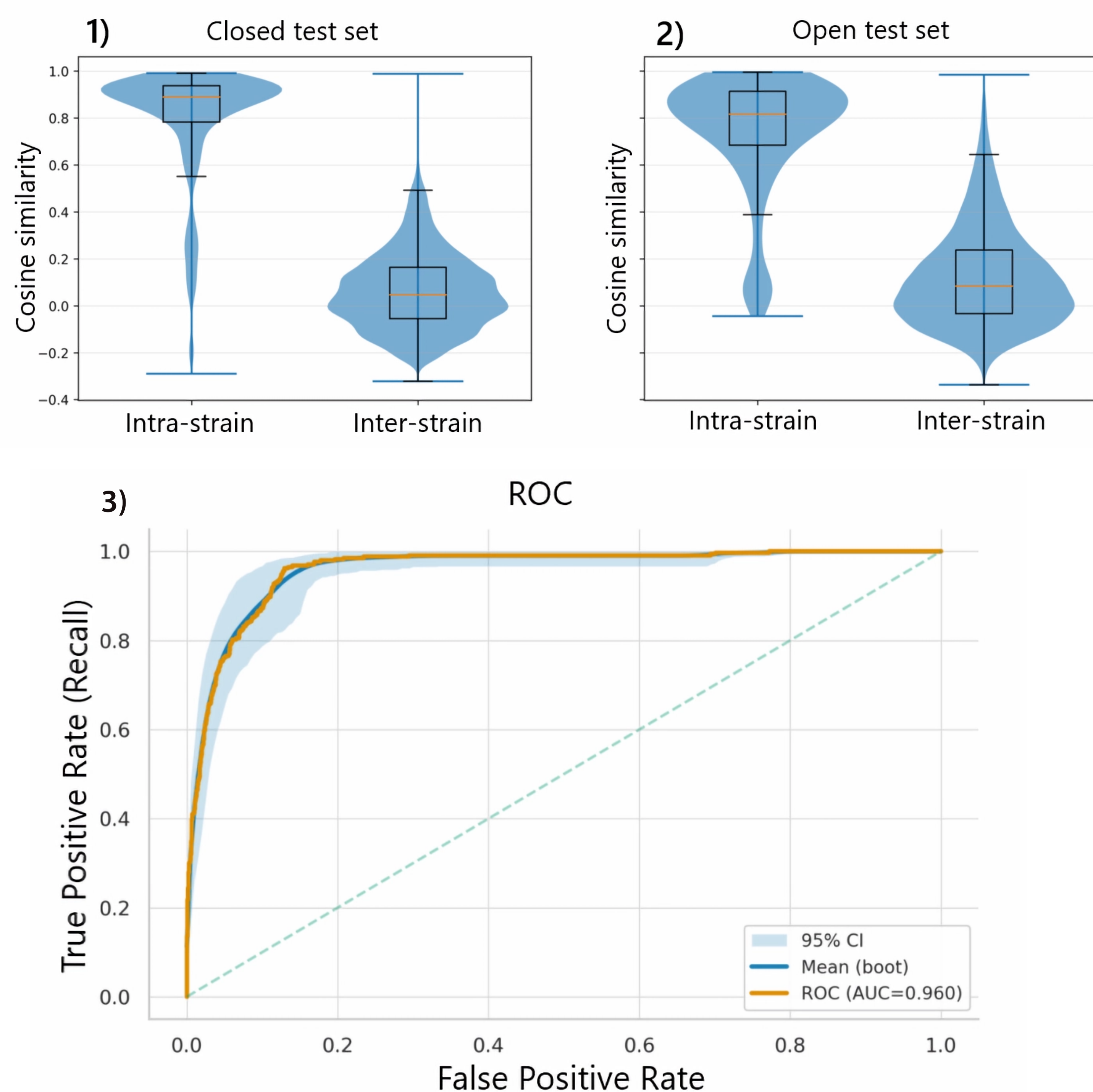
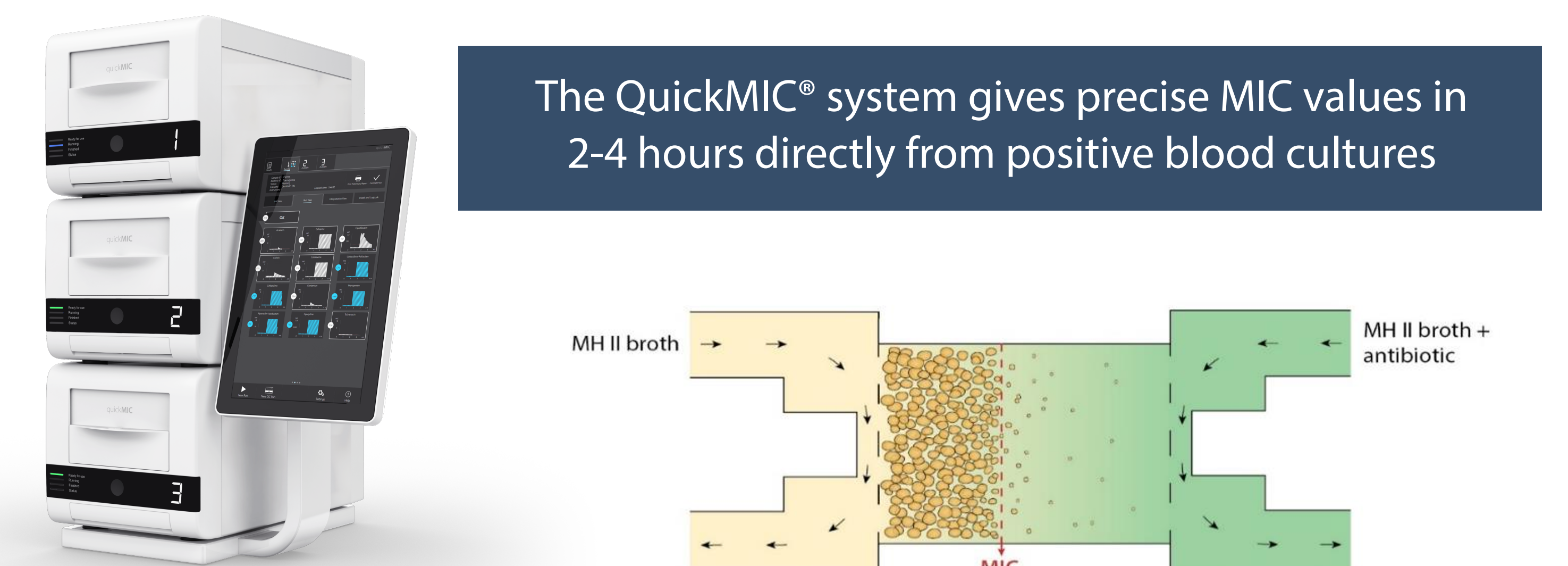


Figure B | (1-2) Violin plots of cosine similarity for intra- and inter-strain pairs in the closed and open test sets, showing higher intra-strain similarity in both. Mean intra-inter differences ($\Delta = \mu_{intra} - \mu_{inter}$) were 0.85 and 0.70, respectively. (3) ROC curve for same- vs different-strain discrimination in the open test set (AUC = 0.960, 95% CI 0.94-0.98; shaded area, bootstrap 95% CI).



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QuickMIC system, 3 modules with control unit. Detail of antibiotic gradient formation in the microfluidic cassette.

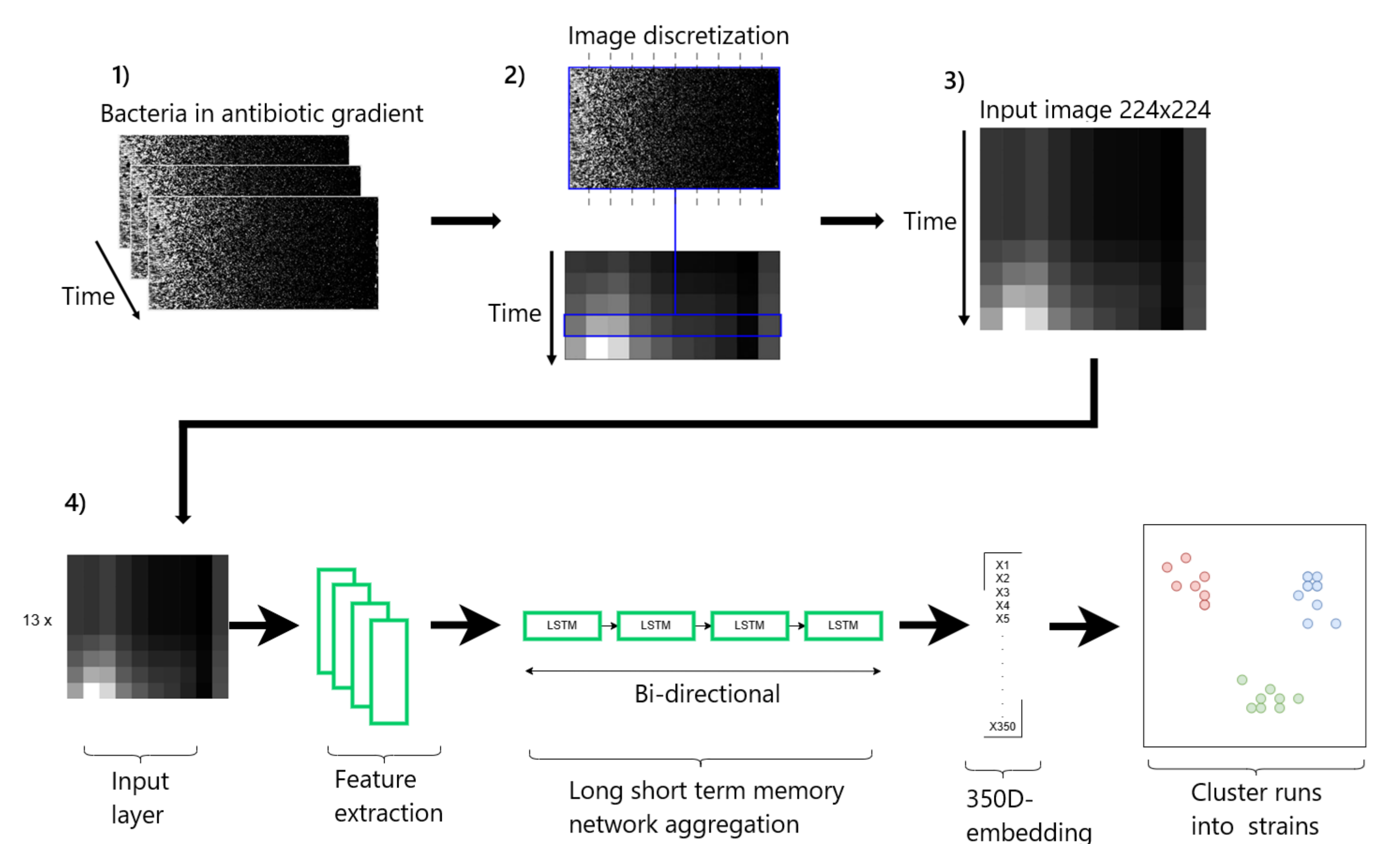


Figure A | (1) Example QuickMIC images over time. (2) Discretization of multiple time points into a single image. (3) 224 x 224 model input. (4) Model workflow: CNN-based feature extraction, bidirectional LSTM aggregation of 13 chamber images into a 350-dimensional run embedding, followed by clustering to identify clonal bacteria.

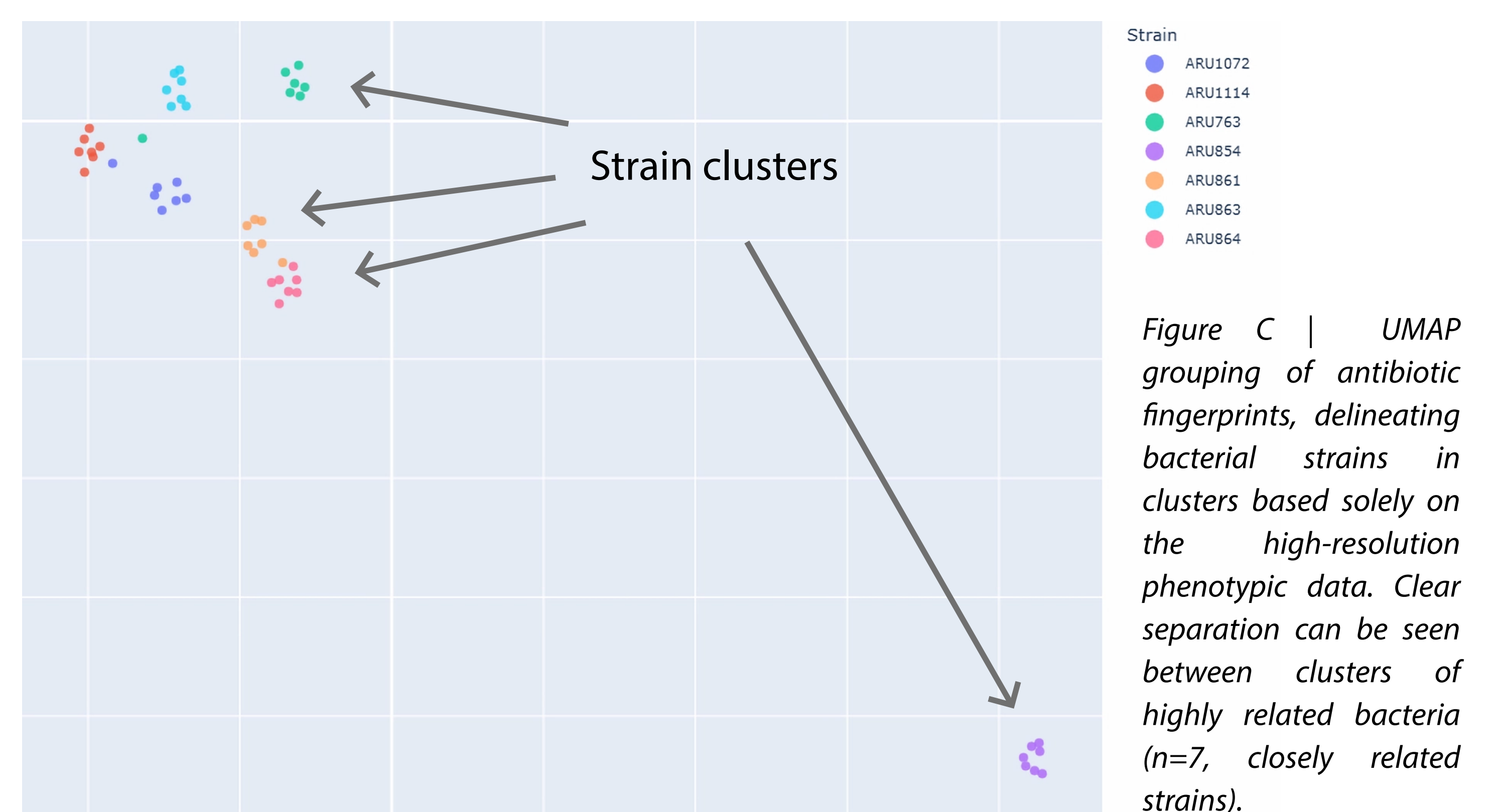


Figure C | UMAP grouping of antibiotic fingerprints, delineating bacterial strains in clusters based solely on the high-resolution phenotypic data. Clear separation can be seen between clusters of highly related bacteria (n=7, closely related strains).

Conclusion

A learned embedding and clustering approach can reliably detect clonal bacterial runs from QuickMIC phenotypic growth data. The method showed high performance in closed-set evaluation and robust performance under open-world conditions. Integration into the QuickMIC platform could enable early detection of potential clonal outbreaks and support faster infection prevention and control responses.



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