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CLINICAL MICROBIOME INTELLIGENCE SYSTEM

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Relevance. Polymicrobial infections with Staphylococcus aureus and Candida albicans are one of the critical problems because biofilms make it difficult and due to this the resistance due to antimicrobe rises and then treatments are not sufficient enough, and mortality increase. Physicians fail to see the jumbled 3D structure of these biofilms and the ways of pathogen infection. What's missing is a tool that pulls all these factors together: pathogen behaviour, biofilm dynamics, host factors. We need combined decision-support that decodes these problems, so we can give true treatment for each patient.

Aim: our aim is to build and test a clinical decision-support system that does it all by leaving no stones unturned. It combines 3D modelling of biofilm design, machine learning analytics, and molecular shaping to mark up the infection severity, predict treatment outcomes, and give us the modified recommendations for patient's care with S. aureus and C. albicans co-infections.

Materials and methods. For the development of this platform, we used Python and used Streamlit for the user interface. This Module simulates the world of microscope like the clusters of the bacterial, fungal hyphae, extracellular matrix by refining Gompertz growth kinetics and shaping the antimicrobial penetration. For the accurate results, we used machine learning algorithms like Random Forest, XGBoost, SVM, Neural Networks. Clustering (K-Means) and PCA found out the patterns in the data. Clinical risks were predicted by the unit of Random Forest and XGBoost, The Treatment Optimization Module brings practical, rule-based guidelines, covering MRSA, VRE, ESBL, with biofilm aiming strategies like DNase and N-acetylcysteine and adjustment of the doses for kidney disease.

Results and their discussion. These machine learning models performed very well, Random Forest and XGBoost gave authentic key predictions. The Biofilm Architecture Module examined resistance mechanisms precisely from physical barriers to quorum sensing and persisted cells. Diabetes, immunocompromised status, and chronic kidney disease became a principal agent, each significantly intensifying the pathogen burden and mortality ($p<0.001$). This system helped us in organizing patients into low (>70%), moderate (40–70%), or high (<40%) risk groups and started giving out the particular recommendations on the basis of risks. Personalized treatment guidelines came out, including biofilm-targeted therapies and crucial renal dose modifications. The results undergo a multilayered verification processes cross-validation, bootstrap, and DeLong's test confirmed trustworthiness, tying every result from authentic clinical guidelines and published literature.

Conclusion. The Clinical Microbiome Intelligence System forged out new directions in managing biofilm-driven infections. With the use of features like 3D modelling, robust machine learning, and molecular detail all built into one platform, physicians and doctors get practical results and to the point treatment advice. This tool helps in improving clinical judgment, enhancing risk grading, and driving personalized care right where it's needed, the inter-cross of complicated biofilms and diverse patient factors.