

Microbiology. Intensive Care Unit.

What is this work about?

The main objective of this study was to evaluate the potential **associations between clinical/epidemiological data and genetical microbial features** in a cohort of patients under mechanical ventilation and isolation of *Staphylococcus aureus* in the respiratory tract .

What problem did we face?

We combined up to 136 variables related to demographics, clinical evolution, severity scores, biomarkers, follow-up and DNA microbial array from 148 patients.

Given the exhaustive exploratory approach of this study, we decided to apply an automated EDA tool like AutoDiscovery.

Which was the contribution of AutoDiscovery ?

AutoDiscovery helped us to identify a clinically relevant **association between the consecutive isolation of *Pseudomonas aeruginosa* and a significantly larger number of days of persistence**. Other associations found involved the presence of specific bacterial genes and clinical variables. Some of these associations were only reported in specific patients subgroups.

The key features of AutoDiscovery applied to this work were:

- 👍 The **non-guided exploratory strategy** proposed by the software, which has proved its effectiveness to analyze and compare multiple variables starting with a set of [exploratory questions](#).
- 👍 The [automated data consolidation](#) tool made combining variables collected in different databases and formats easier and faster.
- 👍 The [post-analysis exclusivity assessment](#), which allowed us to identify unique associations between study subgroups.

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