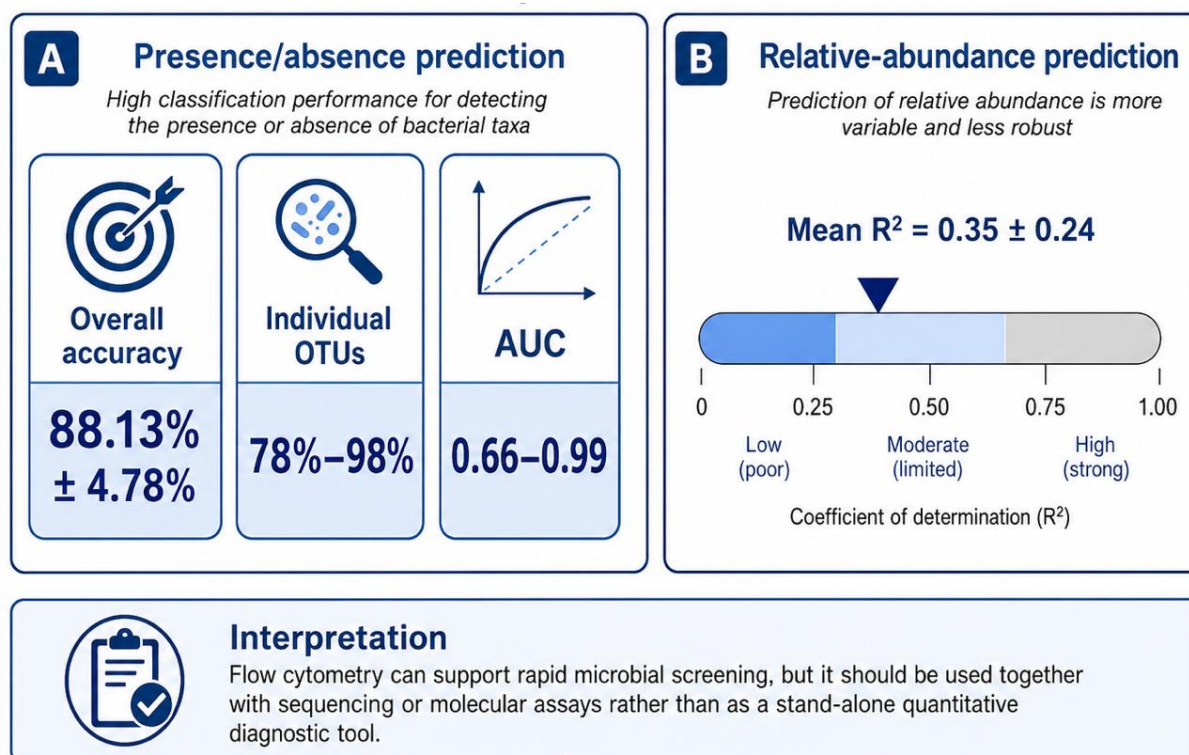


The value of the table is not the creation of fixed thresholds but the linkage of microbial evidence to progressively stronger actions. Such proportionality reduces two opposite errors: ignoring early ecological deterioration and overreacting to ordinary microbiome variability. Evidence from longitudinal aquaculture studies strongly supports this need for contextual rather than single-marker interpretation (Clinton et al., 2024; Lu et al., 2025).

6.5 Data-driven approaches for microbial risk prediction

Multivariate statistics and machine learning are well suited to microbial monitoring because the number of candidate microbial features often far exceeds the number of samples. Random forests, regularized regression, time-series models, and neural networks can combine taxa, cytometric features, environmental variables, and host measurements. Flow-cytometry research has already shown that microbial fingerprints contain enough structure to predict aspects of taxonomic composition, supporting their potential role in rapid screening (Heyse et al., 2021).

The main constraint is not algorithm availability but data quality. Models trained on one farm, season, or analytical pipeline may learn local signatures that fail elsewhere. Tank-level replication, independent validation, temporal testing, transparent feature selection, and calibrated uncertainty are therefore more important than model complexity. For current aquaculture applications, interpretable models that show why a sample was classified as risky may be more useful than opaque systems with marginally higher internal accuracy (Figure 2).



Data summarized from Heyse et al. (2021).

Figure 2 Performance of flow cytometry-based prediction of bacterial taxa in an aquaculture microbial community

7 Microbial Monitoring-Based Health Management Models for Marine Aquaculture

7.1 Routine microbial surveillance model

Routine surveillance begins by establishing what “normal” looks like. This requires repeated sampling during periods of acceptable production, covering major seasons, developmental stages, and management transitions. Baselines should include a manageable set of microbial measures-such as total cell counts, targeted pathogen abundance, community fingerprints, or periodic 16S profiles-alongside temperature, salinity, dissolved oxygen, nitrogen compounds, feeding, biomass, and health records.