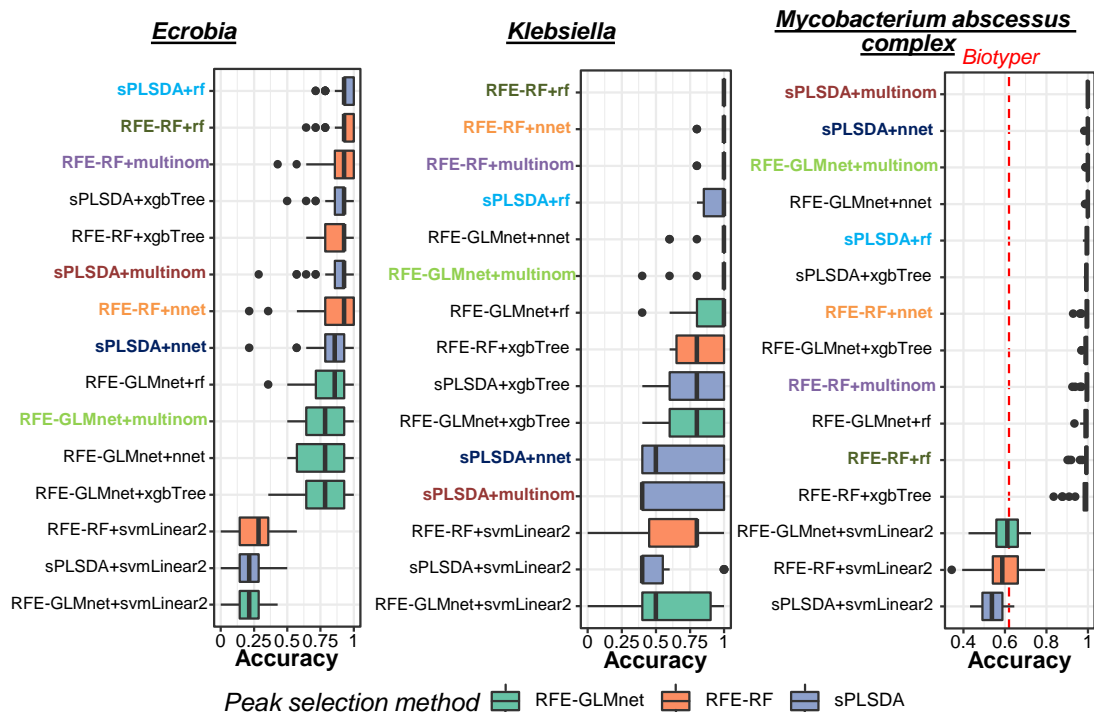


**B** **Comparison of ML-methods to estimate a classification model ranked by mean accuracy on test datasets**



**A:** MSclassifR proposes pipelines to preprocess mass spectra and find discriminant mass-over-charge values. **B:** Accuracies obtained on test sets for the 3 datasets (Wilke et al., 2020), (Lasch, Stämmeler and Schneider, 2016), (Godmer, Aubry, *et al.*, 2021). Top 3 methods are highlighted with different colors. Red dashed line named “Biotyper” is the accuracy level (61%) using Bruker® database (Library Mycobacteria v5.0) coupled to the MALDI Biotyper®.