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The Early detection of frailty syndrome using a model that employs a combination of omic data

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INTRODUCTION & AIM

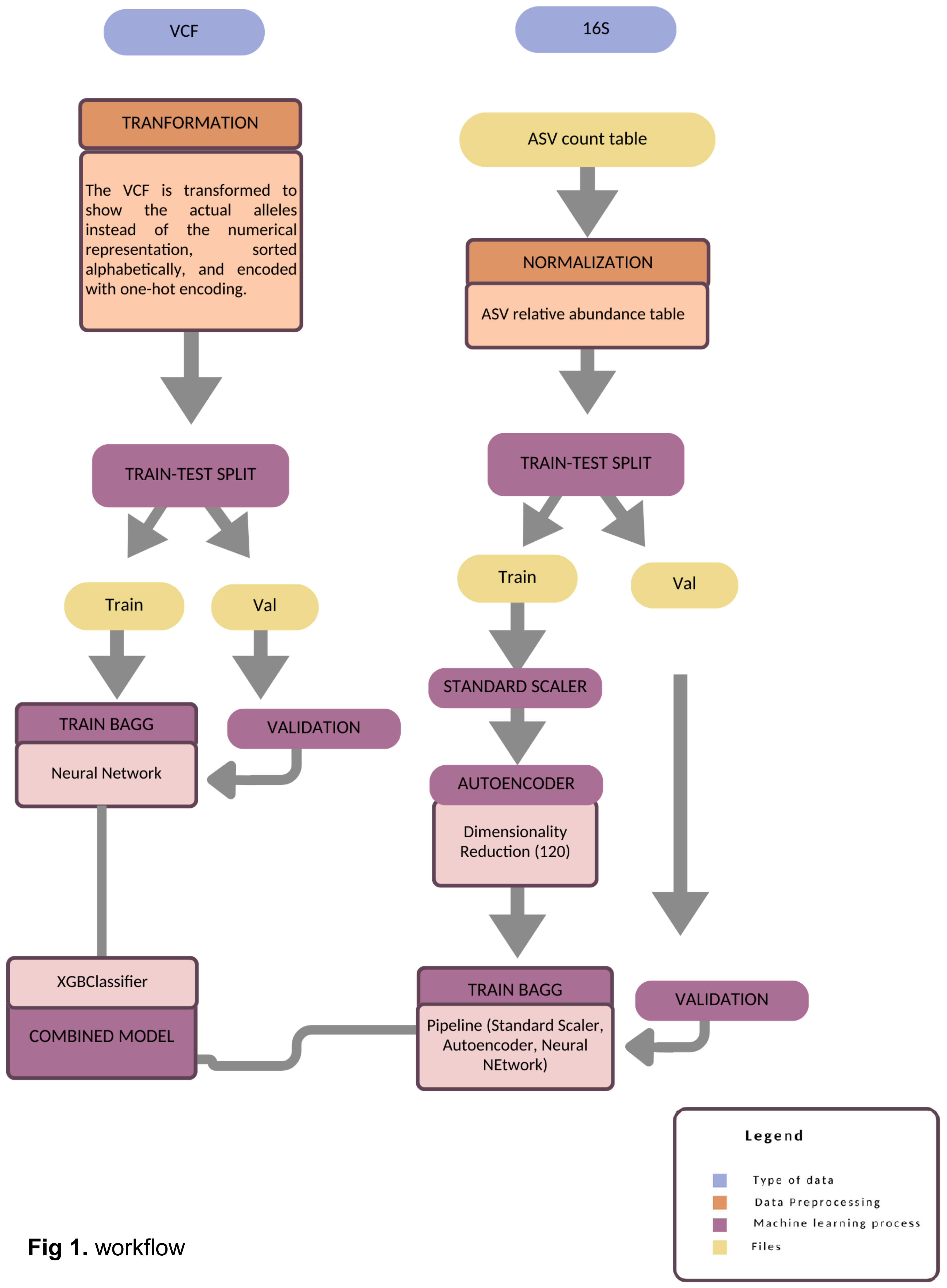
Frailty syndrome (FS) is an age-related disorder characterised by the loss of reserves in numerous organs and systems. Therefore, the ability to diagnose FS is a critical factor that influences patient quality of life and clinical decision-making [1].

In the present study, a stool sample from a cohort of 199 elderly individuals, composed of both frail and non-frail subjects was used to obtain microbiome profiles through metataxonomics (16S), while genomic information from 933 samples was derived from whole genome DNA microarray analyses.

For the 16S rRNA data, a deep autoencoder was employed as a novel nonlinear dimensionality reduction strategy, enabling the extraction of compact latent representations from high-dimensional microbiome profiles.

Predictive models were trained independently for each omic data. For multi-omics integration, we implemented an ensemble approach that improved the predictive capacity.

METHOD



VCF

TRANFORMATION

The VCF is transformed to show the actual alleles instead of the numerical representation, sorted alphabetically, and encoded with one-hot encoding.

TRAIN-TEST SPLIT

Train

Val

TRAIN BAGG

Neural Network

VALIDATION

XGBClassifier

COMBINED MODEL

16S

ASV count table

NORMALIZATION

ASV relative abundance table

TRAIN-TEST SPLIT

Train

Val

STANDARD SCALER

AUTOENCODER

Dimensionality Reduction (120)

TRAIN BAGG

Pipeline (Standard Scaler, Autoencoder, Neural NEtwork)

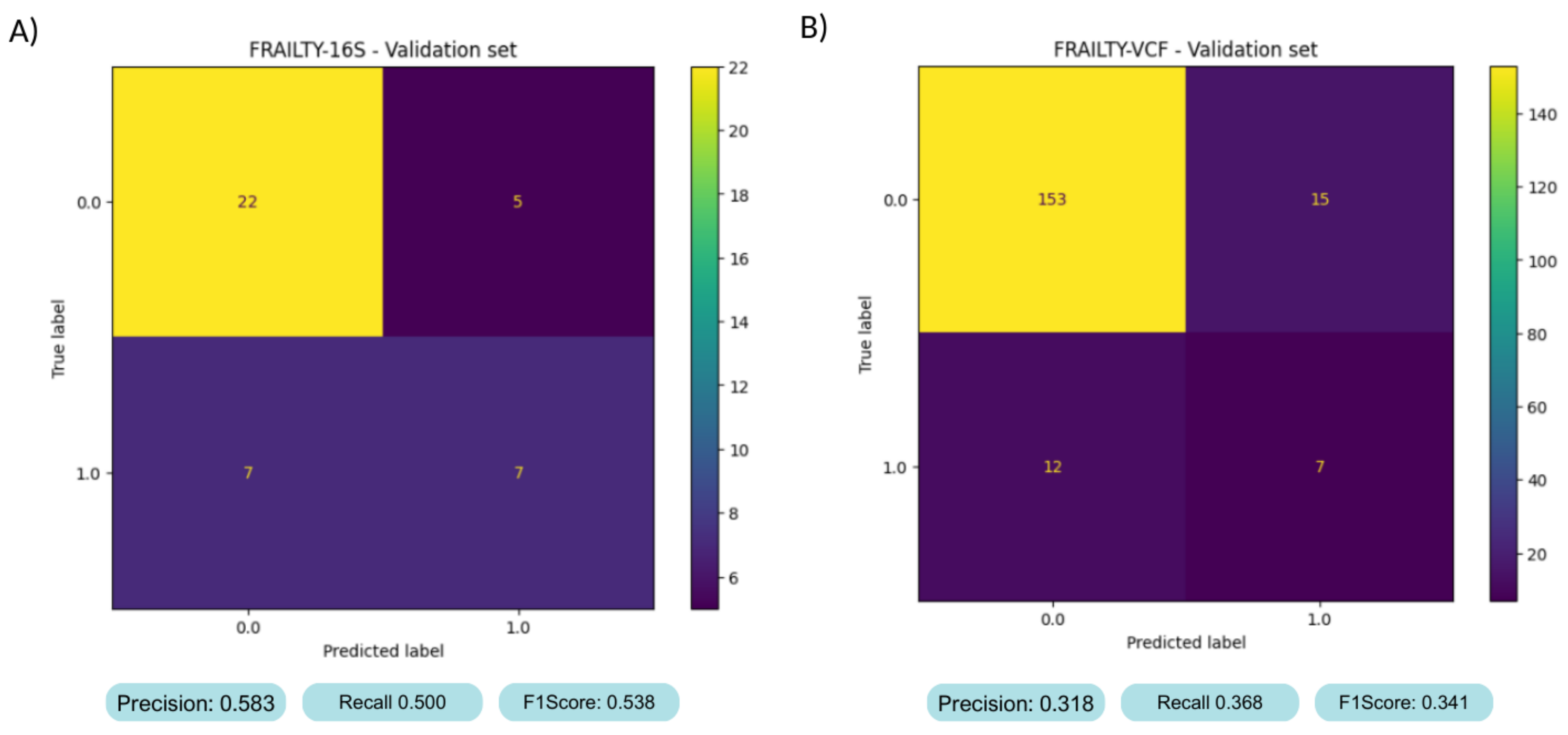
VALIDATION

Legend

- Type of data
- Data Preprocessing
- Machine learning process
- Files

Fig 1. workflow

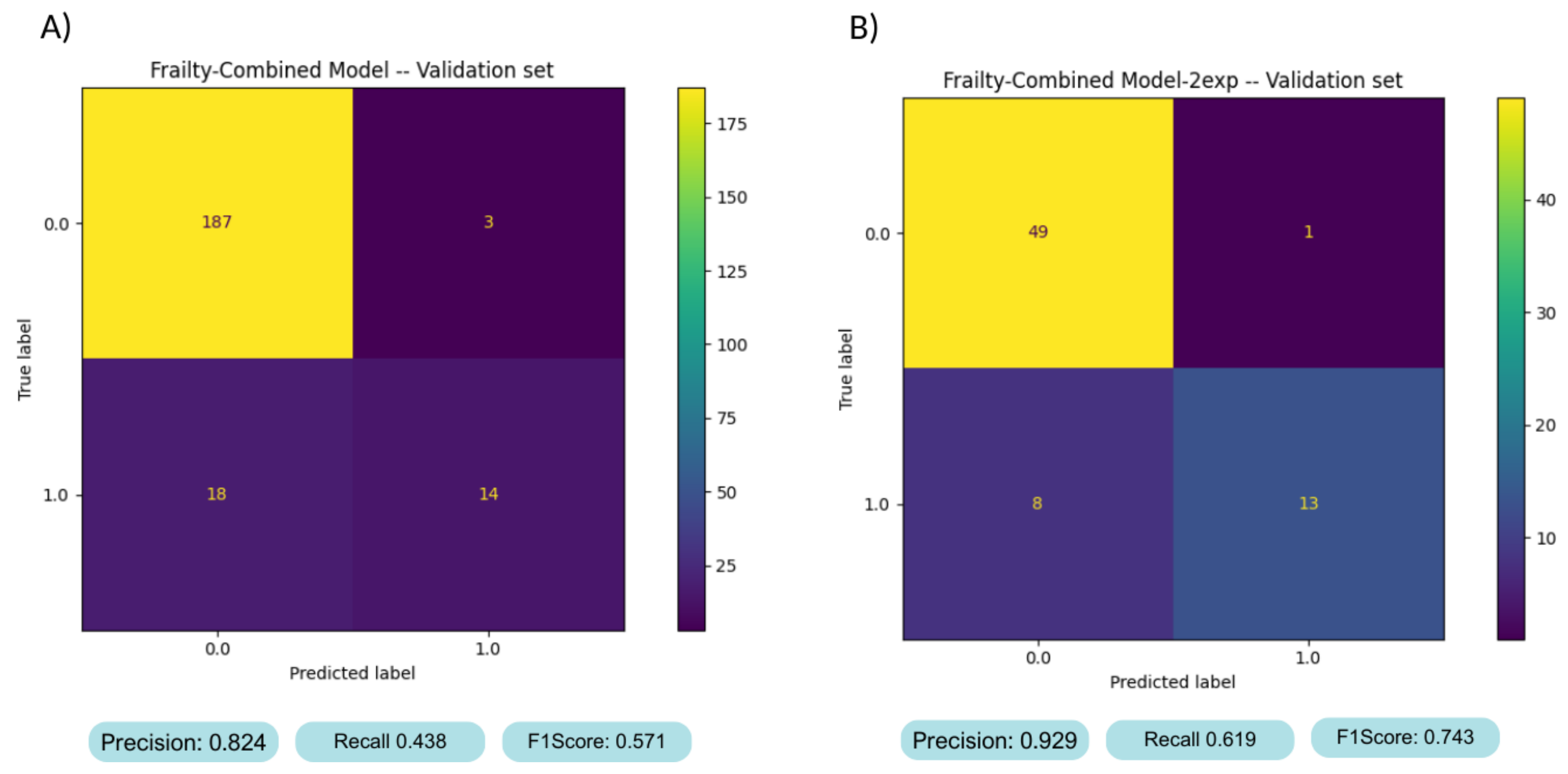
RESULTS & DISCUSSION



Precision: 0.583 Recall 0.500 F1Score: 0.538

Precision: 0.318 Recall 0.368 F1Score: 0.341

Fig 2. Confusion matrices showing the performance of the 16S rRNA (A) and genomic (B) models on the validation set.



Precision: 0.824 Recall 0.438 F1Score: 0.571

Precision: 0.929 Recall 0.619 F1Score: 0.743

Fig 3. Confusion matrices showing ensemble model performance on (A) all samples and (B) paired omics samples (16S + genomic) in the validation set.

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CONCLUSION

Multi-omics ensemble models integrating genomic, 16S rRNA, and clinical data outperformed all single-omics predictors.

The model trained exclusively on paired omics samples achieved superior performance compared to using all available samples, demonstrating the value of integrated molecular datasets.

Future work will extract feature importances to identify frailty-specific biomarkers

FUTURE WORK / REFERENCES

1. van Tongeren SP, Slaets JPJ, Harmsen HJM, Welling GW. Fecal Microbiota Composition and Frailty. Appl Environ Microbiol. 2005;71(10):6438-42. doi:10.1128/AEM.71.10.6438-6442.2005

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