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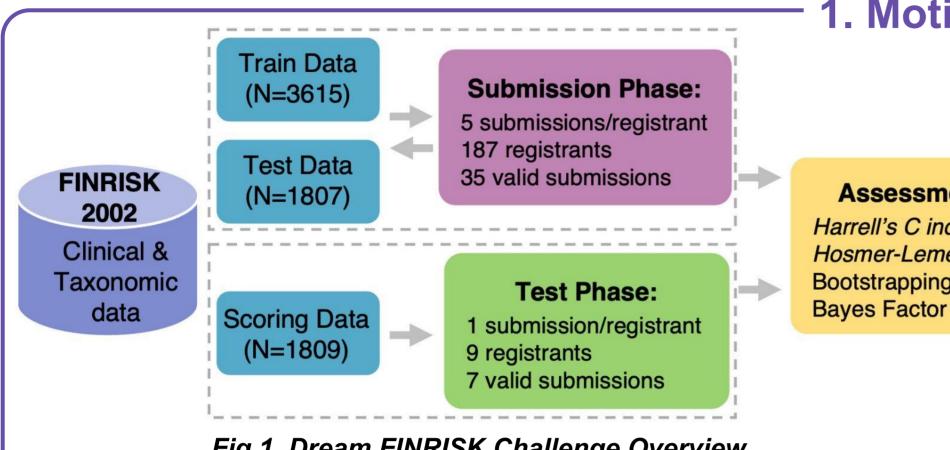


Fig 1. Dream FINRISK Challenge Overview

1. Motivation and Aim

Assessment Harrell's C index Hosmer-Lemeshow Bootstrapping **Bayes Factor**

Heart failure (HF) is a complex clinical syndrome characterized by the heart's inability to meet the body's blood supply needs. Several studies have found differences in the microbiome composition of HF patients compared to controls.

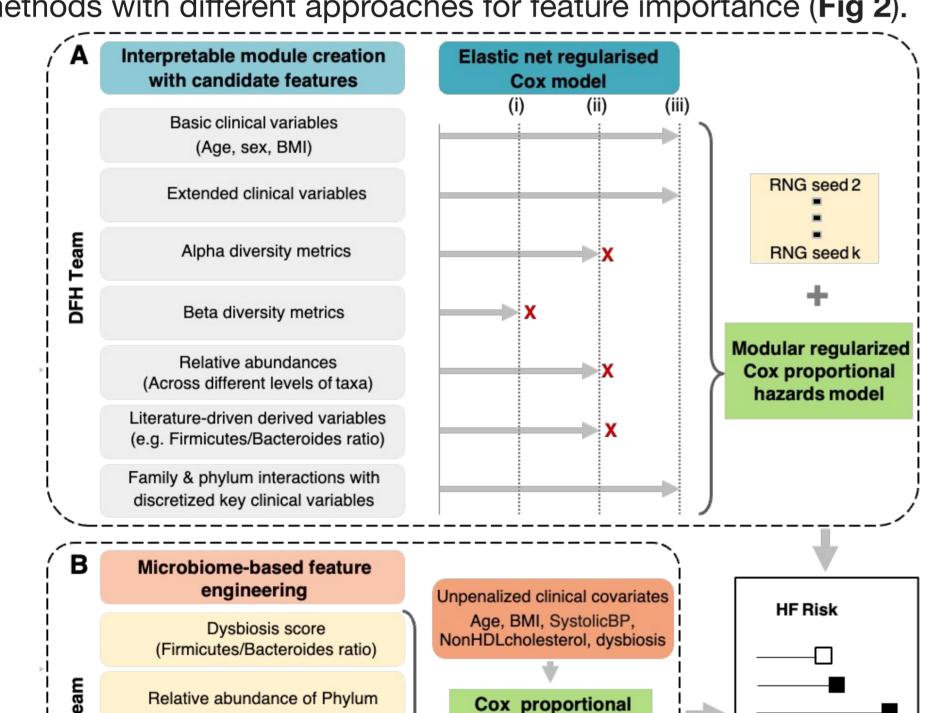
The crowdsourced FINRISK Microbiome DREAM challenge (Fig 1) aimed to investigate the gut microbiome compositions in predicting **HF risk** in a large population of 7,231 Finnish adults¹ (FINRISK 2002, n = 559/7,231 HF). To protect the privacy of individuals, we provided synthetic data that closely mimics the real FINRISK data.

2. Modelling Workflow

Two teams (SB2, DFH) developed superior models that outperformed the baseline and other competing models using regression-based

3. Model Results

- Baseline Age-Sex: Cox model with only Age + Sex as covariates
- Baseline Covariates: Cox model with all clinical covariates



methods with different approaches for feature importance (Fig 2).

Baseline All: Cox model with all clinical covariates + microbiome

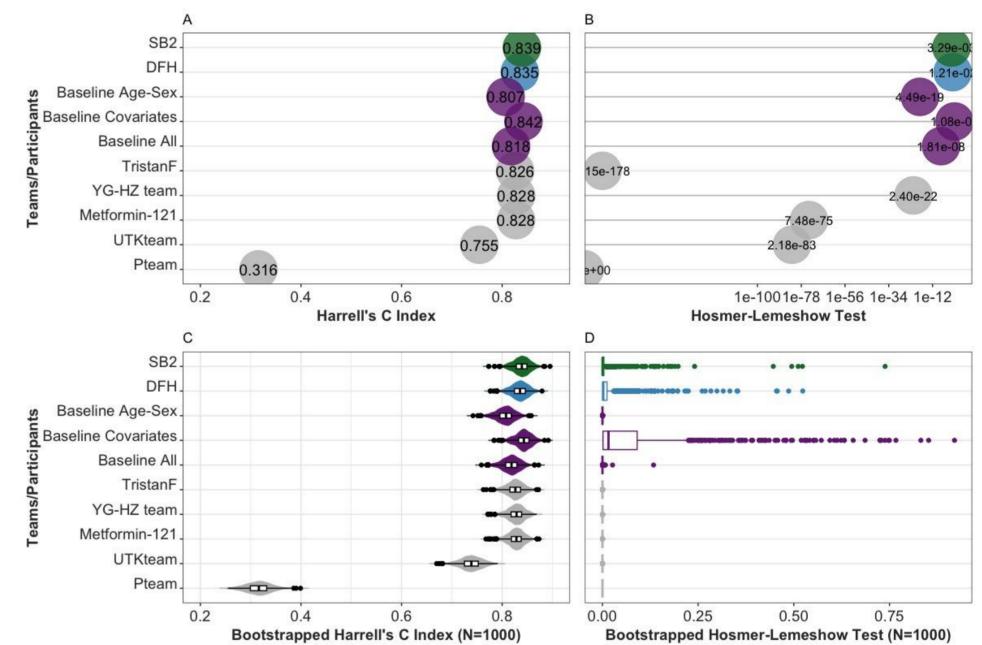
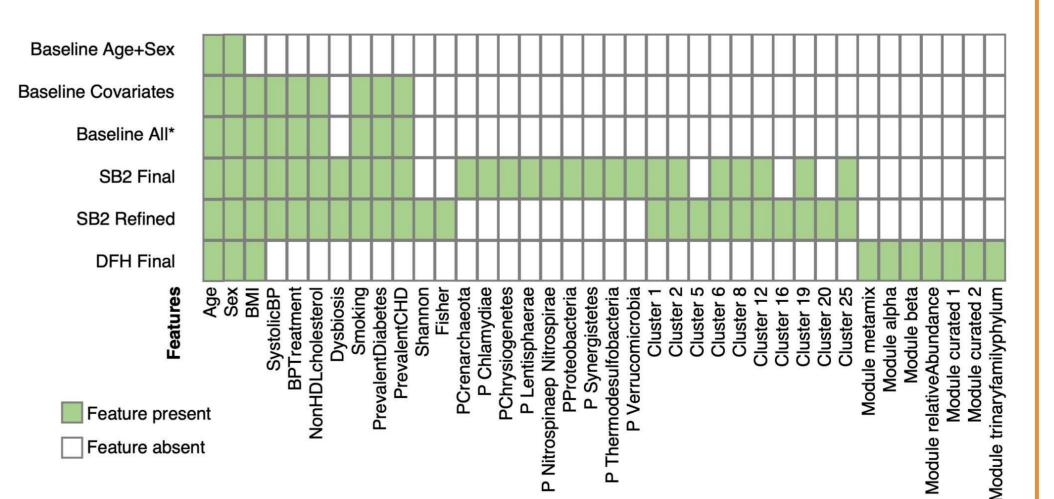


Fig 3. Harrell's C-index and Hosmer-Lemeshow test results



4. Model Refinement

Alpha diversity metrics Shannon, Chao1, Simpson,

InvSimpson, Fisher

Species co-abundances (SpiecEasi R package)

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Post-challenge enhancements included minimizing redundant taxonomic information through species and network analysis, along with combining the final methods (Fig. 5).

Fig 2. Modeling Workflow of the Top Two Performing Teams

hazards model

Feature selection by Lasso

regularized Cox model

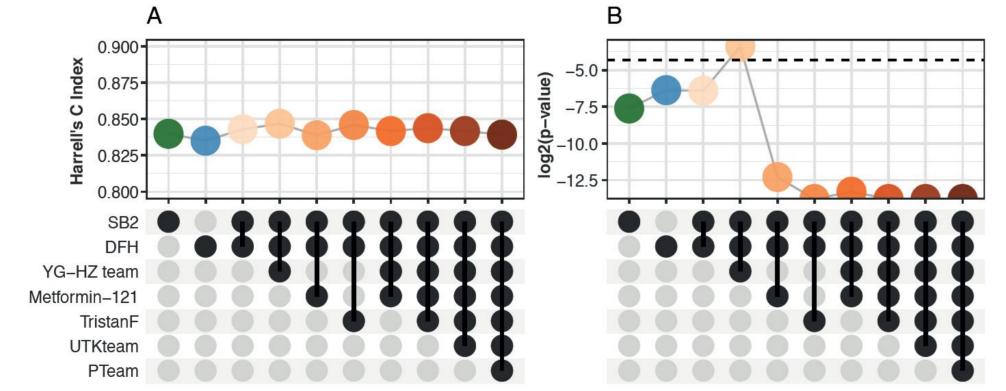


Fig 5. The ensemble model's Harrell's C-index and Hosmer-Lemeshow p-values

Learn More

The DREAM challenge main organizer:

COST action network ML4microbiome (CA18131; ml4microbiome.eu)

Challenge page > **synapse.org/finrisk**

Fig 4. Comparison of Baseline and Top-Performing Models' Features

5. Conclusion

Microbiome species, particularly those associated with inflammation, were found to be valuable predictors of incident HF.

This challenge provides a ground for the scientific community to contribute and advance our current understanding of the incidence of heart failure and its associations with the gut microbiome.

References

Salosensaari A, Laitinen V, Havulinna AS et al., Taxonomic signatures of cause-specific mortality risk in human gut microbiome. Nat Commun 12, 2671 (2021). https://doi.org/10.1038/s41467-021-22962-y