

**MEFE: microbiome signature
identification
based on elastic feature extraction**

Guosen HOU , Yuxiao FEI , Hao GAO, Xiaoquan SU

Frontiers of Computer Science, DOI: [10.1007/s11704-025-50323-1](https://doi.org/10.1007/s11704-025-50323-1)

Problems & Ideas

- Problems of traditional microbiome biomarker discovery:
 - Sensitive to zero-inflated and noisy microbiome data;
 - Ignores biological relationships among microbes (e.g., taxonomy, function).
- Ideas of MEFE: Introduce Elastic Feature Extraction to integrate neighboring microbe signals based on phylogenetic or functional similarity.

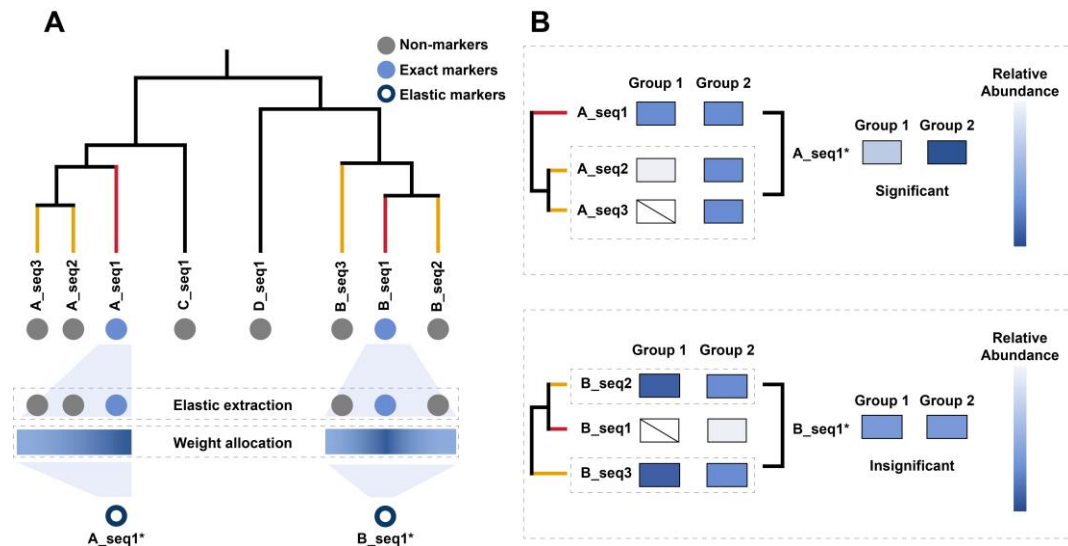
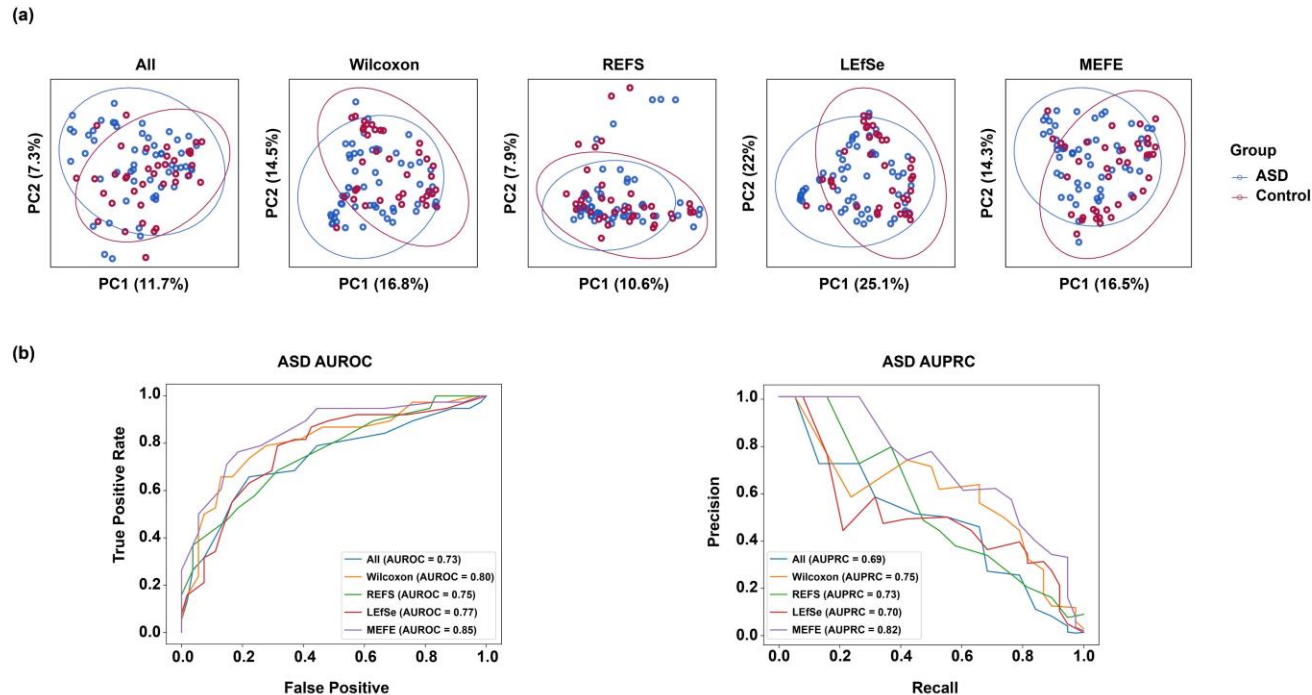


Diagram of the MEFE Algorithm. (A) Elastic feature extraction. (B) Elastic feature extraction reduces errors by microbiome misclassification or data sparsity.

Main Contributions

- Contributions:
 - A novel elastic biomarker extraction algorithm (MEFE), integrating sequence, functional, and taxonomic similarities;
 - Provide a public Python implementation available at: <https://github.com/qdu-bioinfo/MEFE>.



Performance of MEFE on Real Dataset I (ASD) and comparison with other approaches.(a) PCoA analysis.(b) Random Forest-based classification.