# DPS-Tool: An online service platform for disease perturbation scoring

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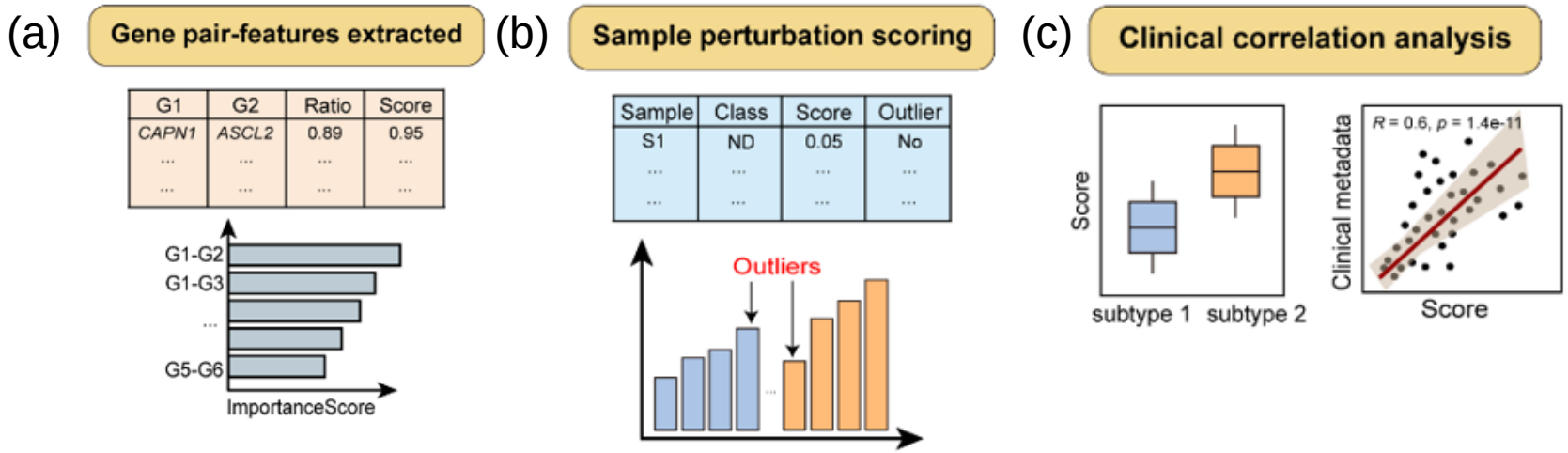
# Problems & Ideas

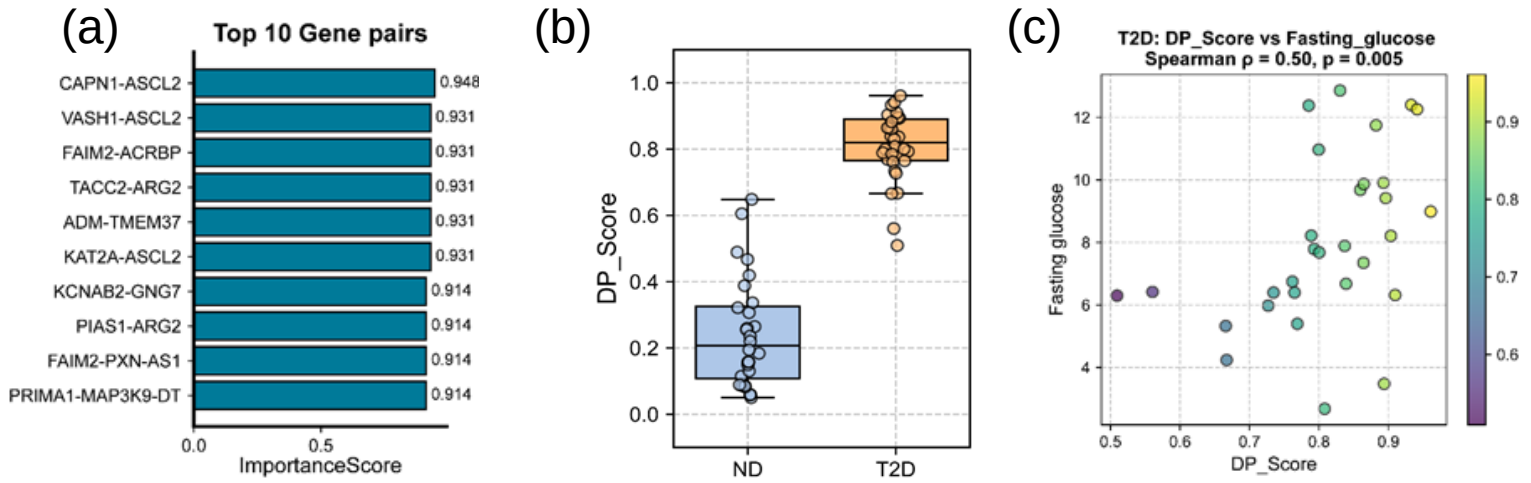
- Problems of current transcriptomic perturbation analysis tools:
  - Existing sample-level perturbation methods rely on absolute gene expression, making them sensitive to batch effects.
  - Limited interpretability in linking molecular global perturbations with disease phenotypes or therapeutic responses.
- Ideas: Develop a gene pair order-based tool to quantify sample-specific global perturbations, enabling identification of key features and their associations with clinical phenotypes




Overview of the DPS-Tool workflow. (a) DPS-Tool first extracts stable gene-pair features from input samples. (b) Sample-specific perturbation scores are then calculated based on changes in the relative expression order of extrated gene pairs. (c) Finally, user-provided clinical information can be used for statistical comparisons between groups or association analyses with perturbation scores.

# Main Contributions

- Contributions:
  - A novel gene pair order-based computational framework that quantifies sample-specific global transcriptomic perturbations and identifies disease-relevant features;
  - A perturbation scoring system that enables statistical comparisons and association analyses between sample-level scores and clinical phenotypes, supporting disease subtyping, risk stratification, and trajectory analysis;
  - A scalable web-based platform with interactive modules and multi-dimensional visualization, facilitating mechanistic studies and translational applications across cohorts and multi-omics datasets.




Application of DPS-Tool to diabetes data. (a) Top 10 features identified by DPS-Tool. (b) Comparison of sample perturbation scores between controls and diabetes. (c) Association between perturbation scores and fasting blood glucose.