Background
Humans have evolved to respond to diverse environmental conditions including various chemicals, mechanical and pathogenic insults. Among these, exposure to chemicals (e.g., cigarette smoke, pollutants, pesticides) induce molecular changes in cells. A subset of exogenous chemicals, chemical-derived metabolites, and endogenous molecules produced by exposed organs (e.g., lung, gut) can pass into the blood stream and induce molecular changes in blood cells manifesting as a discrete exposure response fingerprint that can be examined. While whole blood is an easily accessible matrix, its analysis is challenging owing to its compositional complexity. Moreover, most preclinical in vivo experiments are performed in animals models which raises a question of translatability and relevance of findings to humans.

Goal
To develop blood gene signature-based classification models to predict smoke exposure status or cessation status:
- in human (Sub-challenge 1 - SC1)
- translate across species (Sub-challenge 2 - SC2)

Gene expression data generated from human and mouse

Signatures challenge

Key references

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