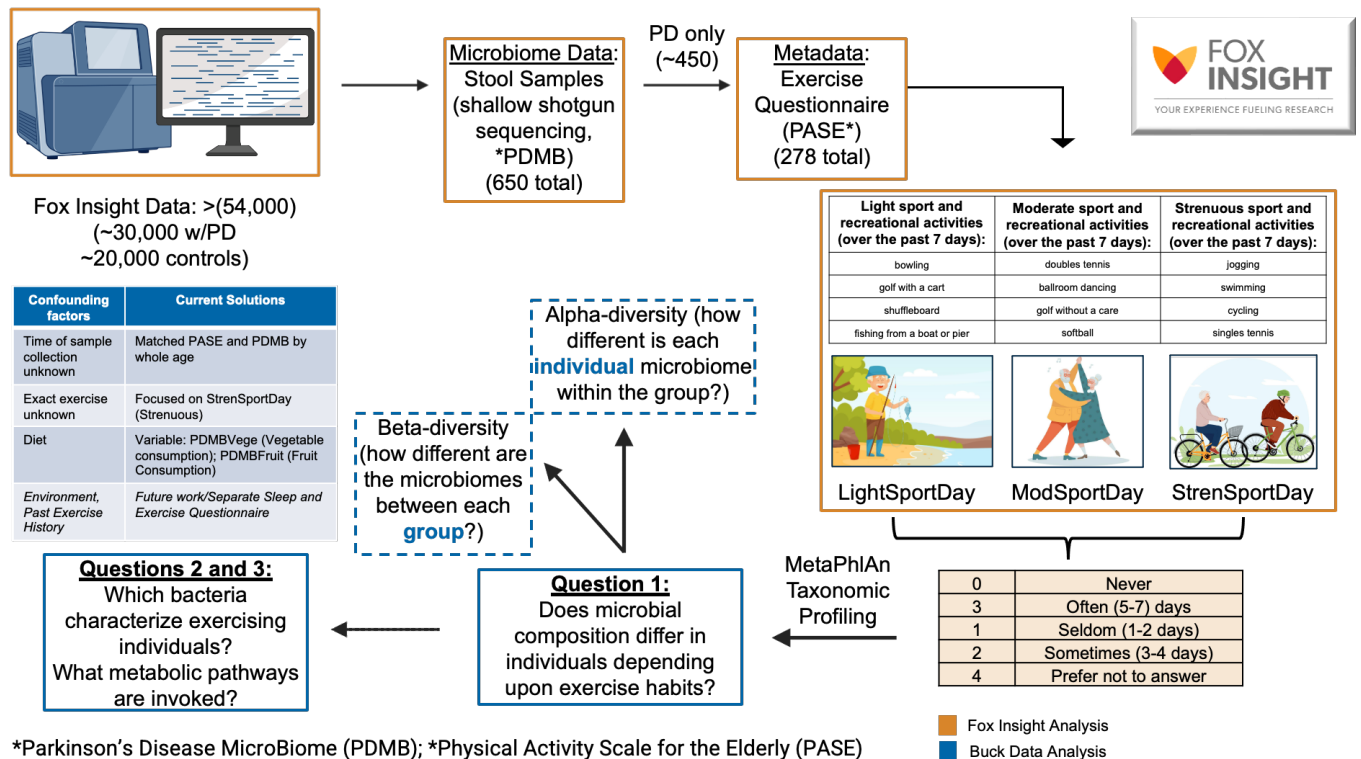




Fox Insight data selection of PASE and PDMB participants and MetaPhlAn bioinformatic analysis.

To date, exercise is one of the only therapeutics shown to effectively ameliorate the progression of Parkinson's disease (PD). One fascinating aspect of exercise is the rapid change which occurs to the physiological state of the gastrointestinal (GI) system where constriction of blood flow results in lower gut oxygen levels and changes in the organ's metabolic demands. Such changes can ultimately alter the gut 'microbiome', the vast community of microorganisms that inhabit the digestive tract. Ingestion of beneficial microbiota in the form of pro-biotics has been shown to improve gut health, brain health, and exercise performance. Over the last decade or so, poor gut health has been established as an important prodromal symptom of Parkinson's, manifesting as early as three decades before diagnosis. Given that exercise slows disease progression in those with PD, this begs the question as to whether administration of 'exercise-probiotics' might provide a targeted benefit. To answer these questions, we have performed bioinformatics analysis and AI-predictive modeling on data from 278 individuals enrolled in Fox Insight, an initiative from the Michael J. Fox Foundation (MJFF). Despite the high diversity of environmental conditions which can influence the microbiome, we have found significant differences in stool microbiomes based on exercise intensity (light, moderate, strenuous) and frequency (never, seldom, sometimes, often). Our results show that participation in strenuous exercise versus no-exercise has the greatest impact on bacterial Beta-diversity ($R^2=0.006$, $p=0.012$) versus moderate and light exercise ($R^2=0.004$, $p=0.13$ and $R^2=0.003$, $p=0.96$, respectively.) Greater significance in Beta-diversity is observed upon comparison of individuals within the strenuous exercise group who exercise often versus sometimes ($R^2=0.014$, $p=0.0025$), while alpha-diversity trends towards lower diversity in often-exercisers (Simpson Index, $p=0.1$), perhaps indicating a reduction in pathogenic bacteria. Using AI-predictive modeling, we were able to further establish substantial differences

between bacterial composition based on exercise behavior. Here, we found four bacteria species which predict strenuous exercise, six which predict moderate exercise, and four which predict light exercise. Our current work is focusing on similar characterization of oral bacteria as well as models which examine correlations between bacteria and disease symptomatology.