

Introduction:

Functional bowel disorders (FBDs) are multi-dimensional diseases varying in demographics, symptomology, lifestyle, mental health, and susceptibility to treatment. The patient lived experience is an integration of these factors, best understood with appropriately multivariate models.

Methods:

In a large patient cohort (n=1175), we developed a machine learning framework to better understand the lived experience of FBDs. Iterating through 59 factors available from routine clinical care, spanning patient demography, diagnosis, symptomatology, life-impact, mental health indices, healthcare access requirements, COVID-19 impact, and treatment effectiveness, machine models were used to quantify the predictive fidelity of one feature from the remainder. Bayesian stochastic block models were used to delineate the network community structure underpinning the lived experience of FBDs.

Results:

Machine models quantified patient personal health rating (R^2 0.35), anxiety and depression severity (R^2 0.54), employment status (balanced accuracy 96%), frequency of healthcare attendance (R^2 0.71), and patient-reported treatment effectiveness variably (R^2 range 0.08-0.41). Contrary to the view of many healthcare professionals, the greatest determinants of patient-reported health and quality-of-life were life-impact, mental wellbeing, employment status, and age, rather than nosology (diagnostic group) and symptom severity (Figure 1). Patients responsive to one treatment were more likely to respond to another, leaving many others refractory to all.

Conclusions:

The assessment of patients with FBD should be less concerned with diagnostic classification than with the wider life impact of illness, including mental health and employment. The stratification of treatment response (and resistance) has implications for clinical practice and trial design, in need of further research.

Stochastic block model

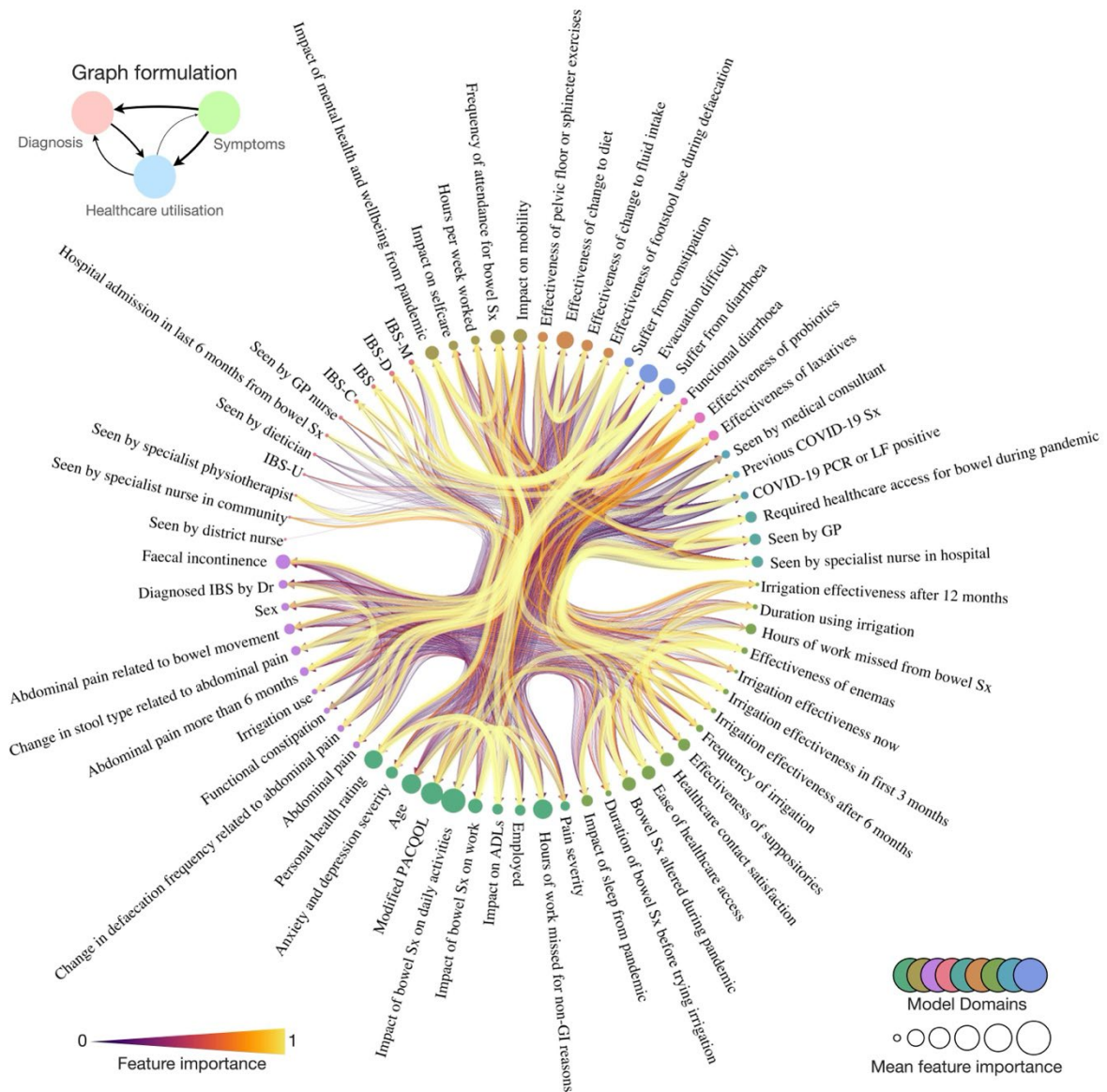


Figure 1: A generative network community structure for the lived experience of functional bowel disorders. Radial network of the nested, generative Bayesian stochastic block model community structure of patient factors. Nodes (circles) are sized according to their importance in predicting all other target nodes. Edges (connections) are weighted by the directional feature importance in predicting one feature over another, where edge width and colour is proportional to the key.