The intestinal microbiome is now recognised as playing an important role in human health and disease, impacting on many host physiological processes from metabolism and immune homeostasis to brain development and even cognitive function. Importantly, many of these physiological processes appear to be affected by early life events. Maternal health during pregnancy, term of birth, mode of delivery (Spontaneous Vaginally Delivered or Caesarean-section), infant diet (breast feeding, infant formula feed, fortified infant formula) and exposure to microorganisms (both pathogenic and commensal) all impact on neonatal physiological development and later life health or disease risk. Many studies, using different microbiological approaches have characterised the successional development of the infant gut microbiota. Some have also correlated microbiota composition with concomitant changes in health status (e.g. incidence of infections) or physiological biomarkers. Studies in animals and using in vitro microbiota models have identified prebiotics capable of modulating the architecture of the infant gut microbiota and intervention studies in healthy infants have also confirmed that infant formula fortified with prebiotics can modulate the gut microbiota of formula fed infants towards that of breast-fed infants. In this presentation we will assess the potential of fructans (inulin and oligo-fructose in particular) as prebiotic ingredients capable of modulating the composition of the infant gut microbiota. We will discuss evidence of safety, tolerability and impact on microbiota metabolic output. Finally, we will discuss the need for wider application of whole systems metabolic profiling or metabolomics to study the metabolic consequences of microbiota modulation, using a specific example data-set. In a collaborative study with University College Cork in Ireland, we have measured the metabolic implications of early life events in terms of urinary metabolite profiles using LC-MS based metabolomics in 199 breast fed infants. Mode of delivery and term v pre-term birth clearly impacted on urinary metabolite profiles, with 5000 statistically significant biomarkers separating infant groups. Remarkably, these shifts in metabolite profiles reflected closely differentiated clustering of faecal microbiota at the same time point, indicating that gut microbiota derived metabolites contribute significantly to the urinary metabolome in infants and more importantly, that changes within the intestinal microbiome brought on by early life events have clear and measurable consequences in terms of infant metabolism. These observations identify metabolomics as a powerfully informative tool for studying diet:microbiota interactions, especially in infants, and a technology likely to provide new mechanistic insight linking microbiota modulation with physiological response or health effects in babies.