Concluding thoughts

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Microbiome is **highly complex** and varied between individuals. We are not yet able to define a “healthy” microbiome i.e. a baseline. Going forward we should perhaps try to define “reference populations”.

Guidelines on specification, or an ‘average’ characterisation including parameters, ranges, diversity and species information. Defining a ‘range’ of microbiomes e.g. structure, function might help identify what types of microbiomes increase the risk of adverse effects.

Investigate how microorganisms process chemicals, considering the **chemical conversions** that occur in the gut including toxicokinetics e.g. metabolism of **xenobiotics into toxic metabolites** and how this might be considered in an assessment.

Continue the **development of integrative multi-omics** approaches, to provide comprehensive and holistic understanding of host microbiome interactions. Functional studies *in vitro* can complement *in vivo* investigations.

Challenge in trying to **distinguish between causality, correlation or association.**

Increase in databases with microbiological, metabolome and genomic data, where AI can be utilised to **process information and extract relevant trends** or results.