**Phenotype switching explains the emergence of alternative stable states in a gut microbial community**

Several human-associated microbial communities occur in more than one configuration and change their composition in response to perturbations, remaining in an altered state even after the perturbation has ceased. Different hypotheses have been proposed to explain this behaviour but have not yet been clearly demonstrated. To identify a mechanism, we first investigated metabolic traits of three common human gut bacteria. A kinetic model parameterised on mono- and co-cultures predicted alternative states as a consequence of phenotype switching in *Blautia hydrogenotrophica*. We confirmed predictions in perturbation experiments and showed that phenotype switching explains alternative states in large communities in simulations. Thus, a transient perturbation combined with metabolic flexibility is sufficient for alternative communities to emerge, implying that they are not necessarily explained by differences between hosts.

One-sentence summary:

We show on the example of a synthetic human gut microbial community that phenotype switching explains the emergence of alternative stable states.