Dear Editors,

We wish to submit the following manuscript to PLOS Computational Biology:

"Process-based modelling of microbial community dynamics in the human colon".

This work uses a mathematical model based on differential equations to produce computer simulations of the microbial communities in the human gut and their response to changes in diet. Gut microbes have an important effect on human health, however, this is a complex ecosystem with huge biodiversity and individual variation and thus any emulation of this system represents a significant scientific challenge. We believe a mathematical modelling approach based on expert knowledge, gained from laboratory and volunteer studies, provides a valuable tool to test current knowledge and highlight knowledge gaps. To aid this we provide the code in an easy to use R package, microPopGut, that can be downloaded from github and thus developed by others in the future as more information is gained about the system.

Yours sincerely,

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