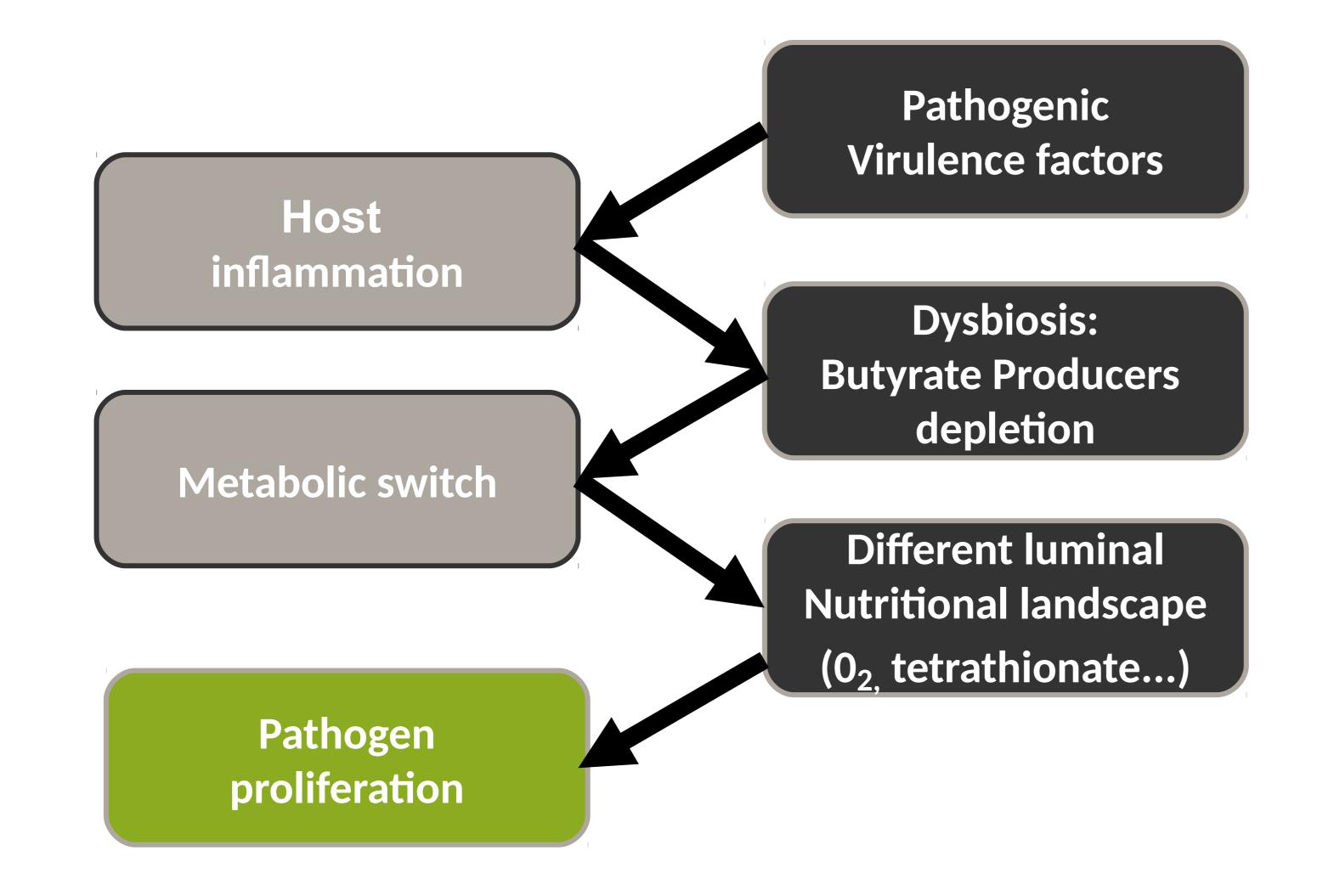


MISTIFY PROJECT. ECOLOGY OF SALMONELLA TYPHIMURIUM INFECTION: A MATHEMATICAL MODELING INSIGHT.

SIMON LABARTHE. MAIAGE, INRA JOUY-EN-JOSAS, FRANCE.
OUTGOING FELLOWSHIP TO ANDREAS BAUMLER'S LAB. AT UC DAVIS.

BIOLOGICAL CONTEXT:

- Salmonella infection is the most common vector of collective food poisoning in the developed world. Deciphering the mechanisms of infection is a key step towards **epidemiological policies** against Salmonella zoonoses.
- Infection mechanism:



•Goal: "whole pathobiome" model to decipher the mechanisms of infection, and characterize the infection mechanisms, together with competition with commensals.

MATHEMATICAL MODEL TYPE: Modeling the ecology of Salmonella infection **Gut section** Spatial motion: Metabolites: Poly/mono- Lactate, Methane, saccharides SCFA Fluid mechanics: Microbial activity: Mucus Peristaltism production Metabolism Trophic motion interactions Viscosity Absorption gradients Model domain Axisymmetry z

PROJECT OVERVIEW: Formalizing Dynamic model: Science front Task 1 host-pathogen host-pathogen interactions interactions Host-microbiota-pathogen Modeling complex interactions during host-pathogen S. Typhimurium infection interactions during infection Dynamic model: Modelling of a Task 2 simplified Host-pathogen-Microbial microbiota metapopulation community interactions simplification to design an **Expected outcome** ecological model Tractable model of hostpathogen-metapopulation interactions during **Exploration of** Numerical Task 3 infection protective scenarii study of the against infection model **Numerical** exploration of the model

