HERMANN EBERL, Univ. Guelph
compuGUT

The compuGUT is a mathematical modeling framework and computer simulation platform for transport processes, anaerobic digestion, and microbial population and resource dynamics in the human colon that we have developed as an in silico tool for studies in gut health. While the model had its origin in the field of food and nutrition, it should also be applicable in health and pharmacological research (e.g. in the the context of PBPK). In this talk we will give an overview of the model and show simple examples how it could be used to study the effects of antibiotics on gut ecology (e.g. supported by probiotics), or in bacteriotherapy. The compuGUT modeling framework is based on the IWA Anaerobic Digestion Model No. 1, adapted to the biological conditions in the colon, spatially extended by accounting for transport along the main flow direction in the lumen, ecologically extended by allowing for multiple representation of functional groups of microorganisms in lumen and mucus. The resulting model is a system of first order partial differential equations that are coupled through the reaction terms. The number of equations is context dependent. In its basic form it consists of 28, if a more complex microbiological description is desired the number of equations can go into the hundreds. This flexibility of the modeling framework poses considerable challenges for the computer implementation, which are addressed in the compuGUT software development (http://compugut.sourceforge.net). This is joint work with Arun Moorthy (Guelph), Martin Kalmokoff (AAFC), Steve Brooks (HC).