Physical modeling of the gut microbiota

In a human body, bacteria have been estimated to be in approximately equal number as human cells, 99% of them in the digestive tract [1]. A question that has just started being addressed is how the physical environment may explain the organization of the microbiota in the gut. Besides the flow in the gut, there are also biotic factors, which mechanism of action may actually be physical. The main effector of the adaptive immune response in the gut is a type of antibodies, which mainly protect the host by binding bacteria together, as we contributed to show [2,3]. We develop models using both analytical calculations and numerical simulations. We have several collaborations with experimentalists, in particular the immunologist Emma Slack (ETH Zürich). Our aim is to develop a more comprehensive model of the physical and mechanical environment in the gut and its consequences for microbiota, to distinguish which aspects can be interpreted with physical arguments, to study the microbiota spatial structure, its interaction with the immune system, and the microbiota evolution [4].

The internship will be located in Laboratoire Jean Perrin, Sorbonne Université, Jussieu, Paris. The advisor will be Claude Loverdo. The internship can be followed by a PhD, but we have no specific funding for a PhD student. There are different possible directions for the internship:

- Inference methods to interpret indirect data
- Multi-scale evolution models of immune escape for gut bacteria (taking into account evolution within a host and spread in the host population)
- Growth of antibody-mediated bacterial clusters: impact of geometry, and of limiting antibody concentration.
- Extension of a preliminary model of bacterial on-dimensional organization along the digestive tract

For more information

Claude Loverdo claude.loverdo@upmc.fr

[1] Sender R., Fuchs S., Milo R. Revised estimates for the number of human and bacteria cells in the body. PLoS biology. 2016;14(8):e1002533.

[2] Moor K., Diard M., Sellin M.E., Felmy B., Wotzka S.Y., Toska A., Bakkaren E., Arnoldini M., Bansept F., Dal Co A., Voller T., Minola A., Fernandez-Rodriguez B., Agatic G., Barbieri S., Piccoli L., Casiraghi C., Corti D., Lanzavecchia A., Regoes R.R., Loverdo C., Stocker R., Brumley D.R., Hardt W.D., Slack E. High-avidity IgA protects the intestine by enchaining growing bacteria. Nature 544:498–502 (2017)

[3] Bansept F., Moor-Schumann K., Diard M., Hardt W-D., Slack E., Loverdo C. Enchained growth and cluster dislocation: a possible mechanism for microbiota homeostasis. Plos Computational Biology 15:e1006986 (2019)

[4] Bansept F., Marrec L., Bitbol A-F., Loverdo C. Antibody-mediated cross-linking of gut bacteria hinders the spread of antibiotic resistance. Evolution 73:1077–1088 (2019)