

## Modelling the gut microbiota ecosystem

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The application of the recent molecular techniques based on massive nucleotide sequencing for the study of the composition of the intestinal microbiota has allowed us to discover an exciting and completely unknown ecosystem. In addition, it has been demonstrated that alterations in their composition or functionality are linked to numerous gastrointestinal and systemic diseases. In recent years, numerous studies have shown the influence of gut microbiota on human health and, consequently, numerous research lines have been established to optimize health influencing this ecosystem. However, the regulation rules of this bionetwork have not yet been deciphered, and this knowledge is crucial to be able to modulate the ecosystem.

The modulation of the microbiota needs not only physician approximations, but also biological, ecological, biochemical and physical. The microorganisms maintain a

close relationship with the host and this complicates the restoration of the ecosystem.

In Spain, our group has been a pioneer in the use of faecal microbiota transference to cure the diarrhoea caused for *Clostridium difficile*. In this pathology, the therapy is completely successful, but has not shown efficacy in other pathologies such as Ulcerative Colitis. The recently publications show that the success of the microbiota transference for the replacement of the gut ecosystem in Ulcerative Colitis patients depends on numerous factors such as the composition of the donor's microbiota, the density of the patient's bacterial ecosystem, the technique of transference, etc. Our proposal is to optimize the management of the gut microbiota modulation to the incorporation of the knowledge of other scientific areas such as mathematical modelling.