Organisms are complex systems that are not easy to study. For example, the gut microbiota is known to play a role in the organism’s brain. Studying these relationships are not straightforward. Information from many different levels needs to be integrated for a coherent picture of the complex interactions. In this talk I will explore the impact of host microbiota on microglia in aging, including transcriptomic and microbiota data. This use-case is also the occasion to think about the daily work of a bioinformatician: analysis of the sequencing data, interaction with collaborators, implementation of best reseach practices (reproducibility, open science), etc.