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Food allergies, gut bacteria and the bioinformatics of the microbiome.

Abstract

The Barwon Infant Study is a prospective cohort study comprising 1074 children born in the Geelong region between 2010 and 2013. The massive amount of data includes challenge-proven food allergy status at 12 months and microbial content of maternal and infant faecal samples. We have established that maternal carriage of a group of bacteria previously shown to be strikingly more common in a rural African population than western Europeans is associated with protection against food allergy.

More interesting from a stochastic modelling point of view is how such a result is discovered. We have used 16S rDNA sequencing to determine the microbial content of our samples, which relies on a clustering algorithm to identify bacterial taxa and may be highly susceptible to uncertainties in sequencing data. The stool samples we use are not fully representative of the microbial environment in the gut, where biological effects manifest. And recent work has indicated that microbiota in the samples can change even in -80 degree storage conditions. I aim to give an overview of the process of microbiome analysis, highlighting questions that may appeal to the applied probabilist.