Microbes are everywhere, including in and on our bodies, and have been shown to play key roles in a variety of prevalent human diseases. Consequently, there has been intense interest in the design of bacteriotherapies or "bugs as drugs," which are communities of bacteria administered to patients for specific therapeutic applications. Central to the design of such therapeutics is an understanding of the causal microbial interaction network and the population dynamics of the organisms. Toward that direction I will present recent work on a Bayesian nonparametric model and associated efficient inference algorithm that addresses the key conceptual and practical challenges of learning microbial dynamics from time series microbe abundance data. These challenges include high-dimensional (300+ strains of bacteria in the gut) but temporally sparse and non-uniformly sampled data; high measurement noise; and, nonlinear and physically non-negative dynamics. In a related work I will discuss a simpler inference problem surrounding the engineering of an interdependent consortia of bacteria. Here we will focus on experimental design for inference and discuss best practices for designing synthetic bacterial consortia for clinical/pharmaceutical applications.