Trillions of bacteria live in our guts, protecting us from infection and aiding our digestion. A bad mixture of bugs, or dysbiosis, may contribute to obesity, diabetes, cancer, Crohn's, and many other diseases, yet each person's gut bacteria are so distinct and diverse that we cannot yet easily identify which microbiomes are "unhealthy." This talk will begin by explaining major computational challenges in using metagenomic data to identify dysbiosis in human disease. The talk will then present contributions to solving several of these challenges using a combination of data mining, statistics, and experimentation.