The analyses of complex biological systems often results in output that may seem just as complex, with little useful knowledge extracted as a result of the multiple layers of information. We present here iterative hierarchical strategies, grounded in latent factor analysis, mixture decomposition and nonlinear extensions that provide interpretation and visualization tools that have proved useful in the analyses of the human microbiome. The use of multi-scale strategies is providing useful predictions of preterm birth and a deeper understanding of resilience of the human microbiome after antibiotic perturbations.