A detailed characterization of the human brain, its structural and functional underpinnings, remains on the frontier of modern science. Neurological research is important not only for its intrinsic interest, but for the purpose of better understanding (diagnosing and treating) neurological disorder as well. Happily, along with many other fields, neuroscience is entering an era of "Big Data" in which a new approach is possible: start from the data to develop a theory (rather than testing a theory by collecting data). In this talk we introduce a strategy involving the analysis of functional Magnetic Resonance Imaging, and employing computational techniques inspired by biological evolution, to discover and characterize interactions among regions of the brain. The technique is applied to two data sets: (1) a single subject performing two different, but related, tasks; and (2) many subjects performing no task, said to be in a "resting state". Preliminary results suggest that the methodology provides meaningful information, in that active regions are correctly predicted and tasks classified in (1), and many of the known resting-state interactions are uncovered in (2). Moreover, the technique characterizes interactions as either linear or nonlinear, providing more information than current methods (which make a linear assumption). Upon further successful testing, the methodology will be employed to enhance the theoretical framework within which we understand and model the human brain.