Understanding the logic of living systems requires knowledge of the mechanisms involved at the levels at which functionality is expressed. This information does not reside in the genome, nor even in the individual proteins that genes code for. No functionality is expressed at these levels. It emerges as the result of interactions between many proteins relating to each other in multiple cascades and in interaction with the cellular environment. To understand functionality there is therefore no alternative to copying nature and computing these interactions to determine the logic of healthy and diseased states. The rapid growth in biological databases, models of cells, tissues and organs and in computing power has made it possible to explore functionality all the way from the level of genes to whole organs and systems. In this lecture I will use models of the heart to demonstrate that we can now go all the way from individual genetic information (on mutations, for example) to exploring the consequences at a whole organ level.
