Changing styles of reasoning in the life sciences have for some time attracted attention from scholars in the history and philosophy of science. For example, it has been argued (Rheinberger 2000) that, whereas early molecular biology aimed at ‘creating the technical means of an extracellular representation of intracellular configurations’ – exemplified perhaps most iconically in Watson and Crick’s stick-and-ball model of the DNA double helix – the advent of recombinant DNA technologies has led to an inversion of this direction of fit. It is now the explicit rewriting of life according ‘extracellular projects’ (e.g., the demands of industrial or medical application) that shapes much of contemporary biomedical research. Similar shifts in focus – from the ‘neutral’ representation of naturally occurring phenomena to the ‘application-driven’ construction of phenomena that blur the line between nature and artifact – have been proposed under the label of ‘technoscientific research’ for other disciplines as well. This calls for an analysis of the interplay between representational projects in science and changes in instrumentation, experimental practice, and available technical infrastructure. The present paper analyzes one such example from cell biology: research into the structure of the cell’s membrane. The first experiments that probed cell membrane structure were performed by Charles Overton in 1895, which led him to believe that cell membranes and lipids bear certain similarities, and that non-polar molecules pass through the membrane by ‘dissolving’ in the membrane’s ‘lipid interior’. Later analysis of the remnants of red blood cells revealed a lipid presence in the membranes themselves, followed by the realization (in the 1930s) of a protein presence alongside the dominant lipids. For several decades to follow, the lipid-protein Davson-Danielli model dominated representations of the cell membrane in the life sciences. Yet, as closer historical and philosophical analysis reveals, none of the preceding discoveries necessitated the particular configuration of protein molecules proposed by the Davson-Danielli model. When technological changes – notably, the advent of electron microscopy – appeared to show a trilaminar structure of the cell membrane, this was taken as a clearcut case of additional confirmation of the protein-lipid-protein structure of the Davson-Danielli model. What contributed to the long-lived attractiveness of the Davson-Danielli model? For one, the model promised a unified account of membrane structure – making it the ‘unit membrane model’ – and thus exhibited what has often been deemed a core theoretical virtue in science: unification. However, we argue that much of the appeal of the model is, in fact, owed to the prestige of the new technology – electron microscopy – that was employed from the 1950s onwards. The great successes of electron microscopy in material sciences and physics, and the tangible materiality of the new technological infrastructure, served as a source of credibility for what, by hindsight, must be considered a theoretical model that was on rather shaky grounds from the start. Not only did the initial model lack sufficient motivation (as well as precedents in other relevant areas), but it also exhibited significant inconsistencies in the way it was used to explain experimental data. Eventually, in the early 1970s new preparation methods for electron microscopy brought out the inconsistencies in a way that could no longer be ignored, giving instead rise to what is still the accepted view of the cell membrane (with only minor modifications) today: namely, the fluid-mosaic view of the model (which postulates proteins being scattered throughout, and bobbing in and out of, a fluid lipid bilayer). The present paper tells the story of this theoretical shift in our understanding of the cell membrane as one that is marked by the (discontinuous) interplay between experimental data, theoretical models, and technological practices.