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In this talk, we will introduce a mathematical model, a system of nonlinear ordinary differential equations, which simulates the MAPK pathway, one of the most important biological cascades within the cell. Although this cascade contains numerous components, not all are accounted for in this model. Instead, we focus on the last and most important biological enzymes, Raf*, MEK and MAPK, whose input is directly derived from the initial hormone, 1-MA, which is added to the cell in order to start the cascade. This is the first model that analyzes the activation of three kinases to 1-MA. In addition, model set up, parametric estimations and numerical simulations will be given. Comparison between the experimental and mathematical results will be discussed. (Received September 22, 2009)