

## **SYSTEMS BIOLOGY ANALYSIS OF THE EGF MAPK PATHWAY: FROM STRUCTURES TO DATA INTEGRATION.**

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Signal transduction in living systems is essential to be able to interact and respond to the changes in the environment. The number of players and the different interactions result in very complex networks (specially in eukaryotes) which cannot be understood in a quantitative manner without the help of computer modeling and simulations. In order to model adequately protein interaction networks we need to incorporate time, space and structural information and move away from a node-edge flat network. Here we have used structural information, quantified all proteins in three different cell lines and localize them in a dynamic fashion to be able to produce a realistic model of the EGF-MAPK pathway that considers around 160 proteins. On top of it we have mapped human SNPs associated to disease on the structural map and analyzed them in terms of their effect on stability, activity and interaction with other proteins.