



# **Computational Systems Biology: Chapter 5. Complexities in Quantitative Systems Analysis of Signaling Networks**

*Christina Kiel, Luis Serrano*

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This chapter brings mammalian signal transduction to the center of quantitative and integrative sciences. Historically imbedded within human physiology, thanks to proteomics, interactomics, and molecular biology approaches, signaling is now far beyond the “black box” principle. However, despite the large amount of data available, we still have only limited insight into general design principles, and we lack knowledge on how cell type-specific signaling is achieved. Here, we summarize recent efforts in elucidating cell type-specific signaling, and in particular the role of protein abundances, signaling complexes and modules. We further discuss the potential of using synthetic biology approaches to decipher signaling networks. All of this is discussed in light of complementary quantitative mathematical modeling approaches. Signaling, more than any other discipline, needs computational biology to capture the dynamic systems behavior, and to reach its final goal: to be truly predictive for both the physiological and disease perturbed cellular conditions.

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