

On the identification of altered signaling pathways in cancer research

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Abstract:

High-throughput methods for measuring gene expression in cancer research, through "old" microarrays or the more recent sequencing-based technologies, generate the sort of data that invite creative systems biology approaches. One important issue along this line is to identify, from gene expression data, how the information processing machinery of the cell is altered in cancer. Within the stringent time constraints of this short talk we will try to describe some of our efforts on this problem.