# Reconstruction Of Intercellular Signaling Network: A Review On The Databases And Methods

S. Azadian[a], J. Zahiri[a]*, S. S. Arab[a], R.Hassan sajedi[b]

[a] Department of Biophysics, School Biological Sciences, Tarbiat Modares University, Tehran, Iran
[b] Department of Biochemistry, School Biological Sciences, Tarbiat Modares University, Tehran, Iran
*zahiri@modares.ac.ir

**Abstract:** One of the most important characteristics of unicellular and multicellular organisms is their ability in respond to environment agents and secretory molecules during the cellular signaling process [1]. This process results in cellular adaptation to different conditions, maintaining cell homeostasis, growth, differentiation, migration and etc. [2][3]. In multicellular organisms, the behavior of cells is more complicated than unicellular organisms because of their communications with other cells and respond to both the environmental factors and the messenger molecules that secreted by other cells.[4] Part of the intercellular communications takes place through the signaling process which is called cell-cell or intercellular signaling, that plays a very important role in coordinating of cell activity and is vital in complex processes such as immune response, growth, and hemostasis. Lack of coordinated activity of these cells lead to diseases such as cancer, autoimmunity and metabolic diseases [5]. Computational methods for network reconstruction can provide an insight into intercellular signaling mechanisms. Two data types is used for network reconstruction: receptor/ligand interactions and the transcriptome or proteome data that is indicated intercellular communications and amount of receptors and ligands expressed in each cell respectively. In this paper, the methods and databases contain related data for reconstruction of intercellular signaling network were reviewed.

**Keywords:** Intercellular signaling; Network reconstruction; Transcriptome; Cell–Cell signaling

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