

A Computational Approach inspired by Simulated Annealing to study the Stability of Protein Interaction Networks in Cancer and Neurological Disorders

Data Mining and Knowledge Discovery

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Deterministic Simulated Annealing Description

Description of the Deterministic Simulated Annealing:

Begin initialize $nE, W_{ij}, S_i, S_j, i, j = 1..N$

$t = 0$

do $t \leftarrow t + 1$

$$nE = \sum_{i=1}^N \sum_{j=1}^N w_{ij} S_i S_j$$

$t = t + 1$

until $t = tmax$

end

whereas:

nE is the system's final energy. t corresponds to a gene expression sample in each dataset and type (Normal, Cancer, Neurological). W_{ij} describes the weight explained in **Equation 2**, representing the existing influence between nodes S_i and S_j . In our approach S_i is the significance level of the expression or no expression of each gene.