

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

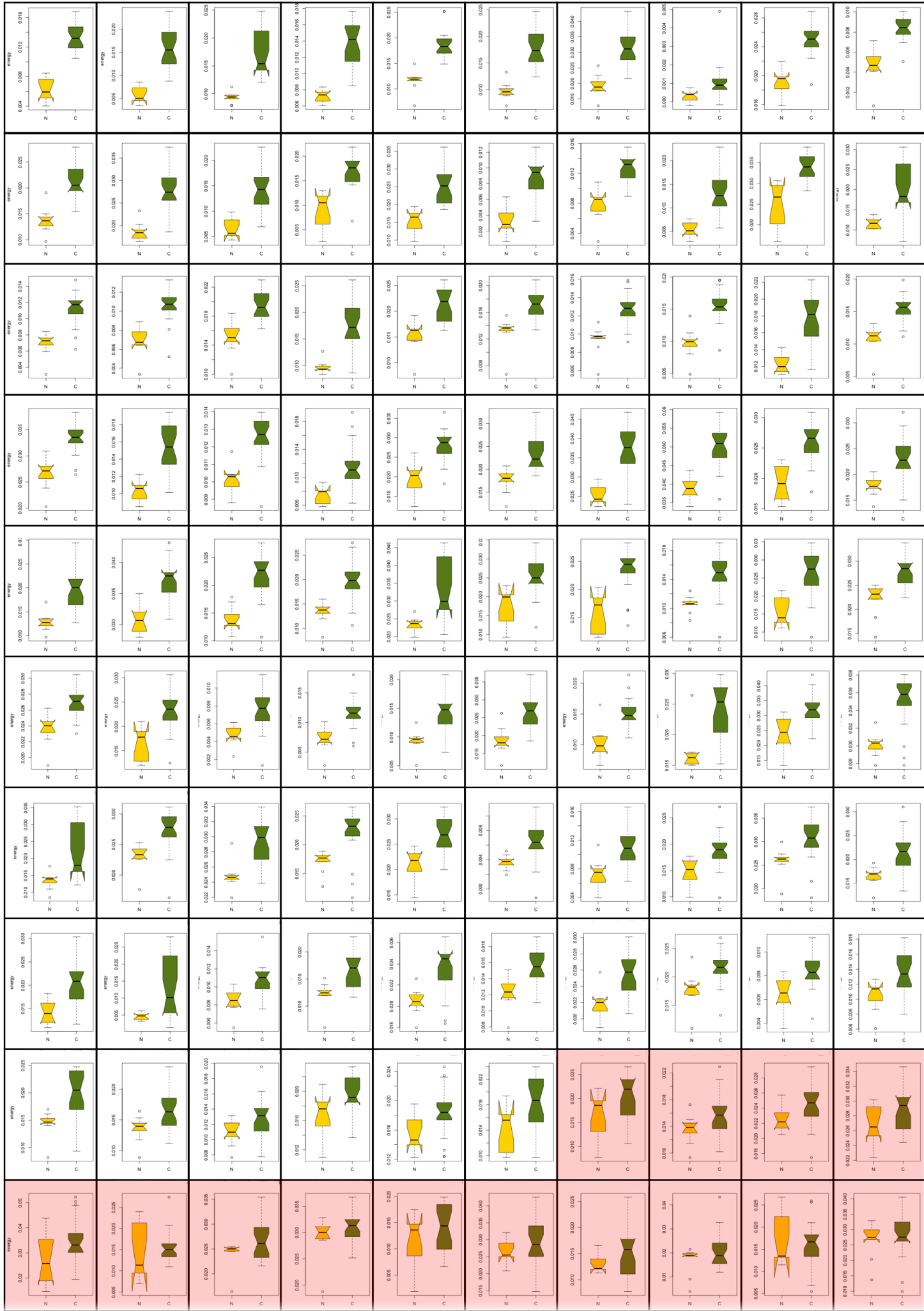
Data Mining and Knowledge Discovery

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**Online Resource 6** The  $nE$  distribution mapping all the genes in normal (N) and cancer (C) conditions in 100 random sub-sample networks. They are sorted by increasing score of p-values, from left to right and from the top to the bottom. In red, cells with non significant differences in the  $nE$  scores between N and C conditions are shown, representing 14% of the random sub-networks