1128-55-320   **Sepideh Nesaei*** (`sepideh.nesaei@wsu.edu`), vancouver, WA , and **Sahar Nesaei**. *Finding Structure In Cancer Gene Expression Data Using Topology.* Preliminary report.

We review a new method in data analysis of gene expression based on information given by tools from algebraic topology. Gene expression data sets are usually high dimensional-giving expressions of 50,000 or more genes for 100-200 subjects. Lockwood and Krishnamoorthy (2015) considered dualizing the data set, i.e., considering genes in the subject space, thus getting a much smaller dimensional problem. The found persistent topological features, i.e., holes, in several different cancer data sets thus dualized. We present the details of their work, and further explore how to analyze the stability and statistical significance of the identified features. (Received February 28, 2017)