This paper introduced a new approach to gain cancer related information by combing gene expression data and protein-protein interaction data. These two datasets are used to build labeled graph, based on which several concepts are defined as well as the corresponding searching algorithms.

Overall, this paper is well written and organized. However, some of the mathematical concepts in this manuscript are a little of overplayed which could have been introduced in simpler and more intuitive ways. Furthermore, the discussion part (Section 4) looks more like conclusion part (which is missing). The way to interpret and understand searching results of the algorithm or more evidences that can prove the conclusion that this method is capable of identifying new potential cancer proteins can be added in this section.