# Personalized Cancer Driver Gene Identification, A Network Based Approach

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**Abstract**: Cancer as one of the most important causes of death in the world, has allocated a lot of studies to itself. This disease is caused as a result of an intracellular genetic change that leads to a change in its normal mechanism. Many of the mutated genes are neutral and are known as "passengers" and their mutations are not an advantage in stimulating the growth of tumors[1, 2]. One of the major challenges in Cancer Genomics is the identification of a small set of active mutated genes called "drivers", which are directly related to the adaptation and growth of the tumor[1, 3]. Cancer driver genes can be classified into two categories: Common driver genes and personalized driver genes[4]. Common driver genes are driver genes that are identified as driver genes in a group of patients, but personalized driver genes are the driver genes identified in a particular person. These genes may also be identified in other individuals as a driver gene, or they are only specific to one patient. In this article, a network based approach is presented for identifying personalized driver genes. In addition to using the available information on the characteristics related to genes and proteins and available communications in genetic networks used in previous approach [4-7], this approach has also used the information available in the Gene Ontology project[8] in the process of identifying driver genes. In this approach, the important mutated gene of each patient is identified once using mutation and expression data, and again using mutation, expression and GO data. For this purpose, important mutated genes have been ranked in the genetic network using the propagation algorithm[9] and enrichment score[10]. Then, these important mutations are combined and personalized driver genes are introduced. Also, a new criterion Patientscore is defined according to identified personalized driver genes, and it is shown that this score is a valid criterion for clinical predictions. In order to evaluate the performance of the proposed approach, firstly, using statistical tests, and it is shown that the calculated Patientscore has a significant relationship with clinical data. Then, using survival analysis[11], and shown that this score has been introduced as a good predictive criterion for each patient, and this indicates the validity of this score.

**Keywords:** Cancer; Cancer driver gene; Personalized driver gene; Gene Ontology; Survival analysis; Clinical prediction.

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