Vision Statement

Cancer is one of the major causes of death in the modern society. It completely changes the patient's life from the moment of diagnosis. While in the 19th century people feared the creeping death by tuberculosis now cancer has taken its place. A variety of oncologic diseases exists and each of them can be considered a different disease. Therefore, more or less specific treatment schemes have been developed for each type of cancer based on surgery, irradiation and chemotherapy. However, scientific studies reveal more and more that even the same type of cancer can be different in each patient. Many doctors believe that the future of cancer treatment is a personalized therapy for each patient based on the traits of disease in this patient [1]. This is complicated by the fact that a biologic system such as cancer cell is very complex. A huge diversity of biomarkers that determine the traits of cancer exists and lots of data showing the correlation between the status of a biomarker and the outcome of therapy has been evaluated in clinical studies. Since this large amount of data makes it impossible for a physician to decide which therapy is the best for his patient I suggest to develop software that would help him with this task. It would store the data from clinical studies, select the most significant biomarkers that affect the outcome and upon determining the status of these biomarkers for a particular patient suggest a therapy that has been successful in patients with the same biomarker pattern. Any physiological process can be considered a biomarker if it determines a trait of cancer. An example is a mutation in a gene that affects the function of its product [2].

The software would consist of four parts.

First, the data from clinical studies has to be acquired. Therefore, a website needs to be developed that screens the www for hospitals performing these studies and sends them a request to share the data.

The second part would be a database. This database would have sections for every particular type of cancer and include the status of biomarkers and the parameter showing the treatment success such as the life span after diagnosis for each patient evaluated by a clinical study.

The third part of the proposed software will be a program that screens the database and selects those biomarkers (for example, DNA mutations, epigenetic alterations), where a different status of this particular marker correlates with a different prognosis/outcome despite the same treatment. This would help to decide which biomarkers the patient should be tested for since their status will affect the outcome.

The fourth and last part of the software will be the one interacting with the physician. Upon entering the diagnosis it would suggest the doctor to test the status of biomarkers that were selected by the previous software part, according to the type of cancer the patient is suffering from. After the laboratory analysis that will determine the status of all significant biomarkers for this patient the program will screen the database again looking for those patients who had the same biomarker status combination. Then it will choose which of these patients had the best outcome and suggest the therapy scheme that those patients received.

Taken together this software will help the physicians to choose the therapy for their patients according to the molecular marker status of their cancer. This would personalize the medicine and revolutionize the concept of cancer treatment.

1. Wistuba, II, et al., *Methodological and practical challenges for personalized cancer therapies.* Nat Rev Clin Oncol. **8**(3): p. 135-41.
2. Rodriguez-Paredes, M. and M. Esteller, *Cancer epigenetics reaches mainstream oncology.* Nat Med. **17**(3): p. 330-9.