

Vision Statement

Cancer is one of the major causes of death in the modern society. For both men and women it is on the second place as the cause of mortality only slightly behind the heart disease. 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. Only few diagnoses are feared as much as cancer and are associated with death.

A lot of hope is placed in new achievements in cancer therapy. And those who have lost their dearest to cancer know what it means to see the therapy failing and longing for an efficient way to treat cancer [1].

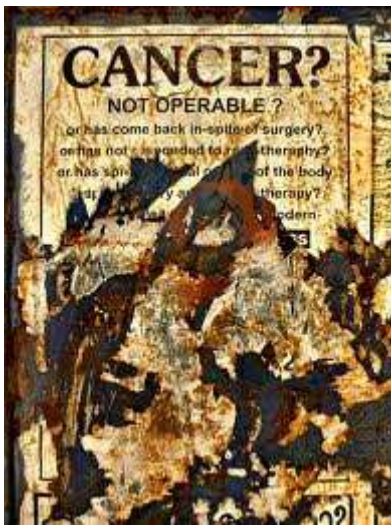


Figure 1. Hopes for a cure are torn into pieces by failure of cancer treatment.

From the medical point of view a variety of oncologic diseases exists and each of them can be considered a different disease making the choice of the right treatment complicated as it is different for every malignant tumor. 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 three 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 of the proposed software would be a database containing the data obtained from clinical studies. For each patient evaluated by a clinical study this database would have sections for the particular type of cancer, the status of biomarkers, the therapy the patient underwent and the parameter showing the treatment success such as the life span after diagnosis.

The third and last part of the software will be the one interacting with the physician and screening the database in order to find the optimal therapy. Upon entering the diagnosis the database will be screened by a program that selects only those biomarkers where a different status of this particular marker correlates with a different prognosis if same treatment was applied. This would indicate that the status of this biomarker affects the efficiency of the therapy. If a difference in the status of one biomarker does not alter the survival of the cancer patients it is unlikely that this biomarker decides about success and failure of a particular therapy. Therefore, this part of our software would help to decide what biomarkers a new cancer patient should be tested for since their status will affect the outcome. Thereafter, the software would suggest the doctor to test the status of biomarkers that were selected by, according to the type of cancer the patient is suffering from. After the laboratory analysis that will determine the status of all significant biomarkers that were suggested by the software 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. The data flow chart and the sequence diagram shown in Figure 2 and 3, respectively, describe parts two and three of the suggested program.

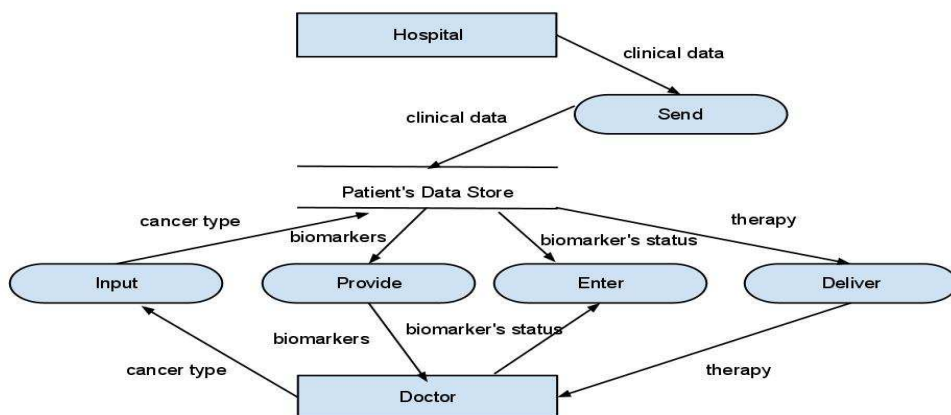


Figure 2. Data flow diagram showing the whole system.

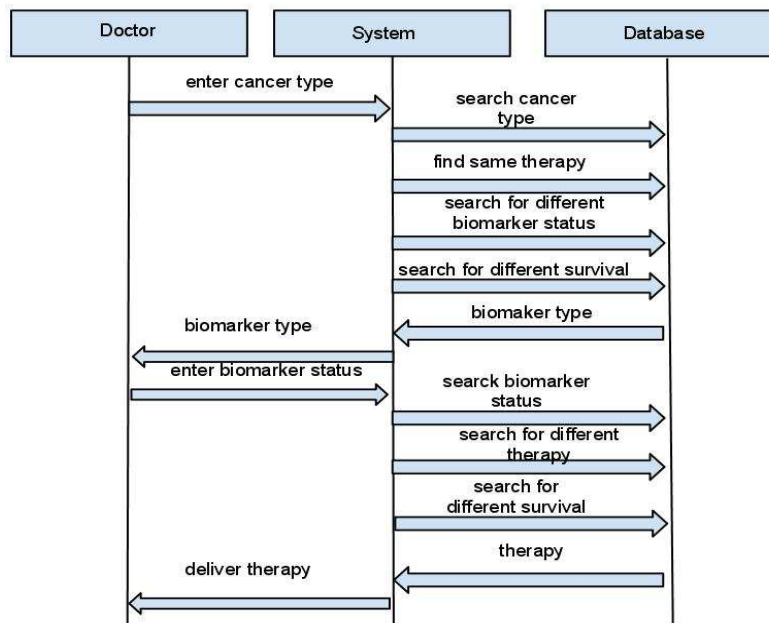


Figure 3. Sequence diagram showing the second and the third part of the system.

Of the systems three parts the second and the third part together are most suitable for immediate implementation. The first part that includes the development of a website requesting from hospitals and receiving this data would take a long time since a lot of hospitals need to be contacted and convinced to cooperate. Without creating the database described in part two there will be no possibility to save the data appropriately. The third part of the software is a step that can only follow the creation of the database. The second and third part that are suggested for implementation require a web server, a database and a program screening the database for appropriate biomarkers to test the patient for based on the criteria described above. After entering the test results the third part of the software will choose the most successful therapy. Its implementation is an interesting and challenging project. Artificial data can be used to test the system.

Since cancer is a very individual disease the only chance to treat it efficiently is to design strategies for a personalized therapy. With a huge amount of data existing on biomarker status correlating with the outcome of a particular cancer therapy a software helping doctors to utilize this data in order to select the best therapy for each patient is desirable. 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.

Sources

1. <http://www.flickr.com/photos/runran/3358075794/>
2. Wistuba, II, et al., *Methodological and practical challenges for personalized cancer therapies*. Nat Rev Clin Oncol. **8**(3): p. 135-41.
3. Rodriguez-Paredes, M. and M. Esteller, *Cancer epigenetics reaches mainstream oncology*. Nat Med. **17**(3): p. 330-9.