MATCH project: Decision support system for improvement of therapy in colon cancer patients

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MATCH project entitles the development of an automatic diagnosis system that aims to support decisional process in clinical practice for the treatment of colon cancer diseases. This computer based platform addresses physician, cancer researchers and pharmaceutical companies.

MATCH philosophy foundation is the integration between medicine and molecular biology by developing a framework where colon cancer diseases will be handled in order to improve effective colon cancer treatment.

Since response to therapy is mainly affected by genetic variability of both the patients as biological system and the tumor tissue of the patient, genetic fingerprinting represent the most suitable way to identify connection between the molecular profile of a patient (and of his neoplastic tissue) and his sensitivity to a particular therapy. Since Single Nucleotide Polymorphisms (SNPs) represent the molecular substrate of this variability, SNPs fingerprinting could provide molecular snapshots of a patient at molecular level with a very high amount of information that can be related to susceptibility to drugs or treatments.

The proposed system is characterized by three phases. Initially, the system will be supplied with quantitative and qualitative clinical and genetic data (mainly SNPs information for tumor suppressor genes). Next, computational process will take place and finally, the results that concern more effective colon cancer treatment and therapy will be available. The process will start with clinical and genetic data input from medical sources concerning a patient with a colon cancer. Genetic data are represented mainly by SNPs information of TSGs (tumor suppressor genes) from: patient normal tissues (non neoplastic mucosa), patient primary tumour, lymph nodes metastasis (when available) and distant metastasis (when available). Clinical and genetic data of all patients will be used to generate homogeneous clusters of patients with the longest subset of features (both clinical and genetic).

All members of a cluster should respond to therapies accord since their molecular profiles indicates small genetic variability among them. The automated decision support system will be then used to match the clinical and genetic profile of a new patient with the clusters representing homogeneous populations in MATCH data set. The new profile will be assigned to the cluster that shows the smallest distance (in terms of features) in its centroid profile. Statistical analysis of cluster population will provide information on the best available therapy for the new patient based on the outcomes of all the cluster members.

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