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A computer program for diagnosing and locating cancer

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A computer program has been developed by a team of researchers at the University of California for detecting and identifying the location of cancer within the patient's body. During the assay, blood sample is taken from the patient's body and the computer program is used for identifying specific molecular patterns in the cancer DNA present in the blood. The pattern is then compared against a database of tumor epigenetics, from different cancer types, to initiate the diagnosis.

The tumor and non-tumor DNA can be differentiated by comparing samples from the database of epigenetic markers. The molecular footprint for non-cancerous samples are also compiled to create a baseline for the cancerous samples.

The new computer program is still in its infancy and is being validated further. However, when it was compared with two other methods, called Random forest and Support Vector Machine, the overall error rate was much less with the new program.
The main advantage of this new program is that it is able to detect cancer at an early stage with an accuracy rate of 80 percent. Tumors present in organs such as liver or lungs are more easily diagnosed as compared to tumors present in breasts with this approach, during the early stage.