MedicalXpress

Sequencing cancer mutations: there's an app for that

April 3 2012

Using precise information about an individual's genetic makeup is becoming increasingly routine for developing tailored treatments for breast, lung, colon and other cancers. But techniques used to identify meaningful gene mutations depend on analyzing sequences of both normal and mutant DNA in tumor samples, a process that can yield ambiguous results. Now, a team of Johns Hopkins researchers says it has developed an easy-to-use online computer software application that can clear up any confusion faster and cheaper than other methods currently used to do the job.

The application, called "Pyromaker," – and soon a related tutorial – are available free-of-charge at http://pyromaker.pathology.jhmi.edu/. The software generates simulated pyrograms, which are readouts from a gene sequencing technique known as pyrosequencing.

Most pyrograms correspond precisely to a person's unique mutation or set of mutations, but some mutations can be more difficult to interpret than others, the Johns Hopkins researchers say. "Pyromaker's value is in rapidly sorting through each of several simulated pyrograms, until there is a clear match with the actual tumor pyrogram," says James R. Eshleman, M.D., Ph.D., a professor in the departments of pathology and oncology at Johns Hopkins. "Pyromaker enables us to do in minutes, essentially at no cost, what otherwise would take days of further, expensive tests."

Pyrosequencing works on shorter stretches of DNA than does the

traditional method, known as "Sanger," named for Frederick Sanger who invented the process. But pyrosequencing is also more sensitive in registering the presence of mutant DNA in a tumor sample, which is a mix of tumor and normal cells. That sensitivity makes it very useful for tumor sequencing, says Eshleman, because the mutant genes that drive a tumor's abnormal growth typically are less prevalent in a tumor sample, compared with normal versions of those genes.

Because a tumor pyrogram is an overlay of both healthy and mutant DNA, identifying the correct sequence may be difficult and further studies to sort it all out can delay diagnosis and add significantly to costs, he says.

Provided by Johns Hopkins Medical Institutions