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# New AI tool accurately identifies lung cancer type

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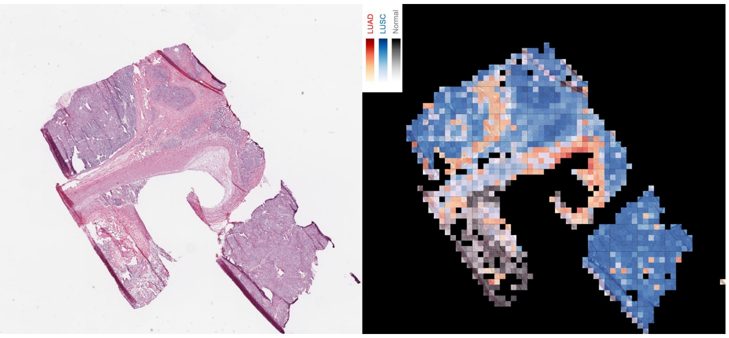
**Approach promises to instantly determine which patients will respond to targeted therapies.**



**Singapore -** A new computer program can analyze images of patients' lung tumors, specify cancer types, and even identify altered genes driving abnormal cell growth, a new study shows.

Led by researchers at NYU School of Medicine and published online in *Nature Medicine*, the study found that a type of artificial intelligence, or "machine learning," program could distinguish -- with 97 percent accuracy -- between adenocarcinoma and squamous cell carcinoma, two lung cancer types that experienced pathologists at times struggle to parse without confirmatory tests.

In addition, the study's AI was also able to, again from analyzing images, determine whether abnormal versions of six genes linked to lung cancer – including EGFR, KRAS and TP53 – were present in cells, with an accuracy that ranged from 73 to 86 percent depending on the gene. Such genetic changes or mutations often cause the abnormal growth seen in cancer, but can also change a cell's shape and interactions with its surroundings, providing visual clues for automated analysis.

Determining which genes are changed in each tumor has become vital with the increased use of targeted therapies that work only against cancer cells with specific mutations, researchers say. About 20 percent of patients with adenocarcinoma, for instance, are known to have mutations in the gene epidermal growth factor receptor or EGFR, which can now be treated with approved drugs.

But the genetic tests currently used to confirm the presence of mutations can take weeks to return results, say the study authors.

"Delaying the start of cancer treatment is never good," says senior study author Aristotelis Tsirigos, PhD, associate professor in the Department of Pathology at NYU School of Medicine and NYU Langone Health's Perlmutter Cancer Center. "Our study provides strong evidence that an AI approach will be able to instantly determine cancer subtype and mutational profile to get patients started on targeted therapies sooner."

Moving forward, the team plans to keep training its AI program with data until it can determine which genes are mutated in a given cancer with more than 90 percent accuracy, at which point they will begin seeking government approval to use the technology clinically, and in the diagnosis of several cancer types.

Along with Tsirigos and Razavian, authors from the NYU School of Medicine were lead investigators Nicolas Coudray of the Applied Bioinformatics Laboratories and Paolo Santiago Ocampo of the Department of Pathology; as well as Navneet Narula, Matija Snuderl, and Andre Moreira in the Department of Pathology, and David Fenyö, in the Department of Biochemistry and Molecular Pharmacology. Also a study author was Theodore Sakellaropoulos in the School of Mechanical Engineering at the National Technical University of Athens in Greece.