Artificial intelligence cuts lung cancer screening false positives

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Lung cancer is the leading cause of cancer deaths worldwide. Screening is key for early detection and increased survival, but the current method has a 96 percent false positive rate. Using machine learning, researchers at the University of Pittsburgh and UPMC Hillman Cancer Center have found a way to substantially reduce false positives without missing a single case of cancer.

The study was published today in the journal *Thorax*. This is the first time artificial intelligence has been applied to the question of sorting out benign from cancerous nodules in lung cancer screening.

"We were able to rule out cancer in about a third of patients, so they wouldn't need biopsies, they wouldn't need PET scans or a short-interval CT scan. They just need to come back in a year," said senior author David Wilson, M.D., M.P.H., associate professor of medicine, cardiothoracic surgery and clinical and translational science at Pitt and co-director of the Lung Cancer Center at UPMC Hillman.

A low-dose CT scan is the standard diagnostic test for lung cancer for those at high risk. Nationwide, about a quarter of these scans turn up shadows indicating nodules in the lung—a positive result—but fewer than 4 percent of those patients actually have cancer.

Right now, it's impossible to know from the scan alone who those 4 percent are, Wilson said. Of course, physicians don't want to miss any real cases of cancer, but they're also trying to reduce the false positive

rate, he noted.

"A positive test creates anxiety, increases health care costs, and the follow-up tests are not risk free," said study coauthor Panayiotis (Takis) Benos, Ph.D., professor and vice chair of computational and systems biology and associate director of the Integrative Systems Biology Program at Pitt. "For the 96 percent of people who have benign nodules, these procedures are unnecessary. So, we try to mine the data to tell which are benign and which are malignant."

Wilson, Benos and colleagues gathered low-dose CT scan data from 218 high-risk UPMC patients who were later confirmed to have either lung cancer or benign nodules. Then they fed the data into a machine learning algorithm—a form of artificial intelligence—to create a model that calculates the probability of cancer. If the probability falls below a certain threshold, the model rules out cancer.

Comparing the model's assessment against the actual diagnoses of these patients, the researchers found that they would have been able to save 30 percent of the people with benign nodules from undergoing additional testing, without missing a single case of cancer.

The three factors that were most important to the model, Benos said, are the number of blood vessels surrounding the nodule, the number of nodules and the number of years since the patient quit smoking.

"While it has been known for some time that tumors recruit more vascular support, this is the first time that we've been able to use computer technology to quantify their contribution and incorporate them into a predictive model that decides, with certainty, that some patients don't have cancer," Wilson said. "The next step is to evaluate this technique in a larger population, and actually it's started already, using about 6,000 scans from the National Lung Screening Trial."

Provided by University of Pittsburgh

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