Medical Xpress

Machines learn to detect breast cancer

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Software that can recognize patterns in data is commonly used by scientists and economics. Now, researchers in the US have applied similar algorithms to help them more accurately diagnose breast cancer. The researchers outline details in the *International Journal of Medical Engineering and Informatics*.

Duo Zhou a biostatistician at pharmaceutical company Pfizer in New York and colleagues Dinesh Mital and Shankar Srinivasan of the University of Medicine and Dentistry of New Jersey, point out that data pattern recognition is widely used in machine-learning applications in science. Computer algorithms trained on historical data can be used to analyze current information and detect patterns and then predict possible future patterns. However, this powerful knowledge discovery technology is little used in medicine.

The team suggested that just such an automated statistical analysis methodology might readily be adapted to a clinical setting. They have done just that in using an algorithmic approach to analyzing data from breast cancer screening to more precisely recognize the presence of malignant tumors in breast tissue as opposed to benign growths or calcium deposits. This could help improve outcomes for patients with malignancy but also reduce the number of false positives that otherwise lead patients to unnecessary therapeutic, chemotherapy or radiotherapy, and surgical interventions.

The machine learning approach takes into account nine characteristics of a minimally invasive fine needle biopsy, including clump thickness,

uniformity of cell size, adhesions, epithelial cell size, bare cell nuclei and other factors. Trained on definitive data annotated as malignant or benign, the system was able to correlate the many disparate visual factors present in the data with the outcome. The statistical model thus developed could then be used to test new tissue samples for malignancy.

More information: "Breast cancer diagnosis: a statistical analysis-based approach" in Int. J. Medical Engineering and Informatics, 2013, 5, 321-333

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