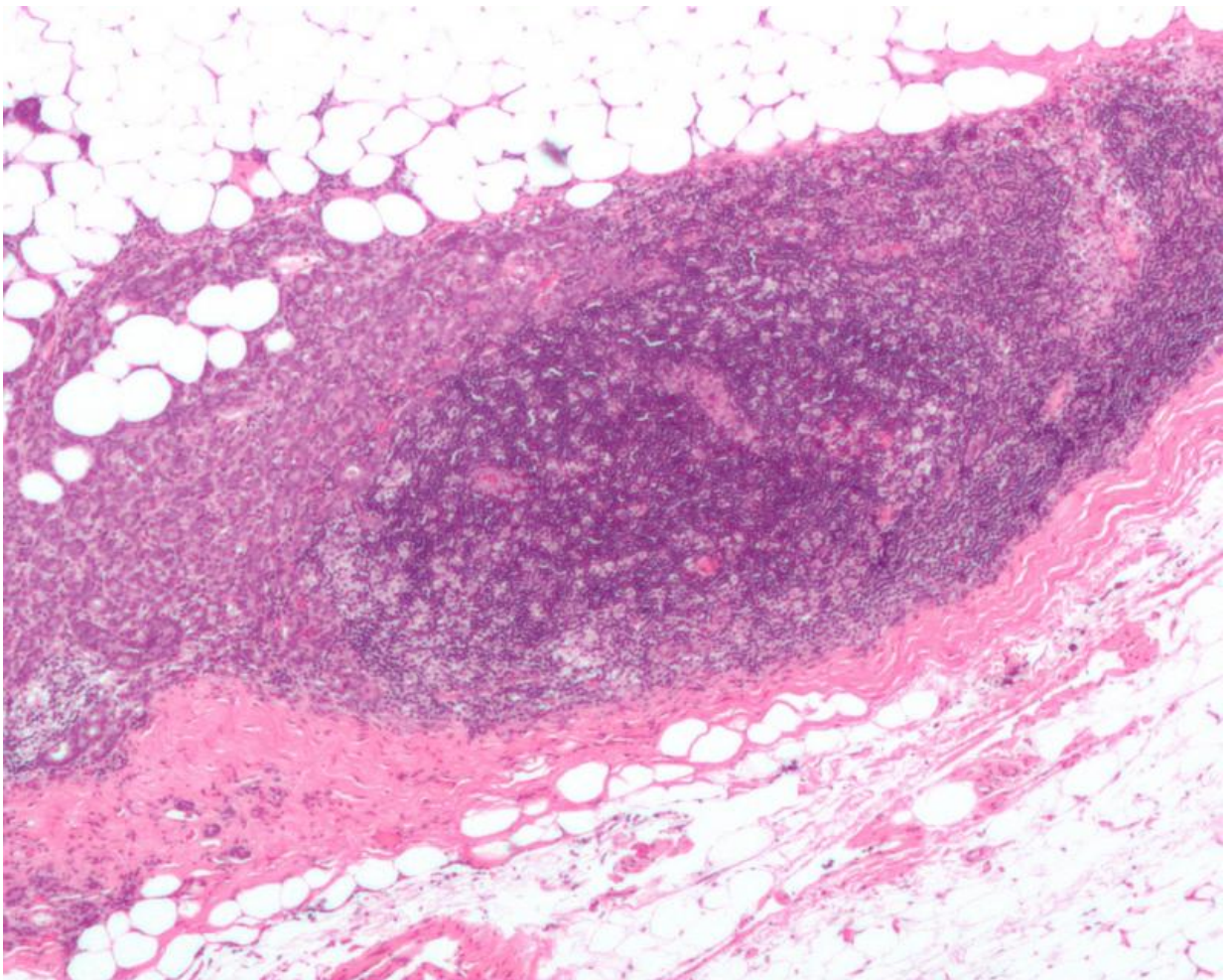


Researchers hope to use artificial intelligence to improve breast cancer patient outcomes

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Micrograph showing a lymph node invaded by ductal breast carcinoma, with extension of the tumour beyond the lymph node. Credit: Nephron/Wikipedia

Western University researchers are working on a way to use artificial intelligence to predict a patient's response to two common chemotherapy medications used to treat breast cancer - paclitaxel and gemcitabine.

Peter Rogan, PhD, and a team of researchers, including Stephanie Dorman, PhD, and Katherina Baranova, BMSc, at Western's Schulich School of Medicine & Dentistry, are hoping to one day remove the guesswork from [breast cancer](#) treatment with this technique.

Based on personal genetic analysis of their tumours, [patients](#) with the same type of cancer can have different responses to the same medication. While some patients will respond well and go into [remission](#), others will develop a resistance to the medication.

Identifying the genetic factors which lead to resistance or remission can help develop better targeted, individualized treatment regimens with better patient outcomes.

"Treating patients with therapies that are the most likely to be successful can help reduce unnecessary toxicity and improve overall outcomes," said Dorman.

Rogan and Joan Knoll, PhD, professor, Schulich Medicine & Dentistry, began by defining a stable set of genes in 90 per cent of breast cancer tumours in 2012.

Beginning with 40 genes including several stable genes, the team then used [artificial intelligence](#) combined with data from cell lines and tumour tissue from cancer patients who had treatment with at least one of the medications to narrow down and identify the genetic signatures most important for determining resistance and remission for each medication. Their study has recently been published in the journal, *Molecular Oncology*.

Using the data, the researchers were able to identify the 84 per cent of women with breast cancer who would go into remission in response to the drug [paclitaxel](#). The genetic signature identified for the drug [gemcitabine](#) was able to predict remission using preserved tumour tissue with 62 to 71 per cent accuracy.

Now, with this data in hand, the researchers are working to further refine the genetic signatures and improve the predictions further.

"Artificial intelligence is a powerful tool for predicting drug outcomes because it looks at the sum of all the interacting genes," said Rogan, professor in the departments of Biochemistry, Oncology and Computer Science, Canada Research Chair in Genome Bioinformatics and president, Cytognomix Inc. "If we can use this technology to improve our knowledge of which medications to use, it could improve patient outcomes. The earlier we treat a patient with the most effective medication, the more likely we can effectively treat or possibly even cure that patient."

More information: Dorman SN, Baranova K, Knoll JH, Urquhart BL, Mariani G, Carcangiu ML, Rogan PK. Genomic signatures for paclitaxel and gemcitabine resistance in breast cancer derived by machine learning. *Mol Oncol*. 2015 Aug 22. pii: S1574-7891(15)00146-5. [DOI: 10.1016/j.molonc.2015.07.006](#). [Epub ahead of print]

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