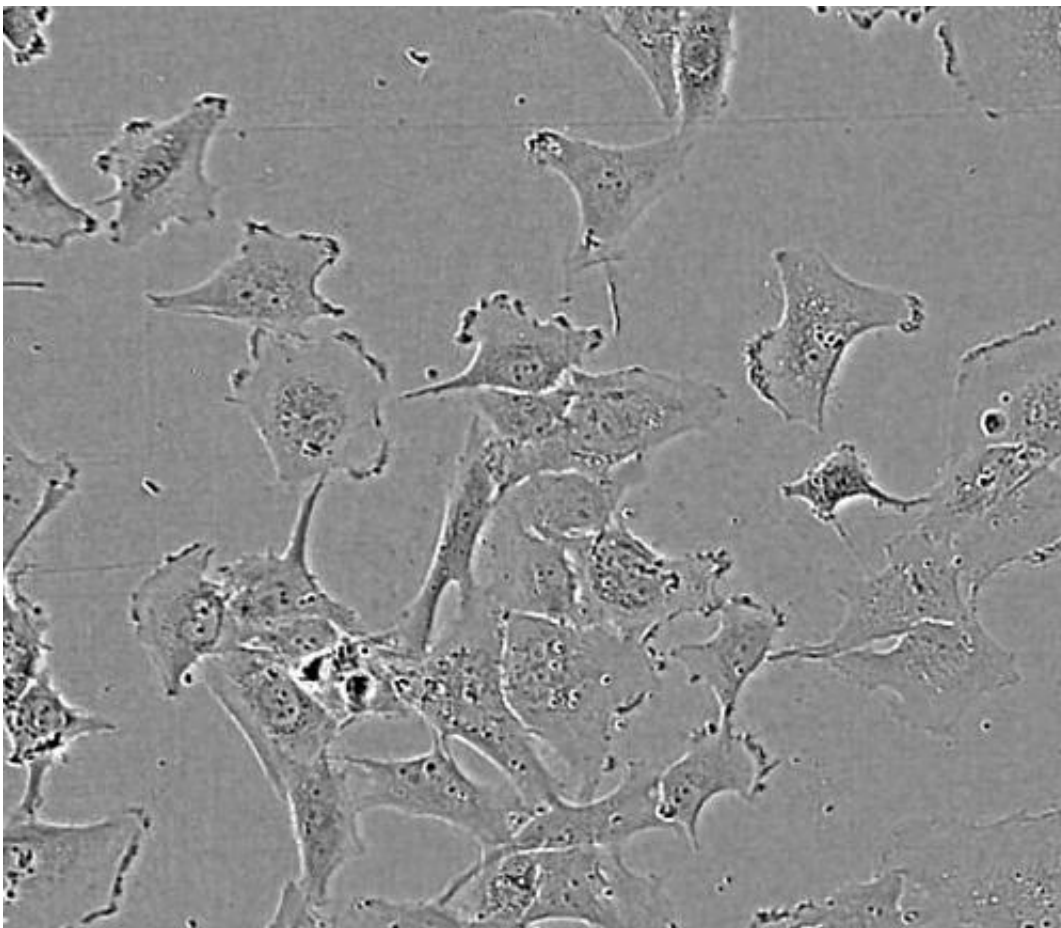# Drug sensitivity predicted computationally

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Culture of HS578 breast cancer cells. Researchers of Aalto University and University of Helsinki have developed a novel computational approach to predict how effectively drugs can inhibit growth of different breast cancer cells.

With modern high-throughput technologies researchers can measure a multitude of molecular properties from cancer cells. A big question of

precision medicine is how computational modelling can be used to predict sensitivity of cancer cells to drugs, and the best cancer treatment. Answers are sought in a study published in *Nature Biotechnology*.

Researchers at Aalto University and University of Helsinki used genomic changes and other measurements in computational modelling, for predicting drug sensitivity of cancer cells as a function of the cells' molecular properties. The enormous number of variables requires innovative statistical solutions, to be able to computationally use the available genomic information in biomedical research. The goal of the research, within the next decade, is to enable better customised treatment decisions for individual patients, and chances to cure specific subtypes of cancer.

 – The goal of computational personalised medicine is to develop computational models with which we can predict effects of drugs in cells based on their genomic profiles. The most difficult challenge is simple in principle: how to choose and combine the molecular properties for the prediction, tells Professor Samuel Kaski of Aalto University.

The top-performing prediction methods used nonlinear models of data, and the different measurement techniques were weighted with coefficients learned from data.

– The most successful approach further applied techniques of statistical machine learning, such as generalizing between similar drugs what was learned from data. Incorporation of prior biological knowledge increased prediction accuracy without additional costly measurements, explains Professor Kaski.

The large method spectrum analysed in this work gives a solid basis for developing models from patient data and refining them in intensive collaboration with cancer biologists and clinicians.

The multidisciplinary Finnish research group from Aalto University and University of Helsinki participated in an international competition of computational [drug sensitivity](#) prediction methods and won the competition. It was organized by the National Cancer Institute (NCI), USA, and the DREAM community (Dialogue on Reverse Engineering Assessment and Methods).

Provided by Aalto University