

Researchers excel in predicting cancer drug sensitivity

November 19 2012

Researchers from Helsinki Institute for Information Technology HIIT and Institute for Molecular Medicine Finland FIMM have developed a triumphant solution for predicting responses of breast cancer cells to a set of cancer drugs. The prediction is based on the genomic profiles of the cancer cells. Harnessing genomic profiles of cells in choosing the best treatment is considered the holy grail of personalised medicine.

The team participated in the seventh annual DREAM competition organised by the U.S. [National Cancer Institute](#) (NCI) and The Dialogue for Reverse Engineering Assessments and Methods (DREAM). Their challenges crowd-source highly demanding scientific problems to top research teams around the world. The best solution will be published in a top journal.

The team led by Professor Samuel Kaski, Director of HIIT, a joint research centre of Aalto University and University of Helsinki, will present its winning solution at the DREAM 2012 conference on November 13 in San Francisco. The team's solution outperformed 47 other teams in the prediction challenge.

Computational methods integrate multiple views of the genomic profile of cancer cells

It is well known that drug therapies may effectively kill cancer cells in one patient, but not in another patient suffering from the same type of

cancer. However, the molecular determinants underlying the differences in drug response are not sufficiently understood.

"A goal of computational personalised medicine is to develop models which predict drug sensitivity of cells from their genomic profiles," explains Kaski.

The organisers of the NCI-DREAM challenge provided data of [breast cancer cells](#) for the training of computational sensitivity [prediction models](#). They evaluated the participants' models on test measurements of drugs that were unknown to the participants.

As in most current biomedical experiments, several types of measurements had been collected on the cancer cells: activity of genes, epigenetics, and [genetic profiles](#). The key problem was to optimally combine the complementary "views" that the different measurements yield.

"We had been developing new machine learning methods for these 'multi-view' problems, which occur in many fields, and they gave us a flying start," tells Kaski.

HIIT and FIMM have also collaborated on personalised medicine well before the competition.

"The challenge was a great additional opportunity for us to put our heads together. People with different backgrounds presented different views on the problem and brought in their own expertise and experience to improve the integrated solution," says HIIT researcher Dr. Elisabeth Georgii.

Although the result is still far from clinical applicability, computational personalised medicine has taken an encouraging, prize-winning step

forward.

Provided by Aalto University

Citation: Researchers excel in predicting cancer drug sensitivity (2012, November 19) retrieved 27 April 2024 from <https://medicalxpress.com/news/2012-11-excel-cancer-drug-sensitivity.html>

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