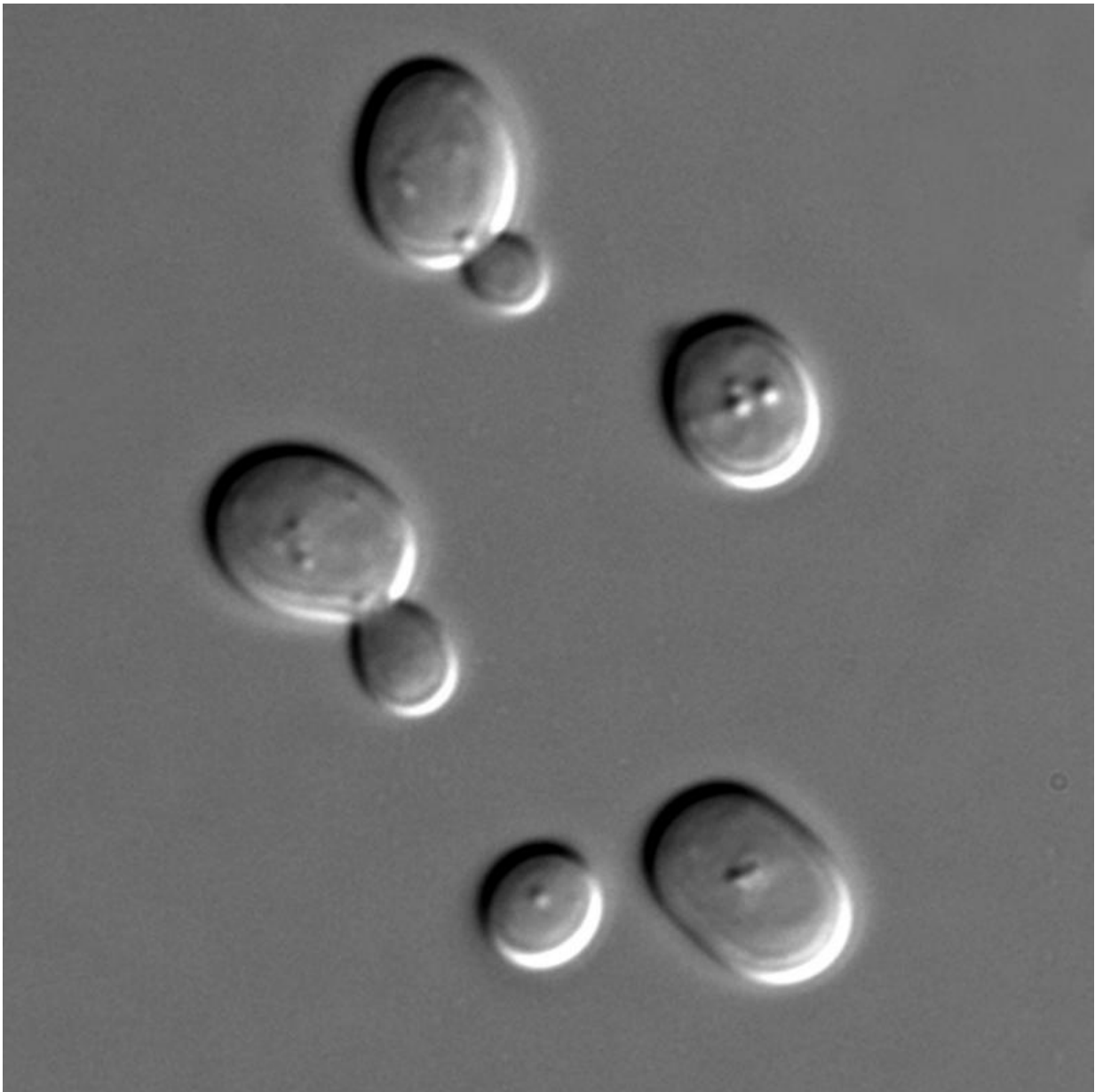


Machine learning predicts metabolism, helping drug developers and brewers

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Cerevisiae cells in DIC microscopy. Credit: public domain

Machine learning algorithms that can predict yeast metabolism from its protein content have been developed by scientists at the Francis Crick Institute. The findings could provide a basis for brewers to have greater control over the flavour of their beer, and scientists to personalise treatments for metabolic disorder patients, in the future.

Metabolism is the process by which organisms convert nutrients into energy and essential molecules, via a series of chemical reactions. When yeast metabolises sugar in the absence of oxygen, it 'ferments' to produce alcohol, acids and gases, including flavour compounds, that make bread, wine and beer taste good.

Within a cell, [metabolism](#) produces hundreds of small molecules, called metabolites. Although yeast is evolutionarily very distant to humans, many of these metabolites are identical, and are made in a similar way. Until now, however, the mechanisms controlling metabolism have not been fully understood.

The latest study, published in *Cell Systems*, shows that to a large extent, the metabolism of brewer's yeast (*S. cerevisiae*) is predictable by machine learning algorithms, if they are provided with large amounts of protein expression information.

"Thanks to machine learning, we now have a better understanding of what controls metabolism, which is good news for brewers looking to create the perfect pint, or for Biotechnologists that use yeast to produce vaccines and other proteins that are medically important " says Aleksej Zelezniak, first author of the paper and researcher at the Crick, and has recently moved to Sweden to establish his independent research group at

the Chalmers University of Technology.

Linking proteins and metabolites

Until now, scientists have been divided over whether metabolism is self-regulating or controlled by gene expression changes; partly because existing methods have failed to detect any strong correlation between the read-out of genes—proteins—and metabolites.

In this study, scientists quantified enzyme expression in 97 different strains of *S. cerevisiae*, known to show differences in metabolism, linking it to changes in metabolite concentrations measured.

They developed machine learning algorithms that could pick up complex relationships between changes in gene expression and metabolites produced. They found that metabolism was controlled by lots of enzymes acting in concert—with no single enzyme having a major effect by itself.

"The relationship between enzyme expression and metabolism in yeast is so complex that previous models have failed to detect it," says Markus Ralser, group leader at the Crick and senior author of the paper.

"Changes in [cellular metabolism](#) are tightly bound to disorders that increase with age, including diabetes, various types of cancer, and neurodegenerative diseases. The fact that one can start to predict metabolism in simple cells like yeast cells, is a milestone for the effort to soon be able to predict metabolism also in human tissues.

"Similar Computational tools are used by tech giants like Amazon and Facebook all the time. But instead of using them to tailor advertisements or recommend friends, we've harnessed their power to predict a yeast cell's metabolism. These insights not only inform our understanding of the basis of beer flavouring, but also some human disorders of

metabolism."

From beer to personalised medicine

The team is hoping to transfer their findings in yeast cells to the clinic in the next few years to help patients with metabolic diseases.

"For non-biologists it might seem strange that one can transfer our knowledge of yeast to humans, but in reality, many fundamental principles of what we know about human biology came from [yeast](#) research," says Aleksej.

"We currently expand our algorithms, so that they will provide us with information also about a person's metabolism, based on which proteins are present in their blood. This information could help doctors decide which treatment option is best for an individual patient."

More information: *Cell Systems* (2018). [DOI: 10.1016/j.cels.2018.08.001](#)

Provided by The Francis Crick Institute

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