Self-learning computer program analyzes cell division process

Daniel Gerlich, a biologist at the IMBA – Institute of Molecular Biotechnology, has developed a new, fully-automated method that allows microscopic images to be analyzed and evaluated without human support. This new technology was introduced in „Nature Methods", a scientific journal.

In modern biological studies, the automated recording of microscopic images is an established standard. This imaging can produce several million pictures per experiment, which then must be analyzed and evaluated so that they can produce relevant findings. Computers help in analyzing these data. But until now, scientists have always had to define the precise criteria by which the computer sorts the data, an approach called „Supervised Machine Learning".

Will computers soon work completely on their own?

Daniel Gerlich, senior group manager at IMBA, is a pioneer in the field of automated microscopy for living cells. With his team, he has now developed a new method that eliminates the need for categorization by a scientist. In this approach, called „Unsupervised Machine Learning", the computer recognizes on its own the criteria by which images must be sorted.

This new method, which requires no human interaction, has two tremendous benefits: greater objectivity, and reproducibility of results. The time-saving factor also plays a major role. „Biologists will of course still be needed in the future. But instead of wasting time on the monotonous work of sorting images, they will be able to focus on their real tasks: formulating hypotheses and designing experiments," said Gerlich.

Daniel Gerlich uses the new technology to examine cell division. „In our experiment we simply told the computer that it should distinguish among six phases of cell division. Without any further input on our part, the system recognized structural changes in the cell during the division process, and sorted images with similar attributes according the individual phases.

Time is the crux

Previous attempts at automated cell recognition were hampered by the tremendous variability of cell structures. The method developed by Gerlich's work group solves this issue by taking time information into account: the computer analyzes filmed processes, not isolated images. The results attained are thus far more precise than those achieved through conventional methods. Even subtle transitions between the individual phases of division could be observed in this study, in which Gerlich monitored the division of human cancer cells. Thus this new approach allows defects that might lead to the degeneration of cancer cells to be examined in detail. „The timeline is what puts the many individual data sets into their proper context," said Gerlich. „Unsupervised Machine Learning" will thus become a valuable tool in modern cellular biology.

Daniel Gerlich:

Daniel Gerlich's research work focuses on the connection between open questions in biology and modern computer technologies. He is a specialist in the field of automated microscopy, which he also uses for his studies of cell division. After completing his post-doctorate at the EMBL in Heidelberg, Germany, Gerlich was an assistant professor at the ETH in Zürich, Switzerland. He became the head of a senior group at IMBA in 2012.

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