

Optimizing cell cycle analysis with the right algorithms

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Scientists of the the Helmholtz Zentrum München have found a new approach improving the identification of cell cycle phases using imaging flow cytometry data. They could avoid the use of stains by applying algorithms from machine learning. With the help of an imaging software they extracted hundreds of features from bright field and dark field images. Using this data they could generate algorithms that can sort the cells digitally.

So far fluorescent stains have been used to assign [cells](#) to their [cell cycle](#) phase. These chemicals damage the cells and may distort the results. Scientists of the Helmholtz Zentrum München in collaboration with the Broad Institute of MIT and Harvard, Swansea University, Newcastle University and The Francis Crick Institute have now found an alternative.

"We used two generally neglected data sources: the bright and the darkfield [images](#)" says Thomas Blasi, PhD student at the ICB and first author of the publication. "We could use the information in these data for [machine learning](#)". This approach makes it possible to not only classify cells, but also to digitally sort them with a high level of specificity. Based on these findings the Broad Institute and the Helmholtz Zentrum München also filed a provisional patent application.

"Computer-based classification of cells based on large population of cell images opens up new perspectives. This approach could also be used in many different contexts, not only for cell cycle analysis", adds Prof. Dr.

Dr. Fabian Theis, head of the ICB.

More information: Thomas Blasi et al. Label-free cell cycle analysis for high-throughput imaging flow cytometry, *Nature Communications* (2016). [DOI: 10.1038/ncomms10256](https://doi.org/10.1038/ncomms10256)

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