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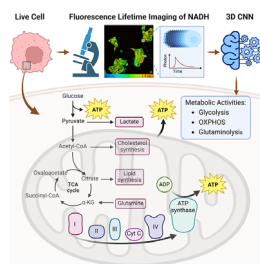


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Machine learning identifies individual cell metabolism from fluorescence lifetime images for informing cancer treatments and immune therapies.



There are many ways a cell can produce its energy. The most common method metabolizes glucose via the citric acid cycle, but some cells employ alternative metabolic pathways. Some cancer cells depend on glutaminolysis or glycolysis to produce additional fuel in the absence of oxygen. Some of the immune cells that fight them also rely on these pathways. Understanding which cells use which metabolic pathways could help boost immune responses or starve tumors.

Hu et al. developed a 3D convolutional neural network to analyze fluorescence lifetime decay data collected from cell samples. Their method can identify metabolic pathways used by individual cells.

Fluorescence lifetime imaging (FLIM) is an existing method that involves collecting fluorescence data from excited NADH, an essential co-enzyme for cellular metabolism. This data is analyzed to calculate the average lifetime of the excited state. Traditionally, however, the lifetime data provided by this method is difficult to relate to metabolic pathways.

“Traditional FLIM analysis reduces the information in the time domain, requires expertise, and is time-consuming,” said author Linghao Hu. “Furthermore, single-cell analysis that averages values across a cell ignores spatial information within the cell.”

The authors trained a neural network on raw NADH fluorescence lifetime images, giving them access to three dimensions of data for each cell. By using data showing changes in fluorescence over time, the neural network was able to identify which of three metabolic pathways each cell employed.

The authors are looking to expand their neural network to provide even more metabolic data in the future.

“We’re not satisfied with only three metabolic pathways,” said author Alex Walsh. “We’d like to incorporate additional pathways like fatty acid synthesis and beta-oxidation.”

Source: “3D convolutional neural networks predict cellular metabolic pathway use from fluorescence lifetime decay data,” by Linghao Hu, Daniela De Hoyos, Yuanjiu Lei, A. Phillip West, and Alex J. Walsh, *APL Bioengineering* (2024). The article can be accessed at <https://doi.org/10.1063/5.0188476>.

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