Okayama University Medical Research Updates （OU-MRU） 2021.12 Vol.96

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Okayama University research: Automated cell image analysis

(Okayama, 24 December) **Researchers at Okayama University present in *Chromosome Research* a tool for automatically classifying light-microscopy images of cells as undergoing cell division or not. The tool, based on deep-learning techniques, is highly important for the field of genetics, as chromosomes (the carriers of genetic code) are most easily observed during cell division.**

Chromosomes are the parts of cells containing DNA, the carrier of an organism's genetic information. Chromosome analysis is a cornerstone of genetics, concerned with the study of heredity in organisms. Observing chromosomes is possible with a light microscope, but only during the process of cell division, when chromosome molecules duplicate and condense. It is therefore necessary to capture the dividing cells, which is typically done by looking for the dividing cells with the eyes using a microscope on a slide with mixture of multiple cells on it, and shoot them manually. Although there is a high demand for automated image analysis, applications are still mostly limited to the analysis of human and laboratory-animal cells, and using them often requires advanced computing skills. Now, Associate Professor NAGAKI Kiyotaka from Okayama University and colleagues have developed an analytic tool based on deep-learning algorithms for processing microscopy images of cells, which is especially useful in the context of plants (for which chromosome number and size vary a lot).

The researchers started from the premise that automated cell image analysis should be user-friendly. Existing deep-learning tools typically involve command-line interfaces, requiring users to have certain computing skills that may go beyond the skill set of geneticists (who are usually not trained as data scientists). Therefore, Associate Professor NAGAKI and colleagues decided to develop a graphical user interface (GUI) using Apple's Create ML application. The latter is a freely available GUI-based developer tool providing a deep-learning framework.

The deep-learning approach requires a 'training' set of images with known content: cells that are either in the process of cell division (called mitosis) or not. Images of mitotic cells display chromosomes, the others do not. The algorithm then 'trains' itself with this set of images, and develops its own criteria for deciding whether a mitotic cell is displayed or not, which can then be applied for processing the images that actually need to be analyzed.

The scientists performed tests with training sets with different numbers of images of mitotic and non-mitotic cells of different species of plants. Datasets with 120 or more images resulted in accuracy of more than 80% in correctly classifying plant cells as mitotic or non-mitotic. Associate Professor NAGAKI and colleagues also found that using images from many

different species improved the classification accuracy, and that the classification also worked for species not occurring in the training sets.

The main limiting factor of the tool is that it does not run on Windows, the world's most widespread operating system. The researchers point out that this limitation can be overcome by obtaining an inexpensive Mac, and that their system "has the potential to be used as a deep learning sorter that anyone can use because it can easily build models for sorting using all kinds of biological images."

Background

Chromosomes

A chromosome is a complex biomolecule build from DNA (containing an organism's genetic material) and protein molecules that help to pack and condense the DNA. Chromosomes are located in the cell nuclei. They can only be observed under a light microscope during a particular phase (called the metaphase) of cell division, just after the duplication of a chromosome has happened, when the two chromosome copies are still joined and in their most condensed form.

Although sequences of images of cells can now routinely be recorded by means of a light microscope, analyzing them still is mainly manual, very tedious task. Associate Professor NAGAKI Kiyotaka from Okayama University and colleagues have now developed a user-friendly computer program with a graphical user interface, based on machine-learning techniques, with which an automated classification of images of cells undergoing, or not undergoing, cell division (i.e., displaying chromosomes, is possible.

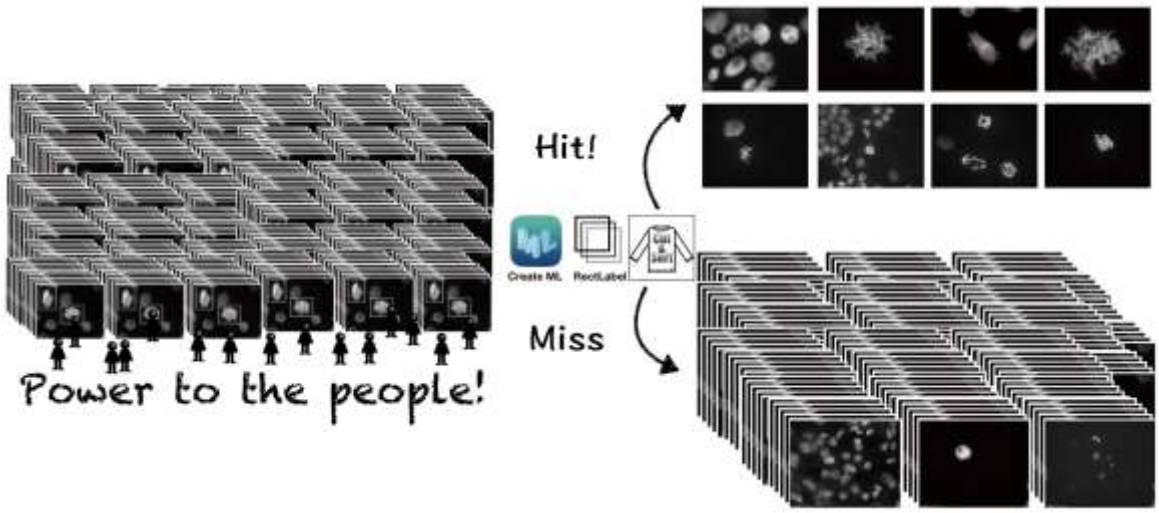

Figure:
Pipelined biological image classifier using Apple's CreateML deep learning application.
Researchers at Okayama University and colleagues have created an artificial intelligence (AI) based image classifier that can be easily customized by non-experts. For example, this classifier instantly detects only those containing the cells of interest from a large number of automatically captured images.

Reference
Kiyotaka Nagaki, Tomoyuki Furuta, Naoki Yamaji, Daichi Kuniyoshi, Megumi Ishihara, Yuji Kishima, Minoru Murata, Atsushi Hoshino and Hirotomo Takatsuka. Effectiveness of Create ML in microscopy image classifications: A simple and inexpensive deep learning pipeline for non-data scientists. *Chromosome Research*. Published: 14 October 2021.
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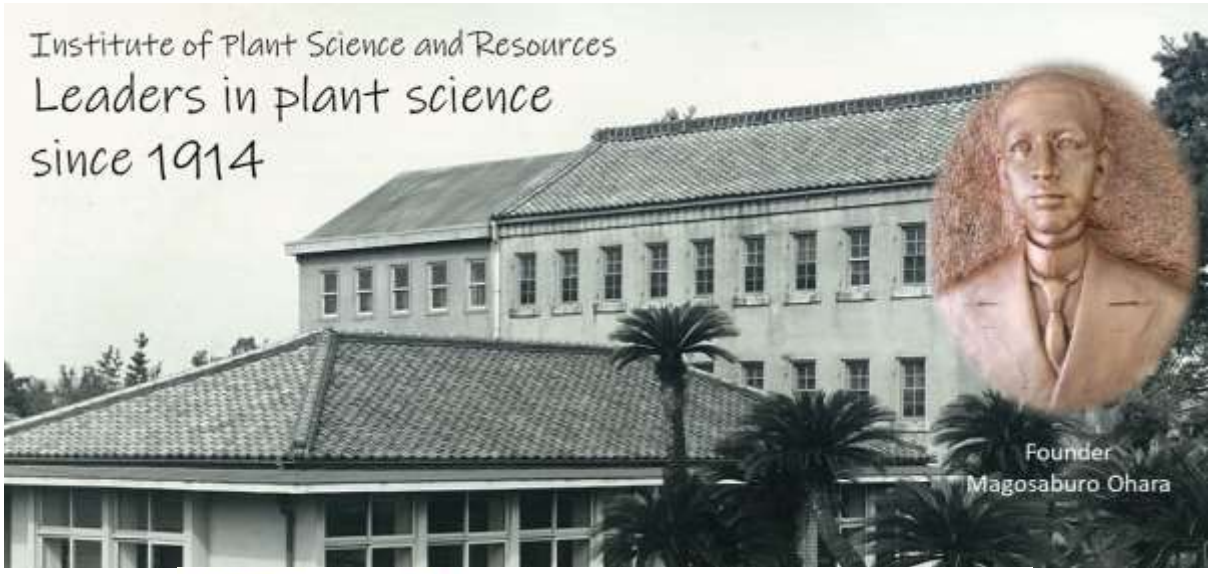

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Okayama University is one of the largest comprehensive universities in Japan with roots going back to the Medical Training Place sponsored by the Lord of Okayama and established in 1870. Now with 1,300 faculty and 13,000 students, the University offers courses in specialties ranging from medicine and pharmacy to humanities and physical sciences.

Okayama University is located in the heart of Japan approximately 3 hours west of Tokyo by Shinkansen.

Website: http://www.okayama-u.ac.jp/index_e.html

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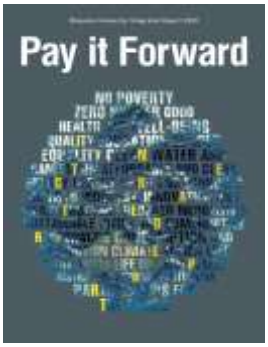

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An integrated report is intended to explain how an organization creates value over time through an organic integration of the vision and the combination of financial information and other information. Through this report we hope to promote greater interest in Okayama University among readers everywhere. In order to help us make improvements in future editions, we encourage you to contact us with any comments and suggestions you may have.

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