From Acapella to ImageJ

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Abstract

In the last two years, we developed several high-throughput image processing algorithms to detect and quantify plant cellular objects on the basis of PerkinElmer's Acapella image analysis software and Opera high content screening system. With one year's development, our algorithms can precisely detect fluorescently labelled plant cells, plasma membrane, stomata, plasmodesmata (PDs), vesicles co-localisation, and different types of membrane compartments. Furthermore, whilst processing tens of thousands images, cellular traits (e.g., size, roundness, width, length, and fluorescence signal intensity) can also be calculated in output fields, which are impossible to be manually identified and scored.

More recently, we have advanced our Acapella scripts to batch process images obtained by conventional confocal microscopy (e.g., TIFF files). Some successful examples of this new application of Acapella are callose detection, calculating pathogen infected area, coloured spots recognition, PDs and cell wall detection, etc.

With an aim of sharing our image analysis algorithms and analysis workflows with the cell research community, we are genuinely interested in translating our Acapella algorithms and scripts into plugins for the JAVA based open-source solution–ImageJ. Hence, we want to make a start on participating Bioimage Analysis Workshop 2012 so that we could commence involving in the ImageJ development from now on.

Keywords

Acapella, high-throughput image processing, confocal microscopy