

Software speeds up the discovery process worldwide

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Biomedical and computational scientists at The University of Queensland have combined forces to create a powerful new tool that will greatly increase the amount of data bio-scientists can expect to process in a week.

Sophisticated software that slashes the processing time required to select high-resolution images is poised to boost biomedical research around the world.

Screening processes that once demanded hundreds of hours from a skilled operator can now be done by a less-skilled operator in a fraction of the time.

The Rapid semi-automated single particle selection software (SwarmPS) speeds-up the painstaking and often laborious process of selecting scientifically 'significant' images from the thousands of 'non-significant' images which routinely accompany them.

Incorporating cross-correlation and edge-detection algorithms, SwarmPS is an improvement on other available technologies because it uses human interaction with images to fine-tune its considerable processing power.

Queensland Brain Institute computational scientist Geoffery Ericksson said the software involved about 20,000 separate lines of computer code and had the potential to save researchers both time and money.

“Essentially, SwarmPS has been designed to provide a user-friendly, powerful and flexible graphical interface to manage and run particle selection jobs,” Dr Ericksson said.

“It's envisaged that users will be able to run the program in a semi-automated mode, with the ability to exert full manual override at any stage, providing maximum flexibility in terms of speed and accuracy of particle selection.

“Shielding people from mundane, repetitive tasks allows them to think about more important aspects of their work.”

Developed by scientists from the Queensland Brain Institute and the Institute for Molecular Bioscience, SwarmPS has been designed to run across most standard computer platforms.

Source: University of Queensland

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