

## Not Sure If Gene Sequence Is Correct? Do A Spell Check!

Thursday, May 10, 2012

<http://www.asianscientist.com/in-the-lab/acacia-spell-checker-for-gene-sequences-2012/>

*AsianScientist* (May 10, 2012) - Researchers from CSIRO and the University of Queensland have developed a new bioinformatics tool called Acacia to 'spell check' gene sequences for their accuracy.

In the May issue of the journal *Nature Methods*, the paper's lead author, Ms. Lauren Bragg, a Ph.D. student at CSIRO and the University of Queensland, highlights her new approach and its software implementation.

Acacia analyzes the output of next-generation gene sequencing instruments, which read the four-letter alphabet of As, Cs, Ts, and Gs – the 'bases' that code for DNA and spell out the genes of different living organisms. The software specifically applies to important parts of microbe genes called amplicons.

The method, or algorithm, that Acacia uses took 18 months for Ms. Bragg to fully develop and test.

Just as a computer spell checker finds typing errors in words, Acacia finds errors in the DNA code of amplicon sequences produced during gene sequencing. According to the authors, Acacia shows clear improvements over the two error-correction tools currently used by biologists for amplicon sequences and is easier to use.

Machine errors in the long lengths of A, C, G, and T code can cause biologists to misinterpret which genes are there, or which microbial species might exist in an environmental sample. Acacia works by using the statistical theory of likelihoods to analyze common errors in sequencing, such as DNA bases which may have been mistakenly added or deleted.

"The Nature article is our way of telling the international biology community that there's a new software tool they can use for error-correcting that's pretty easy to use, quick and reliable. That way, they won't think they've discovered a new microbe species when they haven't or overlooked one they should have found," she said.

The article can be found at: [Bragg L et al. \(2012\) Fast, accurate error-correction of amplicon pyrosequences using Acacia.](#)

-----

Source: [CSIRO](#).

Disclaimer: This article does not necessarily reflect the views of AsianScientist or its staff.