

New genome assembly tool brings complex DNA research to the desktop

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Genome assembly, the construction of DNA sequences from sample sequences, has received a boost with the release of Gossamer, a tool which allows researchers to assemble DNA fragments using cheap commodity computers rather than supercomputers.

New DNA [sequencing technologies](#) are revolutionising biology. These technologies can read billions of short fragments of DNA in a matter of days, producing DNA sequence information in unprecedented volumes and at ever increasing rates. These fragments of DNA come from cells of different types and conditions and can be analyzed to help answer important biological questions. For example, to gain a detailed understanding of many aspects of cancer, it is important to determine how the DNA of the [cancer cells](#) has been rearranged.

To answer such questions it is often necessary to piece together the billions of fragments to reconstruct the underlying DNA sequence – a process called genome assembly. Existing programs for assembling such DNA fragments tend to require very large amounts of computer memory, necessitating large and expensive computing infrastructure. The NICTA Computational Genomics team has developed a prototype assembler called Gossamer that demonstrates how a human genome can be assembled on cheap commodity computers. The Gossamer prototype assembler was demonstrated today at Bio 2011 in Washington, the world's largest biotechnology event. The tool is now available to be trialled for non-commercial use.

Professor Terry Caelli, Director of NICTA's Health Business Area, described Gossamer as a wonderful example of how computer science can play a fundamental role in progressing life sciences research.

“Gossamer is a breakthrough for the genome research community that helps overcome the significant infrastructure requirements the average laboratory is unable to access,” he said. “We are making a prototype version of the tool available to the research community to assist them in progressing their important genome research.”

Provided by Nicta

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