

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
High-speed, parallel DNA sequence assembly	<p>A high-speed DNA sequence assembly algorithm, Assembly by Short Sequences (ABySS), could offer a quick and cost-effective way to identify disease-associated genetic mutations and polymorphisms. ABySS lowers the time needed to assemble large sets of gene sequence reads by distributing the task across a network of computers. The algorithm assembled about 3.5 billion paired-end reads from a sample human genome with 98.8% accuracy. The <i>Escherichia coli</i> K12 genome was also assembled with an accuracy comparable to that of other assembly algorithms. Next steps include increasing the accuracy of ABySS and adapting it for transcriptome analysis.</p> <p>SciBX 2(10); doi:10.1038/scibx.2009.425 Published online March 12, 2009</p>	<p>Software is unpatented; freely available at http://www.bcgsc.ca/platform/bioinfo/software/abyss</p>	<p>Simpson, J.T. <i>et al. Genome Res.</i>; published online Feb. 27, 2009; doi:10.1101/gr.089532.108</p> <p>Contact: Inanc Birol, British Columbia Cancer Agency, Vancouver, British Columbia, Canada e-mail: ibirol@bcgsc.ca</p>