This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Correction and assembly of single-molecule sequencing reads	<p>A computational approach for correcting errors in long-read, single-molecule sequencing could aid in developing applications of the technology for biomedical discovery and guiding treatment. An algorithm that trimmed and corrected individual long-read sequences by first mapping short-read sequences to them and then computing a hybrid consensus sequence improved read accuracy from 80% to more than 99.9%. The method provided long transcripts and assemblies from short reads using sequencing data from both prokaryotic and eukaryotic whole genomes. Ongoing work includes evaluating long reads for the automated filling of sequencing gaps in bacterial genomes and effectively separating mixed sequencing samples.</p> <p>SciBX 5(28); doi:10.1038/scibx.2012.741 Published online July 19, 2012</p>	Source code for the software described in the publication is freely available	<p>Koren, S. <i>et al. Nat. Biotechnol.</i>; published online July 1, 2012; doi:10.1038/nbt.2280 Contact: Adam M. Phillippy, National Biodefense Analysis and Countermeasures Center, Frederick, Md. e-mail: phillippy@nbacc.net Contact: Sergey Koren, same affiliation as above e-mail: korens@nbacc.net</p>