This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
An algorithm for more accurate identification of cancer-associated mutations in genome sequencing studies	<p>An improved algorithm to assess the significance of mutations identified through genome sequencing could be used to more accurately predict cancer-associated genes. A set of 3,083 matched, tumor-normal pairs was used to develop an algorithm to identify cancer-associated genes that includes correcting for heterogeneous rates of mutation across the genome. The algorithm identified cancer-associated genes with higher accuracy than an earlier iteration of the algorithm that did not correct for heterogeneous rates of mutation. Next steps include improving model accuracy using additional sequencing data.</p> <p>SciBX 6(27); doi:10.1038/scibx.2013.699 Published online July 18, 2013</p>	Patent application filed; freely available for not-for-profit use; available for licensing for commercial use	<p>Lawrence, M.S. <i>et al. Nature</i>; published online June 16, 2013; doi:10.1038/nature12213 Contact: Gad Getz, Broad Institute of MIT and Harvard, Cambridge, Mass. e-mail: gadgetz@broadinstitute.org Contact: Eric S. Lander, same affiliation as above e-mail: lander@broadinstitute.org</p>