This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Platypus, a reference genome-free algorithm that rapidly calls variants in clinical sequencing data	<i>In silico</i> studies with available sequence data suggest Platypus can be used for one-step, rapid processing of high throughput clinical sequencing data. The algorithm separates a sensitivity-optimizing candidate generation phase from a specificity-optimizing haplotype-based calling stage. In publicly available whole-genome and whole-exome clinical sequencing data, Platypus achieved 95% sensitivity for <i>de novo</i> mutations in sequence data with an average 35' coverage. Next steps include adapting the algorithm to detect somatic mutations in cancer tissue.	Unpatented; licensing status not applicable	Rimmer, A. <i>et al. Nat. Genet.</i> ; published online July 13, 2014; doi:10.1038/ng.3036 Contact: Gerton Lunter, University of Oxford, U.K. e-mail: gerton.lunter@well.ox.ac.uk
SciBX 7(31); doi:10.1038/scibx.2014.936 Published online Aug. 14, 2014			