This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Case selection-based analysis for the identification of causal gene variants of disease from genomewide association (GWA) studies	<p>A case selection-based analysis of GWA study data could boost the identification of disease causal variants. In a simulated dataset of 500 controls and 500 affected individuals with 3 causal variants present in one gene, the approach, which consists of analyzing co-occurring rare variants in combination, was more effective than conventional fine mapping in identifying the disease-causing gene variants. In a real dataset of hearing loss patients and controls, the case-selection method detected a causal variant in 88% of the 32 patients selected, whereas conventional methods performed on a much larger group of 329 cases only identified the variant in 8.2% of patients. Next steps include using this approach to help identify causal variants for particular diseases.</p> <p>SciBX 3(20); doi:10.1038/scibx.2010.631 Published online May 20, 2010</p>	Unpatented; unavailable for licensing	<p>Wang, K. <i>et al. Am. J. Hum. Genet.</i>; published online April 29, 2010; doi:10.1016/j.ajhg.2010.04.003 Contact: Hakon Hakonarson, University of Pennsylvania, Philadelphia, Pa. e-mail: hakonarson@email.chop.edu Contact: Kai Wang, Children's Hospital of Philadelphia, Philadelphia, Pa. e-mail: kaichop@gmail.com</p>