This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Statistical model for assessing the predictive capacity of personal genome sequencing	<p>A statistical model suggests whole-genome sequencing has limited utility in assessing disease risk. Using data from a cohort of monozygotic twins of Swedish descent, the model predicted that over half the subjects that ultimately developed a disease in 13 of the 27 tested categories would not test positive for the disease via a test based on whole-genome sequencing. Next steps could include using the model to predict the utility of genomic tests in rarer monogenic diseases.</p> <p>SciBX 5(15); doi:10.1038/scibx.2012.399 Published online April 12, 2012</p>	Patent and licensing status unavailable	<p>Roberts, N.J. <i>et al. Sci. Transl. Med.</i>; published online April 2, 2012; doi:10.1126/scitranslmed.3003380 Contact: Victor E. Velculescu, The Sidney Kimmel Comprehensive Cancer Center at The Johns Hopkins University, Baltimore, Md. e-mail: velculescu@jhmi.edu Contact: Bert Vogelstein, same affiliation as above e-mail: vogelbe@jhmi.edu</p>