This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Web-based platform to identify cancer driver mutations across tumor types based on new and existing sequencing data	A computational model called IntOGen-mutations could help to identify mutations that drive tumor formation. The platform integrates sequencing data from tumor genomes and genome analyzers to a scale of hundreds of thousands of genomes. The platform predicts the functional impact of nonsynonymous somatic tumor mutations on protein and pathway function. Next steps include updating the platform with more somatic mutation datasets from tumor genomes and enriching it with data on protein-drug interactions. *SciBX* 6(39); doi:10.1038/scibx.2013.1107 Published online Oct. 10, 2013	Unpatented; available for licensing through the Pompeu Fabra University Technology Transfer Office; platform accessible at http://www.gitools.org/datasets/	Gonzalez-Perez, A. *et al. Nat. Methods*; published online Sept. 15, 2013; doi:10.1038/nmeth.2642 **Contact:** Nuria Lopez-Bigas, Pompeu Fabra University, Barcelona, Spain e-mail: nuria.lopez@upf.edu