This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Whole-cell computational model for predicting phenotype from genotype	A whole-cell computational model could guide development of <i>in silico</i> drug discovery technologies. A whole-cell computational model of <i>Mycoplasma genitalium</i> was generated by integrating 28 models of various bacterial processes. Model simulations were then used to make predictions about DNA-binding protein interactions, the effects of metabolism on cell cycle regulation and energy distribution within the cell. Simulations of single-gene disruptions predicted whether a gene was essential to cell growth and survival with 79% accuracy. Next steps include developing computational models of more complex organisms.	Provisional patent application filed; licensing details available from the Stanford University Office of Technology Licensing	Karr, J.R. <i>et al. Cell</i> ; published online July 20, 2012; doi:10.1016/j.cell.2012.05.044 Contact: Markus W. Covert, Stanford University, Stanford, Calif. e-mail: mcovert@stanford.edu
	SciBX 5(30); doi:10.1038/scibx.2012.794 Published online Aug. 2, 2012		