This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
An algorithm to predict drug combinations to treat genetically heterogeneous tumors	A computational model could help predict drug combinations for genetically heterogeneous tumors. Using published data on drug-genotype interactions, an algorithm predicted effective two-drug combinations. In a model of tumor genetic diversity consisting of mixed cultures of parental and shRNA-expressing subpopulations of lymphoma cells, combinations predicted by the algorithm decreased growth of subpopulations compared with three other drug combinations selected by alternative criteria. In a mouse model of genetically heterogeneous lymphoma, the algorithm-predicted drug combination minimized the emergence of any tumor subpopulation and increased tumor-free survival compared with another differently selected drug combination. Next steps could include testing the algorithm in additional tumor models. <i>SciBX</i> 7(3); doi:10.1038/scibx.2014.100 Published online Jan. 23, 2014	Patent and licensing status unavailable	Zhao, B. <i>et al. Cancer Discov.</i> ; published online Dec. 6, 2013; doi:10.1158/2159-8290.CD-13-0465 Contact: Michael T. Hemann, Massachusetts Institute of Technology, Cambridge, Mass. e-mail: hemann@mit.edu