This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Computational model of synthetic lethality for predicting treatment responses to cancer therapy and identifying drugs for repurposing to treat cancer	<p>A computational model that predicts pairs of synthetically lethal (SL) genes could help guide treatment decisions in patients with cancer and identify drugs that could be repurposed to treat cancer. Computational analyses of genomics data from multiple primary tumors and human cancer cell lines predicted over 3,000 known and previously unknown SL gene pairs. In primary breast tumors, low coexpression of predicted SL gene pairs correlated with overall survival. In human renal cancer cell lines deficient in von Hippel-Lindau tumor suppressor (vHL), noncancer drugs that inhibited proteins encoded by predicted SL partners of vHL decreased growth compared with a negative control drug. Ongoing work includes optimizing the accuracy of the model and testing its predictions in animal cancer models.</p> <p>SciBX 7(35); doi:10.1038/scibx.2014.1053 Published online Sept. 11, 2014</p>	Patented by Ramot at Tel Aviv University; available for licensing	<p>Jerby-Arnon, L. <i>et al. Cell</i>; published online Aug. 28, 2014; doi:10.1016/j.cell.2014.07.027 Contact: Eytan Rupp, Tel Aviv University, Tel Aviv, Israel e-mail: ruppin@post.tau.ac.il Contact: Livnat Jerby-Arnon, same affiliation as above e-mail: livnatje@post.tau.ac.il</p>