

### This week in techniques

Approach	Summary	Licensing status	Publication and contact information
<b>Computational models</b>			
An algorithm to predict cancer subtypes by simplifying complex gene classifiers	A computational model could simplify gene classifiers used to predict molecular subtypes in cancer. Patients with rhabdomyosarcoma are classified as having low, intermediate or high risk of death, which informs the type of chemotherapy they receive. In three separate sets of published gene expression data from patients with rhabdomyosarcoma, the algorithm could distinguish tumors that express the <i>paired box (PAX)</i> - <i>RNA binding protein fox-1 homolog 1 (FOX1)</i> fusion gene from those that do not in >97% of cases based on pairs of markers. The algorithm also distinguished between patients with lung cancer suffering early death and those experiencing long-term survival by using two-gene combinations with an efficiency of >85%. Next steps include generalizing the algorithm, making it available on a public platform and prospectively testing the classifier in clinical trials.	Patent and licensing status not applicable; tool will be available at <a href="http://exhaustive.msvalidator.org">http://exhaustive.msvalidator.org</a>	Wilson, R.A. <i>et al. Cancer Res.</i> ; published online Aug. 2, 2013; doi:10.1158/0008-5472.CAN-13-0324 <b>Contact:</b> Samuel L. Volchenbom, The University of Chicago, Chicago, Ill. e-mail: <a href="mailto:slv@uchicago.edu">slv@uchicago.edu</a>
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