This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Population-specific expression analysis (PSEA) for biomarker identification	An algorithm to analyze cell population-specific gene expression could enable the discovery of biomarkers and targets. PSEA classifies gene expression by cell population based on the expression of cell type-specific markers. In brain tissue samples from patients with Huntington's disease (HD) and from matched controls, PSEA identified differences in the expression of genes associated with myelin formation that were not detected by a standard gene expression analysis method. In whole blood samples from kidney transplant recipients, PSEA identified transplant rejection-associated changes in gene expression in granulocytes. Next steps could include using PSEA to identify new biomarkers for human diseases.	Unpatented; unavailable for licensing	Kuhn, A. <i>et al. Nat. Methods</i> ; published online Oct. 9, 2011; doi:10.1038/nmeth.1710 Contact: Alexandre Kuhn, Swiss Federal Institute of Technology Lausanne, Lausanne, Switzerland e-mail: alexandre.m.kuhn@gmail.com
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