This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Somatic mutation finder (SMUFIN) to identify single-nucleotide variants (SNVs) and structural variants in tumor DNA	The SMUFIN computational approach could help identify different forms of somatic mutations in cancer. SMUFIN uses algorithms that directly compare DNA from tumor and normal cells without requiring alignment with reference DNA. The method identified SNVs with 92% sensitivity and 95% specificity and structural variants with 74% sensitivity and 91% specificity. In patient tumor samples, SMUFIN also detected complex chromosomal rearrangements including chromothripsis and chromoplexy. Next steps could include using SMUFIN to identify new cancer mutations that could be useful as biomarkers.	Patent and licensing status unavailable	Moncunill, V. <i>et al. Nat. Biotechnol.</i> ; published online Oct. 26, 2014; doi:10.1038/nbt.3027 Contact: David Torrents, Barcelona Supercomputing Center, Barcelona, Spain e-mail: david.torrents@bsc.es
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