

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Bayesian tool for methylation analysis (Batman)	Batman may be useful for analyzing dysregulated DNA methylation levels associated with many cancers. Batman analyzed high-resolution, genome-wide methylated DNA immunoprecipitation profiles (MeDIP). The tool estimated absolute methylation levels over a broad range of cytosine guanine (CpG) dinucleotide densities. Batman also achieved about a 20-fold improvement in genome coverage compared with existing profiling methods. Next steps include using Batman with MeDIP to identify DNA methylation biomarkers associated with complex diseases such as cancer.	Not patented; available for use under GNU Lesser General Public License	Down, T.A. <i>et al. Nat. Biotechnol.</i> ; published online July 8, 2008; doi:10.1038/nbt1414 Contact: Stephan Beck, University College London, London, U.K. e-mail: s.beck@ucl.ac.uk Contact: Vardhman Rakyán, Institute of Cell and Molecular Science, Barts and the London School of Medicine, London, U.K. e-mail: v.rakyan@qmul.ac.uk Contact: Thomas A. Down, University of Cambridge, Cambridge, U.K. e-mail: thomas.down@gurdon.cam.ac.uk