This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Computational prediction of competitive endogenous RNA (ceRNA) effect on target expression	A computational model of ceRNA function could help identify new drug targets. ceRNAs are transcripts that contain binding sites for the same microRNA, such that competition between the transcripts for miRNA binding can affect their protein expression. Previous studies have shown that ceRNAs can regulate disease targets including the tumor suppressor PTEN (MMAC1; TEP1). The computational model predicted the regulatory effect of interactions between ceRNAs and miRNAs and generated a window of optimal ceRNA-miRNA expression patterns for which meaningful biological effects are likely to occur. Next steps could include using this model to screen for disease-associated ceRNAs.	Patent and licensing status unavailable	Ala, U. *et al. Proc. Natl. Acad. Sci. USA*; published online March 27, 2013; doi:10.1073/pnas.1222509110 **Contact:** Pier Paolo Pandolfi, Harvard Medical School, Boston, Mass. e-mail: ppandolf@bidmc.harvard.edu

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