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Computational method dramatically speeds up estimates of gene expression

**April 21, 2014**



With gene expression analysis growing in importance for both basic researchers and medical practitioners, researchers at Carnegie Mellon University and the University of Maryland have developed a new computational method that dramatically speeds up estimates of gene activity from RNA sequencing data. [Full Story](#)

### Source

Carnegie Mellon University

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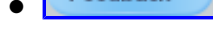
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