

New technique speeds up gene expression analysis from hours to minutes

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 (RNA-seq) data.

With the new method, dubbed Sailfish after the famously speedy fish, estimates of gene expression that previously took many hours can be completed in a few minutes, with accuracy that equals or exceeds previous methods. The researchers' report on their new method is being published online April 20 by the journal Nature Biotechnology.

Gigantic repositories of RNA-seq data now exist, making it possible to re-analyze experiments in light of new discoveries. "But 15 hours a pop really starts to add up, particularly if you want to look at 100 experiments," said Carl Kingsford, an associate professor in CMU's Lane Center for Computational Biology. "With Sailfish, we can give researchers everything they got from previous methods, but faster."

Read the full, original story: [Computational Method Dramatically Speeds Up Estimates of Gene Expression, CMU, UMD Researchers Report](#)