



## TECHNOLOGY

# Sailfish - A System for Estimating Gene Expression from RNA-Seq Reads

## OVERVIEW

Sailfish implements an efficient, accelerated expectation-maximization algorithm for quantifying isoform abundance that produces high-quality results, and is capable of correcting numerous types of systematic bias that are known to occur in RNA-seq experiments. In the paper, we demonstrate that, on both real and synthetic data, Sailfish is as accurate as existing read mapping-based tools such as eXpress and Cufflinks.

Sailfish is available for download at <https://www.cs.cmu.edu/~ckingsf/software/sailfish/index.html>

## CONTACT INFO

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## Additional Information

## INSTITUTION

University of Maryland, College Park

## CATEGORIES

- Software + Algorithm

## EXTERNAL RESOURCES

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