



## 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

UM Ventures  
0134 Lee Building  
7809 Regents Drive  
College Park, MD 20742  
Email: [umdtechtransfer@umd.edu](mailto:umdtechtransfer@umd.edu)  
Phone: (301) 405-3947 | Fax: (301) 314-9502

## Additional Information

### INSTITUTION

University of Maryland, College Park

### CATEGORIES

- Software + Algorithm

### EXTERNAL RESOURCES

IS-2017-155