

# Package ‘countToFPKM’

March 22, 2019

**Type** Package

**Title** Convert counts to Fragments Per Kilobase of transcript per Million (FPKM).

**Version** 1.0

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**Description** Convert a numeric matrix of features (rows) and conditions (columns) with raw feature counts of RNA-seq data to fragments per kilobase of transcript per million mapped reads.

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countToFPKM-package

*Convert counts to Fragments Per Kilobase of transcript per Million (FPKM).*

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## Description

Convert a numeric matrix of features (rows) and conditions (columns) with raw feature counts of RNA-seq data to fragments per kilobase of transcript per million mapped reads.

## Details

The DESCRIPTION file: This package was not yet installed at build time.

This package is to convert a numeric matrix of features (rows) and conditions (columns) with raw feature counts of RNA-seq data to fragments per kilobase of transcript per million mapped reads. @param counts A numeric matrix of raw feature counts i.e. fragments assigned to each gene. @param featureLength A numeric vector with feature lengths. @param meanFragmentLength A numeric vector with mean fragment lengths. @return fpkm A numeric matrix normalized by library size and feature length.

**Author(s)**

Ahmed Alhendi (Dr.) Maintainer: Ahmed Alhendi <asna4@le.ac.uk>

**References**

Trapnell,C. et al. (2010) Transcript assembly and quantification by RNA-seq reveals unannotated transcripts and isoform switching during cell differentiation. Nat. Biotechnol., 28, 511–515. doi: 10.1038/nbt.1621

Lior Pachter. Models for transcript quantification from RNA-Seq. arXiv:1104.3889v2

**Examples**

```
foo <- countToFpkm (counts, featureLength, meanFragmentLength)
```

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## \*Topic **FPKM**

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