

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

NEUMA

RRID:SCR_013324

Type: Tool

Proper Citation

NEUMA (RRID:SCR_013324)

Resource Information

URL: <http://neuma.kobic.re.kr/>

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Description: Software for estimating mRNA abundances from the whole transcriptome shotgun sequencing (RNA-Seq) data based on effective length normalization using uniquely mappable areas of gene and mRNA isoform models. Using the known transcriptome sequence model such as RefSeq, NEUMA pre-computes the numbers of all possible gene-wise and isoform-wise informative reads: the former being sequences mapped to all mRNA isoforms of a single gene exclusively and the latter uniquely mapped to a single mRNA isoform. The results are used to estimate the effective length of genes and transcripts, taking experimental distributions of fragment size into consideration. NEUMA covers a large proportion of genes and mRNA isoforms and offers a measure of consistency ("consistency coefficient") for each gene between an independently measured gene-wise level and the sum of the isoform levels. NEUMA is applicable to both paired-end and single-end RNA-Seq data.

Abbreviations: NEUMA

Synonyms: Normalization by Expected Uniquely Mappable Area

Resource Type: software resource

Defining Citation: [PMID:21059678](#)

Resource Name: NEUMA

Resource ID: SCR_013324

Alternate IDs: OMICS_01281

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260725T190748+0000

Ratings and Alerts

No rating or validation information has been found for NEUMA.

No alerts have been found for NEUMA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Kalaganis FP, et al. (2025) A hybrid neuromarketing approach exploiting EEG graph signal processing and gaze dynamic patterning. Brain informatics, 12(1), 23.

Afzal M, et al. (2020) Legume genomics and transcriptomics: From classic breeding to modern technologies. Saudi journal of biological sciences, 27(1), 543.

Lee S, et al. (2015) EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. BMC bioinformatics, 16, 278.

Roberts A, et al. (2013) Streaming fragment assignment for real-time analysis of sequencing experiments. Nature methods, 10(1), 71.

Kim SC, et al. (2013) A high-dimensional, deep-sequencing study of lung adenocarcinoma in female never-smokers. PloS one, 8(2), e55596.