Resource Summary Report

Generated by RRID on Sep 18, 2026

RECOUNT

RRID:SCR_006118
Type: Tool

Proper Citation

RECOUNT (RRID:SCR_006118)

Resource Information

URL: http://seq.cbrc.jp/recount/

Proper Citation: RECOUNT (RRID:SCR_006118)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on 5/29/14. An Expectation Maximization error correction tool for next generation sequencing data (Solexa/Illumina). The main features of RECOUNT: * Uses quality score to estimate the correct counts, hence potentially more accurate. * It does not use reference genome. * Memory efficient. Next generation sequencing technologies enable rapid, large-scale production of sequence data sets. Unfortunately these technologies also have a non-neglible sequencing error rate, which biases their outputs by introducing false reads and reducing the quantity of the real reads. They have applied RECOUNT to several types of Solexa/Illumina reads from mouse embryo, 5''-end SAGE, and bacterial metagenomic reads. They found that the correction by the tool not only increases the number of mappable reads, but also makes a real difference in the biological interpretation of next generation sequencing data.

Abbreviations: RECOUNT

Resource Type: data processing software, software application, software resource

Defining Citation: PMID:20180274

Keywords: next generation sequencing, c++, error correction, sequence count

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RECOUNT

Resource ID: SCR_006118

Alternate IDs: nlx_151593

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260912T200056+0000

Ratings and Alerts

No rating or validation information has been found for RECOUNT.

No alerts have been found for RECOUNT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Raina P, et al. (2023) GeneFriends: gene co-expression databases and tools for humans and model organisms. Nucleic acids research, 51(D1), D145.

Gohl DM, et al. (2021) Dissecting and tuning primer editing by proofreading polymerases. Nucleic acids research, 49(15), e87.

Karaglani M, et al. (2020) Accurate Blood-Based Diagnostic Biosignatures for Alzheimer's Disease via Automated Machine Learning. Journal of clinical medicine, 9(9).