Resource Summary Report

Generated by dkNET on May 5, 2025

PEMer

RRID:SCR_005263
Type: Tool

Proper Citation

PEMer (RRID:SCR_005263)

Resource Information

URL: http://sv.gersteinlab.org/pemer/

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Description: Software package as computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. Package is composed of three modules, PEMer workflow, SV-Simulation and BreakDB. PEMer workflow is a sensitive software for detecting SVs from paired-end sequence reads. SV-Simulation randomly introduces SVs into a given genome and generates simulated paired-end reads from novel genome.

Synonyms: Paired-End Mapper

Resource Type: software resource

Defining Citation: PMID:19236709

Keywords: structural variation, genome, next-generation sequencing, bio.tools, bio.tools

Funding:

Resource Name: PEMer

Resource ID: SCR_005263

Alternate IDs: biotools:pemer, OMICS_00320

Alternate URLs: https://bio.tools/pemer, https://bio.tools/pemer

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250420T014247+0000

Ratings and Alerts

No rating or validation information has been found for PEMer.

No alerts have been found for PEMer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. Frontiers in genetics, 14, 1277784.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. Frontiers in genetics, 5, 192.

Shyr D, et al. (2013) Next generation sequencing in cancer research and clinical application. Biological procedures online, 15(1), 4.

Zhao M, et al. (2013) Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. BMC bioinformatics, 14 Suppl 11(Suppl 11), S1.

Magi A, et al. (2010) Bioinformatics for next generation sequencing data. Genes, 1(2), 294.