

Resource Summary Report

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DecGPU

RRID:SCR_000585

Type: Tool

Proper Citation

DecGPU (RRID:SCR_000585)

Resource Information

URL: <http://decgpu.sourceforge.net/homepage.htm>

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Description: Software tool as parallel and distributed error correction algorithm for high-throughput short reads using CUDA and MPI parallel programming models.

Synonyms: Distributed short read Error Correction on GPUs

Resource Type: software resource

Defining Citation: [PMID:21447171](#)

Keywords: k-mer based corrector, k-mer spectrum, illumina short read, multistage workflow, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: DecGPU

Resource ID: SCR_000585

Alternate IDs: biotools:decgpu, OMICS_01101, SCR_011850, OMICS_01060

Alternate URLs: <http://musket.sourceforge.net/homepage.htm#latest>,
<https://bio.tools/decgpu>

License: GNU General Public License version 3.0

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260804T043106+0000

Ratings and Alerts

No rating or validation information has been found for DecGPU.

No alerts have been found for DecGPU.

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 [dkNET](#) .

Gallone B, et al. (2016) Domestication and Divergence of *Saccharomyces cerevisiae* Beer Yeasts. *Cell*, 166(6), 1397.

Laehnemann D, et al. (2016) Denoising DNA deep sequencing data-high-throughput sequencing errors and their correction. *Briefings in bioinformatics*, 17(1), 154.

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

Liu Y, et al. (2013) Musket: a multistage k-mer spectrum-based error corrector for Illumina sequence data. *Bioinformatics (Oxford, England)*, 29(3), 308.

Liu Y, et al. (2011) DecGPU: distributed error correction on massively parallel graphics processing units using CUDA and MPI. *BMC bioinformatics*, 12, 85.