

Resource Summary Report

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MesKit

RRID:SCR_020959

Type: Tool

Proper Citation

MesKit (RRID:SCR_020959)

Resource Information

URL: <https://github.com/Niinleslie/MesKit>

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Description: Software R package for dissecting cancer evolution from multi region derived tumor biopsies via somatic mutations. Used for characterizing cancer genomic ITH and inferring history of tumor evolution via implementation of well established computational and statistical methods.

Synonyms: Multi region exome sequencing analysis tool Kit

Resource Type: software toolkit, software resource, data visualization software, data processing software, sequence analysis software, software application, data analysis software

Keywords: Dissecting cancer evolution, region derived tumor biopsies, somatic mutations, cancer genomic ITH, tumor evolution

Availability: Free, Available for download, Freely available

Resource Name: MesKit

Resource ID: SCR_020959

Alternate URLs: <https://bioconductor.org/packages/MesKit/>

License: GPL-3.0

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260803T040802+0000

Ratings and Alerts

No rating or validation information has been found for MesKit.

No alerts have been found for MesKit.

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 [ASWG](#) .

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. Neoplasia (New York, N.Y.), 66, 101180.

Persi E, et al. (2025) Genome-level selection in tumors as a universal marker of resistance to therapy. Nature communications, 16(1), 6535.

Liu M, et al. (2021) MesKit: a tool kit for dissecting cancer evolution of multi-region tumor biopsies through somatic alterations. GigaScience, 10(5).