Resource Summary Report

Generated by NIF on May 15, 2025

PyLOH

RRID:SCR_001511
Type: Tool

Proper Citation

PyLOH (RRID:SCR_001511)

Resource Information

URL: https://github.com/uci-cbcl/PyLOH

Proper Citation: PyLOH (RRID:SCR_001511)

Description: Software for deconvolving tumor purity and ploidy by integrating copy number alterations and loss of heterozygosity. The model resolves the identifiability problem by integrating two types of sequencing information - somatic copy number alterations and loss of heterozygosity - within an unified probabilistic framework.

Resource Type: software resource

Defining Citation: PMID:24695406

Keywords: standalone software, python, bio.tools

Funding:

Availability: GNU General Public License, v2

Resource Name: PyLOH

Resource ID: SCR_001511

Alternate IDs: OMICS_03559, biotools:pyloh

Alternate URLs: https://bio.tools/pyloh

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250420T014030+0000

Ratings and Alerts

No rating or validation information has been found for PyLOH.

No alerts have been found for PyLOH.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Cheng Y, et al. (2025) Stromal architecture and fibroblast subpopulations with opposing effects on outcomes in hepatocellular carcinoma. Cell discovery, 11(1), 1.

Ji D, et al. (2021) Tumor mutation burden in blood predicts benefit from neoadjuvant chemo/radiotherapy in locally advanced rectal cancer. Genomics, 113(1 Pt 2), 957.

Park S, et al. (2019) Paired whole exome and transcriptome analyses for the Immunogenomic changes during concurrent chemoradiotherapy in esophageal squamous cell carcinoma. Journal for immunotherapy of cancer, 7(1), 128.

Li Y, et al. (2015) MixClone: a mixture model for inferring tumor subclonal populations. BMC genomics, 16 Suppl 2(Suppl 2), S1.