Resource Summary Report

Generated by NIF on Apr 20, 2025

QuadGT

RRID:SCR_000073
Type: Tool

Proper Citation

QuadGT (RRID:SCR_000073)

Resource Information

URL: http://www.iro.umontreal.ca/~csuros/quadgt/

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Description: Software package for calling single-nucleotide variants in four sequenced genomes comprising a normal-tumor pair and the two parents. Genotypes are inferred using a joint model of parental variant frequencies, de novo germline mutations, and somatic mutations. The model quantifies the descent-by-modification relationships between the unknown genotypes by using a set of parameters in a Bayesian inference setting. Note that you can use it on any subset of the four related genomes, including parent-offspring trios, and normal-tumor pairs without parental samples.

Abbreviations: QuadGT

Resource Type: software resource

Defining Citation: PMID:23734724

Keywords: single-nucleotide variant, sequenced genome, genotype, genome

Related Condition: Normal, Tumor, Cancer

Funding: Terry Fox Research Institute ;
Canadian Institutes for Health Research ;
Canada National Sciences and Engineering Research Council

Availability: New BSD License

Resource Name: QuadGT

Resource ID: SCR_000073

Alternate IDs: OMICS_02108

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250420T013927+0000

Ratings and Alerts

No rating or validation information has been found for QuadGT.

No alerts have been found for QuadGT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Bao R, et al. (2014) Review of current methods, applications, and data management for the bioinformatics analysis of whole exome sequencing. Cancer informatics, 13(Suppl 2), 67.