Resource Summary Report

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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: 20250410T064507+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 FDI Lab - SciCrunch.org.

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.