

Benchmarking Somatic Copy Number Variation Detection Tools in Cancer Genomes



Lada Krainikova¹, Maria Gridina^{1,2} and Aleksandr Vikhorev^{1,*}

¹Institute of Medicine and Medicine Technologies, Novosibirsk State University, Novosibirsk, Russia

²Laboratory of Genomic Technologies for Medical Genetics, Institute of Cytology and Genetics, Novosibirsk, Russia

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*Address correspondence to this author at the Institute of Medicine and Medicine Technologies, Novosibirsk State University, Novosibirsk, Russia; E-mail: a.vikhorev@g.nsu.ru

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Table S1. Comprehensive performance metrics for somatic CNV detection tools. Sheets 1-4 contain raw values for precision, recall, reproducibility, and concordance across all samples and tool pairs. Sheet 5 provides summarized statistics (mean ± standard deviation) for all metrics and tools evaluated in this study.

Metric	CNV Type	Tool	Mean	Std
Recall	Deletion	CNVkit	0.93	0.037
Recall	Deletion	Sequenza	0.621	0.04
Recall	Deletion	Facets	0.873	0.043
Recall	Deletion	ASCAT	0.732	0.105
Recall	Amplification	CNVkit	0.538	0.006
Recall	Amplification	Sequenza	0.851	0.013
Recall	Amplification	Facets	0.851	0.017
Recall	Amplification	ASCAT	0.453	0.066
Precision	Deletion	CNVkit	0.965	0.038
Precision	Deletion	Sequenza	0.895	0.131
Precision	Deletion	Facets	0.994	0.003
Precision	Deletion	ASCAT	0.816	0.237
Precision	Amplification	CNVkit	0.998	0.003
Precision	Amplification	Sequenza	0.996	0.001
Precision	Amplification	Facets	0.9999	0.0001
Precision	Amplification	ASCAT	0.992	0.009
Reproducibility	Deletion	CNVkit	0.877	0.04
Reproducibility	Deletion	Sequenza	0.941	0.046
Reproducibility	Deletion	Facets	0.934	0.057
Reproducibility	Deletion	ASCAT	0.824	0.063
Reproducibility	Amplification	CNVkit	0.541	0.035
Reproducibility	Amplification	Sequenza	0.969	0.017
Reproducibility	Amplification	Facets	0.974	0.014
Reproducibility	Amplification	ASCAT	0.843	0.076

Metric	CNV Type	Tool	Mean	Std
Concordance	Deletion	CNVkit	0.712	0.125
Concordance	Deletion	Sequenza	0.71	0.089
Concordance	Deletion	Facets	0.768	0.086
Concordance	Deletion	ASCAT	0.731	0.09
Concordance	Amplification	CNVkit	0.508	0.066
Concordance	Amplification	Sequenza	0.698	0.2
Concordance	Amplification	Facets	0.691	0.2
Concordance	Amplification	ASCAT	0.521	0.089

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