

OpenCGA Benchmark Report - Platinum Data Set - Cambridge Test Machine

This benchmark report is generated with "Cambridge Test" with OpenCGA release : "1.4.0-rc3-dev" (git commit: d3e565fbd55a3de075fe594db239b68bdd1f1d11)

Cambridge Test Server Specification:

- Two Tomcat Servers
 - 2 Cores each
 - 12 GB Total Ram
- Single Mongo 3.6 Node
 - 24 Cores
 - 32 GB Ram
- Single Solr 6.4 Node
 - 24 Cores
 - 32 GB Ram

Execution Parameters:

- Number of Concurrent Users : 10
- Number of Repetitions : 05
- Result limit : 100

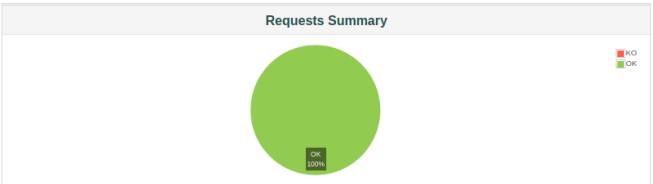
Execution Command:

./opencga-storage-admin.sh benchmark variant --host <http://bioinfodev.hpc.cam.ac.uk/opencga-test> --limit 100 --num-repetition 5 --concurrency 10 -B sid=eyJhbGciOiJIUzI1NiJ9.eyJzdWIiOiJjYWZldGVybyIsImF1ZCI6IkwZW5DR0EgdXNlcnMILCJpYXQiOiJlMzcyODEzNzAsImV4cCI6IjUzNzI4NDk3MH0.8OfajGwcEHuAAgzY6-BIWqW9c7I-vj9jujx5TjftgPo

Benchmark Report:

Complete JMeter report in HTML format is available here to [BenchmarkReport.tar](#)

APDEX (Application Performance Index)			
Apdex	T (Toleration threshold)	F (Frustration threshold)	Label
0.577	500 ms	1 sec 500 ms	Total
0.490	1 sec 500 ms	1 sec 725 ms	MultipleIncludeFilesAndSamples
0.560	1 sec 500 ms	1 sec 725 ms	AllIncludeStudySampleAndFile
0.590	1 sec 500 ms	1 sec 725 ms	TwoFiles
0.630	1 sec 500 ms	1 sec 725 ms	ProteinSubstitution
0.640	1 sec 500 ms	1 sec 725 ms	Info_DP_HaplotypeScore
0.660	1 sec 500 ms	1 sec 725 ms	SampleAndFilterAndGenotype
0.670	1 sec 500 ms	1 sec 725 ms	FileAndFilter-PASS
0.680	1 sec 500 ms	1 sec 725 ms	FileAndSample
0.680	1 sec 500 ms	1 sec 725 ms	EmptyQuery
0.690	1 sec 500 ms	1 sec 725 ms	BiotypeAndLOFAndPFMAF
0.700	1 sec 500 ms	1 sec 725 ms	Qual>50
0.700	1 sec 500 ms	1 sec 725 ms	ThreeGenes
0.710	1 sec 500 ms	1 sec 725 ms	MultipleFiltersAndTwoFiles
0.710	1 sec 500 ms	1 sec 725 ms	SixFilters
0.710	1 sec 500 ms	1 sec 725 ms	FileAndIncludeAllStudiesOneSample
0.730	1 sec 500 ms	1 sec 725 ms	Genotype-NA12877:1/1
0.760	1 sec 500 ms	1 sec 725 ms	FileAndNegatedFilterAndGenotype
0.770	1 sec 500 ms	1 sec 725 ms	Gene-DDX11L1
0.770	1 sec 500 ms	1 sec 725 ms	QualAndFiltersAndFile
0.780	1 sec 500 ms	1 sec 725 ms	FilesFiltersAndGenotype
0.780	1 sec 500 ms	1 sec 725 ms	Genotype-NA12877:0/1
0.800	1 sec 500 ms	1 sec 725 ms	Biotype
0.810	1 sec 500 ms	1 sec 725 ms	Genotype-NA12877:HOM_REF
0.810	1 sec 500 ms	1 sec 725 ms	PopulationFrequencyMaf
0.820	1 sec 500 ms	1 sec 725 ms	TwoGenes
0.820	1 sec 500 ms	1 sec 725 ms	Qual<=5
0.830	1 sec 500 ms	1 sec 725 ms	Qual<50
0.830	1 sec 500 ms	1 sec 725 ms	MultipleGenotype
0.840	1 sec 500 ms	1 sec 725 ms	TwoFiltersAndOneFile
0.930	1 sec 500 ms	1 sec 725 ms	ThreeGenesAndFourCT
0.930	1 sec 500 ms	1 sec 725 ms	ThreeGeneAndLOF
0.980	1 sec 500 ms	1 sec 725 ms	IncludeNone



Requests		Executions				Response Times (ms)							Network (KB/sec)											
Label	^	#Samples	^	KO	Error %	^	Average	^	Min	^	Max	^	90th pct	^	95th pct	^	99th pct	^	Throughput	^	Received	^	Sent	^
Total		1600	0	0	0.00%		1118.59	94			8357	2458.70	2979.20		6532.54		7.47				7651.46		0.00	
AllIncludeStudySampleAndFile		50	0	0	0.00%		2958.68	677			8357	7256.30	7580.65		8357.00		0.27				360.08		0.00	
Biotype		50	0	0	0.00%		905.26	208			2941	2015.60	2427.20		2941.00		0.26				249.50		0.00	
BiotypeAndLofAndPFMAF		50	0	0	0.00%		1152.54	221			2783	2365.10	2696.50		2783.00		0.27				415.05		0.00	
EmptyQuery		50	0	0	0.00%		1214.60	332			3317	2334.70	3108.90		3317.00		0.26				244.86		0.00	
FileAndFilter-PASS		50	0	0	0.00%		1192.30	231			2898	2585.40	2857.80		2898.00		0.26				344.92		0.00	
FileAndIncludeAllStudiesOneSample		50	0	0	0.00%		1019.58	188			2945	2259.40	2429.85		2945.00		0.27				240.60		0.00	
FileAndNegatedFilterAndGenotype		50	0	0	0.00%		1060.46	266			3533	2935.20	3317.20		3533.00		0.27				223.67		0.00	
FileAndSample		50	0	0	0.00%		1133.08	208			3090	2534.20	2648.55		3090.00		0.26				236.24		0.00	
FilesFiltersAndGenotype		50	0	0	0.00%		1002.50	231			3290	2354.60	3116.25		3290.00		0.26				255.02		0.00	
Gene-DDX11L1		50	0	0	0.00%		844.88	178			2721	2145.20	2368.45		2721.00		0.26				222.97		0.00	
Genotype-NA12877-0/1		50	0	0	0.00%		881.84	190			2980	2032.50	2564.20		2980.00		0.26				220.10		0.00	
Genotype-NA12877-1/1		50	0	0	0.00%		1006.22	203			3134	2187.30	2635.00		3134.00		0.27				242.38		0.00	
Genotype-NA12877-HOM_REF		50	0	0	0.00%		881.94	208			2666	2243.30	2514.95		2666.00		0.26				236.41		0.00	
IncludeNone		50	0	0	0.00%		608.96	100			1659	1314.60	1503.60		1659.00		0.26				211.03		0.00	
Info_DP_HaplotypeScore		50	0	0	0.00%		1401.84	253			3707	3108.90	3371.60		3707.00		0.26				244.10		0.00	
MultipleFiltersAndTwoFiles		50	0	0	0.00%		1113.06	260			3522	2228.30	2691.95		3522.00		0.27				188.30		0.00	
MultipleGenotype		50	0	0	0.00%		902.42	294			3446	2429.50	3018.15		3446.00		0.26				254.35		0.00	
MultipleIncludeFilesAndSamples		50	0	0	0.00%		2960.44	516			7270	6713.90	6835.25		7270.00		0.26				286.58		0.00	
PopulationFrequencyMaf		50	0	0	0.00%		838.74	170			2721	1998.50	2515.65		2721.00		0.27				222.55		0.00	
ProteinSubstitution		50	0	0	0.00%		1283.76	267			3272	2459.40	2869.80		3272.00		0.26				715.40		0.00	
Qual<50		50	0	0	0.00%		822.26	165			2412													

Errors			
Type of error	Number of errors	% in errors	% in all samples

[illegible]