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.eyJzdWIiOiJjYWZldGVybyIsImF1ZCI6Ik9wZW5DR0EgdXNlcnMiLCJpYXQiOjE1MzcyODEzNzAsImV4cCI6MjUzNzI4NDk3MH0.8OfajGwcEHuAAgzY6-BlWqW9c7I-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 Summary

Statistics

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**	**0.00%**	**1118.59**	**94**	**8357**	**2458.70**	**2979.20**	**6532.54**	**7.47**	**7651.46**	**0.00**
AllIncludeStudySampleAndFile	50	0	0.00%	2958.68	677	8357	7256.30	7580.65	8357.00	0.27	360.08	0.00
Biotype	50	0	0.00%	905.26	208	2941	2015.60	2427.20	2941.00	0.26	249.50	0.00
BiotypeAndLOFAndPFMAF	50	0	0.00%	1152.54	221	2783	2365.10	2696.50	2783.00	0.27	415.05	0.00
EmptyQuery	50	0	0.00%	1214.60	332	3317	2334.70	3108.90	3317.00	0.26	244.86	0.00
FileAndFilter-PASS	50	0	0.00%	1192.30	231	2898	2585.40	2857.80	2898.00	0.26	344.92	0.00
FileAndIncludeAllStudiesOneSample	50	0	0.00%	1019.58	188	2945	2259.40	2429.85	2945.00	0.27	240.60	0.00
FileAndNegatedFilterAndGenotype	50	0	0.00%	1060.46	266	3533	2935.20	3317.20	3533.00	0.27	223.67	0.00
FileAndSample	50	0	0.00%	1133.08	208	3090	2534.20	2648.55	3090.00	0.26	236.24	0.00
FilesFiltersAndGenotype	50	0	0.00%	1002.50	231	3290	2354.60	3116.25	3290.00	0.26	255.02	0.00
Gene-DDX11L1	50	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	0.00%	881.84	190	2980	2032.50	2564.20	2980.00	0.26	220.10	0.00
Genotype-NA12877:1/1	50	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	0.00%	881.94	208	2666	2243.30	2514.95	2666.00	0.26	236.41	0.00
IncludeNone	50	0	0.00%	608.96	100	1659	1314.60	1503.60	1659.00	0.26	211.03	0.00
Info_DP_HaplotypeScore	50	0	0.00%	1401.84	253	3707	3108.90	3371.60	3707.00	0.26	244.10	0.00
MultipleFiltersAndTwoFiles	50	0	0.00%	1113.06	260	3522	2228.30	2691.95	3522.00	0.27	188.30	0.00
MultipleGenotype	50	0	0.00%	902.42	294	3446	2429.50	3018.15	3446.00	0.26	254.35	0.00
MultipleIncludeFilesAndSamples	50	0	0.00%	2960.44	516	7270	6713.90	6835.25	7270.00	0.26	286.58	0.00
PopulationFrequencyMaf	50	0	0.00%	838.74	170	2721	1998.50	2515.65	2721.00	0.27	222.55	0.00
ProteinSubstitution	50	0	0.00%	1283.76	267	3272	2459.40	2869.80	3272.00	0.26	715.40	0.00
Qual<50	50	0	0.00%	822.26	165	2412	1761.00	2227.55	2412.00	0.27	188.06	0.00
Qual<<5	50	0	0.00%	864.56	254	2507	1932.90	2410.85	2507.00	0.26	342.01	0.00
Qual>50	50	0	0.00%	1125.04	192	2917	2411.40	2583.80	2917.00	0.27	255.50	0.00
QualAndFiltersAndFile	50	0	0.00%	914.54	206	2951	2272.30	2649.65	2951.00	0.27	191.20	0.00
SampleAndFilterAndGenotype	50	0	0.00%	1301.32	257	3770	3034.30	3310.50	3770.00	0.27	227.60	0.00
SixFilters	50	0	0.00%	1126.30	208	3135	2552.00	2645.55	3135.00	0.27	211.06	0.00
ThreeGeneAndLOF	50	0	0.00%	564.42	95	2317	1523.70	1751.75	2317.00	0.26	3.43	0.00
ThreeGenes	50	0	0.00%	1207.82	351	3301	2778.20	3063.30	3301.00	0.27	1009.79	0.00
ThreeGenesAndFourCT	50	0	0.00%	530.68	94	2280	1454.10	2074.05	2280.00	0.26	13.31	0.00
TwoFiles	50	0	0.00%	1383.84	220	3597	2967.90	3343.00	3597.00	0.26	243.14	0.00
TwoFiltersAndOneFile	50	0	0.00%	750.18	181	2565	1962.50	2189.25	2565.00	0.27	188.18	0.00
TwoGenes	50	0	0.00%	840.90	167	2540	1813.40	2135.70	2540.00	0.27	228.78	0.00

Errors

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

Top 5 Errors by sampler

Sample	#Samples	#Errors	Error	#Errors	Error	#Errors	Error	#Errors	Error	#Errors	Error	#Errors
Total	**1600**	**0**										