

Parallelware Analyzer for large codes:

GROMACS case study

Appentra's Parallelware Analyzer is the first static code analyzer that is designed specifically to boost the performance of C/C++ code. Earlier generations of source code analysis are limited to bugs, coding standard enforcement or security, possibly even a combination of these, which while important do nothing to ensure that the code is written to take advantage of modern hardware capabilities offered by chip manufacturers in the low-power multicore processors.

GROMACS is a versatile package to perform molecular dynamics, i.e. simulate the Newtonian equations of motion for systems with hundreds to millions of particles.

About GROMACS

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We have used the <u>GROMACS</u> project to benchmark how Parallelware Analyzer behaves for large code bases. The highlights are summarized below:





340K lines of code across 2.481 C++ files

GROMACS contains 2.481 C++ files accounting for 340.449 lines of code, as reported by the *sloccount* tool.

940 of these C++ files correspond to headers, which are only analyzed when included from .cpp files.



99.6% of files successfully analyzed

We exclude 251 files (17 files that fail due to missing headers plus third-party code).

1.282 out of 1.287 .cpp files were successfully analyzed.



3 secs/file on average, for a total of 1 hour and 7 minutes analysis time

It took a total of 4.204 seconds to run for the 1.287 files¹.

The peak of RAM usage was 518 MBs according to the *valgrind* tool.



0.39% error rate

Parallelware Analyzer successfully analyzed 1.926 loops found in the code. 984 out of those were reported as opportunities to increase performance.

Our R&D team reviewed² 52% of those opportunities and found only 2 of them to be erroneous.

1 On a laptop with an AMD Ryzen 7 4800HS CPU.
2 The review consisted of carefully examining loop variables' compute patterns and data scoping classification.



The above analysis can be reproduced by following the instructions in our GitHub repository.