

Performance of Folding@Home and Distributed Folding cleints

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A question for the folks familiar with the Folding@Home protein folding project.

I have been doing some performance testing of FreeBSD vs Linux in a couple of the Distrubted Computing projects particulary Folding@Home and Distributed folding. The one that I am curios about is Folding@Home where their is no specific FreeBSD client, instead it runs as a Linux client using the linux_base-8 libraries from the ports collection. Under straight linux redhat, CRUX, gentoo it takes about 13hours on a P4C 3.0Ghz for complete a gromacs WU, the same hardware running either FreeBSD 4.9-RELEASE or 5.1-RELEASE is takes about 26hours to do the same task. The only think I have noticed is that under Linux the client says it's using the SSE instructions, where under FreeBSD and the linux_base-8 libraries it does not say that. The cleint runs multi threaded under Linux or FreeBSD.

I have also noticed quite a performance difference, though not as extreme, between the OS's in the distributed folding project where there is a native compile for FreeBSD. The benchmark suite says that FreeBSD is spending more time in sys (I/O) releated ativities than Linux but is still takes more hours to get through set of 250 generations than Linux does, the significant figure is the Foldtraj/ Usr time which seems to relate how long it will take to complete a generation.

Linux Benchmark P4C 3.0Ghz

Summary

Usr time Sys time

Maketraj 2.670 0.710

Foldtraj 28.930 11.000

FreeBSD Benchmark P4 3.16GHz.

Summary

Usr time Sys time

freebsd-performance: Performance of Folding@Home and Distributed Folding clients

Maketraj 5.789 0.234
Foldtraj 36.867 1.523

I am curious if there are any performance tweaks for FreeBSD, other than client settings or nice levels, to get more performance out of either Folding@home or Distributed Folding clients?

I have asked this question on the respective forums, but the people there are generally not FreeBSD gurus.

– Ernie.

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