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bioinformatics-40c-dedicated

Biofinformatics 40c Dedicated

Test Systems:

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Processor: 2 x Intel Xeon (Skylake IBRS) (40 Cores), Motherboard: OpenStack Foundation Nova v21.0.0 (1.13.0-1ubuntu1.1 BIOS), Chipset: Intel 440FX 82441FX PMC, Memory: 16384 MB + 8192 MB RAM, Disk: 50GB, Graphics: Cirrus Logic GD 5446, Network: Red Hat Virtio device

OS: Ubuntu 20.04, Kernel: 5.4.0-74-generic (x86_64), Compiler: GCC 9.3.0, File-System: ext4, Screen Resolution: 1024x768, System Layer: KVM

Kernel Notes: Transparent Huge Pages: madvise
Compiler Notes: --build=x86_64-linux-gnu --disable-vtable-verify --disable-werror --enable-checking=release --enable-clocale=gnu --enable-default-pie --enable-gnu-unique-object --enable-languages=c,ada,c++,go,brig,d,fortran,objc,obj-c++,gm2 --enable-libstdcxx-debug --enable-libstdcxx-time=yes --enable-multiarch

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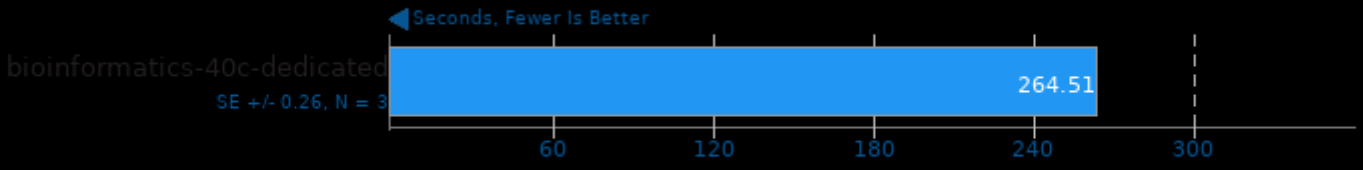
--enable-multilib --enable-nls --enable-objc-gc=auto --enable-offload-targets=nvptx-none=/build/gcc-9-HskZEa/gcc-9-9.3.0/debian/tmp-nvptx/usr,hsa --enable-plugin --enable-shared --enable-threads=posix --host=x86_64-linux-gnu --program-prefix=x86_64-linux-gnu- --target=x86_64-linux-gnu --with-abi=m64 --with-arch-32=i686 --with-default-libstdcxx-abi=new --with-gcc-major-version-only --with-multilib-list=m32,m64,mx32 --with-target-system-zlib=auto --with-tune=generic --without-cuda-driver -v
Processor Notes: CPU Microcode: 0x1
Security Notes: itlb_multihit: Not affected + l1tf: Mitigation of PTE Inversion; VMX: flush not necessary SMT disabled + mds: Mitigation of Clear buffers; SMT Host state unknown + meltdown: Mitigation of PTI + spec_store_bypass: Mitigation of SSB disabled via prctl and seccomp + spectre_v1: Mitigation of usercopy/swapgs barriers and __user pointer sanitization + spectre_v2: Mitigation of Full generic retpoline IBPB: conditional IBRS_FW STIBP: disabled RSB filling + srbds: Not affected + tsx_async_abort: Mitigation of Clear buffers; SMT Host state unknown

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Timed MrBayes Analysis - P.P.A (sec)	264.512
Standard Deviation	0.2%
QMCPACK - simple-H2O (Execution Time - sec)	58.014
Standard Deviation	0.6%
Timed HMMer Search - P.D.S (sec)	198.400
Standard Deviation	0%
Timed MAFFT Alignment - M.S.A - LSU RNA (sec)	12.539
Standard Deviation	1.6%
Himeno Benchmark - P.P.S (MFLOPS)	3105
Standard Deviation	0.2%

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Timed MrBayes Analysis 3.2.7

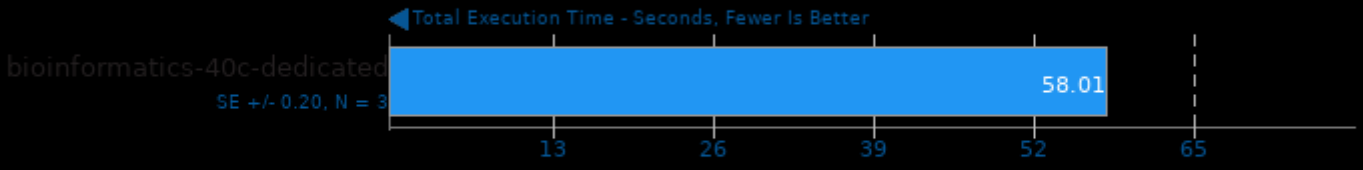
Primate Phylogeny Analysis



1. (CC) gcc options: -mmmx -msse -msse2 -msse3 -mssse3 -msse4.1 -msse4.2 -maes -mavx -mfma -mavx2 -mavx512f -mavx512cd -mavx512vl -mavx512

QMCPACK 3.11

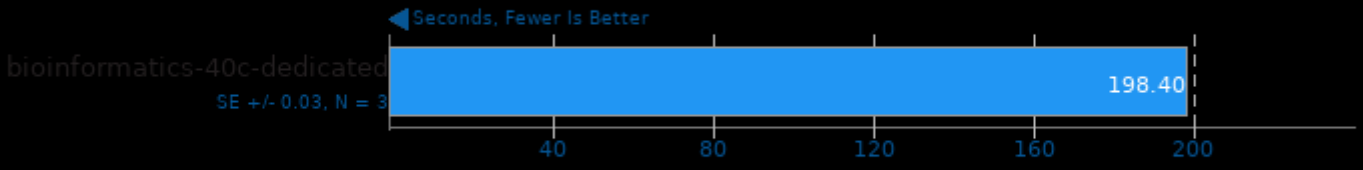
Input: simple-H2O



1. (CXX) g++ options: -fopenmp -finline-limit=1000 -fstrict-aliasing -funroll-all-loops -march=native -O3 -fomit-frame-pointer -ffast-math -pthread -lm

Timed HMMer Search 3.3.2

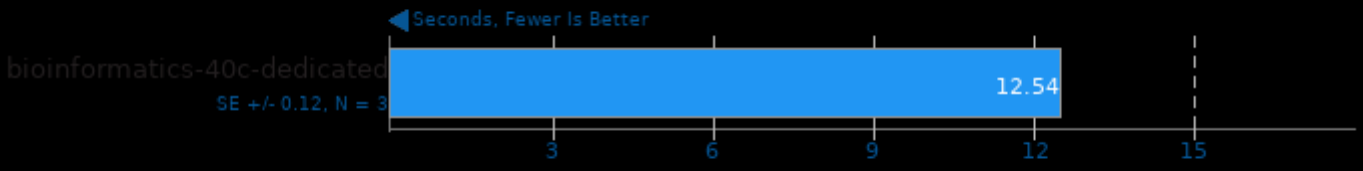
Pfam Database Search



1. (CC) gcc options: -O3 -pthread -lhmmer -leasel -lm -lmpi

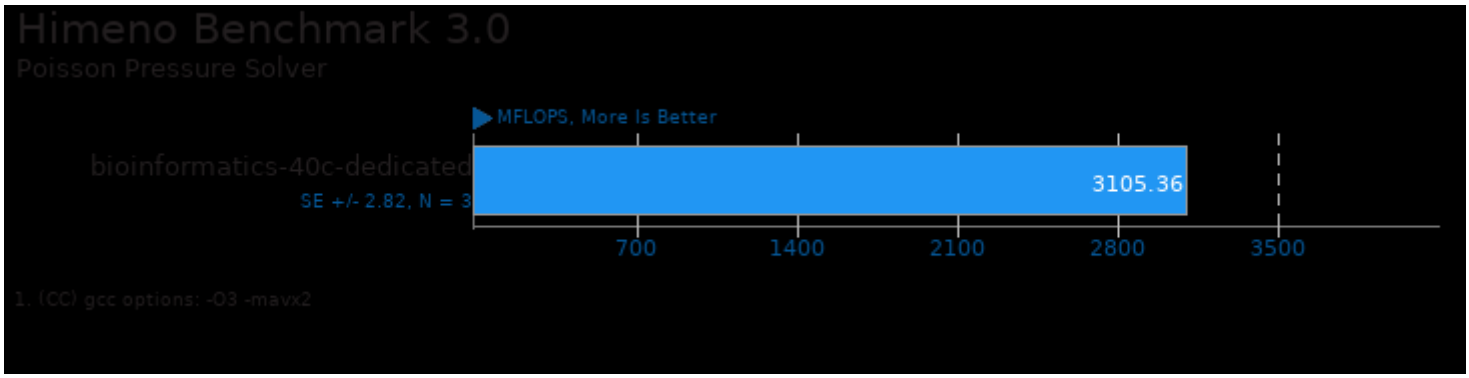
Timed MAFFT Alignment 7.471

Multiple Sequence Alignment - LSU RNA



1. (CC) gcc options: -std=c99 -O3 -lm -lpthread

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This file was automatically generated via the Phoronix Test Suite benchmarking software on Friday, 29 March 2024 01:25.