

Were selected 12 programs contained in the CLBG and then will be presented a brief description according to the project authors, as well as the version used in this study and which inputs were considered.

FASTA

Generate and write random DNA sequences by copying from a given sequence and by weighted random selection from 2 alphabets.

Version selected: 2; Input used: 25000000.

N-BODY

Double-precision N-body simulation. Model the orbits of Jovian planets, using the same simple symplectic-integrator.

Version selected: 4; Input used: 50000000.

FANNKUCH-REDUX

Indexed-access to tiny integer-sequence, as defined in "Performing Lisp Analysis of the FANNKUCH Benchmark"¹. For a given n that tends to infinity, it is conjectured that the count approaches at most $n \cdot \log(n)$.

Version selected: 5; Input used: 12.

SPECTRAL-NORM

Eigenvalue using the power method. Based on the statement in point 3 of the set of challenges published in 2002 by SIAM News called "Hundred-Dollar, Hundred-Digit Challenge Problems"²³.

Version selected: 5; Input used: 5500

MANDELBROT

Generate Mandelbrot set portable bitmap file. Based on the mathematical problem called Mandelbrot Set⁴, which in general terms is a particular set of complex numbers which has a highly convoluted fractal boundary when plotted.

Version selected: 6; Input used: 16000.

REGEX-REDUX

Match DNA 8-mers and substitute magic patterns. In this particular case, through the use of the same simple regex patterns and actions to manipulate FASTA format data.

Version selected: 4; Input used: fasta file input25000000.txt.

K-NUCLEOTIDE

Hashtable update and k-nucleotide strings. Requires mapping of DNA letters and

¹ <http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.35.5124>

² <http://mathworld.wolfram.com/Hundred-DollarHundred-DigitChallengeProblems.html>

³ <http://www.siam.org/siamnews/01-02/challenge.pdf>

⁴ <http://mathworld.wolfram.com/MandelbrotSet.html>

the use of hash functions (built-in or library) that concatenates those codes is an acceptable optimization.

Version selected: 1; Input used: fasta file input25000000.txt.

REVERSE-COMPLEMENT

Read DNA sequences and write their reverse-complement from the sequence of bases of each strand.

Version selected: 6; Input used: input5000000.txt.

BINARY-TREES

Allocate and deallocate a large amount of perfect binary trees, using a simplified adaptation of the method of Hans Boehm's GCBench⁵.

Version selected: 3; Input used: 21.

CHAMENEOS-REDUX

A peer-to-peer cooperation paradigm adapted from what is stated in "Chameneos, a Concurrency Game for Java, Ada and Others"⁶.

Version selected: 5; Input used: 60000000.

METEOR

Algorithmic search of solutions for the Meteor Puzzle (10x5).

Version selected: 1; Input used: 2098.

THREAD-RING

Simplistic adaptation of the process described in "Performance Measurements of Threads in Java and Processes in Erlang"⁷ and "A Benchmark Test for BCPL Style Coroutines"⁸, where messages are passed between N threads/processes that are spawned connected as a ring structure.

Version selected: 3; Input used: 5000000.

⁵ <http://hboehm.info/gc/gc.bench/>

⁶ <http://cedric.cnam.fr/PUBLIS/RC474.pdf>

⁷ <http://archive.is/1droG#selection-129.1-129.204>

⁸ <http://www.cl.cam.ac.uk/~mr10/Cobench.html>