

CREST Open Workshop 3-4th December 2018

Genetic Improvement by Evolving Program Data

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GI 2  19

[GI 2019](#), Montreal, ICSE-2019 workshop

Simple blue example
of grammar based
Genetic Improvement

opencv_gp.tar.gz

[RN/18/06](#)



WIKIPEDIA
Genetic Improvement



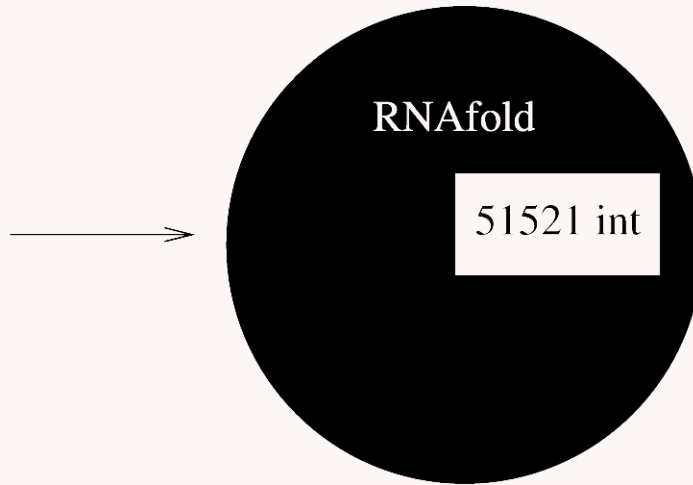
Maintaining Embedded Constants

- [EuroGP 2018](#)
 - RNAfold 7000 lines of code 50000 numbers
 - On average better predictions of RNA folding.
 - Shipped since 2.4.7
- [SSBSE-2018](#) sqrt converted to cube root
 - New functionality, double precision accuracy
- [RN/18/05](#) generate \log_2 from existing open source maths framework

RNAfold

```
> CRW_01446
UUCAAAACGAGGAAA.....
.....
.....
UGAAC
```

RNA sequence



RNA structure



RNAfold reads RNA molecules base sequence.
 Outputs prediction of how molecule will fold up.
 Internally RNAfold uses 51521 parameters.

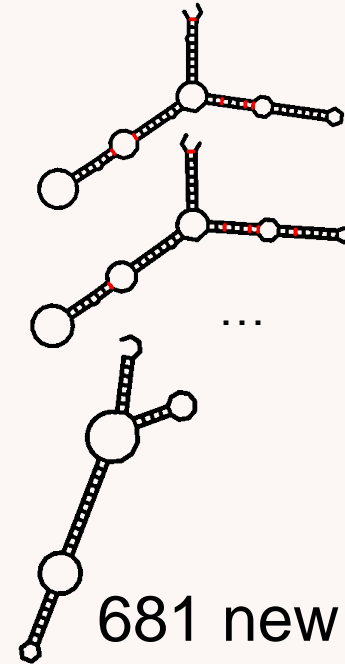
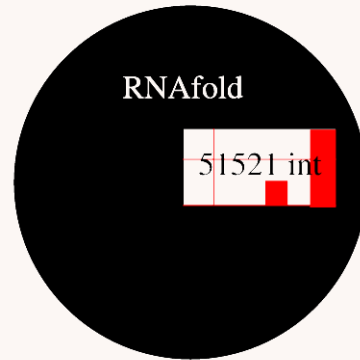
Fitness of Mutated RNAfold

```
> CRW_00550  
NAUUUACGGCGGUC.....  
GACAC
```

```
> CRW_00553  
NNNUUGGUGGCGGAG....  
CAAGC
```

...

```
> TMR_00272  
GGGGAUGAAUU.....  
CACCA
```



681 short training sequences

681 new predictions

- Mutate constants inside RNAfold and recompile
- Run mutated RNAfold on training RNA sequences
- Compare each new prediction with real structure
- Fitness mean Matthew's correlation coefficient on 681 training RNA molecules

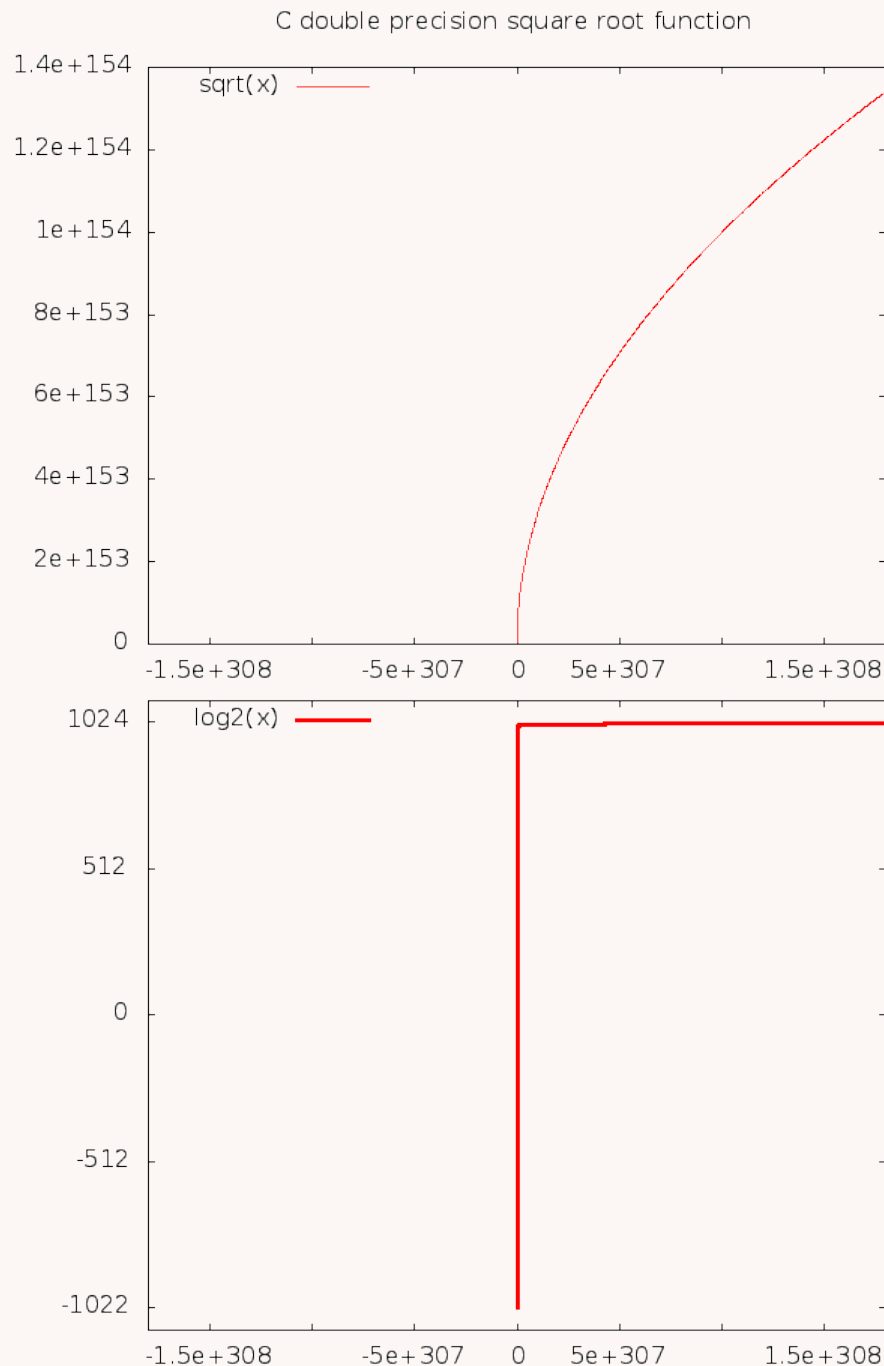
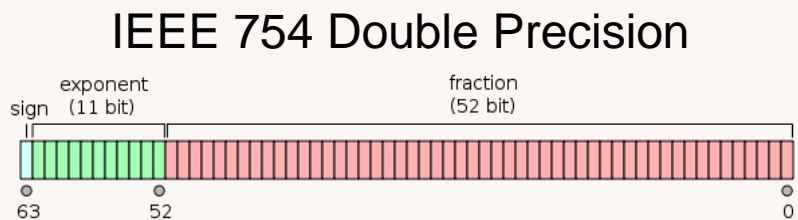
Genetic Improvement of RNAfold

RNAfold state of the art prediction of how RNA molecule will fold up based on its sequence of bases.

- Speed up via Intel SSE parallel instructions [GI 2017](#). Shipped since V2.3.5
- ViennaRNA Package [v2.3.0cuda](#)
- Better predictions by evolving parameters
 - On average better predictions of RNA folding.
 - Shipped since 2.4.7
- AVX speedup will be in release 2.4.11

Use evolution to convert table based **sqrt** into **log₂**

By updating table of **512 floats** (+small code change)



GNU C library sqrt converted to log2

- Chosen implementation of sqrt divides normalised input into 512 bins.
- bin holds start point for Newton-Raphson
- 1 run evolutionary strategy per table value
 - Seed CMA-ES with square root values
 - Run `code` with CMA-ES generated table value
 - Fitness = absolute diff $GI_{\log_2}(x)$, $\log_2(x)$
 - x takes three test values: smallest, mid, max in bin
 - all 512 CMA-ES runs succeed

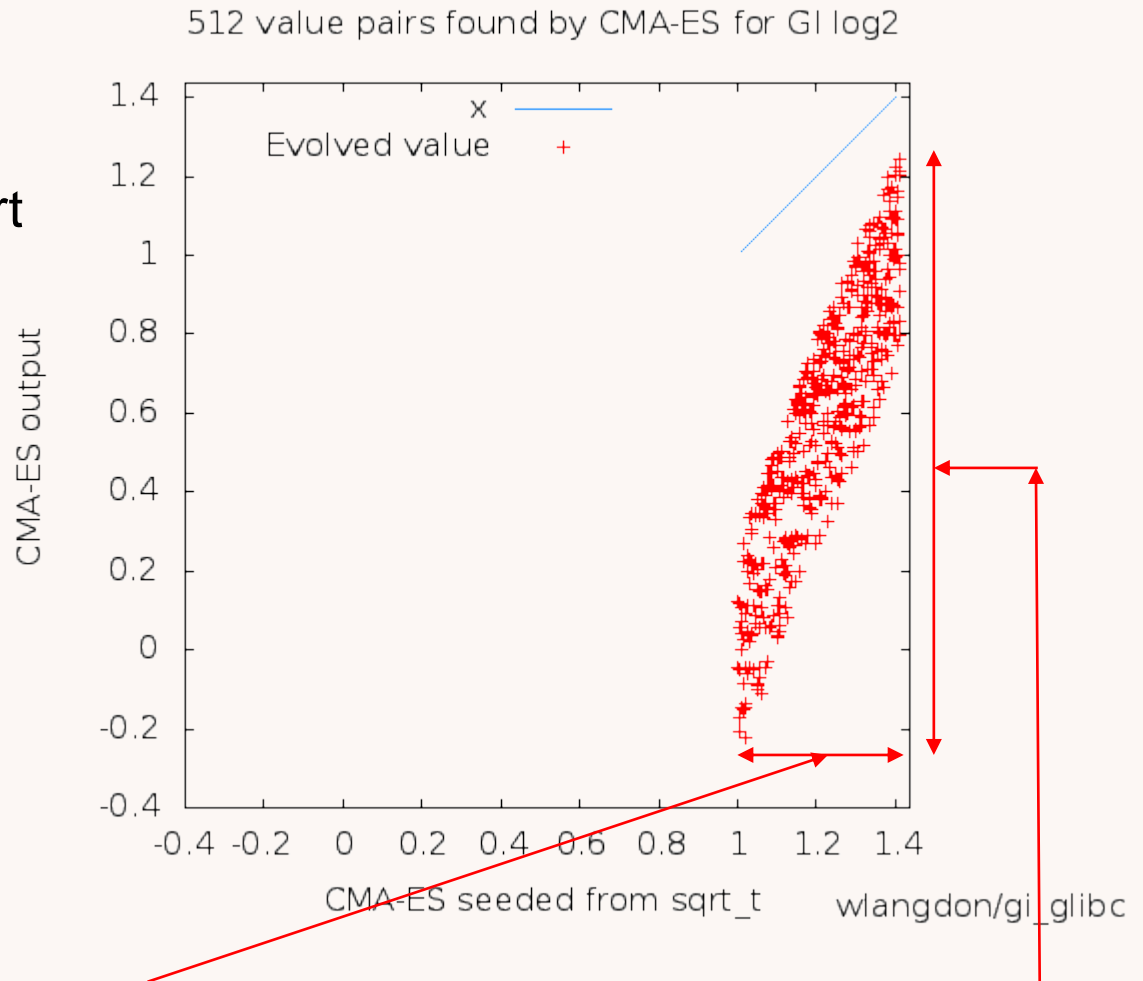
CMA-ES seeded with sqrt values

CMA-ES

evolutionary run
started with

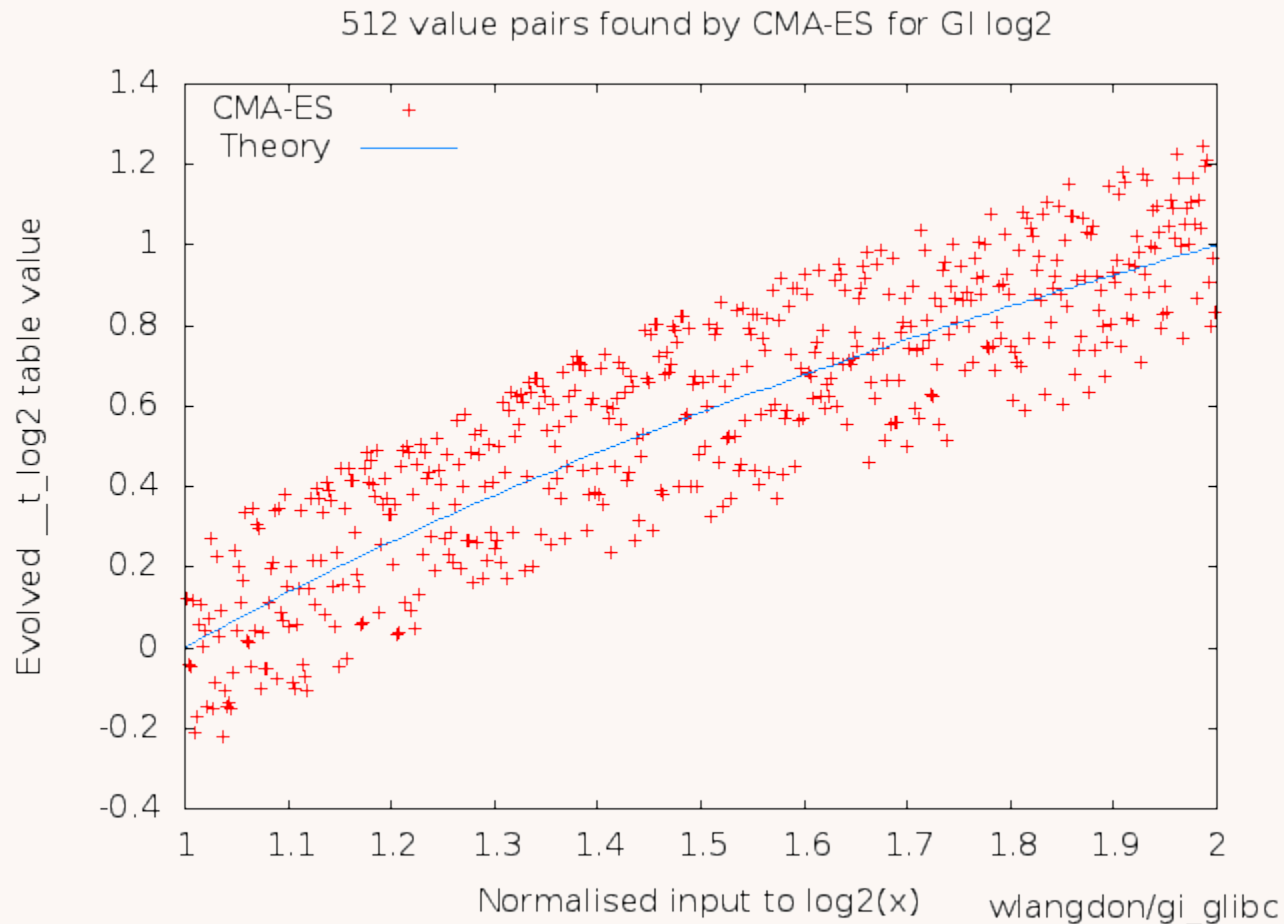
- value from sqrt
- mutation step size from variability of sqrt table

CMA-ES very
easy to solve



Initial seed values are close to \log_2 values

Evolved values for Newton-Raphson



Evolved value scattered about theory

Evolved \log_2

New table driven function tested many thousands of times:

- Same precision as GNU C `sqrt()`:
- Almost always exact
- Worst case last bit double precision $2.2 \cdot 10^{-16}$

Automatic Software Maintenance

- In a world addicted to software, maintenance is the dominant cost of computing.
- Need to keep parameters up to date. Eg:
 - New science (cf. RNAfold), new laws or regulations, new users, new user expectations
 - Change of load, new hardware (eg bigger RAM), automatic porting
 - Search can be fast: cbrt < 5 minutes, log2 6secs
- Little SBSE research
- Great scope for automation

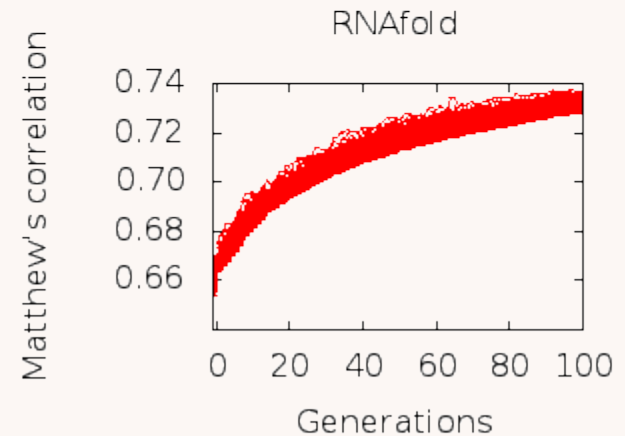
Six impossible things before breakfast



- To have impact do something considered impossible.
- If you believe software is fragile you will not only be wrong but shut out the possibility of mutating it into something better.
- Genetic Improvement has repeatedly shown mutation need not be disastrous and can lead to great things.

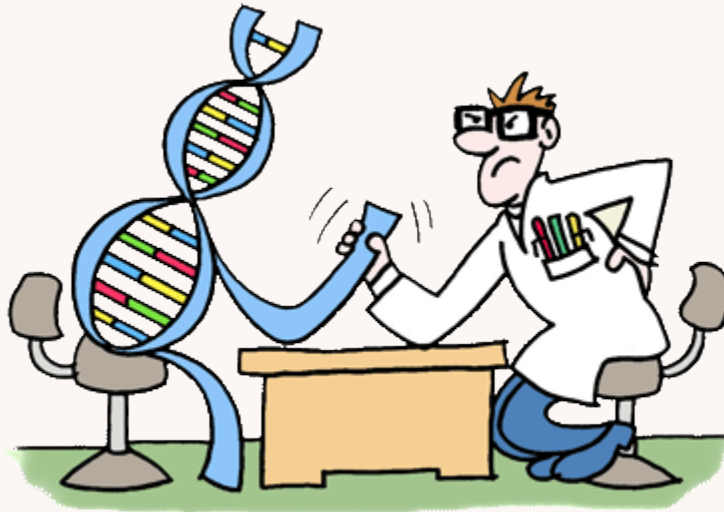
Summary

- Problem of maintaining data in code ignored
- SBSE to optimize data
 - suitable training data
 - treat code as a black box.
- RNAfold on real data
 - 50000 parameters 20% overall better prediction
 - AVX 45% speedup
- Rapidly generated new maths (cbirt, \log_2)
- Need research on Automatic Data Tuning
- **Software is not fragile**



GI 2019

GI 2019, Montreal, ICSE-2019 workshop.
Submission (2 or 8 pages) due 1st February 2019



Humies: Human-Competitive
Cash prizes
GECCO-2019

END OF DAASE



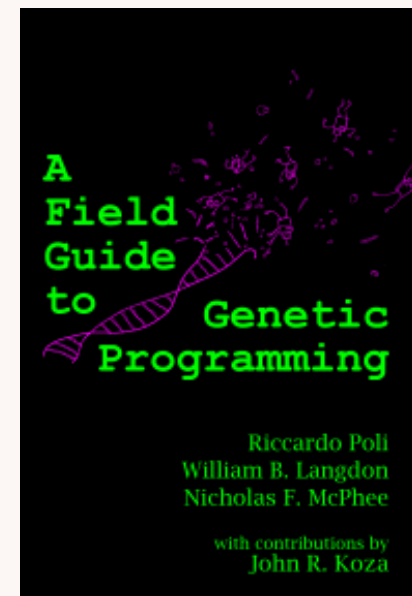
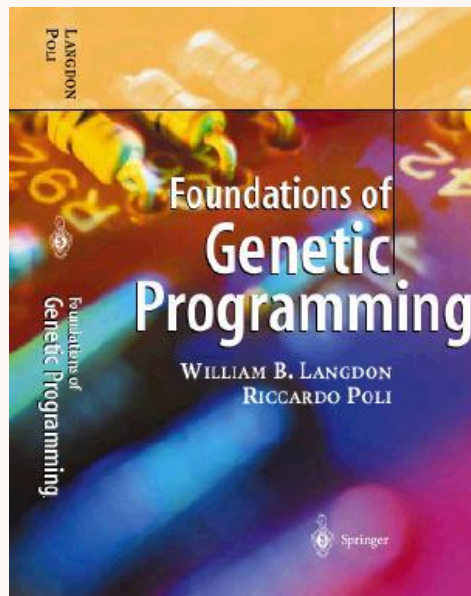
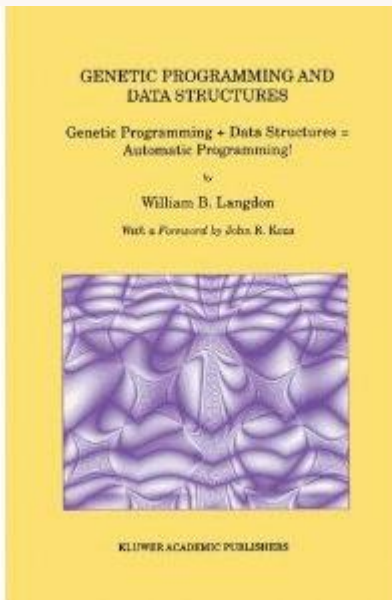
Genetic Improvement



W. B. Langdon

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Department of Computer Science



Improving RNAfold parameters

[EuroGP-2018](#)

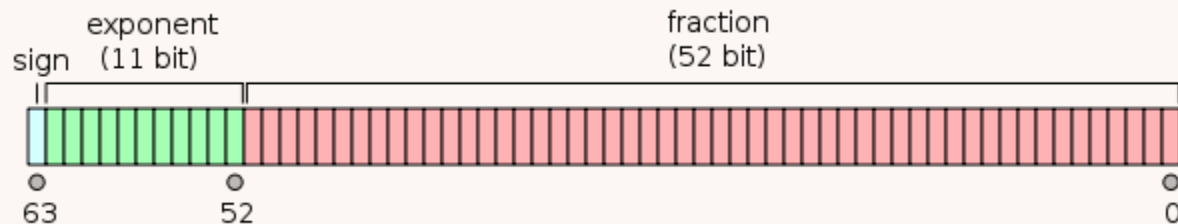
- RNAfold 7100 lines of C source code, 51521 parameters.
- Fitness correlation between prediction and true structure (MCC).
- Post evolution tidy
- 14732 (29%) parameters changed
- Holdout set significant increase in MCC
- Also better than constrained optimisation
- GI parameters [rna_langdon2018.par](#) shipped with ViennaRNA since 13 Jun 2018

Cube Root Code Changes I

- Most implementations of square root use hardware support.
- GNU C library glibc 2.27 also includes Newton-Raphson iterative solution
- Trap bad values, e.g. negative
- Normalise double input to 0.5 .. 2.0
- Guaranteed convergence in three steps:
 - Update both estimate of \sqrt{x} and derivative
- Apply square root to exponent, ie divide by 2

Cube Root Code Changes II

- Remove trap for negative values
- Normalise double precision input to 1.0..2
 - Update both estimate of cube root $x^{1/3}$ and its derivative $\frac{1}{3}x^{-2/3}$
- Apply cube root to exponent, ie divide by 3



Evolved \log_2

New table driven function tested many thousands of times:

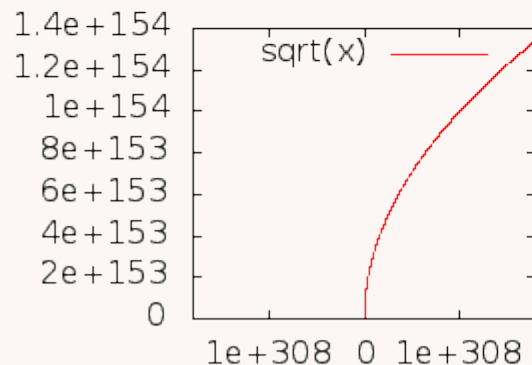
- Almost always exact (double precision).
- **GI log2** always (except on NaN) returned a double y such that GNU C library $\exp2(y)$ is exactly x
 - or y differs only in least significant bit from the closest value which could be inverted by $\exp2$ to yield x .
- Worst case last bit double precision $2.2 \cdot 10^{-16}$
- Same precision as GNU C $\text{sqrt}()$

Square root to binary log [RN/18/05](#)

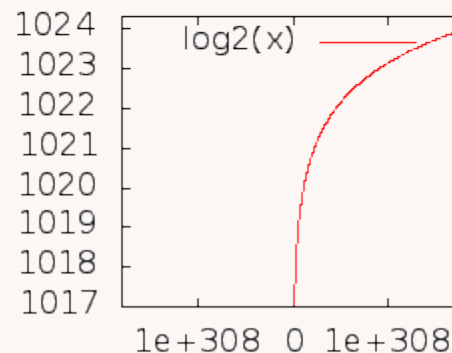
Frame work as sqrt to cbrt but

- Derivative known
- CMA-ES one dimension at a time (512 times)
very easy

C double precision square root function



C double precision binary logarithm function



RN/18/05

The Genetic Programming Bibliography

<http://www.cs.bham.ac.uk/~wbl/biblio/>

12653 references, [11000 authors](#)

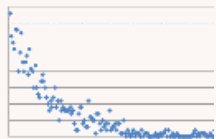
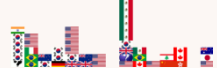
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