CIGPU 2010

Computational Intelligence on Consumer Games and Graphics Hardware

http://www.cs.ucl.ac.uk/external/W.Langdon/cigpu/

IEEE WCCI-2010 Special Session

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A Many Threaded CUDA Interpreter for Genetic Programming

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Introduction

- General Purpose use of GPU (GPGPU) and why we care
- Genetic Programming (GP).
- Running many programs on graphics hardware designed for a single program operating on many data in parallel (SIMD).
- Simultaneously running ¼ million programs
- Actual speed 215 billion GP ops /second
- Lessons

Why Interest in Graphics Cards

- Speed
  - 800 0.8Ghz CPUs
  - Even with multi-threading off-chip memory bottleneck means difficult to keep CPUs busy
- Future speed
  - Faster than Moore’s law
  - nVidia and AMD/ATI claim doubling 12months

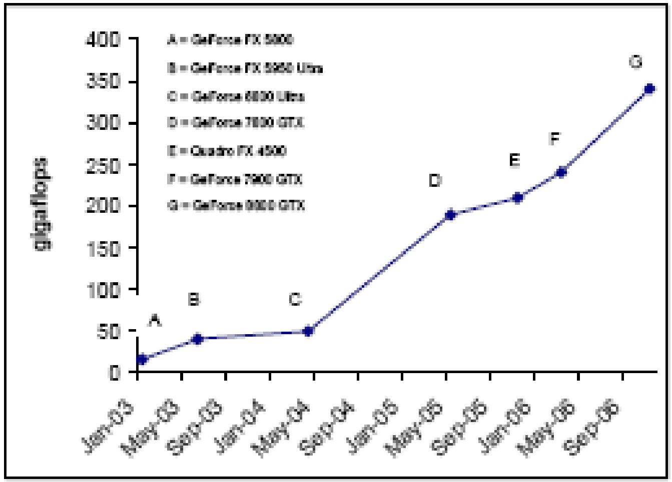
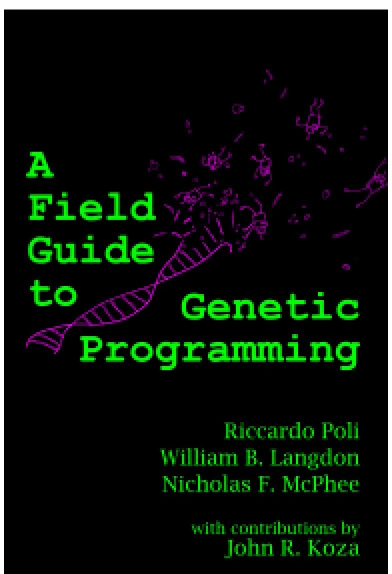


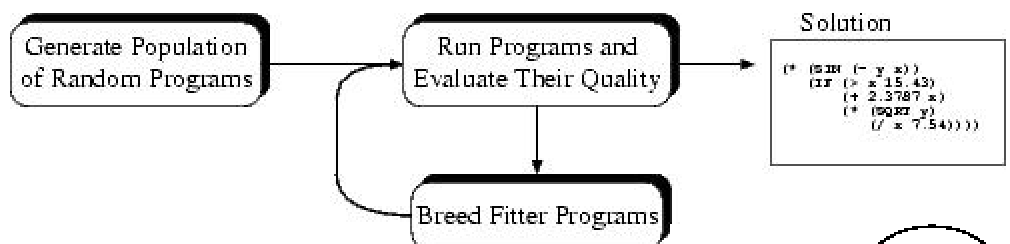
Figure 1-2. Floating-Point Operations/Second on the GPU

NVIDIA Tesla: GPU Compute Tech Brief, Version 1.0.0

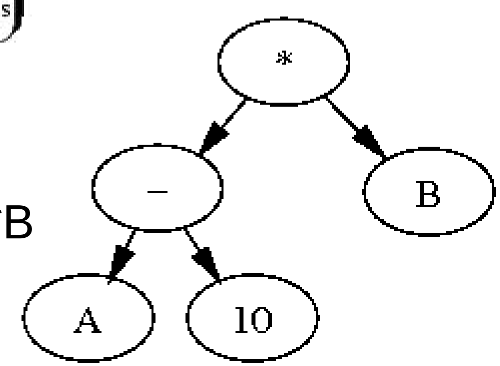
Genetic Programming

- A population of randomly created programs
  - whose fitness is determined by running them
  - Better programs are selected to be parents
  - New generation of programs are created by randomly combining above average parents or by mutation.
  - Repeat generations until solution found.





Tree (A-10)*B



General Purpose GPU Software Options

Most software aimed at graphics. Interest in using them (and CELL processors, XBox, PS3, game consoles) for general purpose computing.

- Microsoft Research windows/DirectX [2007]
- BrookGPU stanford.edu
- GPU specific assemblers
- nVidia CUDA [EuroGP 2008]
- nVidia Cg [GECCO 2007]
- PeakStream
- Sh no longer active. Replaced by RapidMind [EuroGP 2008]
- OpenCL

Missing, Future GPGPU

- Untimely death of tools.
  - Tools no longer supported
  - Tools superceeded or become more commercial
  - Hardware rapid turn over
- The “other” GPU manufacturer AMD/ATI
- OpenCL
- Complete GP on GPU (small gain?)
- Applications with fitness evaluation on GPU
- Improved debug and performance monitoring

nVidia G80 Hardware

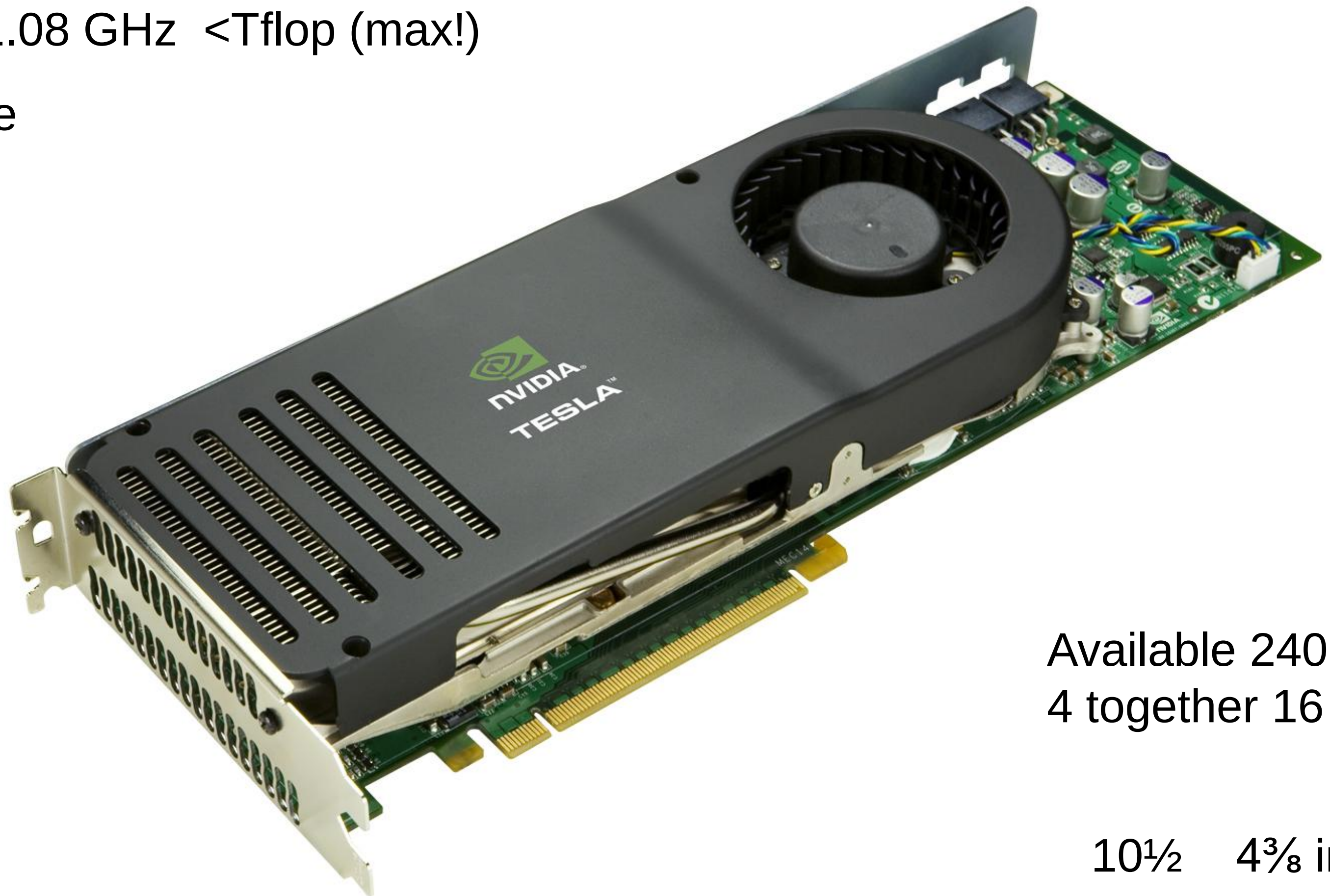
- Connection to host PC computer
- Memory heirarchy
  - On chip: Registers, shared, constants
  - Off chip: Global and “local”
- Scheduling threads
- How many threads?

early nVidia t10p Tesla

192 Stream Processors

Clock 1.08 GHz <Tflop (max!)

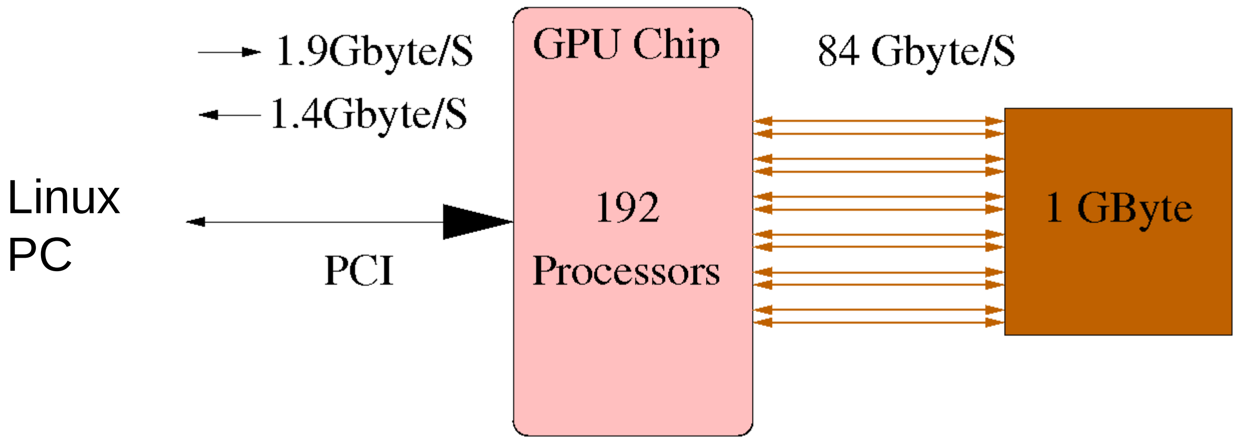
1 GByte



Available 240 1.5GHz
4 together 16 GBytes

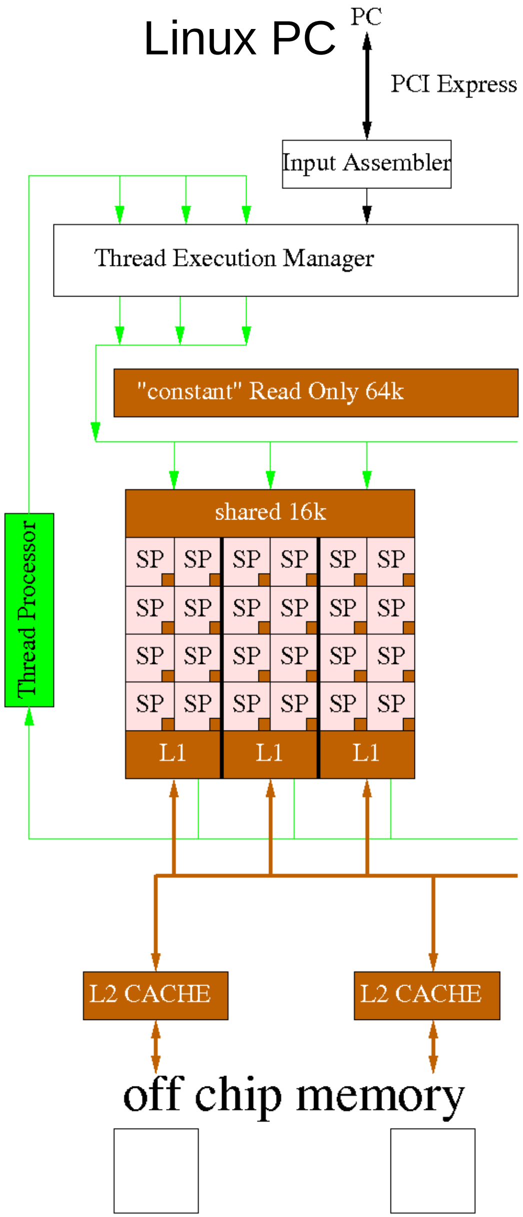
10½   4⅜ inches

Tesla chip connections



Memory, GPU chip, etc. All on one card

CUDA data memory heirarchy



Each stream processor has its own registers

24 SP share 16k. Read/write contention delays threads.

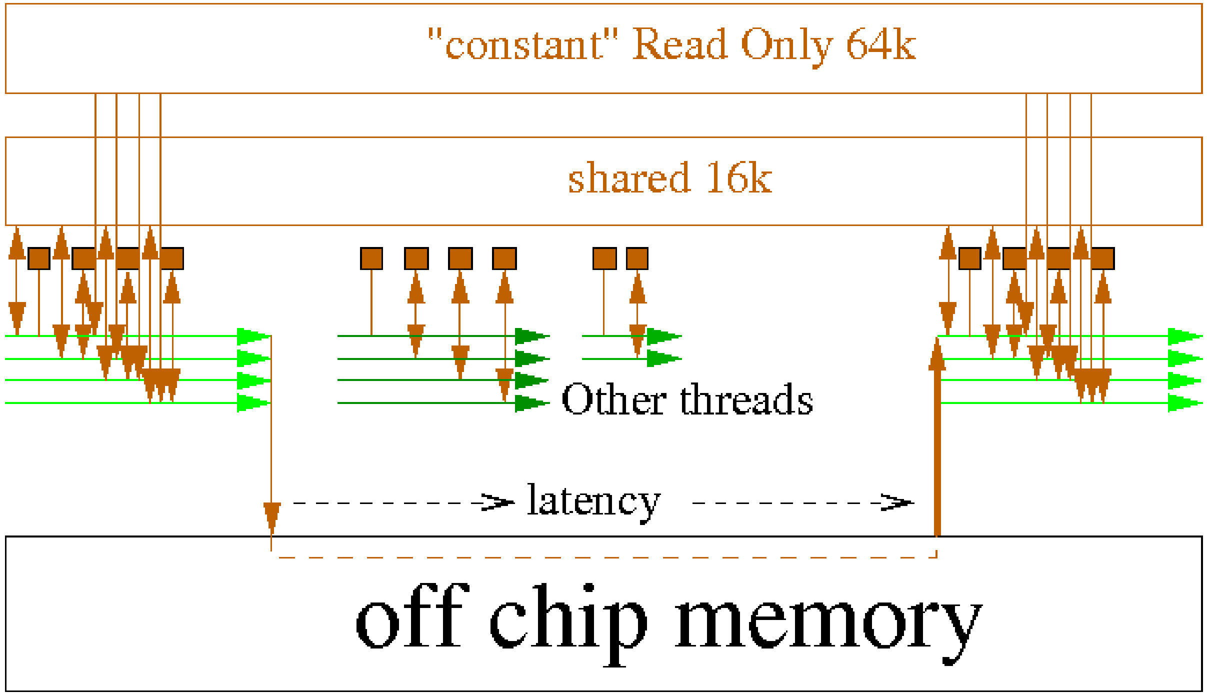
64k can be read by all 8 (10) blocks of SP without contention delays.

Both CUDA "local" and "global" variables are off chip. Latency hundred times more than on chip. Must have thousands of threads to keep SP busy.

Programmer responsible for dividing memory between threads and syncronisation.

Role of caches unclear.

Mega Threading



Each block of 24 stream processors runs up to 24 threads of the same program.

Each thread executes the same instruction.

When program branches, some threads advance and others are held. Later the other branches are run to catch up.

If thread is blocked waiting for off chip memory another set of threads can be started.

New threads could be from another program.

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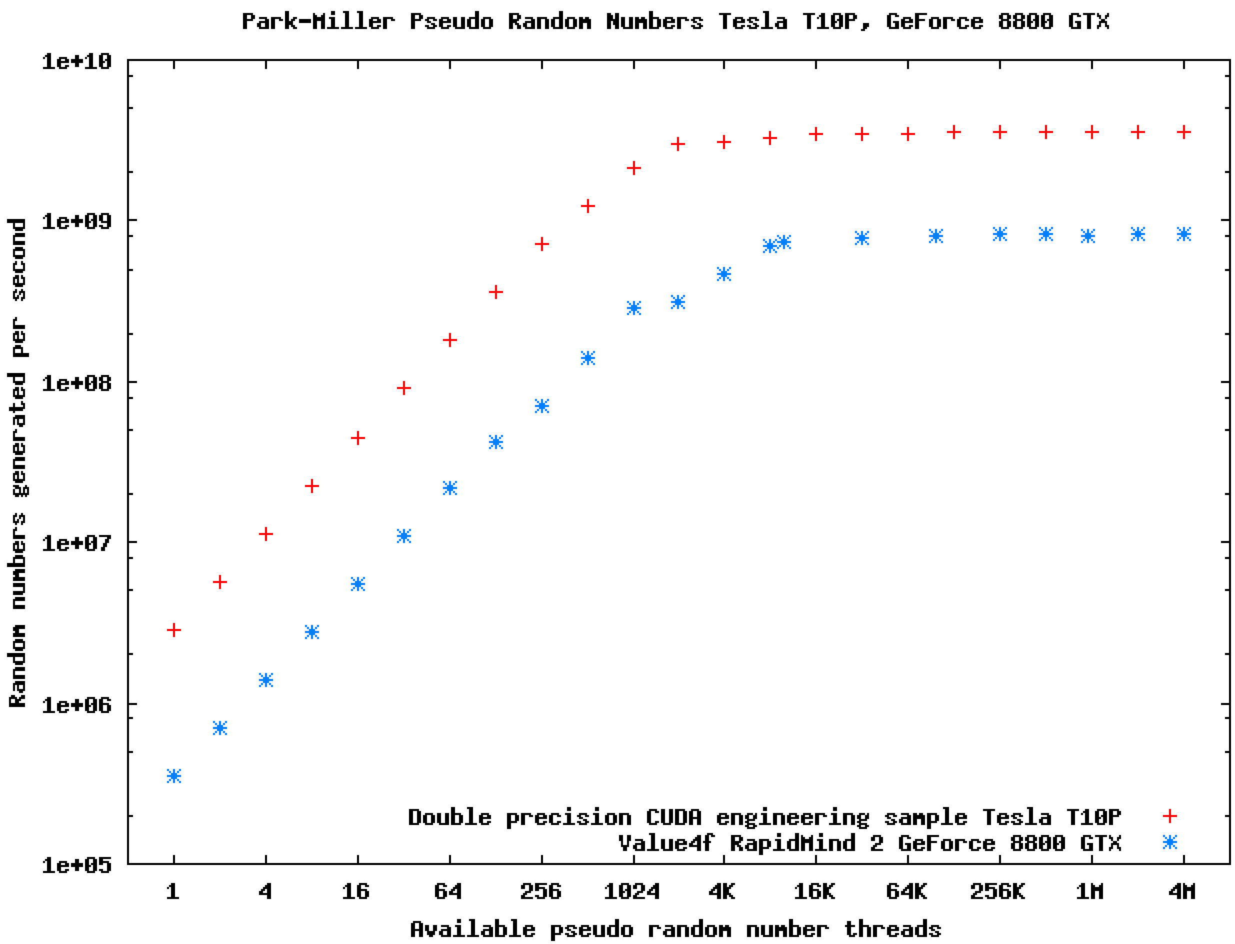
Performance v threads

Speed
(log scale)



Threads (log scale)

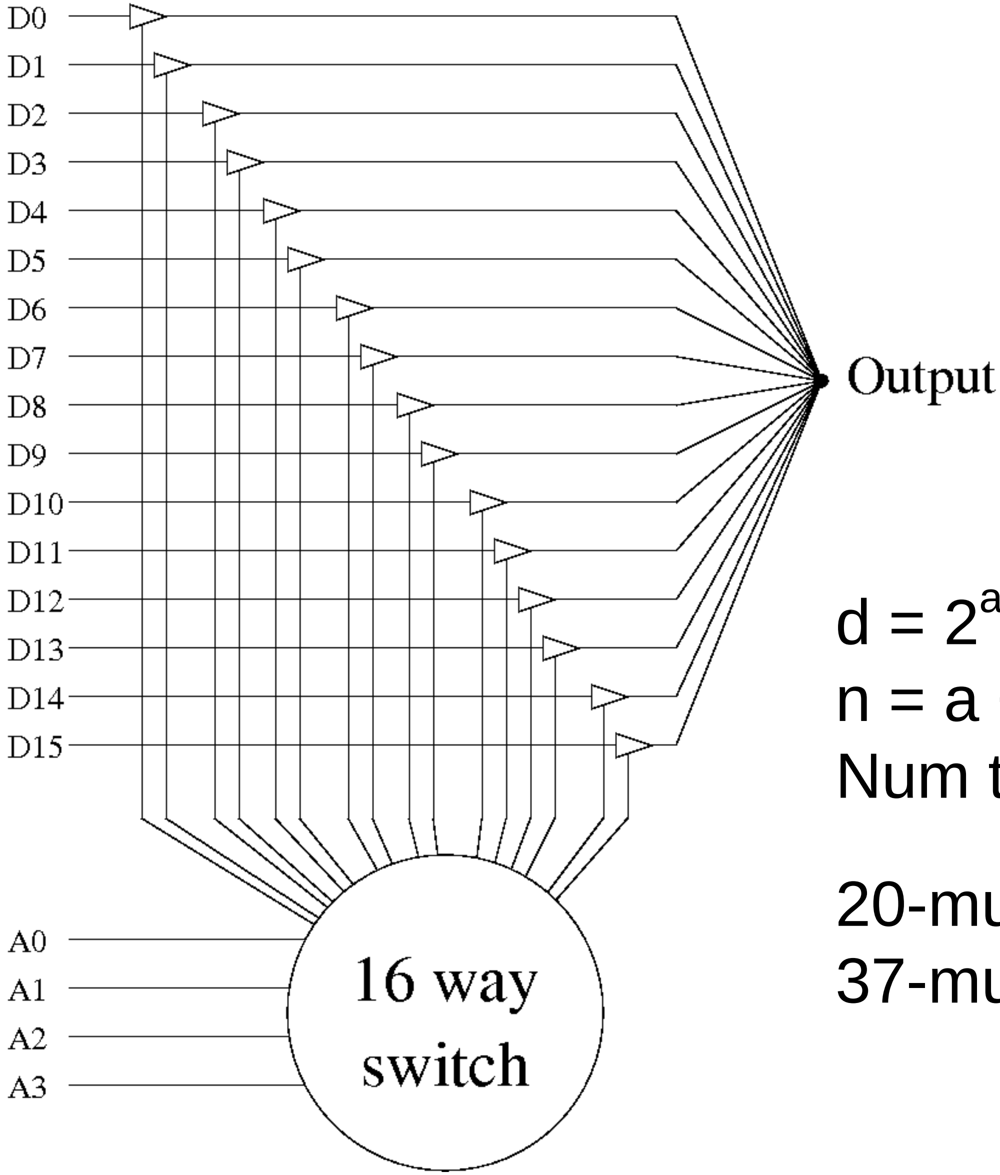
Performance v threads 2

- Graph emphasises the importance of using many threads (minimum 4000).
- When a thread stalls because of waiting for off chip memory another thread is automatically scheduled if ready. Thus access to GPU's main memory bottle neck can be over come.
- At least 20 threads per stream processor
  - 57 10^9 GP op/sec with 12 threads per SP
  - 88 10^9 GP op/sec with 15 threads per SP

Experiments

- Interprets 121 billion GP primitives per second (215 sustained peak)
- How?
  – each integer contains 32 Booleans
  – randomised test case selection
  – simple CUDA reverse polish interpreter
- 20 mux solved
- 37 mux solved. 137 billion test cases

Boolean Multiplexor



$d = 2^a$

$n = a + d$

Num test cases = 2^n

20-mux 1 million test cases

37-mux 137 10^9 tests

Submachine Code GP

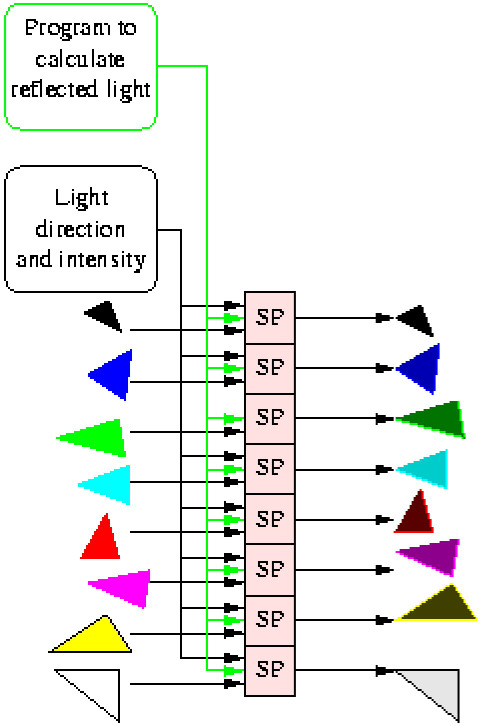
- int contains 32 bits. Treat each as Boolean.
- 32 Boolean (and or, nor, if, not etc) done simultaneously.
- Load 32 test cases
  - $D0 = 01010101\ldots$
  - $D1 = 00110011\ldots$
  - $D_N = 00000000\ldots$ or $11111111\ldots$
- Check 32 answers simultaneously
- CPU speed up 24 fold (32) 60 fold (64 bits)

Randomised Samples

- 20-mux 2048 of 1 million (2 10^{-6})
- 37-mux 8192 of 137 billion (6 10^{-9})
- Same tests for all four programs in each selection tournament
- New tests for new generation and each tournament
- (Statistical significance test not needed)

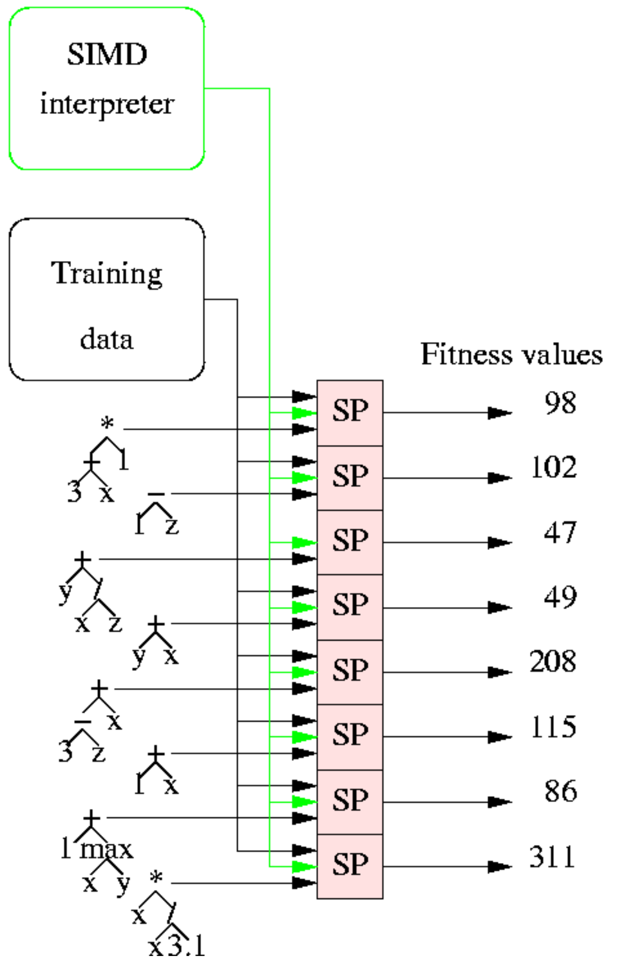
Single Instruction Multiple Data

- GPU designed for graphics
- Same operation done on many objects
  - Eg appearance of many triangles, different shapes, orientations, distances, surfaces
  - One program, many data → Simple (fast) parallel data streams
- How to run many programs on SIMD computer?



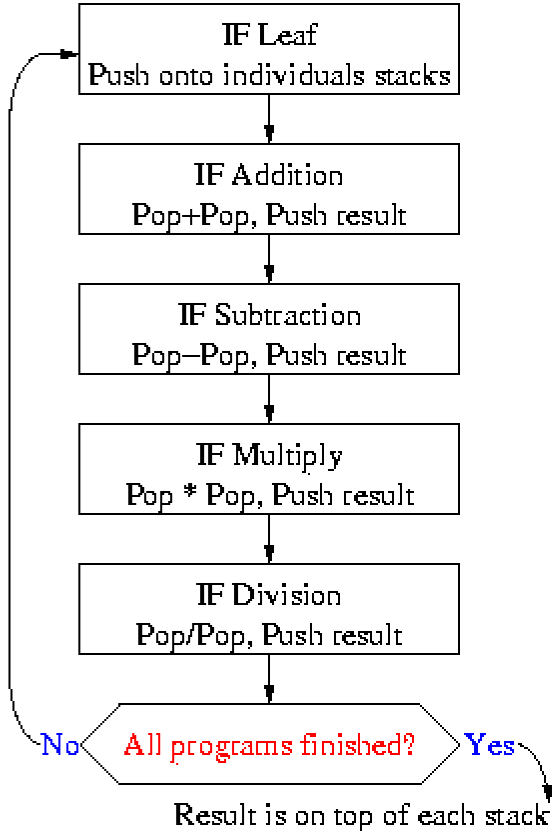
Interpreting many programs simultaneously

- Can compile GP for GPU on host PC. Then run one program on multiple data (training cases).
- Avoid compilation by interpreting tree
- Run single SIMD interpreter on GPU on many trees.
- Better interpret a few trees many test cases



GPU Genetic Programming Interpreter

- Programs wait for the interpreter to offer an instruction they need evaluating.
- For example an addition.
  - When the interpreter wants to do an addition, everyone in the whole population who is waiting for addition is evaluated.
  - The operation is ignored by everyone else.
  - They then individually wait for their next instruction.
- The interpreter moves on to its next operation.
- The interpreter runs round its loop until the whole population has been interpreted.



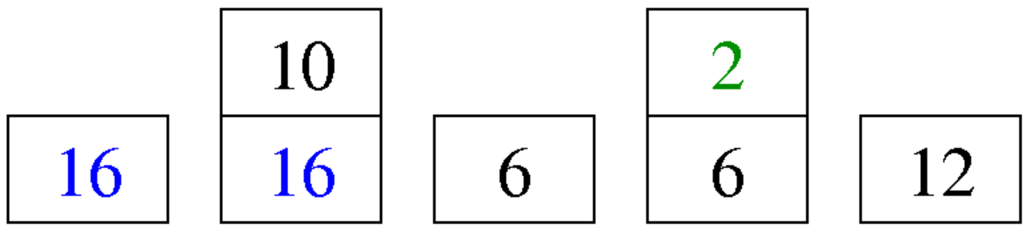
Representing the Population

- Data is pushed onto stack before operations pop them (i.e. reverse polish. x+y $\rightarrow$ $\boxed{x \mid y \mid +}$)
- The tree is stored as linear expression in reverse polish.
- Same structure on host as GPU.
  - Avoid explicit format conversion when population is loaded onto GPU.
- Genetic operations act on reverse polish:
  - random tree generation (eg ramped-half-and-half)
  - subtree crossover
  - 2 types of mutation
- Requires only one byte per leaf or function.
  - So large populations (millions of individuals) are possible.

Reverse Polish Interpreter

$(A-10)*B \quad A=16 \quad B=2$

$A \; 10 \; - \; B \; *$



$(A-10) \; B \; \equiv \; A \; 10 \; - \; B$

Variable: push onto stack

Function pop arguments, do operation, push result

1 stack per program. All stacks in shared memory.

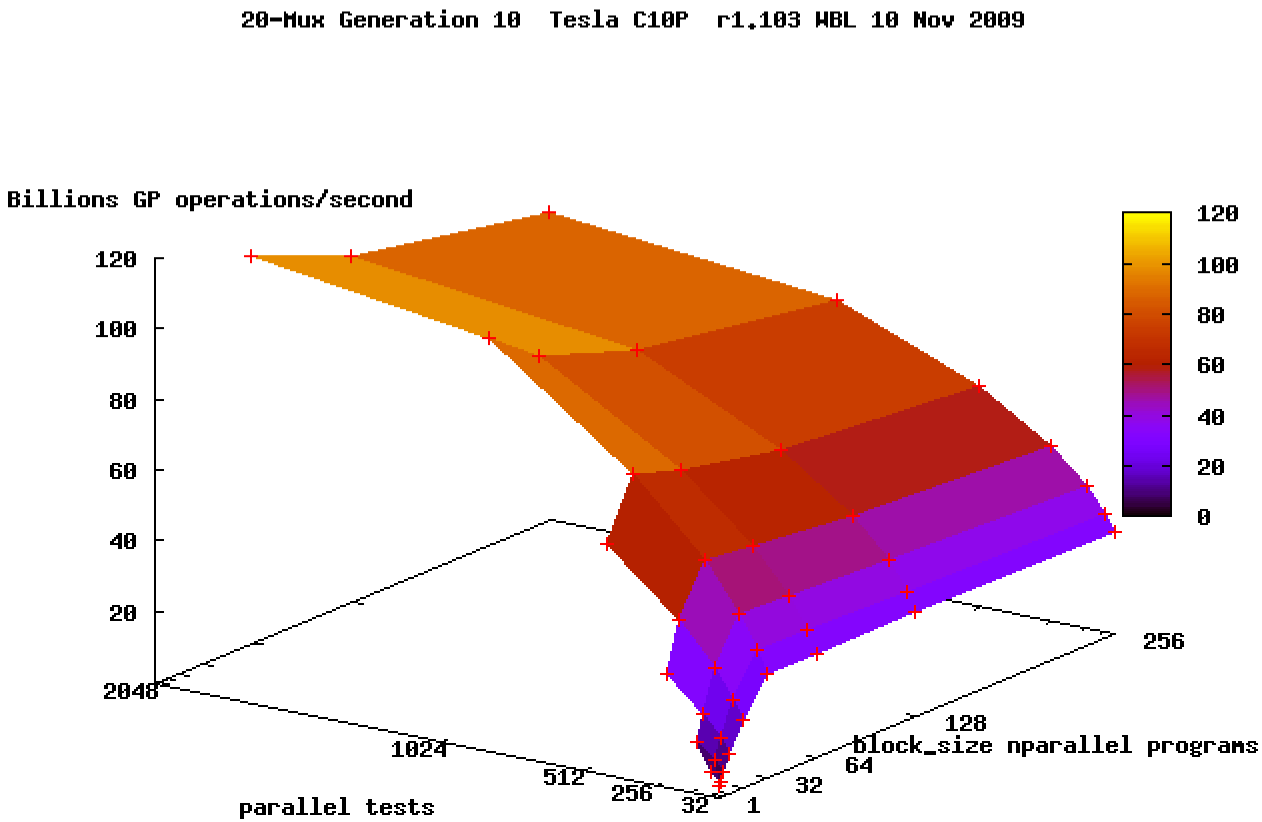
RPN interpreter

```
int SP = 0;
for(unsigned int PC = 0;; PC++){
  Read opcode from global/constant
  if(opcode==OPNOP) break;
  if(type==leaf) push(trainingdata);  // 32 bits
  else { //function
    const unsigned int sp1 = stack(SP-1);
    const unsigned int sp2 = stack(SP-2);
    SP -= 2;
    switch(opcode) {
      case OPAND:   push( AND(sp1,sp2)); break;
      case OPOR:    push(  OR(sp1,sp2)); break;
      case OPNAND: push(~AND(sp1,sp2)); break;
      case OPNOR:  push( ~OR(sp1,sp2)); break;
}}}
```

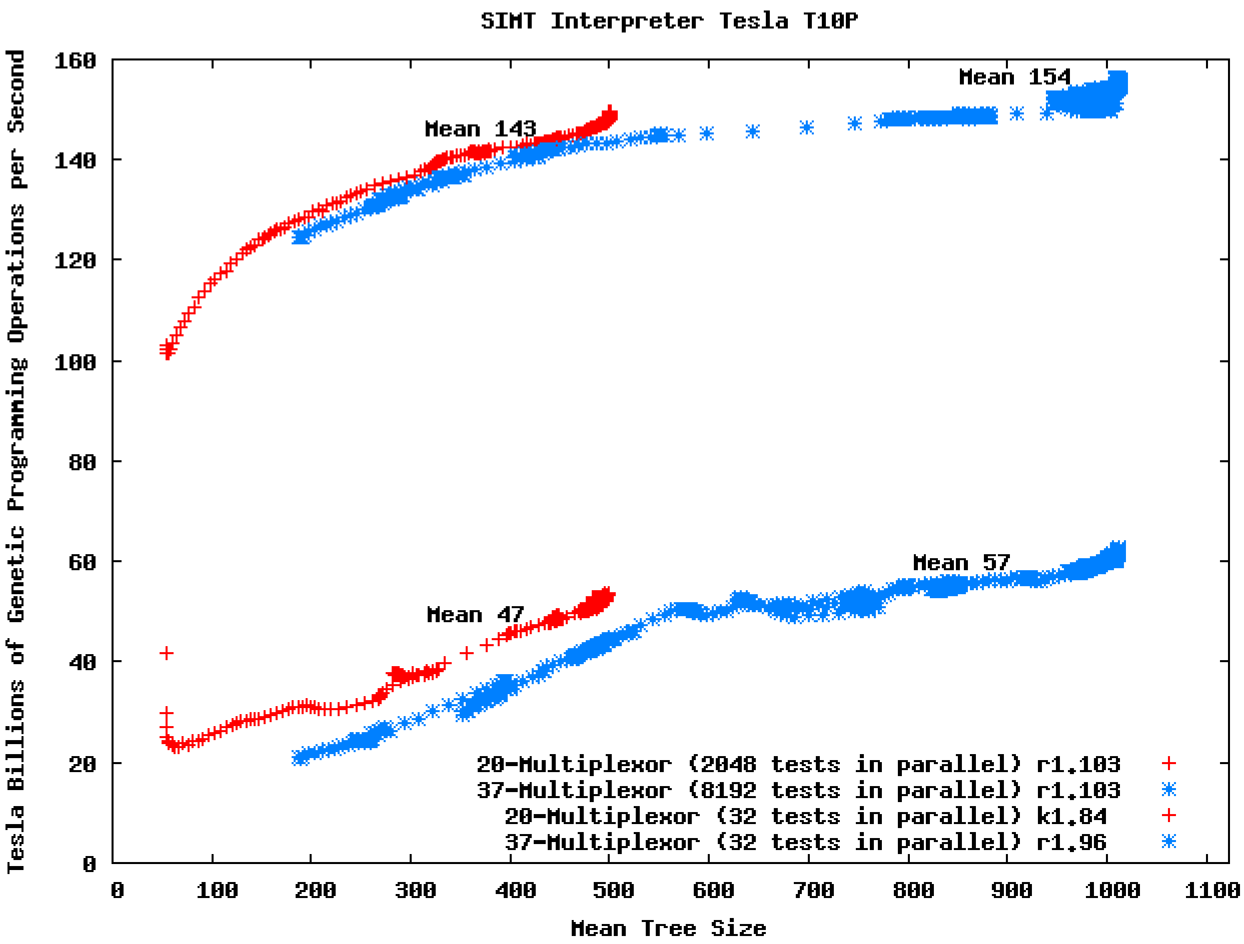
Validation

- Solutions run on all test cases in GPU.
- Evolved 20-mux and 37-mux expressions converted to C code, compiled and run against all tests

Performance v Test v Threads



Performance v RPN size



Performance

- nVidia early engineering sample (192 SP)
- 121 10^9 GP operations/second (peak 215)
- In validation step get big improvement (160 10^9 $\rightarrow$ 215 10^9 GPops) by using "constant" memory
- 100 times [CIGPU 2008]
  - hardware similar nVidia GeForce 8800 GTX (128 SP)

Lessons

- Computation is cheap. Data is expensive.
- Suggest interpreting GP trees on the GPU is dominated by leafs:
  - since there are lots of them and typically they require data transfers across the GPU.
  - adding more functions will slow interpreter less than might have been expected.
- To get the best of the GPU it needs to be given large chunks of work to do:
  - Aim for at least one second
  - GeForce: more than 10 seconds and Linux dies
    - Solved by not using GPU as main video interface??
  - Less than 1millisec Linux task switching dominates
- Poor debug, performance tools

Discussion

- Interpreter faster than compiled GP
  - However using modest number of test cases (8192)
- 32/64-bit suitable for Boolean problems. Also used in regression problems (8 bit resolution), graphics and optical character recognition (OCR)
- Speed up due to 32bits and CUDA
- Main bottle neck is access to GPU's main memory. But GP pop allows many threads.
- No on-chip local arrays; stack in shared memory
  - Limits number of threads to 256.

Conclusions

- GPU offers huge power on your desk
- Interpreted genetic programming (GP) can effectively use graphics cards and Tesla
- 121 billion GP operations per second (0.8 at CIGPU-2008)
- Tesla first to solve two GP benchmarks
  - 20 mux solved (<1 hour v. >4 years)
  - 37 mux solved. 137 billion test cases. <1day

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END

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- Code via ftp
  - http://www.cs.ucl.ac.uk/staff/W.Langdon/ftp/gp-code/gp32cuda.tar.gz
  - gpu_gp_2.tar.gz wbl_gecco2004lb_protein.tar.gz gpu_park-miller.tar.gz
- Movies of evolving populations
  - Evolving π

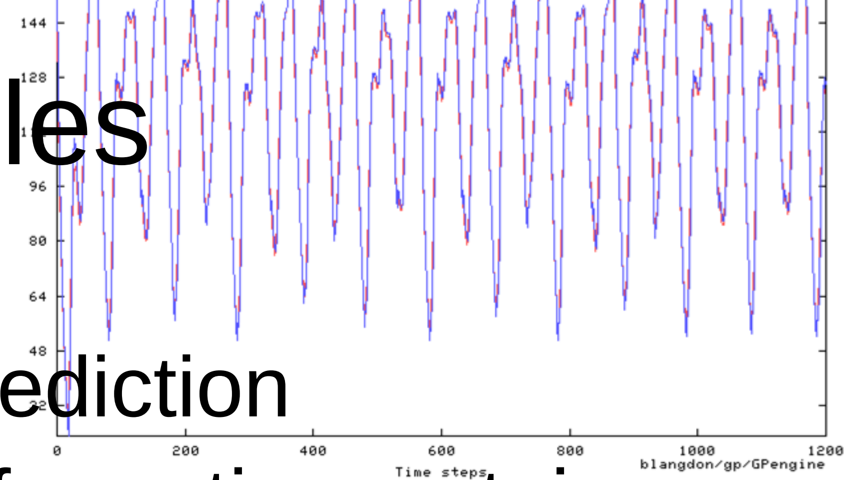
    http://www.cs.ucl.ac.uk/staff/W.Langdon/pi_movie.gif
    http://www.cs.ucl.ac.uk/staff/W.Langdon/pi2_movie.html
  - Evolving Protein Prediction Pop=Million 1000gens http://www.cs.mun.ca/~blangdon/gpu_gp_slides/nuclear.gif
- gpgpu.org GPgpgpu.com nvidia.com/cuda

Speed of GPU interpreter GeForce 8800 GTX.

Experiment	Number of Terminals	|F|	Population	Program size	Stack depth	Test cases	Speed (million OPs/sec)
Mackey-Glass	8+128	4	204 800	11.0	4	1200	895
Mackey-Glass	8+128	4	204 800	13.0	4	1200	1056
Protein	20+128	4	1 048 576	56.9	8	200	504
$Laser_a$	3+128	4	18 225	55.4	8	151 360	656
$Laser_b$	9+128	4	5 000	49.6	8	376 640	190
Cancer	1 013 888+1001	4	5 242 880	≤15.0	4	128	535
GeneChip	47+1001	6	16 384	≤ 63.0	8	⅓M, sample 200	314

CUDA 2.8 billion Compiled on 16 mac 4.2 billion (100 10^6 data points)
[2009] 3.8 billion

Examples



- Approximating Pi
- Chaotic Time Series Prediction
- Mega population. Bioinformatics protein classification
    - Is protein nuclear based on num of 20 amino acids
- Predicting Breast Cancer fatalities
    - HG-U133A/B probes →10year outcome
- Predicting problems with DNA GeneChips
    - HG-U133A correlation between probes in probesets →MM, A/G ratio and A C