Life

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1 Introduction

This report aims to describe a parallel functional implementation for Conway's Game of Life. Conway's Game of Life is a well known cellular automata. Conway's Game of Life is the name of the algorithm which describes the state transitions of a 2D (often toroidal) grid of bits which represent cells which are either Alive or Dead. By the rules of Conway's Game of Life, the next state of each cell on the grid can be derived as a function of the prior state of the cell in question as well as the prior state of every cell adjacent to it (eight total). From Wikipedia:

- 1. Any live cell with fewer than two live neighbours dies, as if by underpopulation.
- 2. Any live cell with two or three live neighbours lives on to the next generation.
- 3. Any live cell with more than three live neighbours dies, as if by overpopulation.
- 4. Any dead cell with exactly three live neighbours becomes a live cell, as if by reproduction

2 Rationale

As seen above, given a grid of cells, the next state of a cell can be found as a function of 9 datapoints, the prior state of the given cell, and the prior state of its 8 adjacent cells. Because of this, this problem is inherently quite parallel and predisposes itself to a parallel solution. The problem also gives us a couple input parameters to play with:

- 1. Starting State
 - Although many configurations have been studied and there are shapes which have been studied extensively and named in the Game of Life community, for this Haskell approach, the input does not actually

matter from a performance standpoint at a high level. Aside from any optimization or caching going on, calculating the N^{th} step of an $X \times Y$ grid will take the same amount of function calls regardless of the original state of that grid.

- 2. Grid Dimension
 - The size of the input grid can be selected such that the overall runtime of the program is fast enough as to be reproducible without a large wait but slow enough to allow any speedup during parallelization to be easily noticeable.
- 3. Steps
 - The amount of steps to simulate can be increased if needed to balance the relative time of reading the input and dumping the output with the time of "actual" computation.

3 Algorithm

3.1 Overview

There exists an algorithm proposed in the 1980's called Hashlife which utilizes a hash-based memoization approach to more quickly be able to compute the future state of the grid at the cost of larger memory usage. For this report, I will focus on the straight-forward brute-force approach which calculates the state of a cell at a given step as a recursive tree of calls to the states of that cell and its adjacent ones.

3.2 Haskell Approach

For the Haskell approach to this, I adapted the approach discussed in this blog. As an input, it takes in a file describing the initial grid state where each character represents a cell with an \times being a live cell and a \cdot being a dead cell.

The parameters are listed as toplevel constants within the Main.hs file:

```
wIDTH :: Integer
wIDTH = 1000
hEIGHT :: Integer
hEIGHT = 1000
sTEP :: Integer
sTEP = 1
```

The grid is represented with the following data structure:

```
— | A point in the grid
type Point = (Integer, Integer)
— | The status of a cell
data Cell = Alive | Dead deriving Eq
— | Description of a grid
type Grid = Point -> Cell
```

The initial grid is parsed from an input file specified via the command line with the following code:

```
parseInitialGrid :: B.ByteString -> Grid
parseInitialGrid s = go
 where
    ls = B. split ' n' s
    maxY = fromInteger wIDTH
    maxX = fromInteger hEIGHT
    go (fromInteger \rightarrow y, fromInteger \rightarrow x)
      | x < 0
                                         = Dead
       y < 0
                                         = Dead
       x \ge maxX
                                         = Dead
        y >= maxY
                                         = Dead
        y \ge (B.length (ls !! x) - 1) = Dead
        B. index (ls !! x) y == '.' = Dead
        otherwise
                                        = Alive
```

The next-step value of a cell is calculate as a function of the old state of the cell and its eight adjacent cell states with the following code:

```
nextStep :: Cell -> [Cell] -> Cell
nextStep Alive adj
| count Alive adj < 2 = Dead --- underpopulation
| count Alive adj > 3 = Dead --- overpopulation
| otherwise = Alive --- Alive and let Alive
nextStep Dead adj
| count Alive adj == 3 = Alive --- reproduction
| otherwise = Dead --- nothing happens
```

The adjacent cells of a given cell are discovered via a kernel approach with the following code:

The count function referenced in the listing of nextStep above contains the following code:

count :: Eq a \Rightarrow a \rightarrow [a] \rightarrow Int count x = length . filter (== x)

The final bit of the algorithm setup is the gameOfLife function:

Note that this approach could be sped up by using memoization from Data.MemoTrie and memo2 or memoFix but the approach above was used for this report as it more obviously predisposed itself to the parallel approach.

3.3 Sequential Approach

For the sequential approach, the main function looks as follows:

```
main :: IO ()
main = do
  [file] <- getArgs
  initialGrid <- parseInitialGrid <$> B.readFile file
  printSetup sTEP wIDTH hEIGHT
  putStrLn "finished parsing"
  let f = gameOfLife initialGrid
     calcCellAndShow point = showCell' (f sTEP point)
     calcRow row = map calcCellAndShow [(y, row) | y <- [0..(wIDTH-1)]]
  mapM_ putStrLn [calcRow x | x <- [0..(hEIGHT-1)]]
  putStrLn "done"
  printSetup sTEP wIDTH hEIGHT</pre>
```

3.4 Parallel Approach

For the parallel approach, an extremely similar approach can be used, swapping from map to parMap from the Control.Monad:

```
calcRow row = runPar
(parMap calcCellAndShow [(y, row) | y <- [0..(wIDTH-1)]])
```

4 Input

4.1 Tuning Parameters

The selection of the parameters discussed above was manipulated until a reasonably tuned selection was made. The input dimensions of 1000×1000 gave a runtime of 10 to 15 seconds. Some experimentation was done with the step of the generation but it made for more complex parallelization as with each additional step, a whole new radius of adjacency is required for each cell calculation.

4.2 inputgen

As discussed above, the input itself does not considerably change the run-time as long as it is run to the same **step** and has the same initial grid dimensions. To test this, a variety of input files were generated using the following python script and 10 of them are included with the file listings:

import random

width = 1000 height = 1000 out = [] for x in range(height): out.append(''.join([random.choice(['X', '.']) for _ in range(width)]))

print('\n'.join(out))

4.3 Actual Input

Because the input does not change the runtime considerably, an input which allowed for easy visual verification of correctness of the output was selected. This was a 20×10 grid which was repeated as many times as necessary across the selected input dimensions. This grid contained two simple "blinkers" which oscillate on a two-step cycle, a slightly more complicated two-step "blinker", two stationary "blocks", and a LWSS (light weight space ship) which was oriented so as to leave the grid within a couple cycles. This input and the next three steps of it's life are shown below

.xxx	XXX	.xxx	xxx
.xxxxxx	XXXXX	.xxxxxx	XXXXX
.xxx	·····xx.	.xxx	xx
XX	xx.	ХХ	XX
	· · · · · · · · · · · · · · · · · · ·		
XX	XX	XX	XX
xxxx	<u>xx</u>	XX	.xxxx
.х	.xx	XXXX	XXXXX
.xxxx	XX.XXXX	xxxx	x.xxxx
. XXXXX	.xxxxx	xxx	xxxx

5 Results

5.1 IO Time

By running with sTEP=0, I found that the input-output time is around 1-1.5 seconds as opposed to the 10-12 second runtime of the N1 algorithm for sTEP=1. On my machine with an AMD Ryzen 5 3600X processor with 6 cores and 12 logical cores. Below are the -s results and threadscope results for various N values.

5.2 N1



5.3 N2



5.4 N4



5.5 N8



/Main (8).eventlog (203526 events, 2.355s)

5.6 N12



(12), even a sig (13) 20 + even as, 2.11 (3)

5.7 N16



5.8 Speedup

Below is a graph of the speedup as a percentage of ideal speedup using the timings reported in the N_{-} sections above. The x axis is the number of cores and the y access is the runtime relative to the N1 runtime.



6 Conclusion

From the results above we can see that speedup is achieved at lower core counts but falls off with higher core counts. We can see from the threadscope results that thread utilization is quite high but there is more and more gaps (possibly due to GC) at the higher thread counts. This is likely due to the amount of duplicated calls between the threads due to the **adjacents** call in the logic. This could be made faster through better slicing of the input and memoization. The largest drawback of the approach is the original data representation adapted from the blog mentioned originally as well as the initial grid parsing which it employs. It makes for large inefficiency and unnecessary random access over the data. By employing a structure which could more easily be traversed and zipped over without the unnecessary access the original algorithm could be made much faster. Re-evaluating the data organization as well as the **parseInitialGrid** could help to achieve this goal.