

# 10. The End

#### Ken Rice Tim Thornton

University of Washington

Seattle, July 2013

## In this session

- Notes on the Special Exercise
- What next?

Cells live on a grid, they can be alive (1) or dead (0). At each generation they have a number of live neighbors. Cells live, die, and become alive according to these rules;

If alive==1 and #neighbors <2, alive <- 0 If alive==1 and #neighbors ==2 or 3, alive <- 1 If alive==1 and #neighbors >3, alive <- 0 If alive==0 and #neighbors ==3, alive <- 1

- other dead cells stay dead.

This is a simple evolutionary model – the simplest Conway could devise that does anything useful. Much of what he learned/proved about it was based on computer simulations, like ours.

An example update;

10.3

An example update;

1	1	2	2	3	2	1
1	0	3	2	3	1	1
2	2	4	3	6	4	2
2	1	3	3	3	2	1
3	3	4	3	3	4	2
2	2	2	2	2	1	1
1	2	2	1	1	1	1

An example update;

# Game of Life: What do we need?

Objects;

- A matrix of cells, each 1 or 0
- A matrix containing # neighbours each cell has
- Another matrix of cells, each 1 or 0 containing the updated values

Code to do the following jobs;

- Count number of neighbors for cells
- Updating the alive/dead status
- Plot the current status, for all cells

First option for neighbors; count based on what's visible.



First option for neighbors; count based on what's visible.



First option for neighbors; count based on what's visible.



Pseudo-code for counting neighbors;

```
neebs <- matrix(NA, nrows, ncols)
for(i in 1:nrows){
  for(j in 1:ncols){
    if(<in corner>){ add up over 3 relevant cells }
    if(<on side>){ add up over 5 relevant cells }
    if(<other>){ add up over 8 relevant cells }
    neebs[i,j] <- #neighbors we just counted
  }
}</pre>
```

- neebs stores the number of neighbors
- $\bullet$  Which cells are relevant depends on i and j

Doing the 'wrap-around' version, always count 8 neighbors;



Same basic commands, 'wrap' with modular arithmetic;

```
> 1:13 %% 7
[1] 1 2 3 4 5 6 0 1 2 3 4 5 6
> ((1:13 - 1) %% 7) + 1
[1] 1 2 3 4 5 6 7 1 2 3 4 5 6
```

## Game of Life: Updating status

Not-so-pseudo code;

```
alive.new <- matrix(0, nrows, ncols) # note full of zeros
for(i in 1:nrows){
    for(j in 1:ncols){
        if(alive[i,j]==1 & neebs[i,j]<2 ){ alive[i,j] <- 0 }
        if(alive[i,j]==1 & neebs[i,j]%in%2:3){ alive[i,j] <- 1 }
        if(alive[i,j]==1 & neebs[i,j]>3 ){ alive[i,j] <- 0 }
        if(alive[i,j]==0 & neebs[i,j]==3 ){ alive[i,j] <- 1 }
    }
}
alive <- alive.new</pre>
```

- Other alive==0 cells stay dead, so no need for another line
- Possible to do fewer updates, if start with alive.new <- alive</li>

## Game of Life: Plotting status

There are many ways to do this. rect() offers one simple way; if i indexes rows and j columns, we need e.g.

xleft	j - 1/2
ybottom	i - 1/2
xright	j + 1/2
ytop	i - 1/2

... and also specify color - e.g. 1 for black/dead, 2 for red/alive.

```
for(i in 1:nrows){
    for(j in 1:ncols){
        rect(j-0.5, i-0.5, j+0.5, i+0.5,
            col=alive[i,j] + 1, border="cyan")
    }
}
```

Also need to set up an 'empty' plot first; type="n"

Other notes;

- Do each task separately, on a small grid (i.e. a small dataset) and make sure it works right
- As per session 9, it helps to write a function for each task

Final pseudo-code;

```
alive <- <initial setup>
<setup empty plot>
refresh.grid(alive) # plot the initial status
```

```
for(k in 1:n.steps){
    alive <- do.update(alive) # counting and updating
    refresh.grid(alive) # plotting
    }</pre>
```

If the arguments to rect() are vectors, it draws multiple rectangles. To do this, we need to make a copy of alive in 'long' format, i.e. in a long tall matrix, where each row corresponds to a cell

This is slightly easier to type, but doesn't actually speed things up much.

A much cuter trick; to count neighbors, slide the grid in all 8 directions, and add;

A much cuter trick; to count neighbors, slide the grid in all 8 directions, and add;











A much cuter trick; to count neighbors, slide the grid in all 8 directions, and add; (it works!)

1	1	2	2	3	2	1
1	0	3	2	3	1	1
2	2	4	3	6	4	2
2	1	3	3	3	2	1
3	3	4	3	3	4	2
2	2	2	2	2	1	1
1	2	2	1	1	1	1

This enables counting neighbors without any explicit loops;

This does notably speed up the code – faster than the graphics can cope, on my laptop. Much of the processor time is spent managing the for() loop, and this 'vectorized' version means all that work is done in C/Fortran instead.

Our final trick is 'logical subscripting'. We can reassign elements of a matrix indexed by the TRUE elements of another matrix, without losing the original matrix structure.

```
alive.new <- alive
 alive.new[alive==0 & neebs==3] <- 1
 alive.new[alive==1 & neebs<2] <- 0</pre>
 alive.new[alive==1 & neebs>3] <- 0
 alive <- alive.new
A simpler example - to show this really is a trick;
> x <- matrix(1:10, 2, 5)
> x
    [,1] [,2] [,3] [,4] [,5]
[1,] 1 3 5 7 9
[2,] 2 4
             6 8 10
> y <- x>5
> x[y]
[1] 6 7 8 9 10
> x[y] <- 0
> x
    [,1] [,2] [,3] [,4] [,5]
[1,] 1 3 5
                    0
                         0
[2,] 2 4 0
                    0
                         0
```

## Game of Life: Nicer output

Standard R graphics are not built for animations. If your code goes too fast for them, export to a file format that does permit animations – e.g. animated GIFs, which the caTools package will write.

Storing every version of alive in a nrows  $\times$  ncols  $\times$  nsteps array object.

```
all.alive <- array(NA, c(nrows, ncols, nsteps))
alive <- <initial setup>
```

## Game of Life: Nicer output

R can't display animated GIFs. So, to open this file in the default application on your computer;

```
shell.exec("gol.gif")
```

Assuming your machine knows what to do with URLs, also try

```
shell.exec("http://www.google.com/")
```

This concludes our course. To learn more;

- Take the next one! 'Elements of R' follows on, with genetics/bioinformatics examples (and lots of programming)
- See the recommended books, on the course site
- To find simple examples/functions, ask Google (in a web browser
- There are several R mailing lists; R-help is the main one. But contributors expect you to have read the documentation – all of it! CrossValidated is friendlier to beginners
- Emailing package authors may also work
- For questions about *any* software, say;
  - What you did (ideally, with an example)
  - What you expected it to do
  - What it did instead

#### What next week?

Calling anyone who can sing (or just read music) – no auditions for two 'open reading' sessions.



www.nwmahlerfestival.org