



## **6. Writing Loops**

**Ken Rice**  
**Thomas Lumley**

Universities of Washington and Auckland

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# Writing loops in R

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We saw that `apply()`, `sapply()` are R's preferred way of **looping** (doing the same thing many times)

Even for expert users, their use requires some careful thought; debugging code may be complex.

In this session we'll talk about some alternatives, and their application to **genome-wide** studies.

# for loops

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Your first computer program?

```
for(i in 1:100){  
  print("Hello world!")  
  print(i*i)  
}
```

- Everything inside the curly brackets {...} is done 100 times
- Looped commands can depend on *i* (or whatever you called the counter)
- R creates a vector *i* with 1:100 in it. You could use **any vector that's convenient**

# for loops

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`for()` loops are very intuitive, but have some drawbacks;

- They can be **slow**;
  - ‘growing’ a large dataset is a bad idea;  
`mydata <- cbind(mydata, rnorm(1000, mean=i))`
  - so set up blank output **first**, then ‘fill it in’
- `apply()` is interpreted slightly faster than `for()` – but typically this will not matter, contrary to some urban myths
- `for()` loops require more typing than `apply()`! For tasks which will be repeated, writing a function really is the Right Thing to do, in the long run.

Using `for(i in 1:N)` sets up a vector (`i`) of length `N`. Do you really need this?

# for loops

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Two alternatives; (see ?Control for details)

```
i <- 1; my.mat <- matrix(NA, N, 3)
while(i <= N){
  z <- work.on.gene(i)
  my.mat[i,] <- summary(z)
  i <- i+1
}
```

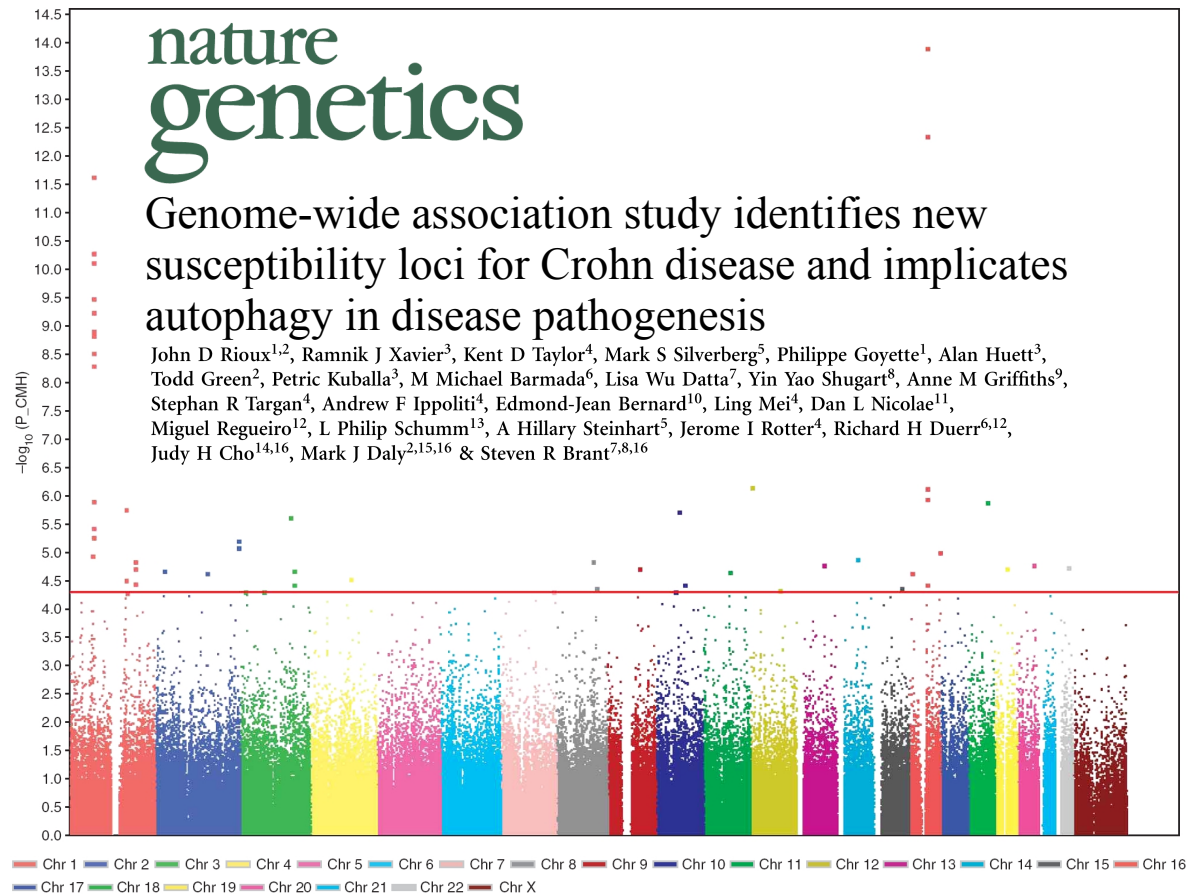
– note that we avoided ‘growing’ the output

```
i <- 1; my.mat <- matrix(NA, N, 3)
repeat{
  z <- work.on.gene(i)
  my.mat[i,] <- summary(z)
  i <- i+1
  if(i>=N) break
}
```

Use `apply()`, `sapply()` to avoid the ‘setup’ stage

# Application to whole-genome study

Whole genome studies look **very intimidating** ...



# Application to whole-genome study

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... however, each  $p$ -value on that picture comes from a single logistic regression.

There may be 304,413 tests in total; if each one takes 1/10 sec, the analysis is done in under an hour;

Time per test	Total time
0.01 sec	51 mins
0.1 sec	8 hours 27 mins
1 sec	3 days 12.5 hrs
5 sec	17 days 15 hrs (!)
5 mins	2 yrs 11 months (!!!)

Cutting time per test from 1 sec  $\rightarrow$  0.1 sec is clearly worthwhile – but proposing analyses where each test takes  $>$  5 secs is silly.

# Making code run faster, part 1

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Some easy 'streamlining' ideas;

- Write a function to do just the analysis you want  

```
> my.output <- apply(my.data, 1, my.function)
```
- Pre-process/'clean' your data before analysis; e.g. `sum(x)/length(x)` doesn't error-check like `mean(x)`
- Similarly, you can streamline `glm()` to just `glm.fit()` [as we'll see, in some examples]
- Use vectorized operations, where possible
- Store data as matrices, not data.frames



# Making code run faster, part 2

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Streamlining, for experts;

- Write small but *important* pieces of code in C, and call these from R
- **Batch mode** processing lets you break down e.g. the whole genome into 23 chromosomes – great if you have 23 processors to use.
  - Save your analysis in 23 output files
  - read in the answers
  - finally produce e.g. multi-color pictures

Various packages help implement this, but use is platform-specific

# Timing

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*“Premature optimization is the root of all evil”*

Donald Knuth

Do you **need** to optimize your code? Running 2 or 3 times faster may **not be worth the time spent coding/debugging!**

But going an **order of magnitude** faster is A Good Thing.

**After** you have code that works, you may need to speed it up. Experienced users may be able to ‘eyeball’ the problem; measurement is an **easier and more reliable** approach

# Timing

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- `proc.time()` returns the current time. Save it before a task and subtract from the value after a task.
- `system.time()` times the evaluation of expression
- R has a **profiler**; this records which functions are being run, many times per second. `Rprof(filename)` turns on the profiler, `Rprof(NULL)` turns it off. `summaryRprof(filename)` reports how much time was spent in each function.

Remember that a 1000-fold speedup in a function used 10% of the time is **less helpful** than a 30% speedup in a function used 50% of the time.

# High-throughput code – caveats

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We saw yesterday that ‘weird’ datasets can crash your code. These **will appear** in genome-wide studies, and a crash at SNP 299,999 will be **very frustrating**.

- Some ‘weirdness’ is easy to spot;
  - Everyone is homozygous
  - All cases missing
  - No variation in outcome ...
- In more complex models, it’s easier to ‘try it and see’. Use `tryCatch()`
- When ‘weirdness’ is found, high-throughput code should;
  - Produce sensible output (NA, -999 etc)
  - Handle these appropriately in summary output