



# **SISG Module 13**

## **Advanced R for Bioinformatics**

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Universities of Washington and Auckland

*Seattle, July 2014*

# Introduction: Course Aims

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- Programming with R
  - Efficient coding
  - Code that other people can use
- Using R for sophisticated analyses
  - Some useful tools for large-scale problems
  - Making R play nicely with others
  - Knowing **where to look** when you need more

# Introduction: About Prof Lumley

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- Prof, University of Auckland
- R Core developer
- Genetic/Genomic research in Cardiovascular Epidemiology
- Sings bass (sometimes)

# Introduction: About Prof Rice

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- Associate Prof, UW Biostat
- Not an author, but a user (and a teacher)
- Genetic/Genomic research in Cardiovascular Epidemiology
- Sings bass (in Seattle!)

... and you?

(who are you, what area of genomics, what are you looking for from the course)

# Introduction: Course structure

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10 sessions over 2.5 days

- Day 0; Programming in R, Graphics
- Day 1; Objects, Packages, XML
- Day 2; C code, large datasets

Download everything from here;

`http://faculty.washington.edu/kenrice/sisg-adv`

# Introduction: Session structure

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We will alternate teaching (questions welcome) and hands-on exercises (questions and discussions welcome!)

For some topics, within a single 90 minute session;

- 45 mins teaching (Questions welcome! Please interrupt!)
- 30 mins hands-on
- 15 mins summary, discussion

For other topics, we'll separate sessions (90 mins) and hands-on exercises (90 mins)



# **1. Introduction to R: First steps**

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# Important pre-takeoff announcement:

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We are assuming you know;

- How to use R from the command line, and how to write and use script files (and spot e.g. missing commas and }'s )
- How to manipulate basic data structures in R; in particular vectors and data frames
- How to write functions
- What NA means, and that `42+NA==NA`
- Enough programming (in R or elsewhere) to recognize loops, and manage files external to your R session
- How to look up help files

Of course, familiarity with (non-advanced) statistical & genetic concepts will also help



# Programmers: what is R?

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- R is a free implementation of a dialect of the S language, the interactive statistics and graphics environment developed at Bell Labs.
- R/S are probably the most widely used software for research in statistical methodology and in genomics, and is popular in financial modelling and medical statistics.
- John Chambers won the 1999 ACM Software Systems award for S, which *will forever alter the way people analyze, visualize, and manipulate data.*
- Ross Ihaka won the Royal Society of New Zealand's 2008 Pickering Medal, recognizing *excellence and innovation in the practical application of technology* for the creation of R.

# Programmers: a little prehistory

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The design of R is largely based on S version 3, which predates Java, Python, JavaScript, Linux, MacOS X, and usable versions of Windows.

Much of the design was fixed in S version 2, which predates C++, Perl, the ANSI C standard, the IBM PC, the GNU project, and Miami Vice.

The basic graphics system is older than Space Invaders.

Yes, some things would be done differently today.

# Simulation

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This really is how calculations and simulation studies were done! Simulations have **always** been part of statistical research.

# Simulations: a simple example?

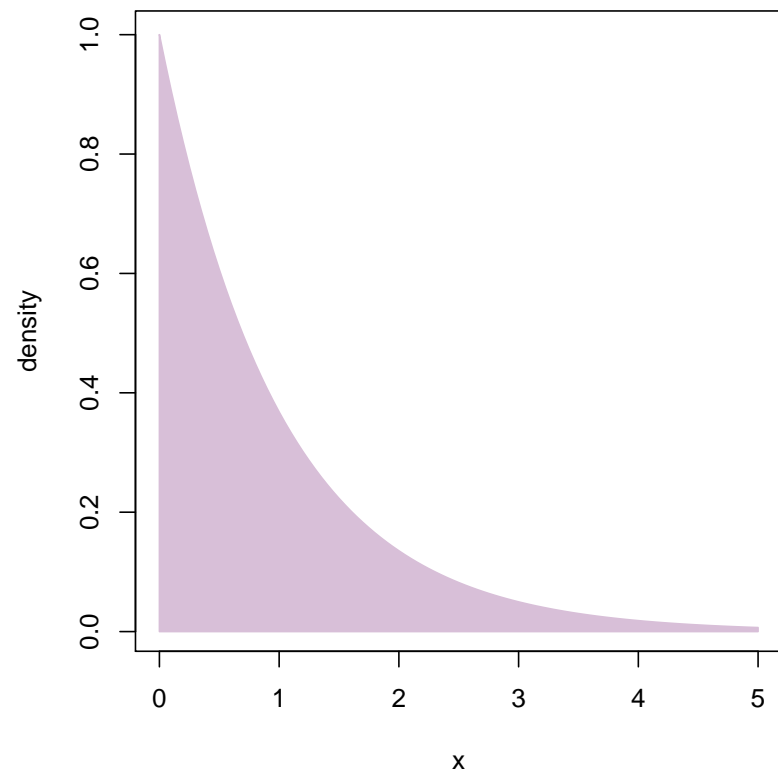
---

Here's a simple problem, for which we *can* work out the exact answer;

*For samples of i.i.d  $Exp(1)$  data with  $n=51$ ...*  
*What is the mean value of the sample median?*  
*What is the mean value of the median-squared?*

If you had, say, 51 survival times to analyze, from a distribution of times not unlike  $Exp(1)$ , these are sane questions.

$Exp(1)$  looks like this (right)  
any guesses?



# Simulations: a simple example?

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...guessing these would require a lot of luck;

$$\mathbb{E}Y = \frac{2178178936539108674153}{3099044504245996706400}$$

$$\mathbb{E}Y^2 = \frac{2467282316063667967459233232139257976801959}{4802038419648657749001278815379823900480000}$$

- They are 0.70286, 0.51380, to 5 d.p.
- They are *about*  $2/3$  and  $1/2$
- 3–4 significant figures is probably enough for most practical purposes. Being *able* compute more accurately is re-assuring
- In the ‘post-genome’ era, being able to compute quickly *is* important (again)

# Simulations: a simple example?

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Brute force provides perfectly acceptable answers; the `replicate()` function replicates evaluation of an expression

```
> bigB <- bazillion <- 10000
> set.seed(4) # a specific "start" value
> many.medians <- replicate(bigB, { median(rexp(51)) } )
> round( mean(many.medians), 3)
[1] 0.702
> round( mean(many.medians^2), 3)
[1] 0.513
```

The 'right' answers averages over an infinite number of replications. `bigB=10,000` here, which  $\approx \infty$ .

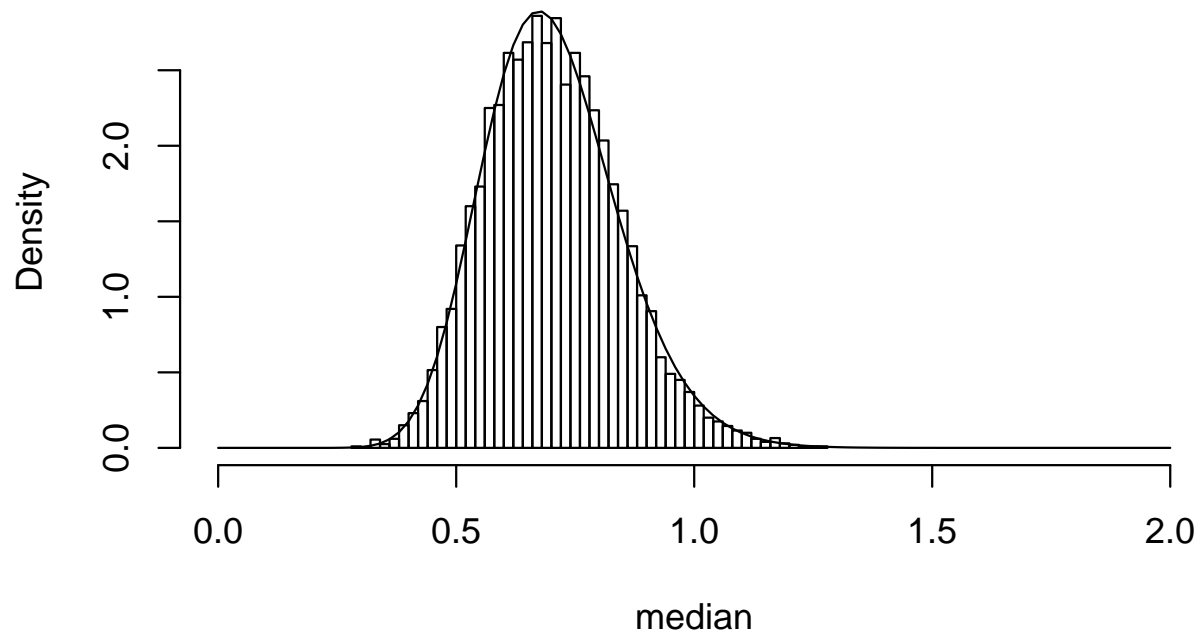
This calculation takes  $< 2$  seconds, on my desktop

# Simulations: a simple example?

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Our simulations get us very close to the true distribution of the median;

**Histogram of many.medians**



Having done the ‘hard work’ of simulation, we can also compute skewness, kurtosis, quantiles, etc – all for ‘free’. This technique is very powerful – and often under-rated by statisticians.

# Simulations: a simple example?

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Here are some other statistical concepts, interpreted in the same way;

- *[If] we simulated data, a bazillion times ( $B \approx \infty$ )..."*
- *...and applied our procedure to each dataset – and recorded the output*
- Does our estimate usually get close? [consistency]
- How close does our estimate typically get? [bias]
- How variable is our estimate? [standard error, efficiency]
- How often does our interval cover the truth? [coverage]
- How often does our test make a Type I/Type II error? [size/power]



# Effective coding

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We need to be able to program simulations effectively. A good default for any simulation study follows this ‘pseudo-code’;

```
do.one <- function(n, beta, f){  
  ... commands to do one analysis  
  ... last command spits out what you want  
}
```

```
many.sim <- replicate(bigB, do.one(my.n, my.beta, my.f))  
  ... commands to work out observed coverage, bias, etc
```

Once this works, wrap it inside further loops, e.g.

```
n.vals      <- c(10, 20, 30, 40, 50, 1000)  
coverage.vals <- sapply(n.vals, function(n){  
  ... commands to do the replication, with my.n=n  
})
```

At each stage, you must first write a function, *then check it*. This requires a bit of sanity-checking (i.e. trying it where you know *at least roughly* what should happen) and debugging.

# Effective coding

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The use of `sapply()` (and `apply()`, `lapply()` ) can be unfamiliar – many programmers have used `for()` loops elsewhere. R does have `for()` loops (see `?Control`) but;

- ‘Growing’ the dataset is a terrible idea;

```
for(i in 1:n){  
  mydata <- cbind(mydata, rnorm(1000, mean=i)) # noooooo!  
}
```

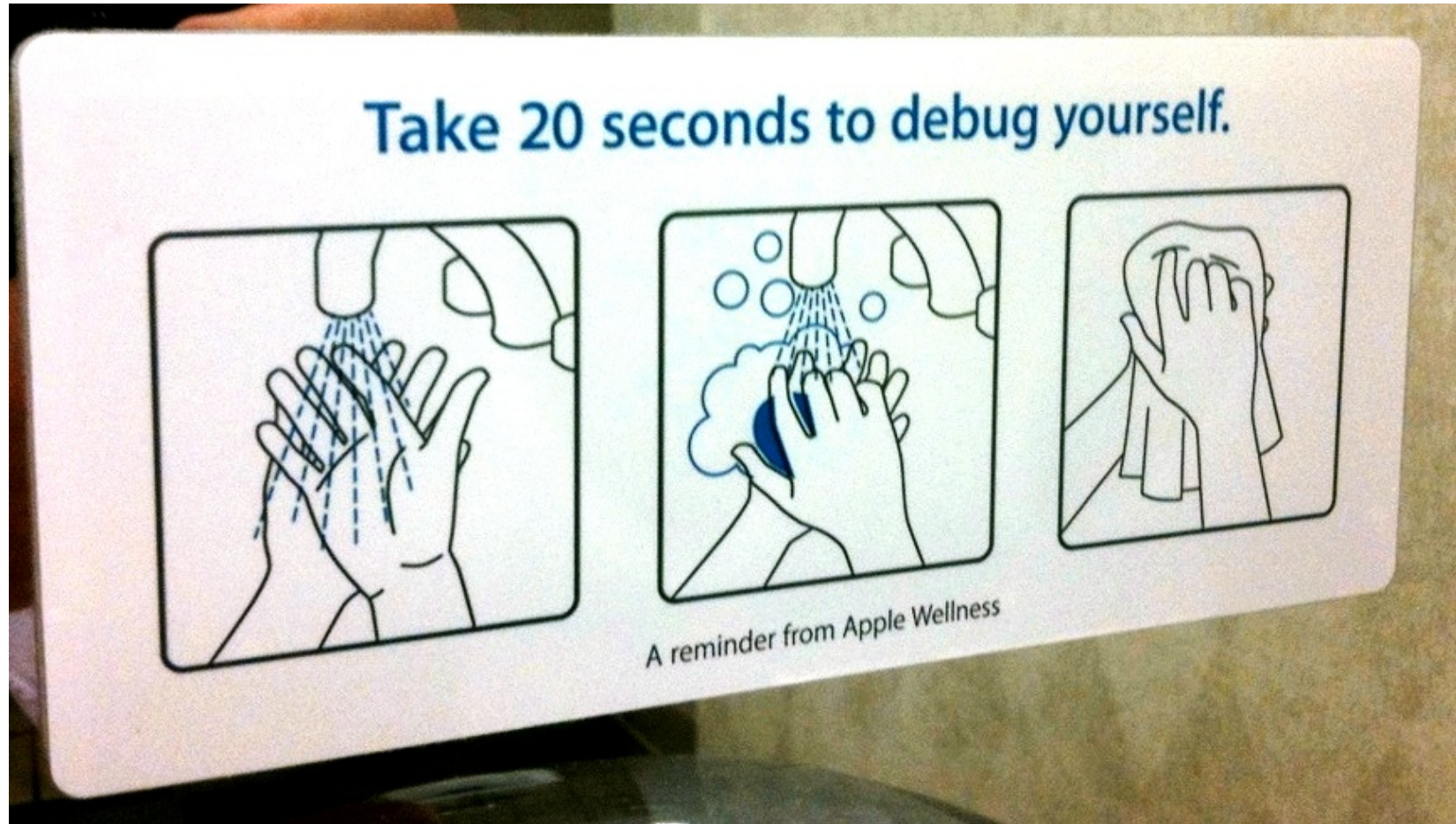
Always set up blank output first, then ‘fill it in’

- Use of `replicate()`, `apply()` etc means slightly faster interpretation of code than `for()` – but not by much. `for()` loops are not *intrinsically* evil
- `for()` requires more typing than `replicate()` etc, and is often more work to edit
- Using functions makes your ultimate R package easier to produce... right?

# Debugging

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A 'handy' hint from the Apple Corporation;



# Debugging

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Beyond the level of spotting missed commas and mis-matching parentheses, debugging is difficult.

We'll discuss use of `traceback()` and `recover()`, which can help;

```
> # a trite example of traceback()
> f1 <- function(x){ print(x); f2(x) }
> f2 <- function(x){ x + i.dont.exist }
> f1(10) # gives this strange error;
[1] 10
Error in f2(x) : object 'i.dont.exist' not found
> traceback()
2: f2(x)
1: f1(10)
```

The error occurred inside the execution of `f2()`

# Debugging

---

If the error's not obvious, try using `recover()`;

```
options(error=recover) # enter c to close
set.seed(4)
replicate(1000, {
  y <- rnorm(10)
  x <- rbinom(10, 1, 0.5)
  lm1 <- lm(y~x) # regress Y on X
  c(coef(lm1)[2], vcov(lm1)[2,2]) # terms of interest
})
```

# Hint: look at the highest number frame first

```
#turn it off! turn it off!
options(error=NULL)
```

Use `ls()` to list local objects; the highest frame number is a good place to start

# Debugging

---

`trace()` adds instrumentation to a function

- `trace(rnorm)` prints a message when `rnorm` is started/ended
- `trace(rnorm, recover)` calls the debugger when `rnorm()` is entered.
- `trace(lm, quote(if(all(mf$x==1)) recover()), at=12)` calls the debugger if `mf$x` is all 1s at line 12 of `lm()`

Use `untrace(rnorm)` to remove tracing from `rnorm()`

# Exceptions

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While you might never see them in practice (due to data cleaning) in simulation studies your replications may produce ‘pathological’ data, e.g. all  $X$  are identical, or all minor allele-carriers smoke. If your regressions estimate differences per allele-copy, adjusting for smoking, it *should* complain.

If this is just too tedious (and rare) to bother fixing, you can use `tryCatch()`;

```
one.glm <- function(outcome, x){  
  tryCatch(  
    {model <- glm(outcome~x, family=binomial())  
      coef(summary(model))[2,]  
    },  
    error=function(e){rep(NA, 4)} # puts 4 NAs in output  
  )  
}
```

... but check your simulation output's rates of NA-ness. It's better to pre-empt these problems – but this is not easy

# Timing

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*Premature optimization is the root of all evil*

Donald Knuth

If you **already have** the capacity to generate reasonably accurate results within a sane time limit, optimizing code is a *waste of effort*

If you need to do things an **order of magnitude** faster, or use your code again (repeatedly) then optimizing your code **may** be worthwhile

To optimize, you need to know;

- What's the bottleneck?
- How much faster can I make that step?



# Timing

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Obvious bottleneck/easy solution;



# Timing

---

*...What's the bottleneck?*

Experienced users may be able to 'eyeball' this from code; measurement is an **easier and more reliable** approach (!)

To find out how long operations are taking;

- `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 a given 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: A 1000-fold speedup in a function used 10% of the time is **less helpful** than a 2-fold speedup in a function used 50% of the time.

# Timing

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A small example of this in action;

```
# what is taking all the time?
Rprof("deleteme.txt")
  many.sim <- replicate(1000, {
    y <- rnorm(10)
    x <- rbinom(10, 1, 0.5)
    if( all(x==0)|all(x==1)) return(c(NA,NA))
    lm1 <- lm(y~x)
    c(coef(lm1)[2], vcov(lm1)[2,2])
  })
Rprof(NULL) # turn it off! turn it off!
summaryRprof("deleteme.txt")
```

# Timing

---

*...How much faster can I make that step?*

Some simple tips;

- Pre-process/clean your data before analysis; e.g. `sum(x)/length(x)` doesn't error-check like `mean(x)`
- Similarly, use `glm.fit` not `glm` – use matrix calculations in place of `lm()`
- Use vectorized operations, where possible
- Store data as matrices, not data frames
- Delete objects you are finished with



# Timing

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More advanced methods;

- Write **small but important** pieces of code in C, and call these from R
- Run multiple batches. Store your commands in one script file (which you should do anyway) and call it with e.g.

```
R CMD BATCH myscript.R myconsoleoutput.txt &
```

... and finally assemble all the (saved) results

The second option applies when there is no available speedup; if your R session is mostly waiting for C to do matrix work, writing the whole thing in C offers no important benefit

## More advanced: short cuts to C

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For a limited number of jobs, it may be worth getting R to send a (large) number of generated datasets to C simultaneously.

- For example, instead of looping over datasets with  $n = 20$  outcomes  $Y$  and  $n = 20$  covariates  $X$ , generate  $B \times 20$  matrices  $\mathbf{Y}$  and  $\mathbf{X}$ ; using `rowSums(X)`, `rowSums(X*Y)` etc to construct  $\hat{\beta}$  avoids `replicate()` or similar
- For large  $n$  or large  $B$  one can quickly run out of memory
- This is a massive pain! I have only used it productively for one real job – doing 2.5 million cookie-cutter meta-analyses
- Less of a pain is `cor(large.matrix)` – for all pairwise correlations of columns of `large.matrix`, where all the looping is done in C

For complex methods, this approach will not help

## Bonus tracks: how big?

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Q. What's the 'Monte Carlo' error in my estimates?

One quick-and-dirty measure of uncertainty is given by these intervals;

```
many.thetahat <- replicate(bigB, {...calculate an estimate...} )
lm1 <- lm(many.thetahat~1)
confint.default(lm1)
```

For binary outcomes, (i.e. when you want coverage, size, power)

```
z <- replicate(bigB, {... calculate theta.hat/est.std.err ...})
mean( z^2 < 1.96^2 ) # how many give p>0.05?
lm2 <- lm( I(z^2 < 1.96^2) ~ 1 )
confint.default(lm2)
```

For GWAS-style levels of e.g.  $5 \times 10^{-8}$ , simulations with e.g.  $B = 10^{10}$  may be needed; efficient coding of them can save many days of processor time.