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It's funny because it's true.

Writing clear code

Tools for Reproducible Research

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Clear code is more likely to be correct.

Clear code is easier to use.

Clear code is easier to maintain.

Clear code is easier to extend.

Basic principles

- ▶ **Code that works**
No bugs; efficiency is secondary (or tertiary)
- ▶ **Readable**
Fixable; extendable
- ▶ **Reuseable**
Modular; reasonably general
- ▶ **Reproducible**
Re-runnable
- ▶ **Think before you code**
More thought \implies fewer bugs/re-writes
- ▶ **Learn from others' code**
R itself; key R packages

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Our first goal should be to get the right answer.

But we also want to write code that we (and others) will be able to use again. Efficiency is way down on the list of needs.

Write clearly, and re-write for greater clarity.

Break things down into small, re-usable functions, written in a general way, but not **too** general. You want to actually solve a particular problem.

Step 1: stop and think.

Step 2: write re-usable functions rather than a script.

By reproducible/re-runnable, I mean: don't have a bunch of code from which you copy-and-paste in a special way.

Break code into small functions

```
sampleone <-  
function(vec)  
  ifelse(length(vec)==1, vec, sample(vec, 1))  
  
get_grid_index <-  
function(vec, step)  
{  
  grid <- seq(min(vec), max(vec), by=step)  
  index <- match(grid, vec)  
  
  if(any(is.na(index)))  
    index <- sapply(grid, function(a,b) {  
      d <- abs(a-b);  
      sampleone(which(d == min(d)))  
    }, vec)  
  
  index  
}
```

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This is a bit of code that was originally part of a larger function. I pulled out the `get_grid_index` and then further pulled out the `sampleone` function.

Separated as functions, the code is more likely to be reused. And the smaller and more focused the function, the more likely you'll use it again.

Avoid having scripts that are long streams of code. Write functions. Give each function a single, focused task. Break long functions into pieces.

Comment on the input and output; ideally, these are obvious from the names.

Another example

```
# retain just the indicated markers
pull.markers <-
function(cross, markers)
{
  mn <- markernames(cross)

  m <- match(markers, mn)
  if(any(is.na(m)))
    warning("Some markers couldn't be found: ",
            paste(markers[is.na(m)], collapse=" "))

  drop.markers(cross, mn[is.na(match(mn, markers))])
}
```

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Note that this function calls other functions I wrote, **markernames** and **drop.markers**.

The reliance on **drop.markers** might be less efficient, but it's more efficient to write, and it's easier to maintain.

Yet another example

```
# rmvn: simulate from multivariate normal distribution
rmvn <-
function(n, mu=0, V=matrix(1))
{
  p <- length(mu)

  if(any(is.na(match(dim(V),p))))
    stop("Dimension problem!")

  D <- chol(V)

  matrix(rnorm(n*p),ncol=p) %*% D + rep(mu,each=n)
}
```

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Perhaps this is more understandable.

Note the use of default values.

Still more examples

```
# colors from blue to red
revrainbow <-
function(n=256, ...)
  rev(rainbow(start=0, end=2/3, n=n, ...))

# move values above/below quantiles to those quantiles
winsorize <-
function(vec, q=0.006)
{
  lohi <- quantile(vec, c(q, 1-q), na.rm=TRUE)
  if(diff(lohi) < 0)
    lohi <- rev(lohi)

  vec[!is.na(vec) & vec < lohi[1]] <- lohi[1]
  vec[!is.na(vec) & vec > lohi[2]] <- lohi[2]

  vec
}
```

If there's a bit of code that you write a lot, turn it into a function.

Don't repeat yourself (or others)

- ▶ Avoid having repeated blocks of code.
- ▶ Create functions, and call those functions repeatedly.
- ▶ This is easier to maintain.
 - If something needs to be fixed/revised, you just have to do it the one time.
- ▶ Look at others' libraries/packages.
 - Don't write what others have already written (especially if they've done it better than you would have).

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Don't repeat yourself (DRY) is one of the more important concepts for programmers.

I'm particularly bad at making use of others' code.

Don't make things too specific

- Write code that is a bit more general than your specific data

- Don't assume particular data dimensions.
- Don't forget about the possibility of missing values (even if **your** data doesn't have any).
- Aim for re-use.

- Use function arguments

- Don't assume particular data file names
- Don't hard-code tuning parameters
- R scripts can take **command-line arguments**:

```
Rscript myscript.R input_file output_file  
args <- commandArgs(TRUE)
```

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Don't make things too general, either. You want to actually solve your particular problem.

You don't want to have to edit the code for different data.

No global variables, ever!

- ▶ Don't refer directly to objects in your workspace.
- ▶ If a function needs something, pass it as an argument.
- ▶ (But what about really big data sets?)

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Global variables make code unreadable.

Global variables make code difficult to reuse.

No magic numbers

- ▶ Name numbers and use the names

```
max_iter <- 1000  
tol_convergence <- 0.0001
```

- ▶ **Even better:** include them as function arguments

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You'll later ask yourself, "Why 12?"

When you include such things as function arguments, include reasonable default values.

Indent!

```
# move values above/below quantiles to those quantiles
winsorize <-
function(vec, q=0.006)
{
  lohi <- quantile(vec, c(q, 1-q), na.rm=TRUE)
  if(diff(lohi) < 0)
    lohi <- rev(lohi)
  vec[!is.na(vec) & vec < lohi[1]] <- lohi[1]
  vec[!is.na(vec) & vec > lohi[2]] <- lohi[2]
  vec
}
```

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I taught part of a course on statistical programming at Johns Hopkins. It included a lecture like this one. Still, many students submitted their programming assignment flush left.

Most people recommend indenting by 4 spaces. Still, I prefer 2. (4 spaces are easier to track.)

Don't use tabs, as they get messed up when moving between computers.

Use white space

```
# move values above/below quantiles to those quantiles
winsorize<-function(vec,q=0.006)
{lohi<-quantile(vec,c(q,1-q),na.rm=TRUE)
if(diff(lohi)<0)lohi<-rev(lohi)
vec[!is.na(vec)&vec<lohi[1]]<-lohi[1]
vec[!is.na(vec)&vec>lohi[2]]<-lohi[2]
vec}
```

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The computer doesn't care about white space, but people do.

Don't let lines get too long

```
get_grid_index <-  
function(vec, step)  
{  
  grid <- seq(min(vec), max(vec), by=step)  
  index <- match(grid, vec)  
  
  if(any(is.na(index)))  
    index <- sapply(grid, function(a,b) { d <- abs(a-b); sampleone(whi  
  
  index  
}
```

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< 72 characters per line

Use parentheses to avoid ambiguity

```
if( (ndraws1==1) && (ndraws2>1) ) {  
  ...  
}  
leftval <- which( (map - start) <=0 )
```

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Even if they aren't **necessary**, they can be helpful to you (or others) later.

Names: meaningful

- ▶ Make name descriptive but concise
- ▶ Avoid `tmp1`, `tmp2`, ...
- ▶ Only use `i`, `j`, `x`, `y` in the simplest situations
- ▶ If a function is named `fv`, what might it do?
- ▶ if an object is called `nms`, what could it be?
- ▶ Functions as verbs; objects as nouns

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I'm terrible at coming up with good names. But it's really important.

Descriptive names make code self-documenting.

If functions are named by what they do, you may not need to explain further.

If the object names are meaningful, the code will be readable as it stands. If the objects are named `g`, `g2`, and `gg`, it'll need a lot of comments.

I admit, I'm a terrible offender in this regard, especially when I'm coding in a hurry. Do as I say, not as I do.

Names: consistent

- ▶ `markers` VS `mnames`
- ▶ `camelCase` VS. `pothole_case`
- ▶ `nind` VS `n.var`
- ▶ If a function/object, there shouldn't be a function/object with the other

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Consistency makes the names easier to remember.

If the names are easier to remember, you're less likely to use the wrong name and so introduce a bug.

And, of course, other users will appreciate the consistency.

Names: avoid confusion

- ▶ Don't use both `total` and `totals`
- ▶ Don't use both `n.cluster` and `n.clusters`
- ▶ Don't use both `result` and `results`
- ▶ Don't use both `Mat` and `mat`
- ▶ Don't use both `g` and `gg`

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Don't use similar but different names, in the same function or across functions.

Don't be cute



Richie Cotton
@richierocks



Giving myself Best Named Function Award for
`drop_the_bom` that removes byte order marks from
UTF-8 files.

5:17 AM - 11 Oct 2013

1 RETWEET 1 FAVORITE



@richierocks

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`drop_the_bom` might actually be quite memorable, which would make it a good choice.

And think of knitr: `knit`, `purl`, `spin`, `stitch`. Those work.

But generally I'd say: be direct rather than cute. Perhaps
`remove_byteorder_marks`

Comments

- ▶ Comment the tricky bits and the major sections
- ▶ Don't belabor the obvious
- ▶ Don't comment bad code; rewrite it
- ▶ Document the input/output and purpose, not the mechanics
- ▶ Don't contradict the code
 - this happens if you revise the code but don't revise the related comments
- ▶ Comment code as you are writing it (or before)
- ▶ Plan to spend 1/4 of your time commenting

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Some things are tricky and deserve explanation, so that when you come back to it, you have a guide.

But in many cases, code can be rewritten to be clear and self-documenting.

Commenting takes time. And no one ever goes back and adds comments later. It's another one of those "invest for the future" type of things.

Error/warning messages

- ▶ Explain what's wrong (and where)
 - `error("nrow(X) != nrow(Y)")`
- ▶ Suggest corrective action
 - You need to first run `calc.genoprob()`.
- ▶ Give details
 - `error("nrow(X) (", nrX, ") != nrow(Y) (", nrY")`
- ▶ Don't give warning messages that the users won't understand.
 - `X'X is singular.`
- ▶ Don't let users do something stupid without warning
- ▶ Include error checking even in personal code.

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Meaningful error messages are hard.

Writing them to give detailed information takes time.

And of course **you** wouldn't be making these errors, right?

But remember that you, six months from now, will be like a whole new person.

Check data integrity

- ▶ Check that the input is as expected, or give warnings/errors.
- ▶ Write these in the first pass (though they're dull).
 - You may not remember your assumptions later
- ▶ These are useful for **documenting** the assumptions.

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You can't include enough such checks.

Hadley Wickham's `assertthat` package is great for this. We'll talk about it in a couple of weeks.

Program organization

- ▶ Break code into separate files (say 300 lines?)
- ▶ Each file includes related functions
- ▶ Files should be named meaningfully
- ▶ Include a **brief** comment at the top.

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My R/qlt package has some **really** long files, like `util.R`, which seemed like a good idea at the time. I have to use a lot of **grep** to find things. And there are plenty of functions in there that I have totally forgotten about.

I used to make really long boiler-plate comments at the top of each file. That means that you **always** have to page down to get to the code. Now I try to write really minimal comments.

Create an R package!

- ▶ Make a personal package with bits of your own code
- ▶ Mine is R/broman, github.com/kbroman/broman

```
# qqline corresponding to qqplot
qqline2 <- function(x, y, probs = c(0.25, 0.75), qtype = 7, ...)
{
  stopifnot(length(probs) == 2)
  x <- quantile(x, probs, names=FALSE, type=qtype, na.rm = TRUE)
  y <- quantile(y, probs, names=FALSE, type=qtype, na.rm = TRUE)
  slope <- diff(y)/diff(x)
  int <- y[1L] - slope*x[1L]
  abline(int, slope, ...)
  invisible(c(intercept=int, slope=slope))
}
```

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R packages are great for encapsulating and distributing R code with documentation.

Every R programmer should have a personal package containing the various functions that they use day-to-day.

We'll talk about writing R packages next week. It's really rather easy.

I give an example here of one function in my R/broman package. Some of the earlier examples are in this package.

Complex data objects

- ▶ Keep disparate data together in a more complex structure.
 - lists in R
 - I also like to hide things in object **attributes**
- ▶ It's easier to pass such objects between functions
- ▶ Consider object-oriented programming

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Complex data objects allow you to think about complex data as a **single thing**. And they make it easier to pass the data into a function.

R has two systems for object-oriented programming: S3 and S4. They can make your code easier to use and understand. But they can also make things more opaque and harder to understand.

Avoiding bugs

- ▶ Learn to type well.
- ▶ Think before you type.
- ▶ Consider commenting before coding.
- ▶ Code defensively
 - Handle cases that "can't happen"
- ▶ Code simply and clearly
- ▶ Use modularity to advantage
- ▶ Think through all special cases
- ▶ Don't be in too much of a hurry

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Writing clear code will make it easier to find bugs, but we also want to **avoid** introducing bugs in the first place. These are my strategies: Useful when **applied**.

Basic principles

- ▶ **Code that works**
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It seems useful to repeat these basic principles.

Summary

- ▶ Get the correct answers.
- ▶ Find a clear style and stick to it.
- ▶ Plan for the future.
- ▶ Be organized.
- ▶ Don't be too hurried.
- ▶ Learn from others.

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Our primary goal, as scientific programmers, is to get the right answer.

We all write differently. That's okay. But be consistent. If every function is named in a different way, it will be that much harder to remember.

Plan for the future: write code that is readable and easy to maintain. And write things in a modular and reasonably general way, so that you (or others) will be more likely to be able to re-use your work.

Be organized. Well-organized software is easier to understand and maintain.

It's when I'm hurried that I write crap code. It means more work later.

There are a lot of great programmers out there; read their code and learn from it.