Why Benchmark? Well maybe you don't need to if your code runs well and fast enough for your requirements.

On the other hand there are many different ways to do things in R and sometimes you wind up doing things that take a very long time.

So you need ways to do comparisons and pick the approach that is "best" and most efficient.

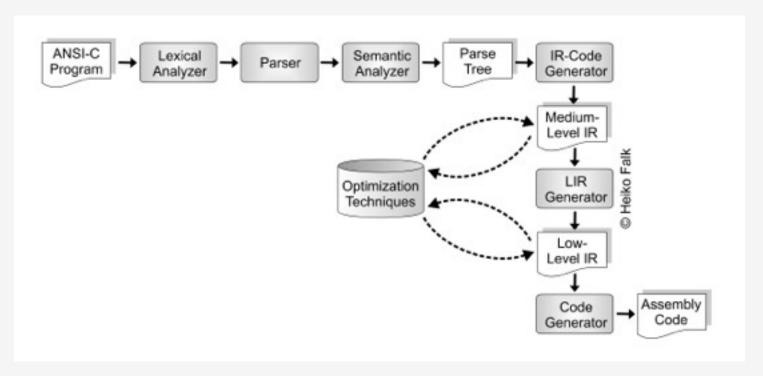
C, C++, FORTRAN are "compiled" languages (there are many others)
FORTRAN was introduced in 1957, C was introduced in 1969, C++ in 1983

Programs/"source code" created in these languages are "read" by another program, called a compiler, that translates the entire program in to "machine code" that can then be passed to the operating system for rapid execution. T

Modern compliers can make improvements and optimizations to the code automatically giving even better performance.

A problem with this approach is that users need to recompile their programs for every change they make to the code.

This shows us what is involved in compilation. Note that the compiler handles all of the steps for us so its not like we have to do them all separately. But it takes a lot to take "source code" and turn it into "machine code" - a computer's "native language".



http://ls12-www.cs.tu-dortmund.de/daes/de/forschung/source-code-optimization/motivation.html

R is an "interpreted" language as is Python, Perl, Ruby, and many others.

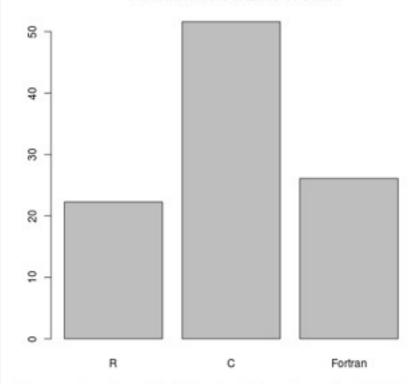
Interpreted languages have some advantages such as platform independence and a quicker development cycle since there is no compilation step involved. However, they tend to be slower since there is no direct translation into "machine code" before execution.

Each line is "interpreted" in sequence which is easier on the user but doesn't result in great efficiencies.

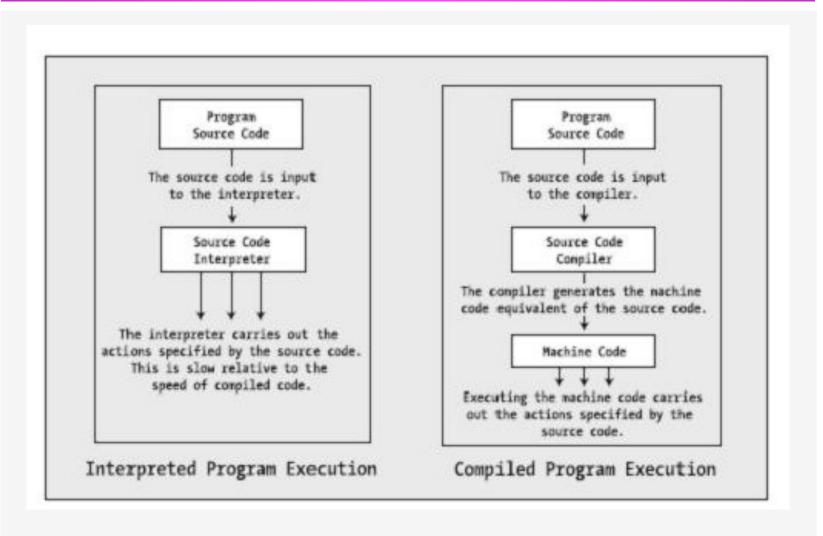
The language R is written in R with a large portion being written in C and FORTRAN. Certain functions are written in C and FORTRAN to speed up computation.



#### Percent of Core R Lines of Code



For comparison, about 50% of R is written in C, and just under 30% in Fortran -- for the current 2.13.1 release, at least. Of course, these ratios have changed over time with each release of R, as this <u>analysis of the R codebase from Ohloh</u> shows:

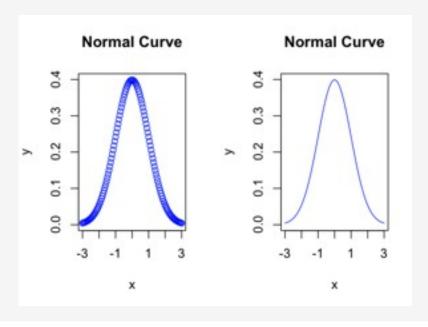


http://www.devshed.com/c/a/Practices/Basic-Ideas/1/

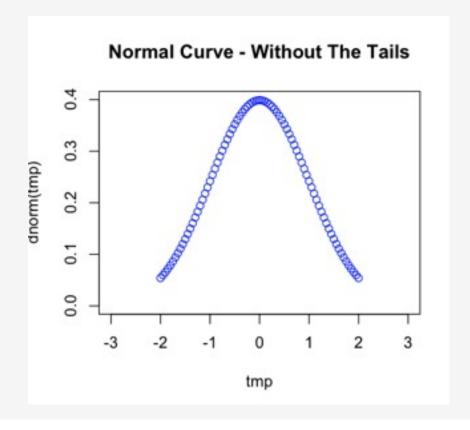
```
Let's set up a test case:
x = seq(-3, 3, by=0.05)
# The "by" argument let's us specify a "step" or "interval" value
Х
 [1] -3.00 -2.95 -2.90 -2.85 -2.80 -2.75 -2.70 -2.65 -2.60 -2.55 -2.50 -2.45
 [13] -2.40 -2.35 -2.30 -2.25 -2.20 -2.15 -2.10 -2.05 -2.00 -1.95 -1.90 -1.85
 [25] -1.80 -1.75 -1.70 -1.65 -1.60 -1.55 -1.50 -1.45 -1.40 -1.35 -1.30 -1.25
 [37] -1.20 -1.15 -1.10 -1.05 -1.00 -0.95 -0.90 -0.85 -0.80 -0.75 -0.70 -0.65
[49] -0.60 -0.55 -0.50 -0.45 -0.40 -0.35 -0.30 -0.25 -0.20 -0.15 -0.10 -0.05
[61] 0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.35 0.40 0.45 0.50 0.55
[73] 0.60 0.65 0.70 0.75 0.80 0.85 0.90 0.95 1.00 1.05 1.10 1.15
[85]
      1.20 1.25 1.30 1.35 1.40 1.45 1.50 1.55 1.60 1.65
                                                               1.70 1.75
[97] 1.80 1.85 1.90 1.95 2.00 2.05 2.10 2.15 2.20 2.25
                                                               2.30 2.35
[109] 2.40 2.45 2.50 2.55 2.60 2.65 2.70 2.75 2.80 2.85 2.90 2.95
[121] 3.00
```

```
x = seq(-3, 3, by=0.05)
y = dnorm(x)

# Now we plot the data
par(mfrow=c(1,2))  # Set the plot region to be one row and two columns
plot(x, y, xlim=c(-3,3), ylim=c(0,0.4), main="Normal Curve", col="blue")
plot(x,y,xlim=c(-3,3),ylim=c(0,0.4),main="Normal Curve",col="blue",type="l")
```



And we could look at points between -2 and 2 also just as easily.



Note that in other programming languages we would use a for loop structure to do this. We can also do this in R. It isn't particularly difficult.

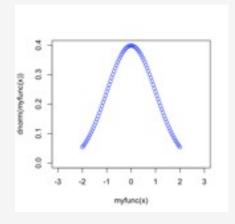
```
x = seq(-3, 3, by=0.05)
hold = vector()
for (ii in 1:length(x)) {
    if ( (x[ii] >= -2) & (x[ii] <= 2) ) {
        hold[ii] = x[ii]
    }
}
# Same "tails" plot as before

plot(hold,dnorm(hold),xlim=c(-3,3),ylim=c(0,0.4),col="blue")</pre>
```

```
# We could put this into a function also. It doesn't change the results

myfunc <- function(x) {
  hold = vector()
  for (ii in 1:length(x)) {
    if ( (x[ii] >= -2) & (x[ii] <= 2) ) {
      hold[ii] = x[ii]
    }
  }
  return(hold)
}

plot(myfunc(x),dnorm(myfunc(x)), xlim=c(-3,3),ylim=c(0,0.4),col="blue")</pre>
```



So now let's generate a lot more points and pull out the tails. We also want to get an idea about how long it takes to do this. What could we do to get the timings? One way is to use Sys.time() as a "stopwatch".

```
Sys.time()
[1] "2013-11-09 20:01:00 EST"

# Wait 5 seconds

Sys.time()
[1] "2013-11-09 20:01:05 EST"

now = Sys.time()

# Wait for some period of time

later = Sys.time()

later - now
Time difference of 5.272433 secs
```

This is just okay. However, there is some delay between the first call to sys.time() and when tmp = x[(x >= -2) & (x <= 2)] is executed, and then the last call to sys.time(). But overall it does give us some idea of how long the process took.

```
Sys.time()
[1] "2013-11-08 15:57:53 EST"
x = seq(-3, 3, by=0.0001)
length(x)
[1] 60001
start.time = Sys.time()
tmp = x[(x \ge -2) \& (x \le 2)]
Sys.time() - start.time
```

Time difference of 0.008060932 secs

```
package:base
                                                       R Documentation
system.time
CPU Time Used
Description:
     Return CPU (and other) times that 'expr' used.
Usage:
     system.time(expr, gcFirst = TRUE)
     unix.time(expr, gcFirst = TRUE)
Arguments:
   expr: Valid R expression to be timed.
gcFirst: Logical - should a garbage collection be performed
          immediately before the timing? Default is 'TRUE'.
Details:
     'system.time' calls the function 'proc.time', evaluates 'expr',
     and then calls 'proc.time' once more, returning the difference
     between the two 'proc.time' calls.
     'unix.time' is an alias of 'system.time', for compatibility with
     s.
     Timings of evaluations of the same expression can vary
     considerably depending on whether the evaluation triggers a
     garbage collection. When 'gcFirst' is 'TRUE' a garbage collection
     ('gc') will be performed immediately before the evaluation of
     'expr'. This will usually produce more consistent timings.
: 1
```

system.time() is better. It allows us to pass R code directly as an argument so the timing is more precise. And we can repeat the testing to see if the timing is consistent.

```
x = seq(-3, 3, by=0.0001)
length(x)
[1] 60001
system.time( tmp <- x[(x >= -2) & (x <= 2)] )
   user system elapsed
        0.000 0.003
  0.003
system.time( tmp \langle -x[(x >= -2) \& (x <= 2)] \rangle
   user system elapsed
  0.004
        0.000
                0.004
system.time( tmp \leftarrow x[(x \ge -2) \& (x \le 2)])
   user system elapsed
  0.003 0.000 0.003
```

If we wanted to replicate this many times, say 5, R has a function just for that purpose. Each column represents one execution of the system.time command. The results are stored in the columns.

Okay, how long would the comparable for loop take? x = seq(-3, 3, by=0.0001)length(x) [1] 60001 myfunc <- function(x) {</pre> hold = vector() for (ii in 1:length(x)) { if  $(x[ii] >= -2) & (x[ii] <= 2)) {$ hold[ii] = x[ii]return(hold) system.time( myfunc(x) ) user system elapsed 6.362 3.160 9.528 system.time( $x[(x \ge -2) \& (x \le 2)]$ ) # Big difference! user system elapsed 0.004 0.000 0.004

Actually, the bracket character is a function written in C which is why it is fast

```
> `[`
.Primitive("[")
```

Let's double the size of the vector and see how fast/slow the timings are.

```
x = seq(-3,3,by=0.000025)
length(x)
[1] 240001

system.time( x[(x >= -2) & (x <= 2)] )
   user system elapsed
   0.014   0.000   0.014

system.time( myfunc(x) )
   user system elapsed
109.284   45.376   154.782</pre>
```

Is there a tool that helps us do benchmarking? Yes. Several in fact. We will focus only on one here which is the rbencmark function.

You will have to install it since it is an add-on package. Use RStudio or the Windows GUI to do this or you can use the **install.packages** command. This package contains the function called **benchmark** which allows you to time the execution of any R function including those that you have written.

It replicates the function a specified number of times. You can also compare the performance of more than one function at a time. Let's start out simple. Here we will time how long it takes to square the x vector.

As mentioned this will be replicated some number times with the default being 100. We will get back a variety of information.

We can compare how long it takes to square it vs cubing it. We can also specify the information to be returned

```
benchmark( square = x^2, cube = x^3, replications=5, columns=c("test","elapsed"))
   test elapsed
2   cube   0.006
1   square   0.001
```

So it takes longer to cube the vector than it does to square it - That makes sense. Let's look back at our original problem now.

```
x = seq(-3,3,by=0.01)
length(x)
[1] 601
```

We can use the benchmark function to time the performance of the bracket notation vs. the for loop although we already have some ideas about that.

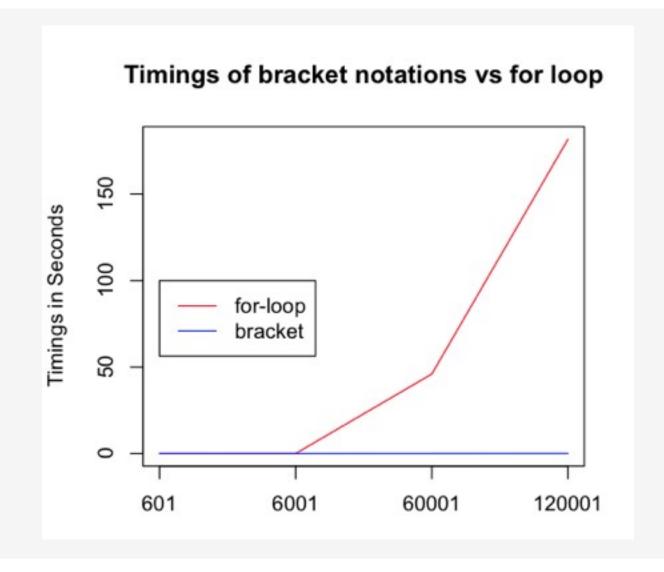
```
# Okay let's try it on a larger vector
x = seq(-3,3,0.01)
length(x)
[1] 601
t600 = benchmark(bracket = x[(x \ge -2) & (x \le 2)],
            forloop = myfunc(x),replications=10, columns=c("test","elapsed"))
t600
     test elapsed
1 bracket
            0.000
2 forloop
            0.023
```

```
# Okay let's try it on a larger vector
x = seq(-3,3,0.001)
# length(x)
# [1] 6001
t6K = benchmark(bracket = x[(x >= -2) & (x <= 2)],
            forloop = myfunc(x),replications=10, columns=c("test","elapsed"))
t6K
      test elapsed
1 bracket
            0.003
2 forloop 0.511
```

```
# Okay let's try it on a larger vector
x = seq(-3,3, 0.0001)
length(x)
[1] 60001
t60K = benchmark(bracket = x[(x >= -2) & (x <= 2)],
            forloop = myfunc(x),replications=10, columns=c("test","elapsed"))
t60K
     test elapsed
1 bracket
         0.034
2 forloop 46.021
```

```
# Okay let's try it on a larger vector
x = seq(-3,3, 0.00005)
length(x)
[1] 120001
t120K = benchmark(bracket = x[(x \ge -2) & (x \le 2)],
            forloop = myfunc(x),replications=10, columns=c("test","elapsed"))
t120K
     test elapsed
1 bracket
         0.067
2 forloop 179.109
```

```
mtimings = cbind(t600[,2],t6K[,2],t60K[,2],t120K[,2])
colnames(mtimings)=c("601","6001","60001","120001")
mtimings
       601 6001 60001
                         120001
[1,] 0.001 0.000 0.033
                          0.066
[2,] 0.024 0.027 46.009 181.679
plot(1:4, mtimings[2,], pch=18, col="red", type="1", xaxt="n",
           main="Timings of bracket notations vs for loop",
           ylab="Timings in Seconds")
points(1:4,mtimings[1,],type="1",col="blue")
axis(1,1:4,labels=colnames(mtimings),xlab=c("vector size in elements"))
legend(1,100,c("for-loop","bracket"),col=c("red","blue"),lty=c(1,1))
```



Use vectorized functions where-ever possible. These are functions that know how to handle vectors as arguments. Add up the elements of a vector:

#### Not vectorized:

```
total = 0
x = rnorm(100, mean=100, sd=2)
for (ii in 1:length(x)) {
    total = total + x[ii]
}
total
[1] 9985.895
Vectorized:
sum(x)
[1] 9985.895
sum
function (..., na.rm = FALSE) .Primitive("sum") # Written in C or FORTRAN
```

```
Given a vector find the maximum value:
```

```
set.seed(233)
x = rnorm(10000)
# Not vectorized:
maxval = x[1]
for (ii in 1:length(x)) {
   if (x[ii] > maxval) {
      maxval = x[ii]
maxval
[1] 3.983584
# Vectorized:
max(x)
[1] 3.983584
> max
function (..., na.rm = FALSE) .Primitive("max") # Written in C or FORTRAN
```

Given a data frame, exclude any rows that contain a missing value as indicated by the presence of NA. the built in data frame airquality has records like this:

```
airquality[5:6,]
 Ozone Solar.R Wind Temp Month Day
5
            NA 14.3
    NA
                      56
            NA 14.9 66 5 6
6
    28
Not vectorized:
                 Ugh!
jj = 1
mylist = list()
for (ii in 1:nrow(airquality)) {
   numofnas = grep("NA", airquality[ii,])
   if (length(numofnas) == 0) {
      mylist[[jj]] = airquality[ii,]
      jj = jj +1
   } else {
      next
nonadf = do.call(rbind, mylist)
```

Given a data frame, exclude any rows that contain a missing value as indicated by the presence of NA. The built in data frame airquality has records like this:

```
airquality[5:6,]
  Ozone Solar.R Wind Temp Month Day
5   NA   NA 14.3   56   5   5
6   28   NA 14.9   66   5   6

Vectorized: So much easier !

nonasdf = airquality[ complete.cases(airquality), ]
```

Given two vectors of the same length find the maximum between the corresponding elements.

```
v1 = c(1,2,3,4,5)
v2 = c(5,4,3,2,1)
# So we would get back 5,4,3,4,5
# Not vectorized: Please - No!
resvec = vector()
for (ii in 1:length(v1)) {
    if (v1[ii] >= v2[ii]) {
       resvec[ii] = v1[ii]
    } else {
       resvec[ii] = v2[ii]
resvec
[1] 5 4 3 4 5
```

Given two vectors of the same length find the maximum between the corresponding elements.

```
v1 = c(1,2,3,4,5)
v2 = c(5,4,3,2,1)

# So we would get back 5,4,3,4,5

# Vectorized: Ah yes !

pmax(v1,v2)
[1] 5 4 3 4 5
```

Always try to find a function that looks like it might do the job.

for loops aren't necessarily "evil" they just get slow when you use large input vectors. knowing how to write for loops will help you when learning other languages

Many times the vectorized solution requires little or no knowledge of programming.

Study the problem - determine what is being asked of you and then try to find functions that can help. Do some googling and/or use "??" within R

```
Need to do sums ? rowSums, colSums, sum,

Need to do statistics ? mean, sd, var, quantile, fivenum

Need to find missing values ? complete.cases, is.na

Need to find values in a vector based on conditions ? subset or bracket

Need to do something to each row/column of a matrix ? Use apply
```

Given these two vectors, find the element numbers in vec1 where the elements of vec2 match any element in vec1. So "b1" in vec2 matches the second element in vec1. "d3" in vec2 matches the fourth element in vec1. so we return 2 and 4

#### Not vectorized:

Given these two vectors, find the element numbers in vec1 where the elements of vec2 match any element in vec1. So "b1" in vec2 matches the second element in vec1. "d3" in vec2 matches the fourth element in vec1. so we return 2 and 4

#### **Vectorized:**

```
vec1 = c("a1", "b1", "c2", "d3")

vec2 = c("b1", "d3")

vec1 %in% vecb
[1] FALSE TRUE FALSE TRUE

is.element(vec1, vec2)
[1] FALSE TRUE FALSE TRUE

which(vec1 %in% vec2) # Pretty cool huh ?
[1] 2 4
```

In R you don't really have to think about allocating memory to structures before you use them. This is good and bad: Let's create a "blank" vector and then extend it to have 400000 elements which we will fill using a for loop:

```
somevec = vector() #
for (ii in 1:400000) {
    somevec[ii] = ii
}
```

Is this any different, better, or worse than preallocating space for the 400000 elements?

```
somevector = vector()
length(somevector) = 400000
for (ii in 1:400000) {
   somevec[ii] = ii
}
```

```
func1 <- function(size=400000) {</pre>
   somevec = vector()
   for (ii in 1:size) {
     somevec[ii] = ii
   return(somevec)
func2 <- function(size=400000) {</pre>
  somevec = vector()
  length(somevec) = size # We tell R explicitly the size of the vector
  for (ii in 1:400000) {
    somevec[ii] = ii
  return(somevec)
```

```
system.time(func1())
  user system elapsed
130.905 46.591 177.634

system.time(func2())
  user system elapsed
0.607 0.001 0.609
```

So preallocating memory does help this situation. Even if you don't know exactly how long the structure will be, you can always estimate it in advance and it will improve performance. But to really do this why not use the power of vectors:

```
system.time(somevec <- 1:400000) # Much faster
user system elapsed
0.000 0.000 0.001</pre>
```