Analysis of Algorithms I

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Algorithms

- Procedure to perform a task or solve a problem
- We have seen some examples: find primes, compute factorials / binomial coefficients
- Important theoretical questions:
  - Is an algorithm correct? (Does it *always* work?)
  - How much resource does the algorithm need?
- These questions are particularly interesting when multiple algorithms are available

Correctness

- When is an algorithm correct?
- The answer may depend on the input
- An algorithm may be correct for some inputs, not for others
- A specific input for a general problem is often called an *instance* of the problem
- To be correct, an algorithm must
  - Stop (after a finite number of steps), and
  - produce the *correct output*
- This must happen for *all possible inputs*, i.e., all *instances* of the problem

Efficiency

- *How efficient is an algorithm?*
- That is, how much of resources does the algorithm need?
- We are usually interested in efficiency in terms of
  - Time needed for the algorithm to execute
  - Amount of memory / storage needed while the algorithm runs
- The answer may again depend on the specific instance of the problem

Sorting

- We will study these questions mainly in the context of one specific problem, namely *sorting*
- The basic problem:
  - Input: A sequence of numbers $(a_1, a_2, ..., a_n)$
  - Desired output: A permutation of the input, $(b_1, b_2, ..., b_n)$ such that $b_1 \leq b_2 \leq ... \leq b_n$

- Sometimes we are interested in the *permutation* rather than the *permuted output*
- The a_i-s are known as *keys*.

Arrays

- The analysis of algorithms is both a practical and a theoretical exercise
- For a theoretical analysis of algorithms, we need
  - Abstract data structures to represent the input and output (and possibly intermediate objects)
  - Some rules or conventions regarding how these structures behave
- These structures and rules should reflect actual practical implementations
- For sorting, we usually need a simple data structure known as an *array*:
  - An array $A[1, ..., n]$ of length n is a sequence of length n.
  - The i-th element of an array A is denoted by $A[i]$
  - Each $A[i]$ acts as a *variable*, that is, we can assign values to it, and query its current value
  - The sub-array with indices i to j (inclusive) is often indicated by $A[i, ..., j]$

Insertion sort

- *Insertion sort* is a simple and intuitive sorting algorithm
- Basic idea:
  - Think of sorting a hand of cards
  - Start with an empty left hand and the cards face down on the table
  - Remove one card at a time from the table and insert it into the correct position in the left hand
  - To find its correct position, compare it with each of the cards already in the hand, from right to left
- Insertion sort is a good algorithm for sorting a small number of elements
- The following pseudo-code represents the insertion sort algorithm
- Here the input is an already-constructed array `A`
- The length of the array is given by the attribute `A.length`

```
insertion-sort(A)

for (j = 2 to A.length) {
    key = A[j] // Value to insert into the sorted sequence A[1,...,j-1]
    i = j - 1
    while (i > 0 and A[i] > key) {
        A[i+1] = A[i]
        i = i - 1
    }
    A[i+1] = key
}
```

Exercise

- Is it obvious that this algorithm works?
- Can you think of any other sorting algorithm?
- Is your algorithm more efficient than insertion sort?

Insertion sort in R

```
insertion.sort <- function(A, verbose = FALSE)
{
    if (length(A) < 2) return(A)
    for (j in 2:length(A)) {
        key <- A[j]
        i <- j - 1
        while (i > 0 && A[i] > key) {
            A[i+1] <- A[i]
            i <- i - 1
        }
        A[i+1] <- key
        if (verbose) cat("j =", j, ", i =", i,
                         ", A = (", paste(format(A), collapse = ", "), ")\n")
    }
    return (A)
}
```

- More or less same as the algorithm pseudo-code
- Addition `verbose` argument to print intermediate steps
- Due to R semantics, the result must be *returned* (not modified *in place*)
- This last behaviour has important practical implications (to be discussed later)

```
(A <- sample(10))
```

```
 [1]  2  1 10  6  4  8  5  7  9  3
```

```
insertion.sort(A)
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

```
(A <- round(runif(10), 2))
```

```
 [1] 0.67 0.33 0.92 0.84 0.35 1.00 0.55 0.18 0.90 0.05
```

```
insertion.sort(A)
```

```
 [1] 0.05 0.18 0.33 0.35 0.55 0.67 0.84 0.90 0.92 1.00
```

```
A
```

```
 [1] 0.67 0.33 0.92 0.84 0.35 1.00 0.55 0.18 0.90 0.05
```

```
insertion.sort(A, verbose = TRUE)
```

```
j = 2 , i = 0 , A = ( 0.33, 0.67, 0.92, 0.84, 0.35, 1.00, 0.55, 0.18, 0.90, 0.05 )
j = 3 , i = 2 , A = ( 0.33, 0.67, 0.92, 0.84, 0.35, 1.00, 0.55, 0.18, 0.90, 0.05 )
j = 4 , i = 2 , A = ( 0.33, 0.67, 0.84, 0.92, 0.35, 1.00, 0.55, 0.18, 0.90, 0.05 )
j = 5 , i = 1 , A = ( 0.33, 0.35, 0.67, 0.84, 0.92, 1.00, 0.55, 0.18, 0.90, 0.05 )
j = 6 , i = 5 , A = ( 0.33, 0.35, 0.67, 0.84, 0.92, 1.00, 0.55, 0.18, 0.90, 0.05 )
j = 7 , i = 2 , A = ( 0.33, 0.35, 0.55, 0.67, 0.84, 0.92, 1.00, 0.18, 0.90, 0.05 )
```

```
j = 8 , i = 0 , A = ( 0.18, 0.33, 0.35, 0.55, 0.67, 0.84, 0.92, 1.00, 0.90, 0.05 )
j = 9 , i = 6 , A = ( 0.18, 0.33, 0.35, 0.55, 0.67, 0.84, 0.90, 0.92, 1.00, 0.05 )
j = 10 , i = 0 , A = ( 0.05, 0.18, 0.33, 0.35, 0.55, 0.67, 0.84, 0.90, 0.92, 1.00 )
```

```
 [1] 0.05 0.18 0.33 0.35 0.55 0.67 0.84 0.90 0.92 1.00
```

Correctness

- Examples suggest that this algorithm works
- How can we formally prove correctness for all possible input (all instances)?
- Note that the algorithm works by running a loop
- The key observation is the following:

  > At the beginning of each loop (for any particular value of j), The first $j-1$ elements in $A[1,...,j-1]$ are the same as the first $j-1$ elements originally in the array, but they are now sorted.

Loop invariant

- This kind of statement is known as a *loop invariant*
- Such loop invariants can be used to prove correctness if we can show three things:
  - Initialization: It is true prior to the first iteration of the loop
  - Maintenance: If it is true before an iteration of the loop, it remains true before the next iteration
  - Termination: Upon termination, the invariant leads to a useful property
- The first two properties are similar to induction
- The third is important in the sense that a loop invariant is useless unless the third property holds

Loop invariant for insertion sort

Statement

> At the beginning of each loop (for any particular value of j), The first $j-1$ elements in $A[1,...,j-1]$ are the same as the first $j-1$ elements originally in the array, but they are now sorted.

Initialization

- Before starting the for loop for $j=2$, $A[1,...,j-1]$ is basically just $A[1]$, which is
  - trivially sorted, and
  - the same as the original $A[1]$

Maintenance

- At the beginning of the for loop with some value of j, $A[1,...,j-1]$ is sorted
- Informally, the while loop within each iteration works by
  - comparing $key = A[j]$ with $A[j-1], A[j-2], ..., A[1]$ (in that order)
  - moving them one position to the right, until the correct position of key is found
- Clearly, this while loop must terminate within at most j steps
- After the while loop ends, $key = A[j]$ is inserted in the correct position

- At the end, $A[1, ..., j]$ is a sorted version of the original $A[1, ..., j]$.
- Thus, the loop invariant is now true for index $j + 1$
- To be more formal, we could prove a loop invariant for the while loop also
- Will not go into that much detail

Termination

- The for loop essentially increments j by 1 every time it runs
- The loop terminates when $j > n = A.length$
- As each loop iteration increases j by 1, we must have $j = n + 1$ at that time
- Substituting $n + 1$ for j in the loop invariant, we have
  - $A[1, ..., n]$ has the same elements as it originally had, and is now sorted.
- Hence, the algorithm is correct.

Run time analysis

- It is natural to be interested in studying the efficiency of an algorithm
- Usually, we are interested in running time and memory usage
- Both these may depend on the size of the input, and often on the specific input
- If we have a practical implementation, we can simply run the algorithm to study running time
- Let's try this with the R implementation

Run time of R implementation

- We expect running time to depend on size of input
- To average out effect of individual inputs, we can consider multiple random inputs, e.g.,

```
x <- replicate(20, runif(100), simplify = FALSE) # list of 20 vectors
system.time(lapply(x, insertion.sort))
```

```
   user  system elapsed 
  0.008   0.000   0.008 
```

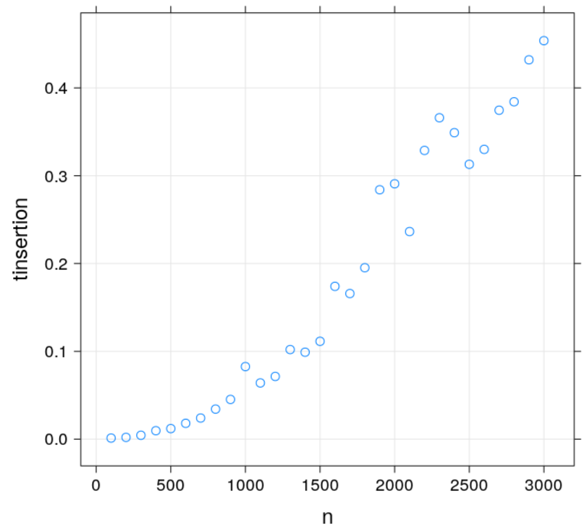
```
x <- replicate(20, runif(1000), simplify = FALSE)
system.time(lapply(x, insertion.sort))
```

```
   user  system elapsed 
  0.548   0.000   0.549 
```

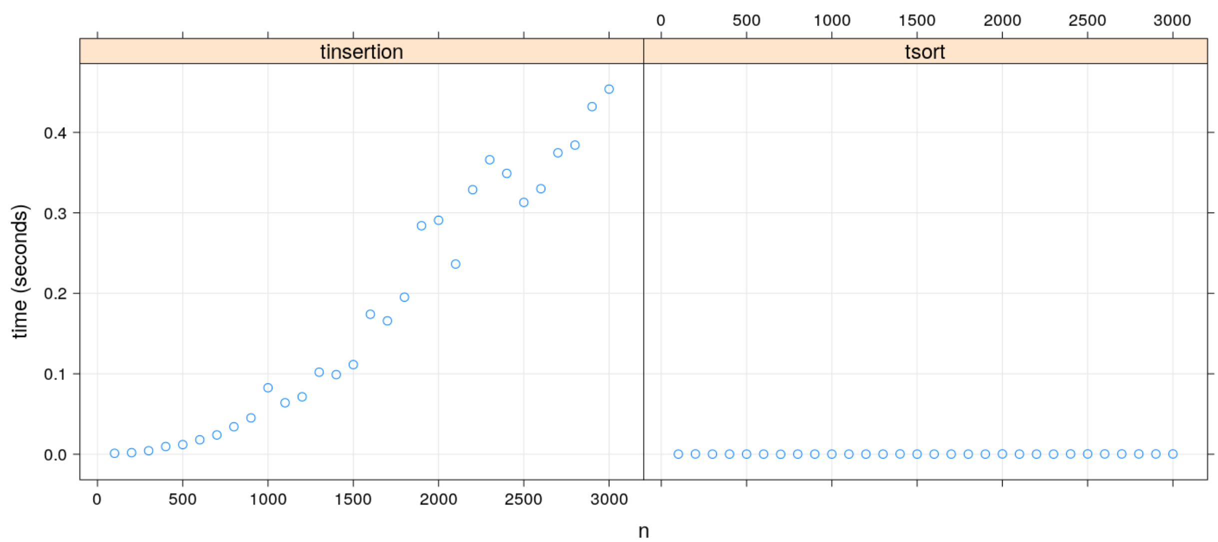
- Do this systematically for various input sizes

```
timeSort <- function(size, nrep = 20, sort.fun = insertion.sort)
{
    x <- replicate(nrep, runif(size), simplify = FALSE)
    system.time(lapply(x, sort.fun))["elapsed"] / nrep
}
n <- seq(100, 3000, by = 100)
tinsertion <- sapply(n, timeSort, nrep = 5, sort.fun = insertion.sort)
```

```
xyplot(tinsertion ~ n, grid = TRUE, aspect = "xy")
```




```
tsort <- sapply(n, timeSort, nrep = 5, sort.fun = sort) # built-in sort() function
xyplot(tinsertion + tsort ~ n, grid = TRUE, outer = TRUE, ylab = "time (seconds)")
```



Insertion sort in Python

- We can also implement the algorithm in Python
- Arrays are not copied when given as arguments, so changes modify original
- Python array index starts from 0, so need to suitably modify

```
def insertion_sort_py(A):
    for j in range(1, len(A)):
        key = A[j]
        i = j - 1
        while i > -1 and A[i] > key :
```

```
            A[i+1] = A[i]
            i = i - 1
        A[i+1] = key
```

```
import numpy as np
import time
x = np.random.uniform(0, 1, 10).round(2)
x
```

```
array([0.01, 0.84, 0.02, 0.06, 0.65, 0.17, 0.85, 0.26, 0.75, 0.93])
```

```
t0 = time.time()
insertion_sort_py(x)
t1 = time.time()
x
```

```
array([0.01, 0.02, 0.06, 0.17, 0.26, 0.65, 0.75, 0.84, 0.85, 0.93])
```

```
t1 - t0 # elapsed time in seconds
```

```
0.00815129280090332
```

Run time of Python implementation

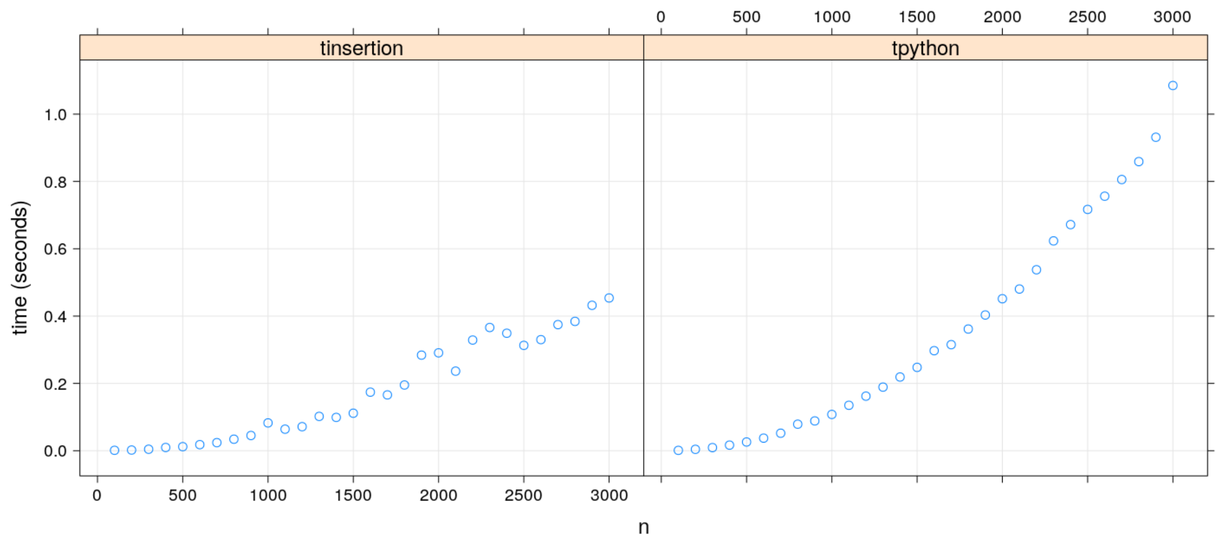
```
def time_sort(size, nrep, sortfun):
    total_time = 0.0
    for i in range(nrep):
        x = np.random.uniform(0, 1, size)
        t0 = time.time()
        sortfun(x)
        t1 = time.time()
        total_time += (t1 - t0)
    return total_time / nrep

nvals = range(100, 3001, 100)
tvals = [time_sort(i, 5, insertion_sort_py) for i in nvals]
print(tvals)
```

```
[0.0007145404815673828, 0.0027111530303955077, 0.005713224411010742, 0.010121440887451172, 0.01595230101
```

Run time comparison

```
library(reticulate) # to communicate between R and Python (ignore for now)
tpython <- py$tvals
xyplot(tinsertion + tpython ~ n, grid = TRUE, outer = TRUE, ylab = "time (seconds)")
```



Insertion sort in C++

- Yet another possibility is to implement the algorithm in C / C++
- We will use `Rcpp` so that we can easily call the function from R
- Array indexing starts from 0 (like Python), so similar modifications needed

```
#include <Rcpp.h>
using namespace Rcpp;

// [[Rcpp::export]]
NumericVector insertion_sort_rcpp_bad(NumericVector A)
{
    int i, j, n = A.size();
    double key;
    for (int j = 1; j < n; j++) {
        key = A[j];
        i = j - 1;
        while (i > -1 && A[i] > key) {
            A[i+1] = A[i];
            i = i - 1;
        }
        A[i+1] = key;
    }
    return A;
}
```

```
(A <- round(runif(10), 2))
```

```
 [1] 0.74 0.69 0.62 0.39 0.57 0.94 0.27 0.53 0.99 0.32
```

```
insertion_sort_rcpp_bad(A)
```

```
 [1] 0.27 0.32 0.39 0.53 0.57 0.62 0.69 0.74 0.94 0.99
```

```
A # changed!
```

```
 [1] 0.27 0.32 0.39 0.53 0.57 0.62 0.69 0.74 0.94 0.99
```

- C++ also does not copy arrays when given as arguments, so changes modify original
- This violates implicit contract of R functions, so we need to explicitly copy

```
#include <Rcpp.h>
using namespace Rcpp;

// [[Rcpp::export]]
NumericVector insertion_sort_rcpp(NumericVector x)
{
    int i, j, n = x.size();
    double key;
    NumericVector A = clone(x);
    for (int j = 1; j < n; j++) {
        key = A[j];
        i = j - 1;
        while (i > -1 && A[i] > key) {
            A[i+1] = A[i];
            i = i - 1;
        }
        A[i+1] = key;
    }
    return A;
}
```

```
(A <- round(runif(10), 2))
```

```
 [1] 0.50 0.13 0.95 0.18 0.23 0.83 0.01 0.42 0.05 0.42
```

```
insertion_sort_rcpp(A)
```

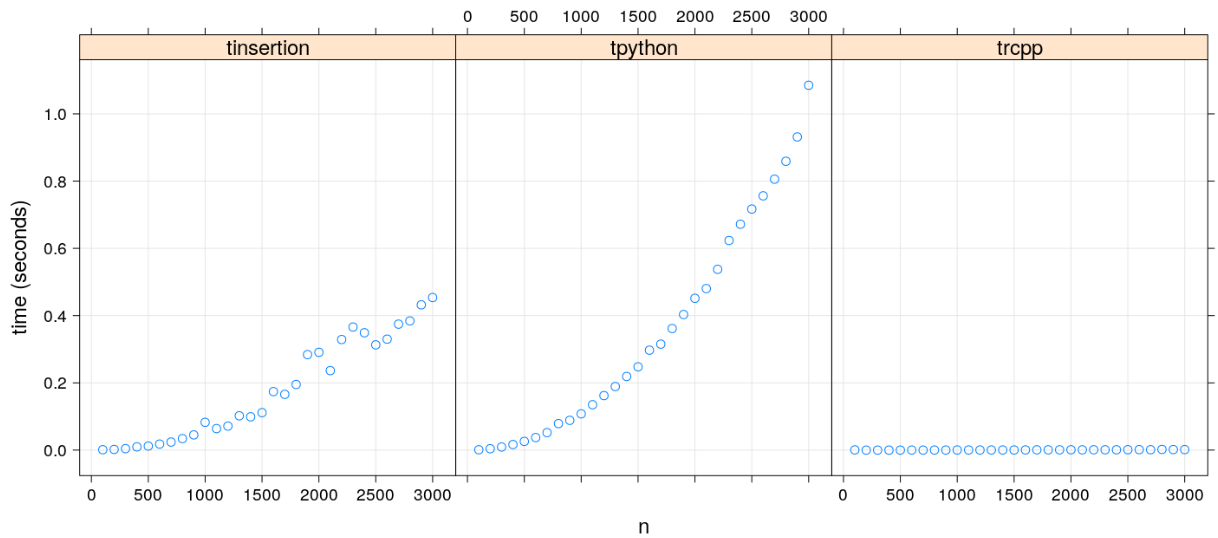
```
 [1] 0.01 0.05 0.13 0.18 0.23 0.42 0.42 0.50 0.83 0.95
```

```
A # unchanged
```

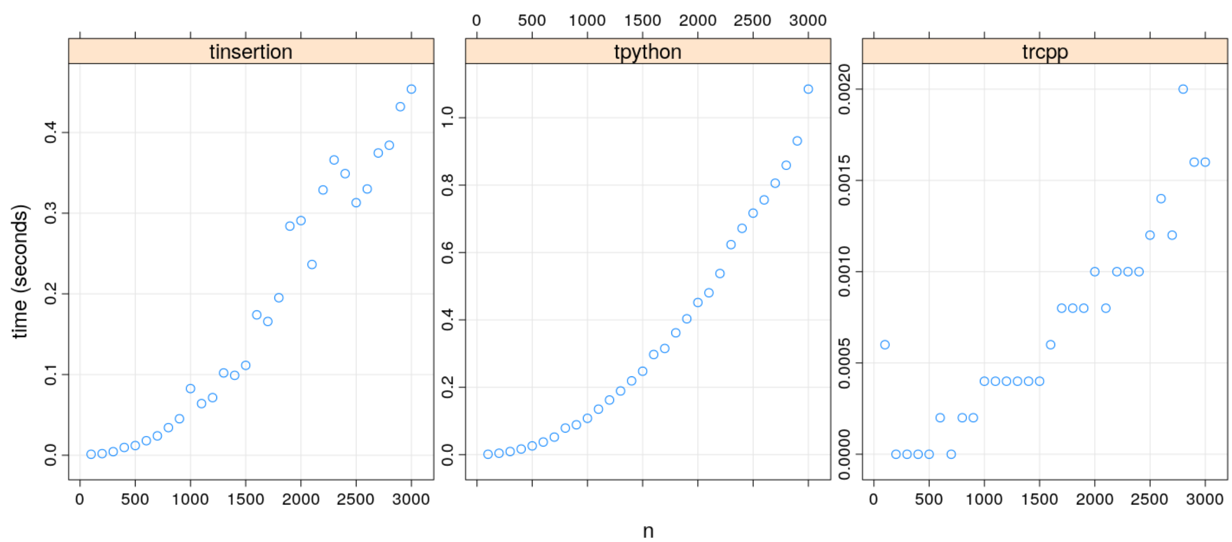
```
 [1] 0.50 0.13 0.95 0.18 0.23 0.83 0.01 0.42 0.05 0.42
```

Run time comparison

```
trcpp <- sapply(n, timeSort, nrep = 5, sort.fun = insertion_sort_rcpp)
xyplot(tinsertion + tpython + trcpp ~ n, grid = TRUE, outer = TRUE, ylab = "time (seconds)")
```

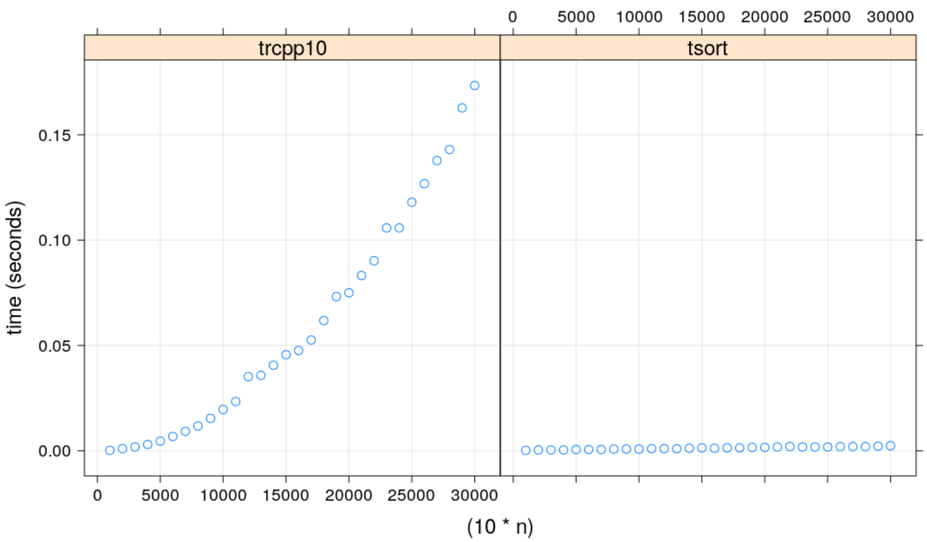



```r
xyplot(tinsertion + tpython + trcpp ~ n, grid = TRUE, outer = TRUE,
       scales = list(y = "free"), ylab = "time (seconds)")
```

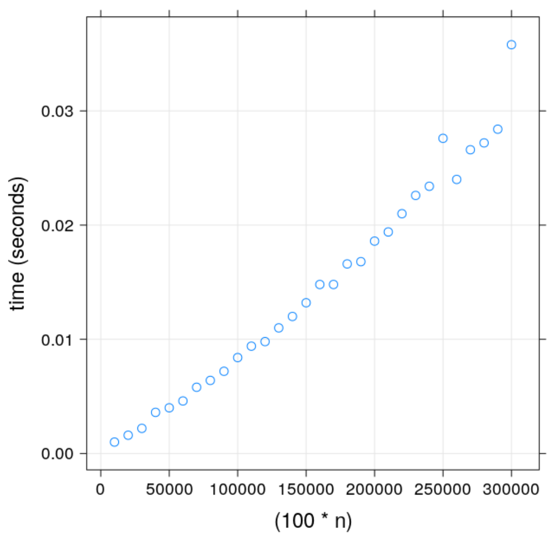


Run time comparison (for larger inputs)

```r
trcpp10 <- sapply(10 * n, timeSort, nrep = 5, sort.fun = insertion_sort_rcpp)
tsort <- sapply(10 * n, timeSort, nrep = 5, sort.fun = sort)
xyplot(trcpp10 + tsort ~ (10 * n), grid = TRUE, outer = TRUE, ylab = "time (seconds)", aspect = 1)
```




```
tsort <- sapply(100 * n, timeSort, nrep = 5, sort.fun = sort)
xyplot(tsort ~ (100 * n), grid = TRUE, outer = TRUE, ylab = "time (seconds)", aspect = 1)
```



Run time comparison: summary

- Run time may vary substantially depending on implementation
- Even a C++ implementation of insertion sort is mich slower than built in `sort()` in R
- As a crude approximation, run time of insertion sort seems to be roughly quadratic in input size
- Can we validate this observation theoretically?

Theoretical analysis of algorithms

- Analysis of an algorithm means predicting the resources requires by it, e.g.,

  - amount of memory
  - amount of input-output
  - (most commonly) amount of computational time
- This helps identify efficient algorithms when multiple candidates available
- Such analysis may indicate multiple viable candidates, but helps to discard inferior ones

Theoretical model

- Analysis of an algorithm requires a *model* of the implementation technology
- Specifically, we need model for the resources and their associated costs
- We will assume a *single-processor random access machine (RAM)* model
- This has a precise technical meaning, but for our purposes, it means that
  - Instructions are executed one after another, with no concurrent operations
  - Accessing any location in memory has the same cost, regardless of the location
- In particular, accessing variable values (memory look-up) requires constant time
- Arrays are assumed to occupy contiguous locations in memory
- In other words, location of $A[i]$ = location of $A[1]$ + constant * $(i - 1)$
- So accessing any $A[i]$ has same cost
- Drawback: arrays cannot be resized without incurring significant cost (by copying)
- We can be more precise, by
  - listing the set of basic instructions the machine can perform
  - E.g., add, multiply, data copy, move, branching, etc.
  - Model the cost of each such operation
- We will not try to be that precise
- With reasonable assumptions, we will still be able to do reasonable analysis

Runtime analysis of insertion sort

- Intuitively clear that time taken by insertion sort depends on several factors:
  - Size of the input (longer arrays will need more time)
  - Whether the array is already (almost) sorted (then the position of the key is found quickly in every step)
- We need to formalize both these dependencies
- Notion of *input size* depends on the context
  - For sorting problem, length of the input array is the natural notion
  - For multiplying two numbers, a reasonable notion may be their magnitudes
- To take the nature of input into account, we usually consider
  - worst case
  - best case
  - average case

How should we define "running time"?

- Ideally, sum of the times taken (or *cost*) for each basic instruction in the machine.
- We take a slightly different approach
- Instead of assigning a cost to each basic instruction, we assign a cost to each *step* in our algorithm
- Then, count the number of times each step is executed

Runtime analysis of insertion sort

- Try this for insertion sort
- Assume a cost for each line of the algorithm

`insertion-sort(A)`	cost
for (j = 2 to A.length) {	c_1
key = A[j]	c_2
i = j - 1	c_3
while (i > 0 and A[i] > key) {	c_4
A[i+1] = A[i]	c_5
i = i - 1	c_6
} \	
A[i+1] = key	c_7
}	

- We need to count the number of times each step is executed
- This depends on the number of times the while loop runs, which depends on the input
- Let t_j denote the number of times the while condition is tested for index j
- The test will be false for the last iteration (and the loop will not run)

`insertion-sort(A)`	cost	times
for (j = 2 to A.length) {	c_1	n
key = A[j]	c_2	$n-1$
i = j - 1	c_3	$n-1$
while (i > 0 and A[i] > key) {	c_4	$\sum_{j=2}^{n} t_j$
A[i+1] = A[i]	c_5	$\sum_{j=2}^{n}(t_j-1)$
i = i - 1	c_6	$\sum_{j=2}^{n}(t_j-1)$
} \		
A[i+1] = key	c_7	$n-1$
}		

- The total running time (cost) is

$$T(n) = c_1 n + (c_2 + c_3 + c_7)(n-1) + c_4\left(\sum t_j\right) + (c_5 + c_6)\left(\sum t_j - 1\right)$$

- Runtime of insertion sort

$$T(n) = c_1 n + (c_2 + c_3 + c_7)(n-1) + c_4\left(\sum t_j\right) + (c_5 + c_6)\left(\sum t_j - 1\right)$$

- Depends on the values of t_j
- If input is already sorted, then $t_j = 1$ for all j, and hence

$$T(n) = c_1 n + (c_2 + c_3 + c_7 + c_4)(n-1) = an + b,$$

- In other words, $T(n)$ is linear in n, with coefficients a and b that depend on the costs c_i
- This is the *best case* scenario
- Runtime of insertion sort

$$T(n) = c_1 n + (c_2 + c_3 + c_7)(n-1) + c_4 \left(\sum t_j\right) + (c_5 + c_6)\left(\sum t_j - 1\right)$$

- The *worst case* scenario is when the array is reverse sorted
- In that case, $t_j = j$ for all j
- Noting that $\sum_2^n j = \frac{n(n+1)}{2} - 1$ and $\sum_2^n (j-1) = \frac{n(n-1)}{2}$, we have

$$T(n) = an^2 + bn + c$$

- In other words, $T(n)$ is quadratic, with coefficients a, b, c that depend on the costs c_i
- The best case scenario is usually not of interest
- An algorithm is typically evaluated based on its worst case running time
- Another reasonable definition is the *average case* running time
- For the sorting problem, this is defined as the
  - Expected running time if the input is randomly ordered
  - More precisely, "randomly ordered" means all permutations are equally likely

Exercises

- Derive the average case running time of insertion sort
- Modify the insertion sort algorithm to return a *permutation* that will sort the input
- Specifically, `p <- insertion_order(A)` should give an index vector `p` such that `A[p]` is sorted
- Implement this modified algorithm using both R and Rcpp
- To use Rcpp, you must first install a compiler and other tools from here
- See also the RStudio page for Rcpp for other resources

Order of growth

- Note that we have ignored the exact costs c_i for each step
- Instead, we express the worst-case running time as $T(n) = an^2 + bn + c$
- As n grows larger, this is dominated by the n^2 term
- Lower order terms (linear and constant) are asymptotically insignificant compared to n^2
- For this reason, we usually simplify further and say that the *order of growth* of $T(n)$ is like n^2
- This is indicated using the notation

$$T(n) = \Theta(n^2)$$

- One algorithm is considered better than another if it has lower order of growth
- This is true even if the second one is faster for small input (as it will be slower for large enough input)
- If two algorithms have same order of growth, the coefficients may be important in practice

- However, theoretical analysis will usually consider them to be equivalent

Divide and Conquer

- Insertion sort is an *incremental algorithm*: modifies the input one step at a time
- Another common approach is known as "divide-and-conquer"
- Depends on a technique called *recursion* (an algorithm calling itself)
- The basic idea is:
  - **Divide** the problem into a number of subproblems that are smaller instances of the same problem
  - **Conquer** the subproblems by solving them recursively
  - **Combine** the solutions to the subproblems into the solution for the original problem

Merge sort

- The first example of this we study is called merge sort
- Loosely, it operates as follows
  - Divide: Divide the n-element sequence to be sorted into two subsequences of $n/2$ elements each
  - Conquer: Sort the two subsequences
    - If a subsequences is of length 1, it is already sorted, and there is nothing more to do
    - Otherwise, sort it recursively using merge sort
  - Combine: Merge the two sorted subsequences to produce the sorted answer
- The first two steps are essentially trivial
- Key operation: merge two sorted sequences in the "combine" step

The merge step

- Done using an auxiliary procedure MERGE(A, p, q, r), where
  - A is an array
  - p, q, and r are indices into the array such that $p \leq q < r$
  - Assumes that subarrays $A[p, ..., q]$ and $A[q+1, ..., r]$ are in sorted order
  - Goal is to merge them to into single sorted subarray that replaces the current subarray $A[p, ..., r]$
- The essential idea of MERGE is the following:
  - Suppose we have two sorted piles on the table, with the smallest cards on top
  - Start with a new empty pile
  - Look at the top two cards, pick the smaller one, and add to new pile
  - Repeat (if one pile empty, choose always from the other)

`merge(A, p, q, r)`

n_1 = q - p + 1
n_2 = r - q
Create new arrays L[1, ... , n_1+1] and R[1, ... , n_2+1]
for (i = 1, ... , n_1) { L[i] = A[p+i-1] }
for (j = 1, ... , n_2) { R[j] = A[q+j] }

```
L[ n₁+1 ] = ∞     ## sentinel values
R[ n₂+1 ] = ∞     ## ensures that L and R never become empty
i = 1
j = 1
for (k = p, . . . , r) {
    if (L[i] ≤ R[j]) {
        A[k] = L[i]
        i = i + 1
    }
    else {
        A[k] = R[j]
        j = j + 1
    }
}
```

- It is easy to see that the runtime of merge is linear in $n = r - p + 1$
- One comparison needed to fill every position
- To prove correctness, consider the loop invariant

  At the start of each iteration of the main for loop, the subarray $A[p, ..., k-1]$ contains the $k - p$ smallest elements of $L[1, ..., n_1 + 1]$ and $R[1, ..., n_2 + 1]$ in sorted order. Also, of the remaining elements, $L[i]$ and $R[j]$ are the smallest elements in their respective arrays.

Correctness of `merge`

Initialization

- Prior to the first iteration, we have $k = p$, so that the subarray $A[p, ..., k-1]$ is empty
- This empty subarray contains the $k - p = 0$ smallest elements of L and R
- As $i = j = 1$, $L[i]$ and $R[j]$ are the respective smallest elements not copied back into A

Maintenance

- Suppose that $L[i] \leq R[j]$
- Then $L[i]$ is the smallest element not yet copied back into A
- $A[p, ..., k-1]$ already contains the $k - p$ smallest elements of L and R
- So, after $L[i]$ is copied into $A[k]$, $A[p, ..., k]$ will contain the $k - p + 1$ smallest elements
- Incrementing k (in for loop) and i reestablishes the loop invariant for the next iteration
- If instead $L[i] > R[j]$, then the other branch maintains the loop invariant

Termination

- At termination, $k = r + 1$
- By loop invariant,

  the subarray $A[p, ..., k-1] \equiv A[p, ..., r]$, contains the $k - p = r - p + 1$ smallest elements of $L[1, ..., n_1]$ and $R[1, ..., n_2]$, in sorted order
- The arrays L and R together contain $n_1 + n_2 + 2 = r - p + 3$ elements
- All but the two largest have been copied back into A, and these two largest elements are the sentinels

Merge sort

- Using merge, the merge sort algorithm is now implemented as

```
merge-sort(A, p, r)

if (p < r) {
    q = floor( (p+r)/2 )
    merge-sort(A, p, q)
    merge-sort(A, q+1, r)
    merge(A, p, q, r)
}
```

- In general, this sorts the subarray $A[p, ..., r]$
- It is initially called as merge$(A, 1, n)$ for an n-element input array

Analysis of divide and conquer algorithms

- The runtime of merge sort can be expressed as a recurrence

$$T(n) = \begin{cases} \Theta(1) & n \leq 1 \\ 2T(\lceil n/2 \rceil) + \Theta(n) & \text{otherwise} \end{cases}$$

- $\Theta(1)$ represents a constant cost of sorting a 0 or 1-element array
- The $\Theta(n)$ term is the cost of merging, including the (constant) cost of computing the split
- We will later see a general result that helps to solve recurrences of this form
- For now, we will derive the solution for merge sort based on heuristic arguments

Analysis of merge sort

- We do this by constructing a so-called *recursion tree*
- For convenience, we assume that the input size n is an exact power of 2
- This means that each split is of exactly half the size
- This lets us rewrite the recurrence in a simpler form:

$$T(n) = \begin{cases} c & n = 1 \\ 2T(n/2) + cn & n > 1 \end{cases}$$

Recursion tree for merge sort

- Main observations:
  - Each level of the tree requires cn time
  - There are $1 + \log_2 n$ levels in total
- This gives a total runtime of

$$T(n) = cn(1 + \log_2 n) = \Theta(n \log n)$$

Growth of functions

- Before moving on, we will briefly discuss asymptotic growth notation
- Formally, we are interested in the behaviour of a function $f(n)$ as $n \to \infty$
- All functions we consider are from $\mathbb{N} \to \mathbb{R}$
- Sometimes we may abuse notation and consider functions with domain $\mathbb{R}$

Θ-notation

- Given a function $g : \mathbb{N} \to \mathbb{R}$, we define the *set*

$$\begin{aligned}\Theta(g(n)) = \{f(n) \quad | \quad & \exists\, c_1, c_2 > 0 \text{ and } N \in \mathbb{N} \text{ such that} \\ & n \geq N \implies 0 \leq c_1 g(n) \leq f(n) \leq c_2 g(n)\}\end{aligned}$$

- That is, $f(n) \in \Theta(g(n))$ if $f(n)$ can be asymptotically bounded on both sides by multiples of $g(n)$
- We will usually write $f(n) = \Theta(g(n))$ to mean the same thing.
- Note that this definition implicitly requires $f(n)$ to be asymptotically non-negative
- We will assume this here as well as for other asymptotic notations used in this course.
- The Θ notation is used to indicate *exact* order of growth
- The next two notations indicate upper and lower bounds

O-notation

- The O-notation (usually pronounced "big-oh") indicates an asymptotic upper bound

$$O(g(n)) = \{f(n) \mid \exists\, c > 0 \text{ and } N \in \mathbb{N} \text{ such that } n \geq N \implies 0 \leq f(n) \leq cg(n)\}$$

- As before, we usually write $f(n) = \Theta(g(n))$ to mean $f(n) \in \Theta(g(n))$
- Note that $f(n) = \Theta(g(n)) \implies f(n) = O(g(n))$, that is, $\Theta(g(n)) \subseteq O(g(n))$
- The O-notation is important because upper bounds are often easier to prove (than lower bounds)
- That is often a sufficiently useful characterization of an algorithm

Ω-notation

- The Ω-notation (pronounced "big-omega") similarly indicates an asymptotic lower bound

$$\Omega(g(n)) = \{f(n) \mid \exists\, c > 0 \text{ and } N \in \mathbb{N} \text{ such that } n \geq N \implies 0 \leq cg(n) \leq f(n)\}$$

- The proof of the following theorem is an exercise:

$$f(n) = \Theta(g(n)) \iff f(n) = \Omega(g(n)) \text{ and } f(n) = O(g(n))$$

- So, for example, if $T(n)$ is the running time of insertion sort, then we can say that

$$T(n) = \Omega(n) \text{ and } T(n) = O(n^2)$$

- But *not* that

$$T(n) = \Theta(n) \text{ or } T(n) = \Theta(n^2)$$

- However, if $T(n)$ denotes the worst-case running time of insertion sort, then

$$T(n) = \Theta(n^2)$$

Arithmetic with asymptotic notation

- We will often do casual arithmetic with asymptotic notation
- Most of the time this is OK, but we should be careful about potential ambiguity
- Example: Consider the statement

$$an^2 + bn + c = an^2 + \Theta(n)$$

- Here we use $\Theta(n)$ to actually mean a *function* $f(n) \in \Theta(n)$ (in this case, $f(n) = bn + c$)
- Similarly, we could write

$$2n^2 + \Theta(n) = \Theta(n^2)$$

- This means that whatever the choice of $f(n) \in \Theta(n)$ in the LHS, $2n^2 + f(n) = \Theta(n^2)$
- This kind of abuse of notation can sometimes lead to amiguity
- For example, if $f(n) = \Theta(n)$, then

$$\sum_{i=1}^{n} f(i) = \Theta(n(n+1)/2) = \Theta(n^2)$$

- We may write the following to mean the same thing:

$$\sum_{i=1}^{n} \Theta(i)$$

- But this is not the same as $\Theta(1) + \Theta(2) + \cdots + \Theta(n)$
  - This may not even make sense (what is $\Theta(2)$?)
  - Each $\Theta(i)$ may represent a different function

o- and ω-notation

- The O- and Ω-notations indicate bounds that may or may not be asymptotically "tight"
- The "little-oh" and "little-omega" notations indicate strictly *non-tight* bounds

$$o(g(n)) = \{f(n) \colon \text{ for all } c > 0, \ \exists \ N \in \mathbb{N} \text{ such that } n \geq N \implies 0 \leq f(n) \leq cg(n)\}$$

- and

$$\omega(g(n)) = \{f(n) \colon \text{ for all } c > 0, \ \exists \ N \in \mathbb{N} \text{ such that } n \geq N \implies 0 \leq cg(n) \leq f(n)\}$$

- Essentially, as $f(n)$ and $g(n)$ are asymptotically non-negative,

$$f(n) = o(g(n)) \implies \limsup \frac{f(n)}{g(n)} = 0 \implies \lim \frac{f(n)}{g(n)} = 0$$

- Similarly, $f(n) = \omega(g(n)) \implies \lim \frac{f(n)}{g(n)} = \infty$
- Refer to *Introduction to Algorithms* (Cormen et al) for further properties of asymptotic notation
- We will use these properties as and when necessary

Analyzing Divide and Conquer algorithms

- As seen for merge sort, the runtime analysis of a divide-and-conquer algorithm usually involves solving a recurrence
- Let $T(n)$ be the running time on a problem of size n
- We can write

$$T(n) = \begin{cases} \Theta(1) & \text{if } n \leq c \\ aT(n/b) + D(n) + C(n) & \text{otherwise} \end{cases}$$

- where $T(n)$ is constant if the problem is small enough (say $n \leq c$ for some constant c), and otherwise
  - the division step produces a subproblems, each of size n/b
  - $D(n)$ is the time taken to divide the problem into subproblems,
  - $C(n)$ is the time taken to combine the sub-solutions.
- There are three common methods to solve recurrences.
  - The *substitution method*: guess a bound and then use mathematical induction to prove it correct
  - The *recursion-tree method*: convert the recurrence into a tree, and use techniques for bounding summations to solve the recurrence
  - The *master method* provides bounds for recurrences of the form $T(n) = aT(n/b) + f(n)$ for certain functions $f(n)$ that cover most common cases

The substitution method

- The substitution method is basically to
  1. Guess the form of the solution, and
  2. Use mathematical induction to verify it
- Example (similar to merge sort): Find an upper bound for the recurrence

$$T(n) = 2T(n/2) + n$$

- Suppose we guess that the solution is $T(n) = O(n \log_2 n)$
- We need to prove that $T(n) \leq cn \log_2 n$ for some constant $c > 0$
- Assume this holds for all positive $m < n$, in particular,

$$T(n/2) \leq \frac{cn}{2} \log_2 \frac{n}{2}$$

- Substituting, we have (provided $c \geq 1$)

$$
\begin{aligned}
T(n) = & \quad 2T(n/2) + n \\
\leq & \quad 2\frac{1}{2}cn\log_2(n/2) + n \\
= & \quad cn\log_2 n - cn\log_2 2 + n \\
= & \quad cn\log_2 n - cn + n \\
\leq & \quad cn\log_2 n
\end{aligned}
$$

- Technically, we still need to prove the guess for a boundary condition.
- Let's try for $n = 1$:
  - Require $T(1) \leq c\ 1\log_2 1 = 0$
  - Not possible for any realistic value of $T(1)$
  - So the solution is not true for $n = 1$
- However, for $n = 2$:
  - Require $T(2) \leq c\ 2\log_2 2 = 2c$
  - Can be made to hold for some choice of $c > 1$, whatever the value of $T(2) = 2T(1) + 2$
- Similarly for $T(3)$
- Note that for $n > 3$, the induction step never makes use of $T(1)$ directly
- Remark: be careful not to use asymptotic notation in the induction step
- Consider this proof to show $T(n) = O(n)$, assuming $T(m) \leq cm$ for $m < n$

$$
\begin{aligned}
T(n) = & \quad 2T(n/2) + n \\
\leq & \quad 2cn/2 + n \\
\leq & \quad cn + n \\
= & \quad O(n)
\end{aligned}
$$

- The last step is invalid
- Unfortunately, making a good guess is not always easy, limiting the usefulness of this method

The recursion tree method

- This is the method we used to calculate the merge sort run time
- Usually this is helpful to derive a guess that we can then formally prove using recursion

The master method

- **The Master theorem**: Let $a \geq 1$ and $b > 1$ be constants, let $f(n)$ be a function, and

$$T(n) = aT(n/b) + f(n)$$

- Here n/b could also floor or ceiling of n/b
- Then $T(n)$ has the following asymptotic bounds:
  1. If $f(n) = O(n^{\log_b a - \varepsilon})$ for some constant $\varepsilon > 0$, then $T(n) = \Theta(n^{\log_b a})$
  2. If $f(n) = \Theta(n^{\log_b a})$, then $T(n) = \Theta(n^{\log_b a}\log_2 n) = \Theta(f(n)\log_2 n)$
  3. If $f(n) = \Omega(n^{\log_b a + \varepsilon})$ for some constant $\varepsilon > 0$, and if $af(n/b) \leq cf(n)$ for some constant $c < 1$ and all sufficiently large n, then $T(n) = \Theta(f(n))$

- We will not prove the master theorem
- Note that we are essentially comparing $f(n)$ with $n^{\log_b a}$
- whichever is bigger (by a polynomial factor) determines the solution
- If they are the same size, we get an additional $\log n$ factor
- Additionally, the third case needs a regularity condition on $f(n)$
- Exercise: Use the master theorem to obtain the asymptotic order for

$$T(n) = T(n/2) + cn$$