# Lists

**Douglas Wilhelm Harder, M.Math. LEL**
Department of Electrical and Computer Engineering
University of Waterloo
Waterloo, Ontario, Canada

ece.uwaterloo.ca
dwharder@alumni.uwaterloo.ca



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# Outline

We will now look at our first abstract data structure

- Relation: explicit linear ordering
- Operations
- Implementations of an abstract list with:
  - Linked lists
  - Arrays
- Memory requirements
- Strings as a special case
- The STL `vector` class

3.1

# Definition

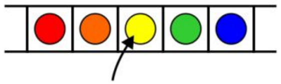
An Abstract List (or List ADT) is linearly ordered data where the programmer explicitly defines the ordering

We will look at the most common operations that are usually
- The most obvious implementation is to use either an array or linked list
- These are, however, not always the most optimal

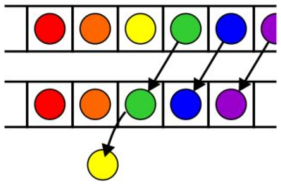
# Operations

Operations at the $k^{\text{th}}$ entry of the list include:

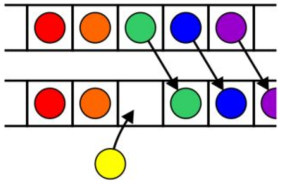
Access to the object



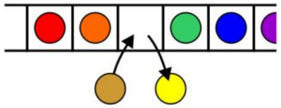
Erasing an object



Insertion of a new object



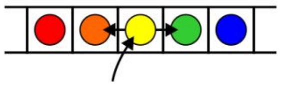
Replacement of the object



3.1.1

# Operations

Given access to the $k^{\text{th}}$ object, gain access to either the previous or next object



Given two abstract lists, we may want to

- Concatenate the two lists
- Determine if one is a sub-list of the other

3.1.2

# Locations and run times

The most obvious data structures for implementing an abstract list are arrays and linked lists

- We will review the run time operations on these structures

We will consider the amount of time required to perform actions such as finding, inserting new entries before or after, or erasing entries at

- the first location (the *front*)
- an arbitrary ($k^{\text{th}}$) location
- the last location (the *back* or $n^{\text{th}}$)

The run times will be $\Theta(1)$, $\mathrm{O}(n)$ or $\Theta(n)$

3.1.3

# Linked lists

We will consider these for

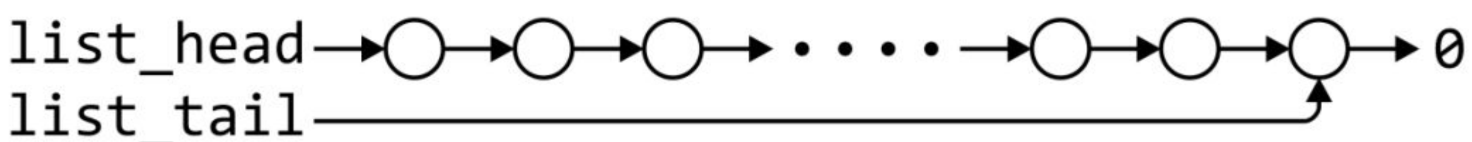
- Singly linked lists
- Doubly linked lists

3.1.3.1

# Singly linked list

| | Front/$1^{st}$ node | $k^{th}$ node | Back/$n^{th}$ node |
|---|---|---|---|
| Find | $\Theta(1)$ | $O(n)$ | $\Theta(1)$ |
| Insert Before | $\Theta(1)$ | $O(n)$ | $\Theta(n)$ |
| Insert After | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Replace | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Erase | $\Theta(1)$ | $O(n)$ | $\Theta(n)$ |
| Next | $\Theta(1)$ | $\Theta(1)^*$ | n/a |
| Previous | n/a | $O(n)$ | $\Theta(n)$ |

$^*$ These assume we have already accessed the $k^{th}$ entry—an $O(n)$ operation

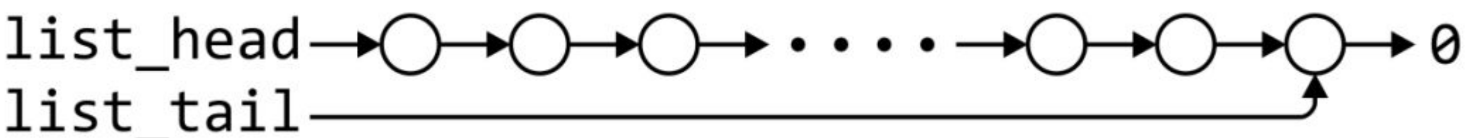


3.1.3.1

# Singly linked list

| | Front/$1^{st}$ node | $k^{th}$ node | Back/$n^{th}$ node |
|---|---|---|---|
| Find | $\Theta(1)$ | $O(n)$ | $\Theta(1)$ |
| Insert Before | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Insert After | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Replace | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Erase | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(n)$ |
| Next | $\Theta(1)$ | $\Theta(1)^*$ | n/a |
| Previous | n/a | $O(n)$ | $\Theta(n)$ |

By replacing the value in the node in question, we can speed things up
– useful for interviews

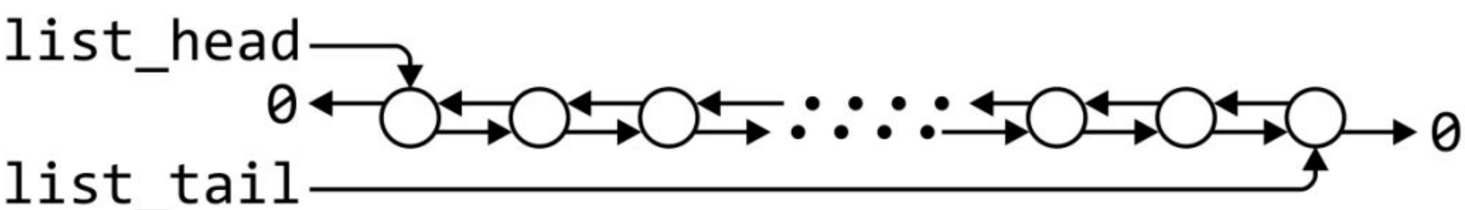


3.1.3.2

# Doubly linked lists

| | Front/$1^{st}$ node | $k^{th}$ node | Back/$n^{th}$ node |
|---|---|---|---|
| Find | $\Theta(1)$ | $O(n)$ | $\Theta(1)$ |
| Insert Before | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Insert After | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Replace | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Erase | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ |
| Next | $\Theta(1)$ | $\Theta(1)^*$ | n/a |
| Previous | n/a | $\Theta(1)^*$ | $\Theta(1)$ |

* These assume we have already accessed the $k^{th}$ entry—an $O(n)$ operation

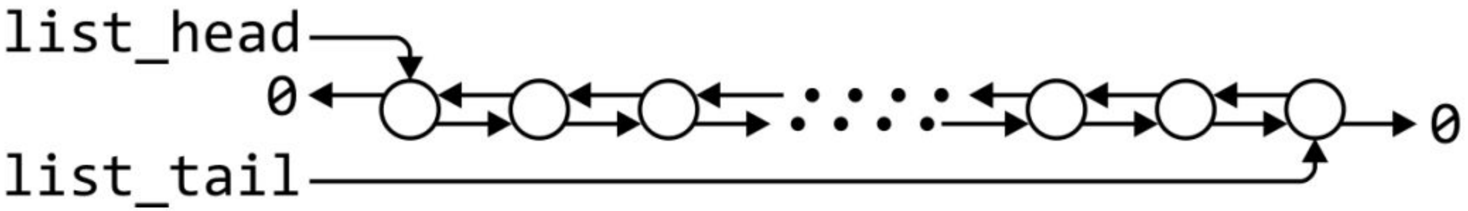


3.1.3.2

# Doubly linked lists

Accessing the $k^{\text{th}}$ entry is $\mathrm{O}(n)$

| | $k^{\text{th}}$ node |
|---|---|
| Insert Before | $\Theta(1)$ |
| Insert After | $\Theta(1)$ |
| Replace | $\Theta(1)$ |
| Erase | $\Theta(1)$ |
| Next | $\Theta(1)$ |
| Previous | $\Theta(1)$ |



# 3.1.3.3 Other operations on linked lists

Other operations on linked lists include:

- Allocation and deallocating the memory requires $\Theta(n)$ time
- Concatenating two linked lists can be done in $\Theta(1)$
  - This requires a tail pointer

# Arrays

We will consider these operations for arrays, including:

- Standard or one-ended arrays
- Two-ended arrays

3.1.4

# Standard arrays

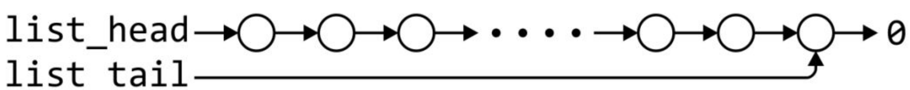
We will consider these operations for arrays, including:

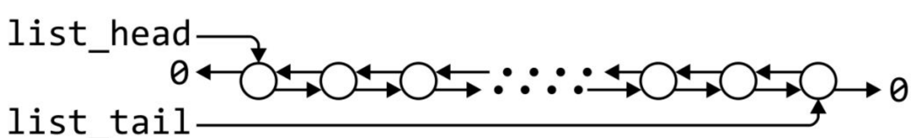
- Standard or one-ended arrays
- Two-ended arrays

# Run times

| | Accessing the $k^{\text{th}}$ entry | Insert or erase at the Front | Insert or erase at the $k^{\text{th}}$ entry | Insert or erase at the Back |
|---|---|---|---|---|
| Singly linked lists | $O(n)$ | $\Theta(1)$ | $\Theta(1)^*$ | $\Theta(1)$ or $\Theta(n)$ |
| Doubly linked lists | | | | $\Theta(1)$ |
| Arrays | $\Theta(1)$ | $\Theta(n)$ | $O(n)$ | $\Theta(1)$ |
| Two-ended arrays | | $\Theta(1)$ | | |

* Assume we have a pointer to this node




# Data Structures

In general, we will only use these basic data structures if we can restrict ourselves to operations that execute in $\mathbf{\Theta}(1)$ time, as the only alternative is $\mathbf{O}(n)$ or $\mathbf{\Theta}(n)$

Interview question: in a singly linked list, can you speed up the two $\mathbf{O}(n)$ operations of

- Inserting before an arbitrary node?
- Erasing any node that is not the last node?

If you can replace the contents of a node, the answer is "yes"

- Replace the contents of the current node with the new entry and insert after the current node
- Copy the contents of the next node into the current node and erase the next node

# Memory usage versus run times

All of these data structures require $\Theta(n)$ memory

- Using a two-ended array requires one more member variable, $\Theta(1)$, in order to significantly speed up certain operations
- Using a doubly linked list, however, required $\Theta(n)$ additional memory to speed up other operations

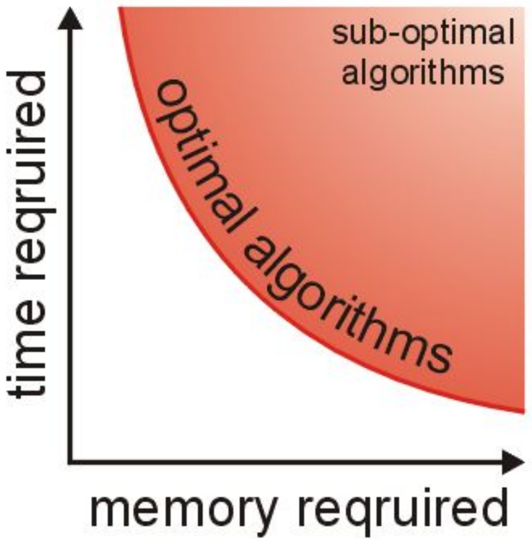
# Memory usage versus run times

As well as determining run times, we are also interested in memory usage

In general, there is an interesting relationship between memory and time efficiency

For a data structure/algorithm:

- Improving the run time usually requires more memory
- Reducing the required memory usually requires more run time



# Memory usage versus run times

Warning: programmers often mistake this to suggest that given any solution to a problem, any solution which may be faster must require more memory

This guideline not true in general: there may be different data structures and/or algorithms which are both faster and require less memory

- This requires thought and research

# The `sizeof` Operator

In order to determine memory usage, we must know the memory usage of the various built-in data types and classes

- The **`sizeof`** operator in C++ returns the number of bytes occupied by a data type
- This value is determined at compile time
  - It is **not** a function

# The **sizeof** Operator

```
#include <iostream>
using namespace std;

int main() {
	cout << "bool      " << sizeof( bool )     << endl;
	cout << "char      " << sizeof( char )     << endl;
	cout << "short     " << sizeof( short )    << endl;
	cout << "int       " << sizeof( int )      << endl;
	cout << "char *    " << sizeof( char * )   << endl;
	cout << "int *     " << sizeof( int * )    << endl;
	cout << "double    " << sizeof( double )   << endl;
	cout << "int[10]   " << sizeof( int[10] )  << endl;

	return 0;
}
```

```
{eceunix:1} ./a.out # output
bool       1
char       1
short      2
int        4
char *     4
int *      4
double     8
int[10]    40
{eceunix:2}
```

# Abstract Strings

A specialization of an Abstract List is an Abstract String:

- The entries are restricted to *characters* from a finite *alphabet*
- This includes regular strings "Hello world!"

The restriction using an alphabet emphasizes specific operations that would seldom be used otherwise

- Substrings, matching substrings, string concatenations

It also allows more efficient implementations

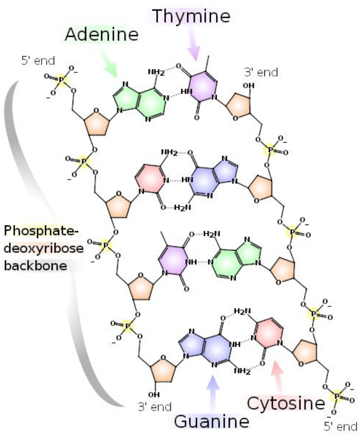
- String searching/matching algorithms
- Regular expressions

# Abstract Strings

Strings also include DNA

- The alphabet has 4 *characters*: A, C, G, and T
- These are the nucleobases:

  adenine, cytosine, guanine, and thymine




Bioinformatics today uses many of the algorithms traditionally restricted to computer science:

- Dan Gusfield, *Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology*, Cambridge, 1997

  http://books.google.ca/books?id=STGlsyqtjYMC
- References:

  http://en.wikipedia.org/wiki/DNA

  http://en.wikipedia.org/wiki/Bioinformatics

# Standard Template Library

In this course, you must understand each data structure and their associated algorithms

- In industry, you will use other implementations of these structures

The C++ Standard Template Library (STL) has an implementation of the `vector` data structure

- Excellent reference:

  http://www.cplusplus.com/reference/stl/vector/

# Standard Template Library

```
#include <iostream>
#include <vector>
using namespace std;
int main() {
    vector<int> v( 10, 0 );

    cout << "Is the vector empty?  " << v.empty() << endl;
    cout << "Size of vector:  "      << v.size()  << endl;

    v[0] = 42;
    v[9] = 91;

    for ( int k = 0; k < 10; ++k ) {
        cout << "v[" << k << "] = " << v[k] << endl;
    }

    return 0;
}
```

```
$ g++ vec.cpp
$ ./a.out
Is the vector empty?  0
Size of vector:  10
v[0] = 42
v[1] = 0
v[2] = 0
v[3] = 0
v[4] = 0
v[5] = 0
v[6] = 0
v[7] = 0
v[8] = 0
v[9] = 91
$
```

# Summary

In this topic, we have introduced Abstract Lists

- Explicit linear orderings
- Implementable with arrays or linked lists
  - Each has their limitations
  - Introduced modifications to reduce run times down to $\Theta(1)$
- Discussed memory usage and the `sizeof` operator
- Looked at the String ADT
- Looked at the `vector` class in the STL

# References

[1] Donald E. Knuth, *The Art of Computer Programming, Volume 1: Fundamental Algorithms*, 3rd Ed., Addison Wesley, 1997, §2.2.1, p.238.

[2] Weiss, Data Structures and Algorithm Analysis in C++, 3rd Ed., Addison Wesley, §3.3.1, p.75.

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Sincerely,

Douglas Wilhelm Harder, MMath
**dwharder@alumni.uwaterloo.ca**