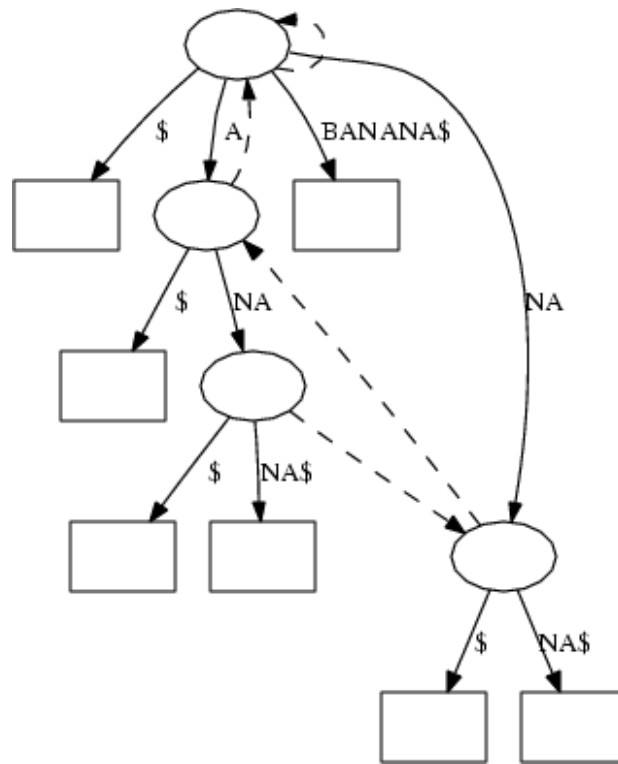


# Algorithms and Analysis

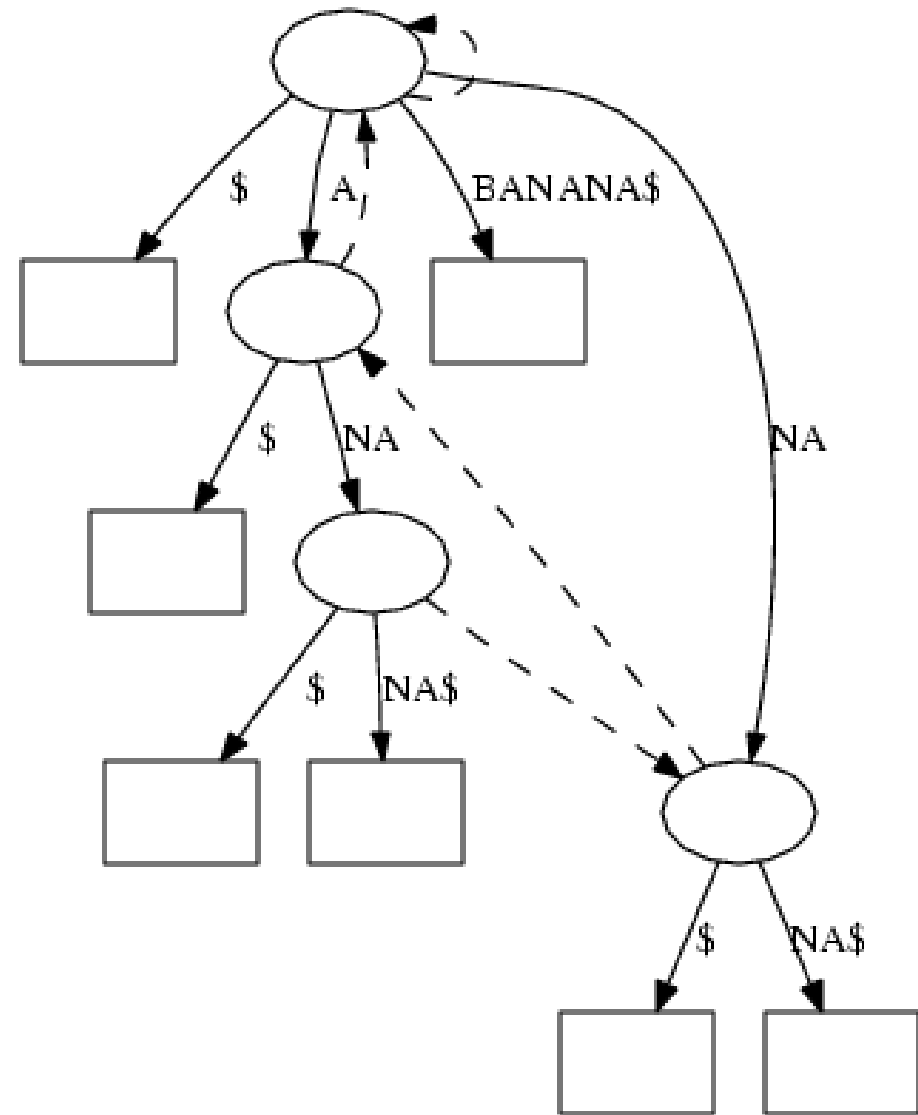
## Lesson 1: *Use Data Structures and Algorithms!*



*Course structure, examples of data structures and algorithms*

# Outline

1. **Course structure**
2. Example of Using DSA
3. Sophisticated Program
4. State-of-the-Art



# Welcome to Further Mathematics and Algorithms

- First 7 weeks Daniela and I will be teaching you about algorithms
- The last 4 weeks you will learn some further maths
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# Quick Survey on C++

- Who considers themselves a competent coder in C++?



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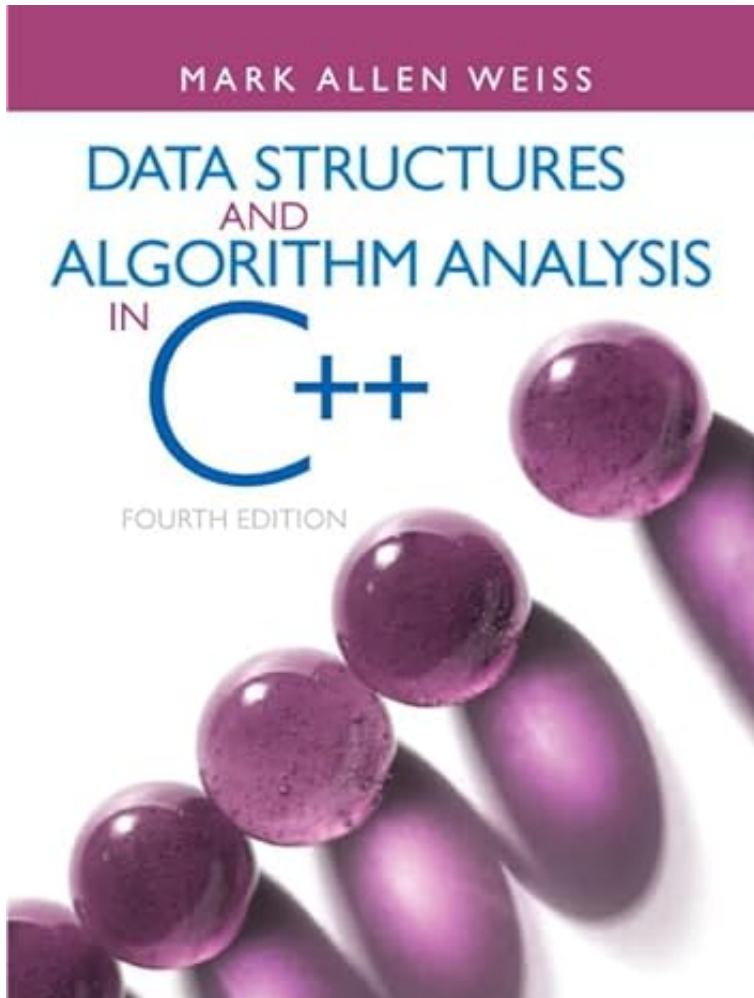
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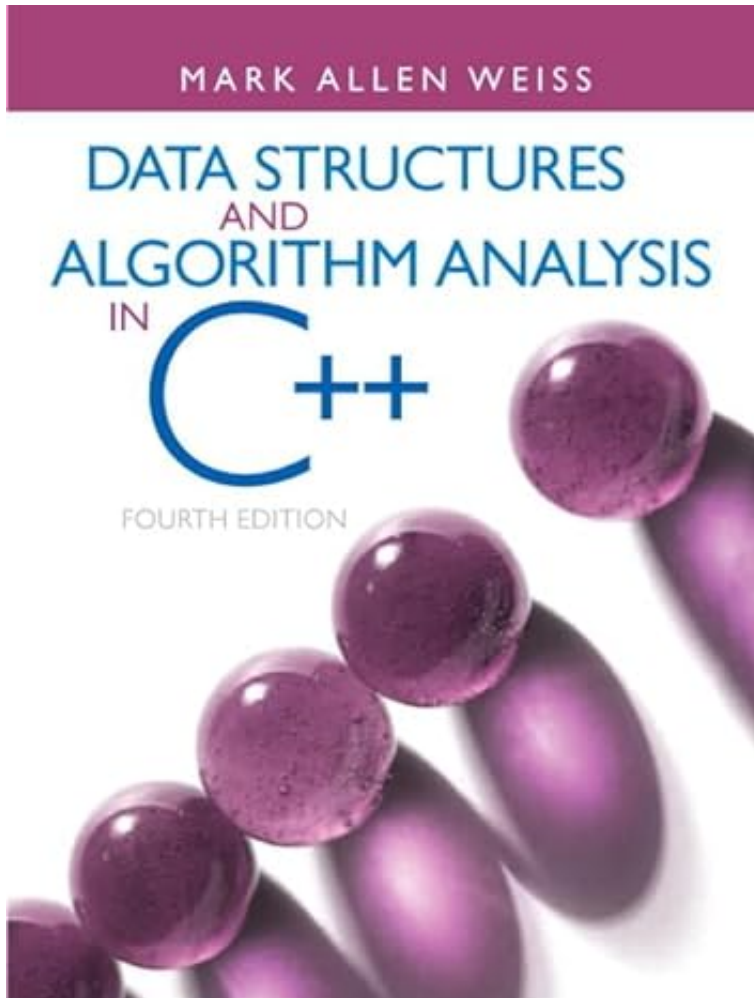
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- Who has heard of *resource acquisition is initialisation (RAII)*?

# Recommended Course Text



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  - ★ Not huge, but covers all the basics
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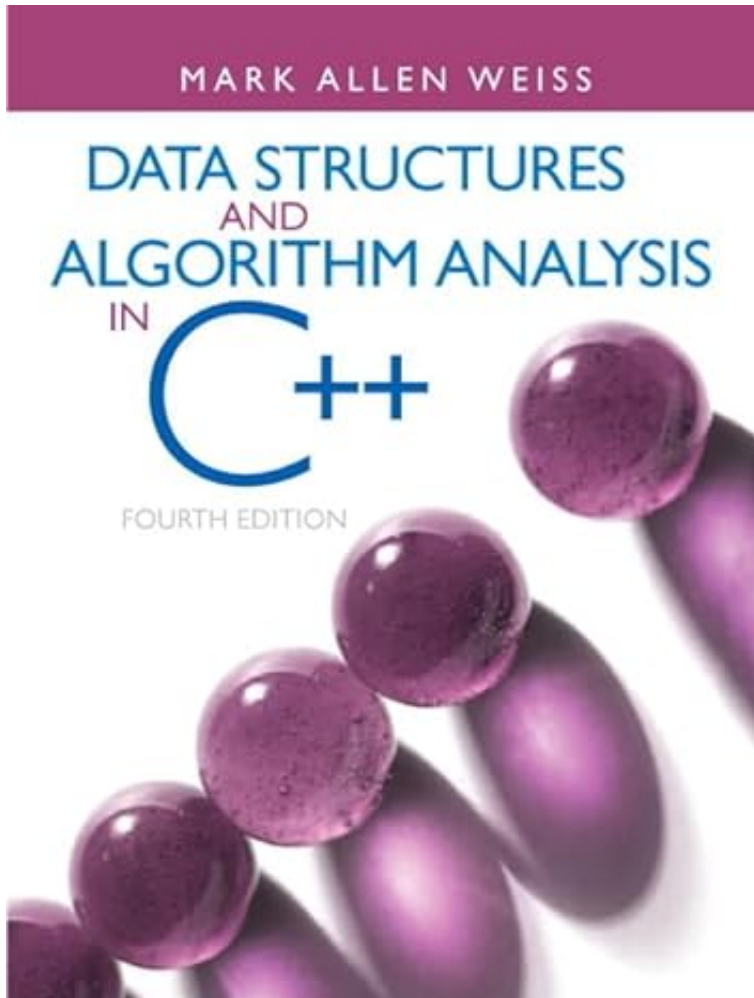
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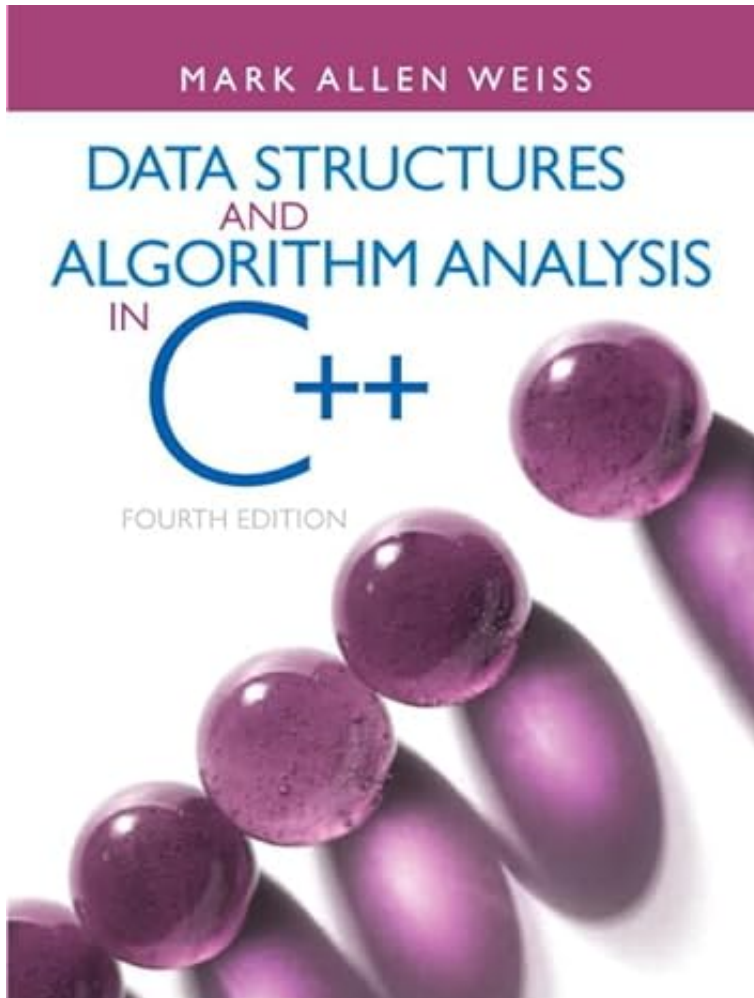


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# What is a Data Structure?

*any of various methods of organising data items (as records) in a computer*

- Container for data
- E.g. sets, stacks, lists, trees, graphs
- Clean interface, e.g. `push`, `pop`, `delete`
- Usually designed for fast or convenient access

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# Exemplary OO-Software

- Abstraction from details of problem
- Declaration of intention
- Clean interfaces
- Hidden implementations
- Makes programs readable and maintainable
- Reuse code—don't even have to write it yourself

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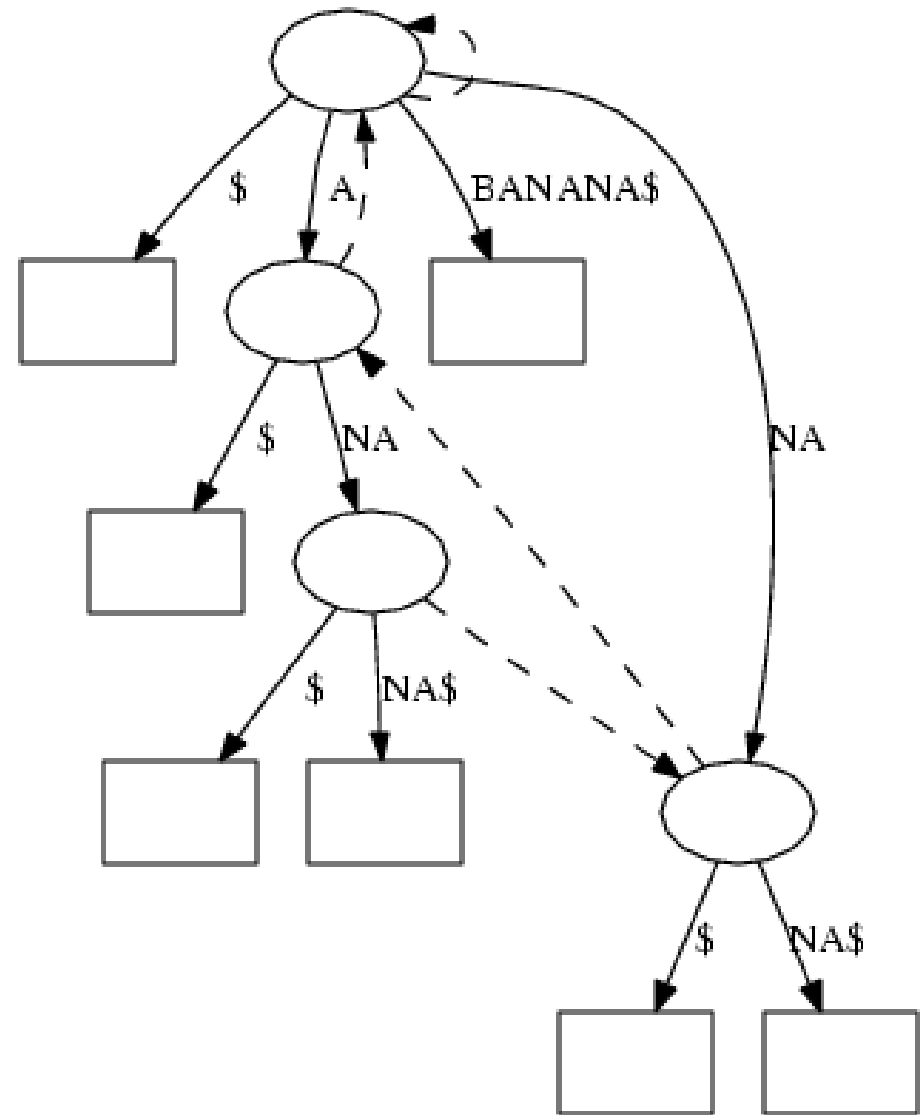
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*Thou shall not re-implement common data structures*

# Outline

1. Course structure
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# Example: Sort program

- Suppose we want to write a program to
  - ★ read an input file of integers
  - ★ sort the integers
  - ★ write a list of integers to standard out
- In Unix there is a command called `sort` which does just this
- Note that you don't know the number of inputs

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# Code for sort

```
#include <iostream>
#include <fstream>

int main(int argc, char** argv) {
    std::ifstream myfile(argv[1]);

    int array_size = 10;
    int* array = new int[array_size];
    int cnt = 0;
    while(myfile.good()) {
        if (cnt==array_size) {
            int* new_array = new int[2*array_size];
            for(int i=0; i<array_size; ++i)
                new_array[i] = array[i];
            delete[] array;
            array = new_array;
            array_size *= 2;
        }
        myfile >> array[cnt++];
    }
}
```



```
for(int i=0; i<cnt; ++i) {  
    int index = 0;  
    for(int j=1; j<cnt-i; ++j) {  
        if (array[j]<array[index])  
            index = j;  
    }  
    std::cout << array[index] << std::endl;  
    array[index] = array[cnt-i-1];  
}  
}
```

# Notes on Code

- Details of code don't matter
- Simple program ( $\sim 20$  lines of code)
- Uses a simple array
- Difficult to see what is going on
- On 100 000 inputs it takes 10 seconds to run

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# Using Data Structures and algorithms

```
#include <iostream>
#include <fstream>
#include <iterator>
#include <vector>
#include <algorithm>
using namespace std;

int main(int argc, char *argv[])
{
    ifstream in(argv[1]);
    vector<int> data;
    copy(istream_iterator<int>(in), istream_iterator<int>(),
        back_inserter(data));
    sort(data.begin(), data.end());
    copy(data.begin(), data.end(), ostream_iterator<int>(cout, "\n"));
}
```

# Sorting Doubles

```
#include <iostream>
#include <fstream>
#include <iterator>
#include <vector>
#include <algorithm>
using namespace std;

int main(int argc, char *argv[])
{
    ifstream in(argv[1]);
    vector<double> data;
    copy(istream_iterator<double>(in), istream_iterator<double>(),
        back_inserter(data));
    sort(data.begin(), data.end());
    copy(data.begin(), data.end(), ostream_iterator<double>(cout, "\n"));
}
```



# Notes on C++

- `vector<int>` is the C++ standard resizable array
- input/output is treated as a copy
- Code is easy to read
  - ★ Declare `vector<int>` or `vector<double>`
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Data structure version is

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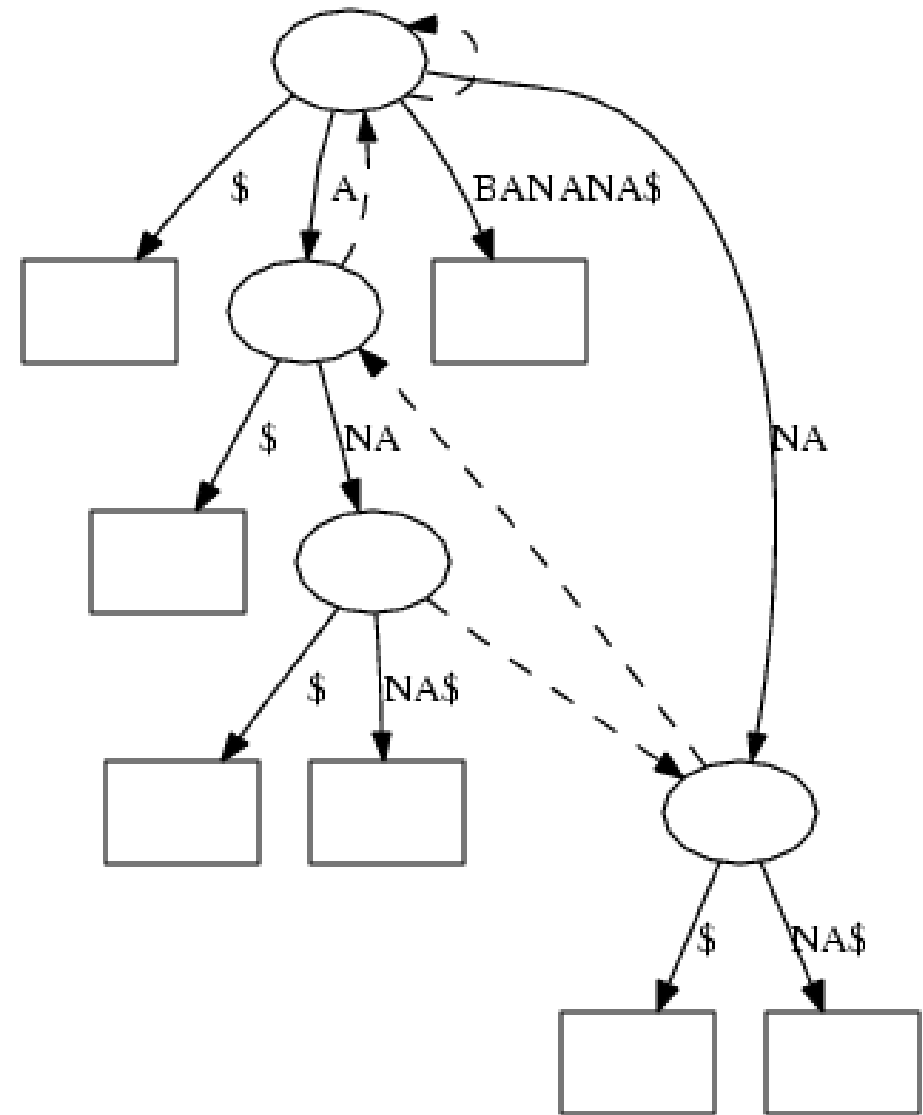
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# Sophisticated Programs

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# countWords

```
#include <stuff>

int main(int argc, char** argv) {
    ifstream in(argv[1]);
    map<string, int> words;

    string s;
    while(in >> s) {
        ++words[s];
    }

    vector<pair<string,int> > pairs;
    copy(words.begin(), words.end(), back_inserter(pairs));
    sort(pairs.begin(), pairs.end(),
        [](auto& a, auto&b){return a.second>b.second;});

    for(auto w=pairs.begin(); w!=pairs.end(); ++w) {
        cout << w->first << "_occurs_" << w->second << "_times\n";
    }
}
```

# Using countWords

```
> countWords text.dat | more
the occurs 97 times
of occurs 96 times
to occurs 57 times
and occurs 42 times
a occurs 36 times
be occurs 31 times
will occurs 26 times
we occurs 23 times
that occurs 23 times
is occurs 21 times
have occurs 19 times
freedom occurs 18 times
```

# Programming Challenge

- Run on “I have a dream” speech with 1550 words in 0.02 seconds
- Challenge for good programmers

*Write a program without use data structures in less than 10 times as much code that runs in less than 10 times as long*

- Probably possible, but certainly not easy



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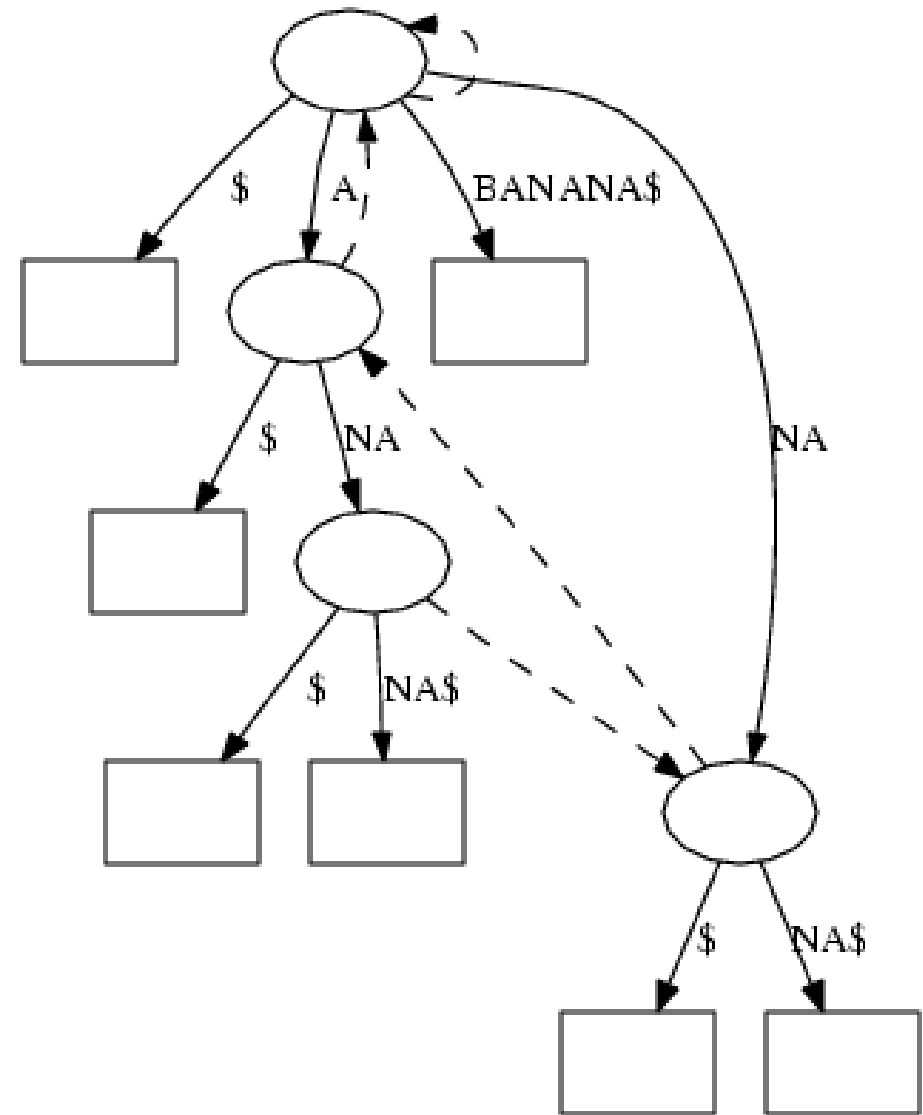
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# Sequencing and Assembly

A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

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ATACCAACCATGCCTCCTTTGCTCCAATATTAAATTCAGGCG  
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TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
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ATACC

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TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
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CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
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ATACCAACCAT

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CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
TACCA	CACCA	CCTTG	CTCCA	TATTA	AATTC

# Sequencing and Assembly

ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG

ATACCAACCATGCCTCC

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
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ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG

ATACCAACCATGCCTCCTT

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
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ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG

ATACCAACCATGCCTCCTTT

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
TACCA	CACCA	CCTTG	CTCCA	TATTA	AATTC

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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
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ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG

ATACCAACCATGCCTCCTTTGCT

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AAAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AAAT	CAAGG	TGCCT
TACCA	CACCA	CCTTG	CTCCA	TATTA	AAATTC

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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G C T C

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
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ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG  
ATACCAACCATGCCTCCTTTGCTCCCAATATTAAATTCAGGCG

ATACCAACCATGCCTCCTTTGCTCC

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AAAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AAAT	CAAGG	TGCCT
TACCA	CACCA	CCTTG	CTCCA	TATTA	AAATTC

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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G C T C C A

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
TACCA	CACCA	CCTTG	CTCCA	TATTA	AATTC

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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G C T C C A A T A T

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
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ATACCAACCATGCCTCCTTTGCTCCCAATATTAA

TTGCT	TACCA	CAAGG	TTAAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
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TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
TACCA	CACCA	CCTTG	CTCCA	TATTA	AATTC

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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
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TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
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A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G  
A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

A T A C C A C C A T G C C T C C T T G C T C C A A T A T T A A T T C A A G G C G

TTGCT	TACCA	CAAGG	TTAAT	TTCAA	TCCTT
TGCCT	AATAT	CCTCC	AGGCG	ATACC	ACCAT
CTCCT	CCTTG	ATGCC	GCTCC	TGCCT	TTGCT
TGCTC	ACCAC	TTGCT	AATAT	CAAGG	TGCCT
TACCA	CACCA	CCTTG	CTCCA	TATTA	AATTC

# New Generation Sequencers

- The estimated cost of sequencing the human genome in 2005 was \$10 000 000
- To reduce the cost there was and is a drive to produce new sequencing machines
- These tend to read much shorter sections of DNA (e.g. 20-100nt)
- Can these be assembled?

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# Repeats

- The difficulty of assembly is caused by repeats

A T A C C A C C A T G C C T C C T T G C T C C A A T C C A C C A T C A A G G C G

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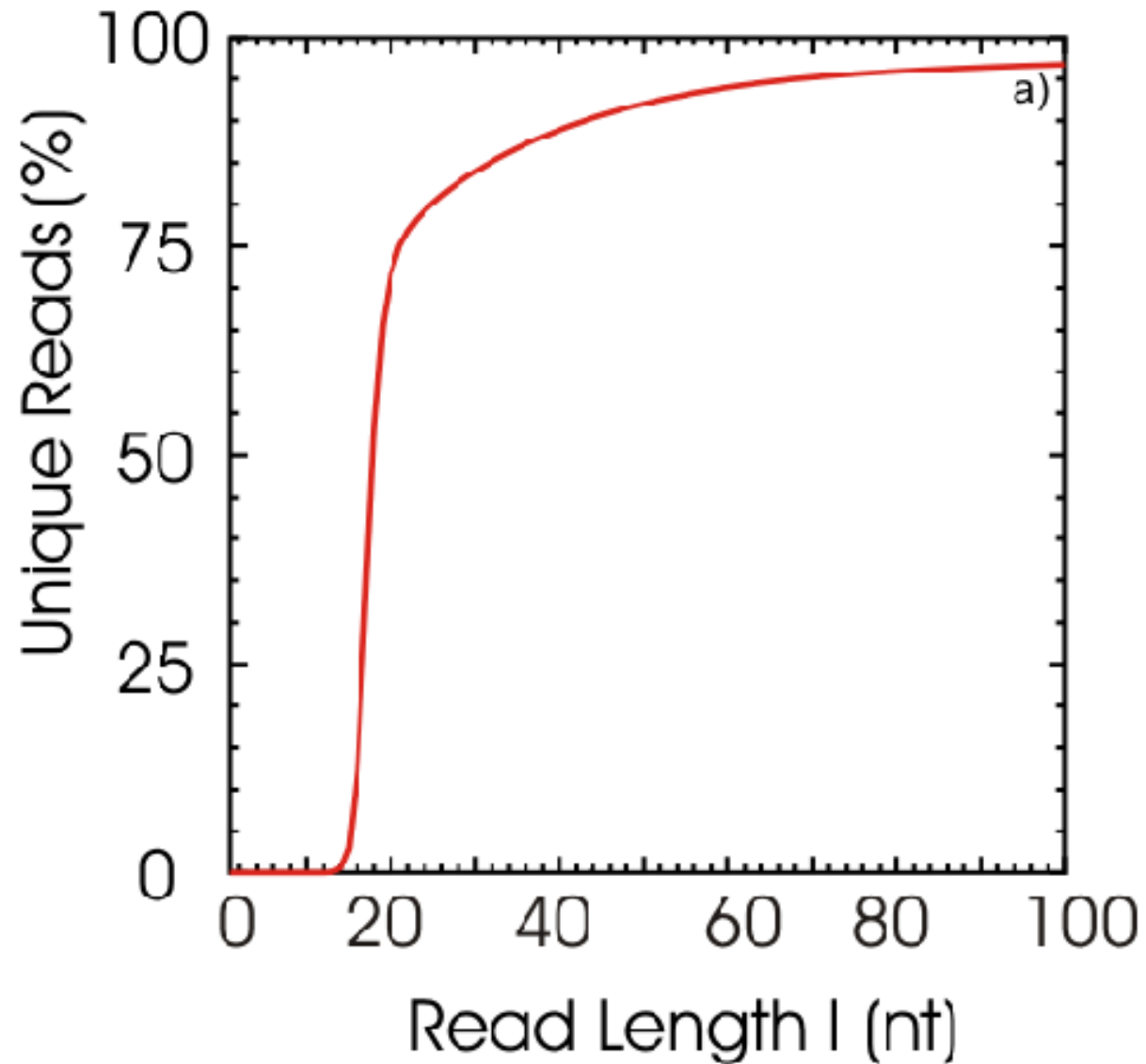
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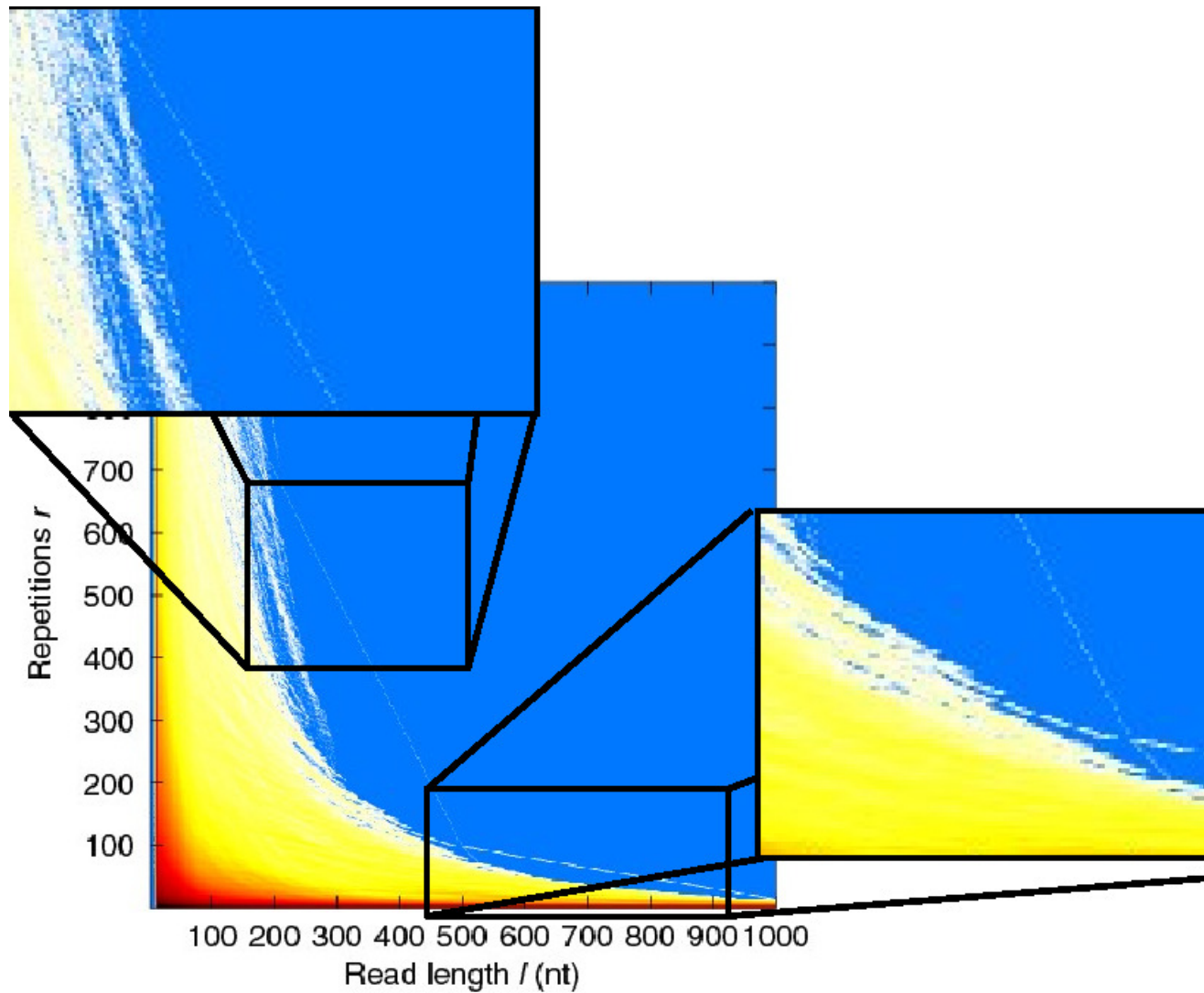
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# Repeats in Human Genome



# Repeats Structure



# Computing Repeats

- A naive program would take  $n^2$  operations where  $n = 6.4 \times 10^9$
- If we used this we would still be waiting for the program to finish
- Could not answer this question a few years ago
- Used state-of-the-art suffix arrays
- Smart algorithms allow you to do things which you cannot do otherwise

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# To Use DSA You Need To

- Know what common data structures and algorithm do
- Understand the implementations enough to modify existing data structures to be fit for purpose
- Understand time/space complexity to select the right data structure or algorithm
- Understand software interfaces for DSA
- Be able to combine data structures
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