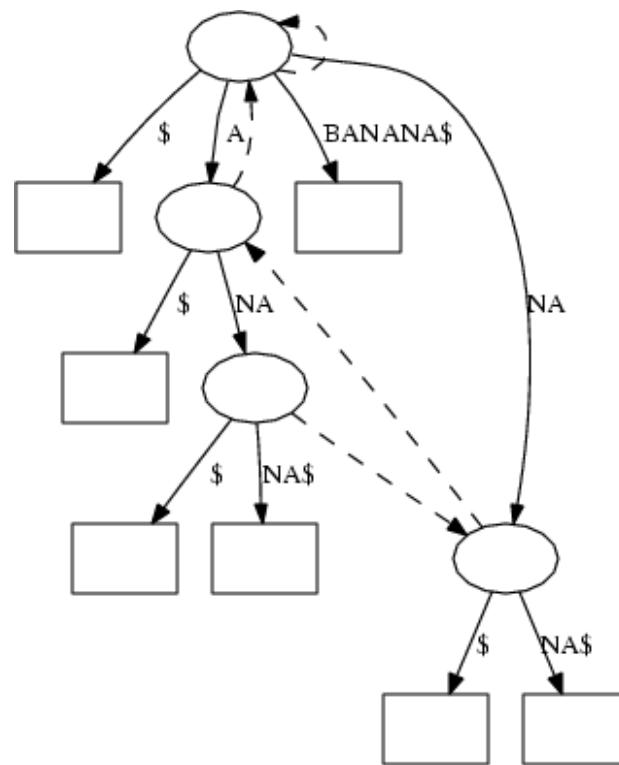


Algorithms and Analysis

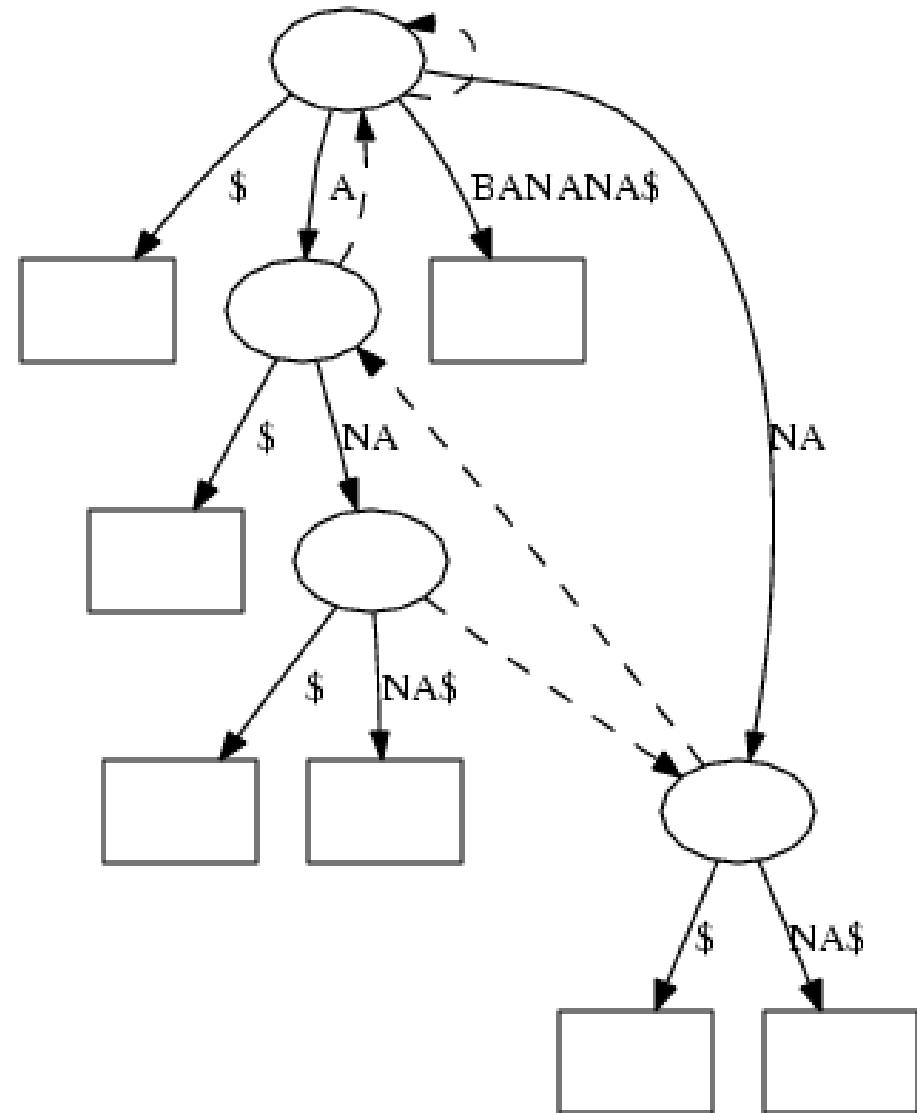
Lesson 1: *Use Data Structures and Algorithms!*



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 Algorithms and Analysis

- Taught by Dr Daniela Mihai and me (Adam Prügel-Bennett)
- I'm teaching you algorithms
- The analysis is an ability to reason about programming
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Course Structure

- 30ish lectures

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- 4 labs (worth 10%)

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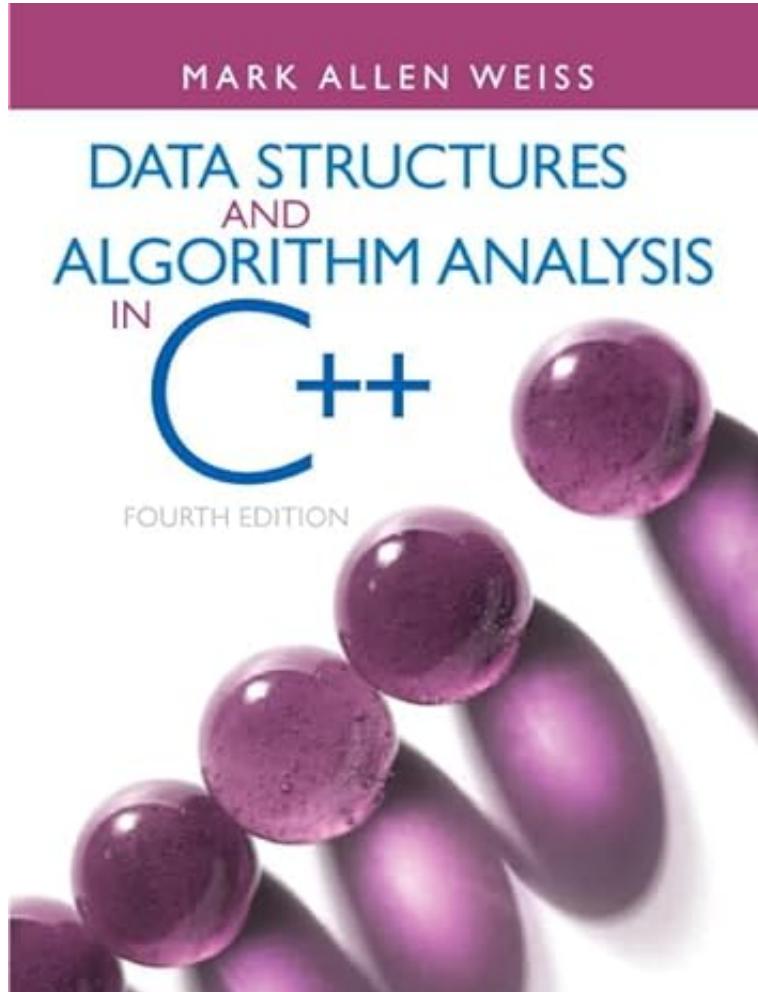
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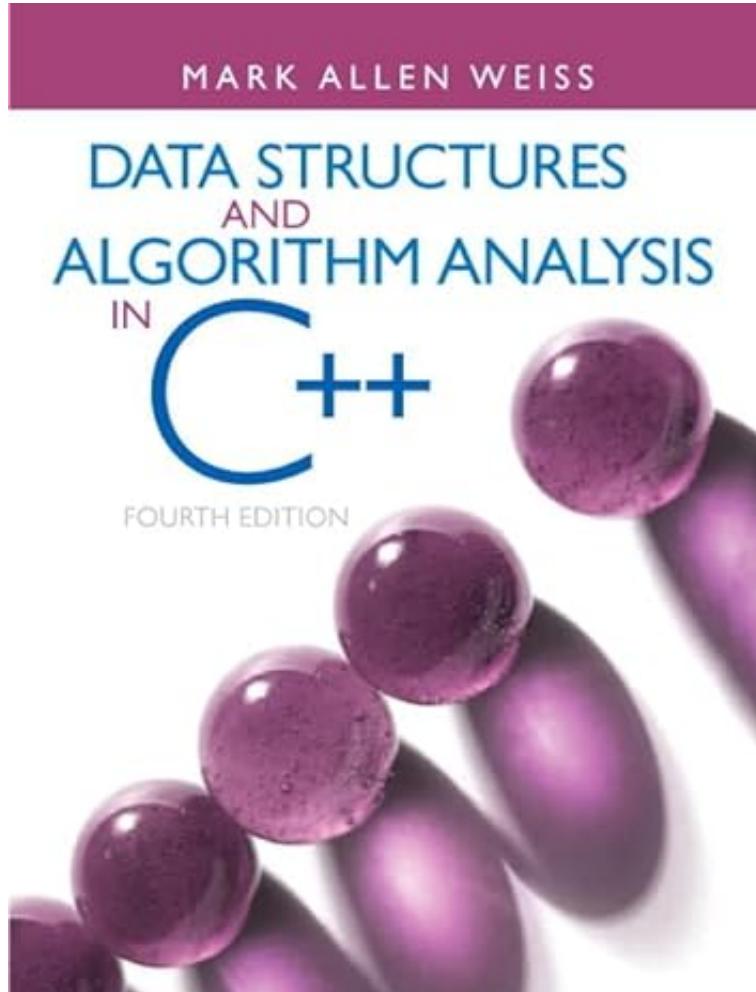
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- Final exam (worth 70%)
- This is different to last year

Recommended Course Text



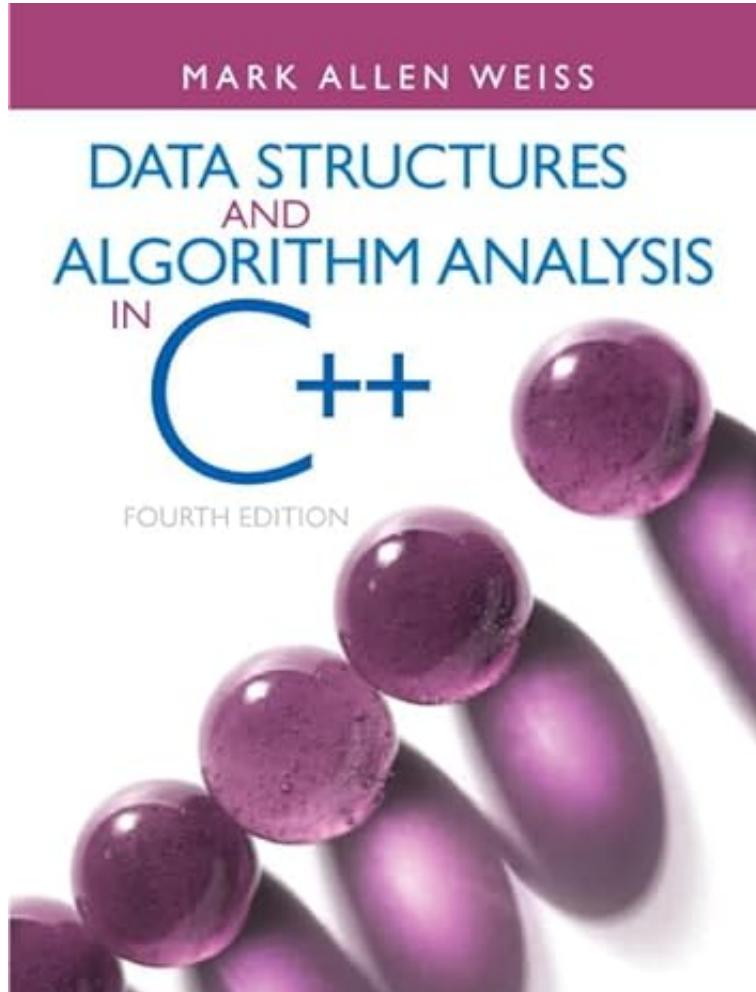
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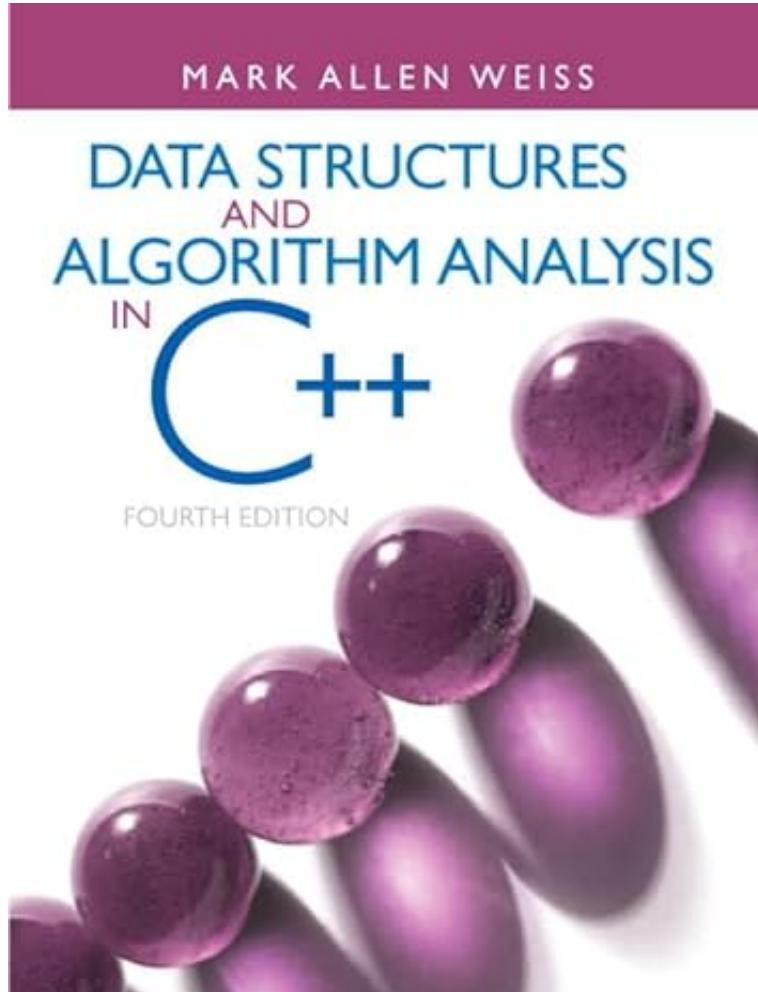
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What is a Data Structure?

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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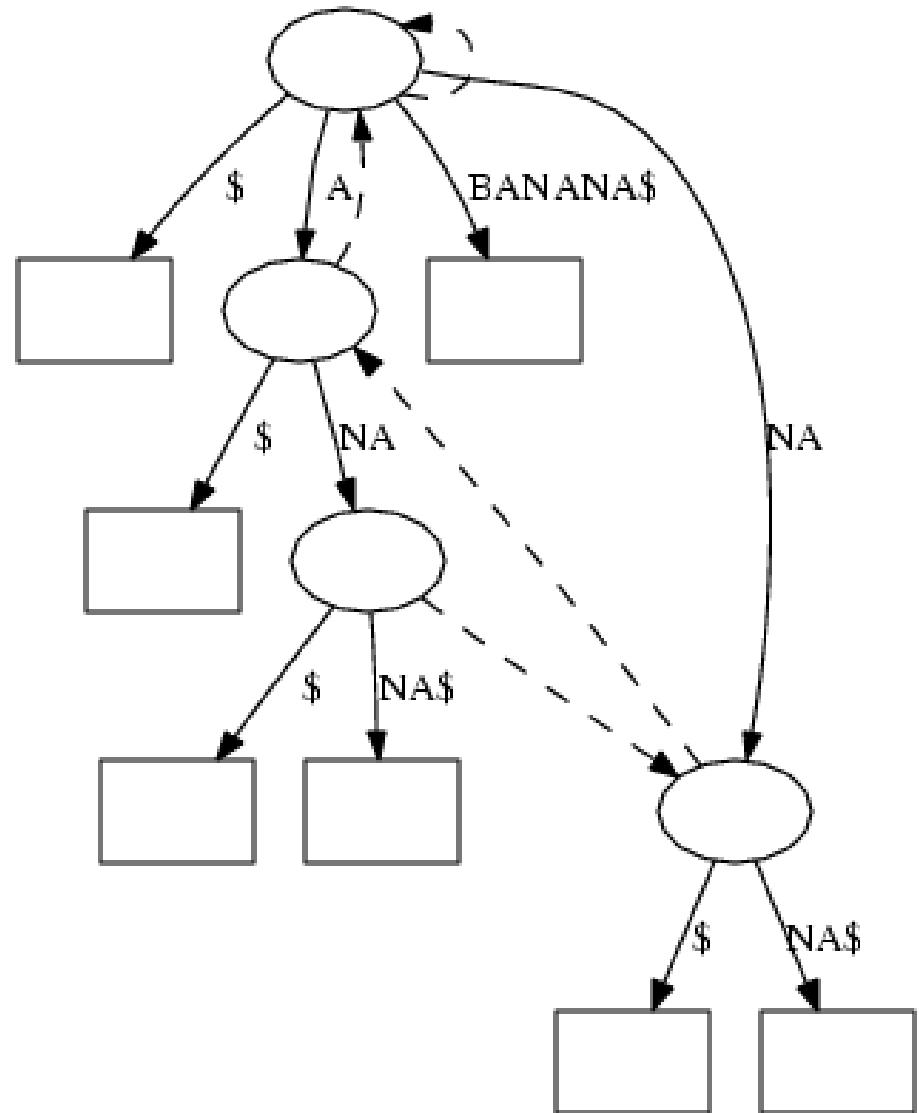
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Thou shall not re-implement common data structures

Outline

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2. **Example of Using DSA**
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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 (~ 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>`
 - ★ copy input file into vector
 - ★ sort vector
 - ★ copy sorted vector to standard output stream
- On 100 000 inputs takes 10ms to run

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Summary: Why use Data Structures?

Data structure version is

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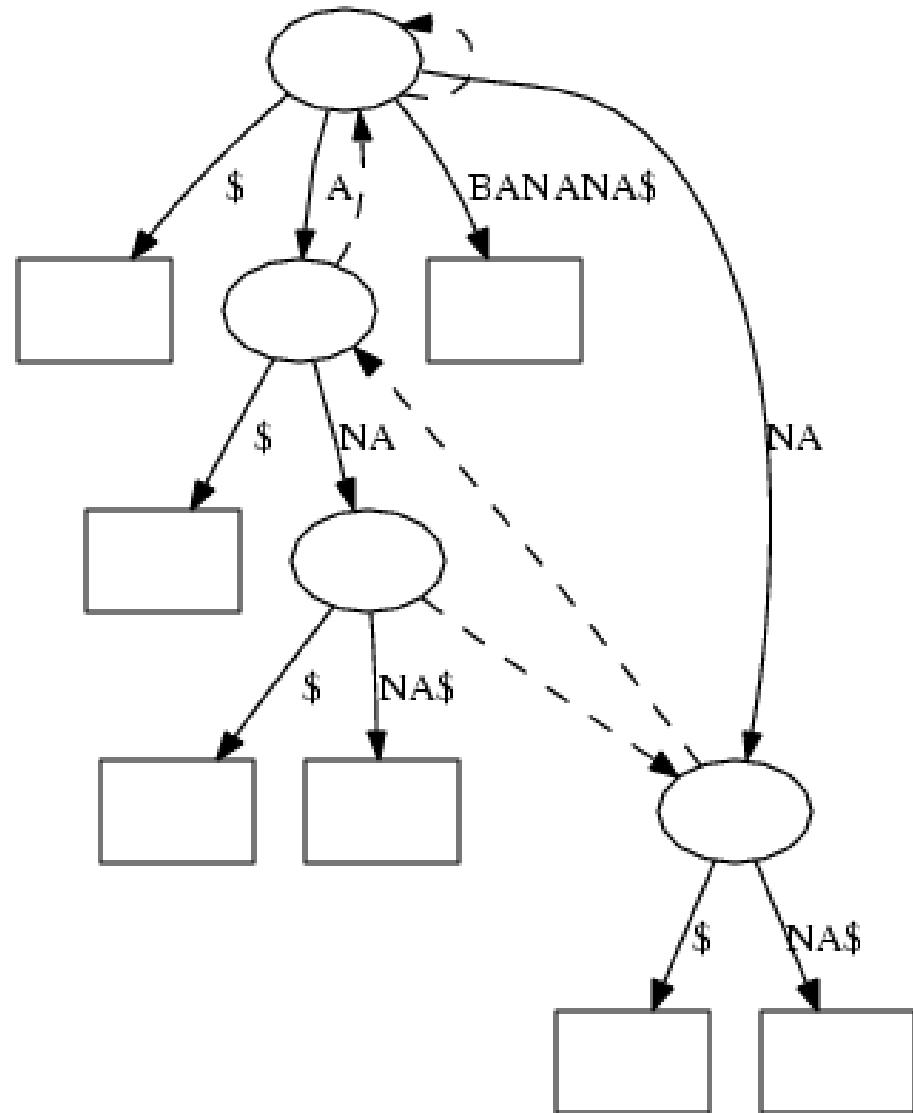
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Sophisticated Programs

- Data structures and algorithms allow moderately competent programmers to write some very impressive programs
- E.g. consider a program to count all occurrences of words in a document
- We want to output the words in sorted order

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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 that 10 times as much code that runs in less than 10 times as long

- Probably possible, but certainly not easy

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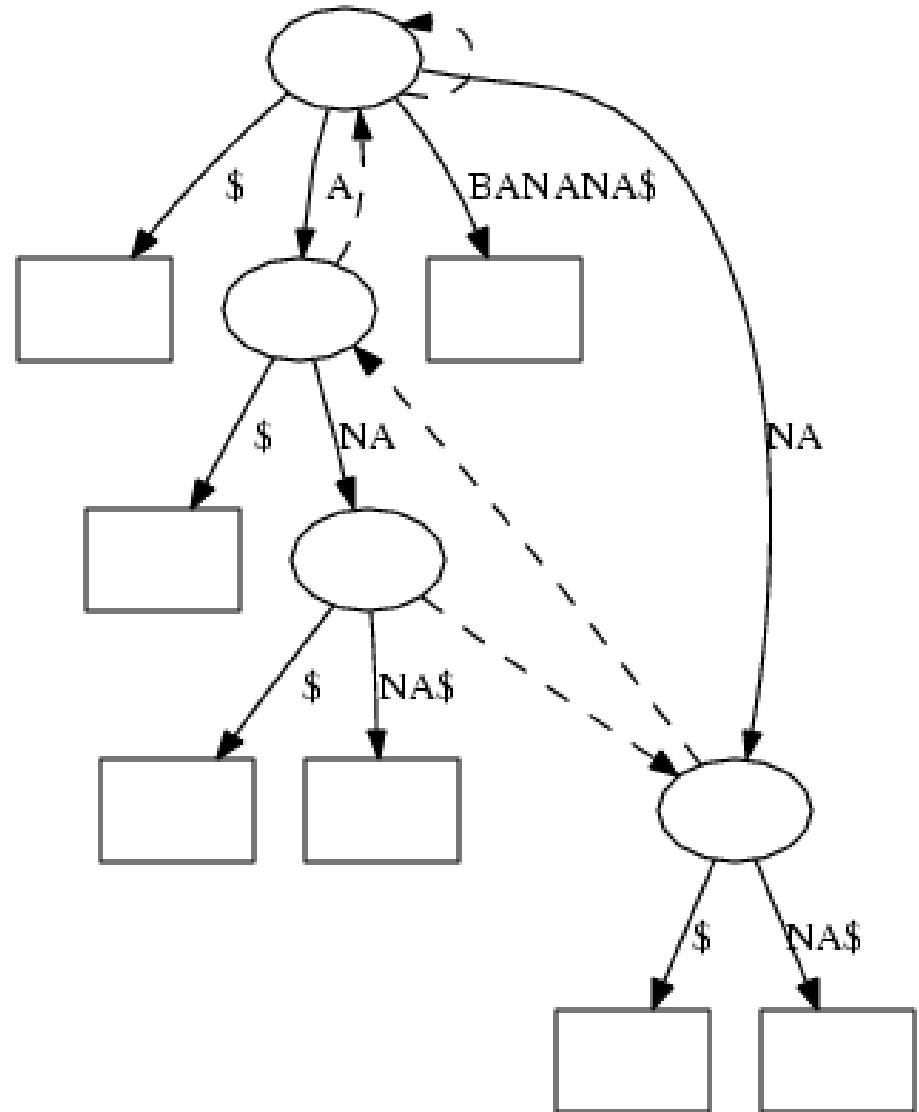
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DNA Sequencing

- In modern whole shotgun genome sequencing the full genome is broken into small pieces
- The pieces are then read by a sequencing machine
- This reads short sections (around 1000) bases
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AAAAGAGGTGCAATAGTAGGTA
CTGTACGGATTAAACAT

Sequencing and Assembly

AAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
CACAT
AAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
CACAT
AAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
CACAT
AAAAGAGGTGCATATAGTAGGTA
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ACTGTACGGATTAA
ACAT
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCAT
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATTT

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ACAT
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT

AAAGA

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATTT

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CTGTACGGATTAA
ACAT
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ACAT
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CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT

AA|AGA|GG

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATT T

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ACAT
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT

AAA|GAGGT

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
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ACTGTACGGATTAA
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA

AAA|GAG|GTGC

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATT

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AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA

AAA|GAGG|TGCA|T

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCA T	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATT

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ACAT
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ACAT
AAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT

AA|AGAGGTGCATATA

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
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CTGTACGGATTAA
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AA|AGAGGTGCATATAG

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATT

Sequencing and Assembly

AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT

AA|AGAGGTGCATATAGT

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATT

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ACAT
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ACAT
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CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
CTGTACGGATTAA
ACAT

AA|AGAGGTGCATATAGT|A

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
AGTAG	ATAGT	ATTTA	CGGAT	AAAGA	GATT

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AAAAGAGGTGCATATAGTAGGTA
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ACTGTACGGATTAA
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
AAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA

AAAAGAGGTGCATATAGTAGGTA

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
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ACTGTACGGATTAA
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ACAT

AAAGAGGTGCATATAGTAGTACTG

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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ACAT
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ACTGTACGGATTAA
ACAT
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ACTGTACGGATTAA
ACAT

AAAAGAGGTGCATATAGTAGT
ACTGT

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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TACTGTACGGAT

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ACAT
AAAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT
AAAAAGAGGTGCATATAGTAGGTA
ACTGTACGGATTAA
ACAT

AAA|AGAGGTGCATATAGT|AG
TACTGTAC|GGATT

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
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AAAAGAGGTGCATATAGTAGGTA
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CACAT
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ACTGTACGGATTAA
CACAT

AAAAGAGGTGCATATAGTAG	TACTGTACGGATTAAAC				
AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCA T
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
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- The estimated cost of sequencing the human genome in 2005 was \$10 000 000
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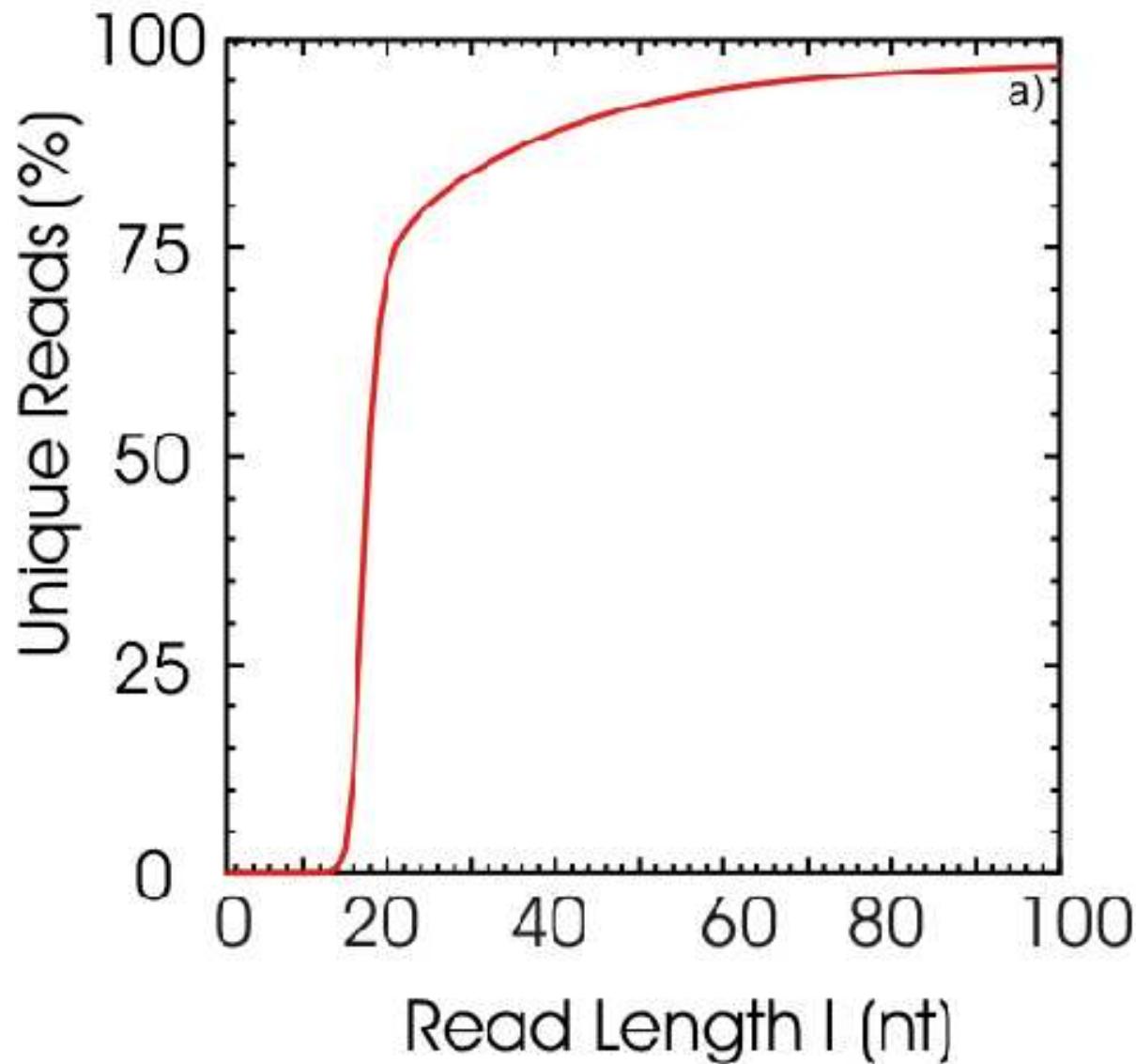
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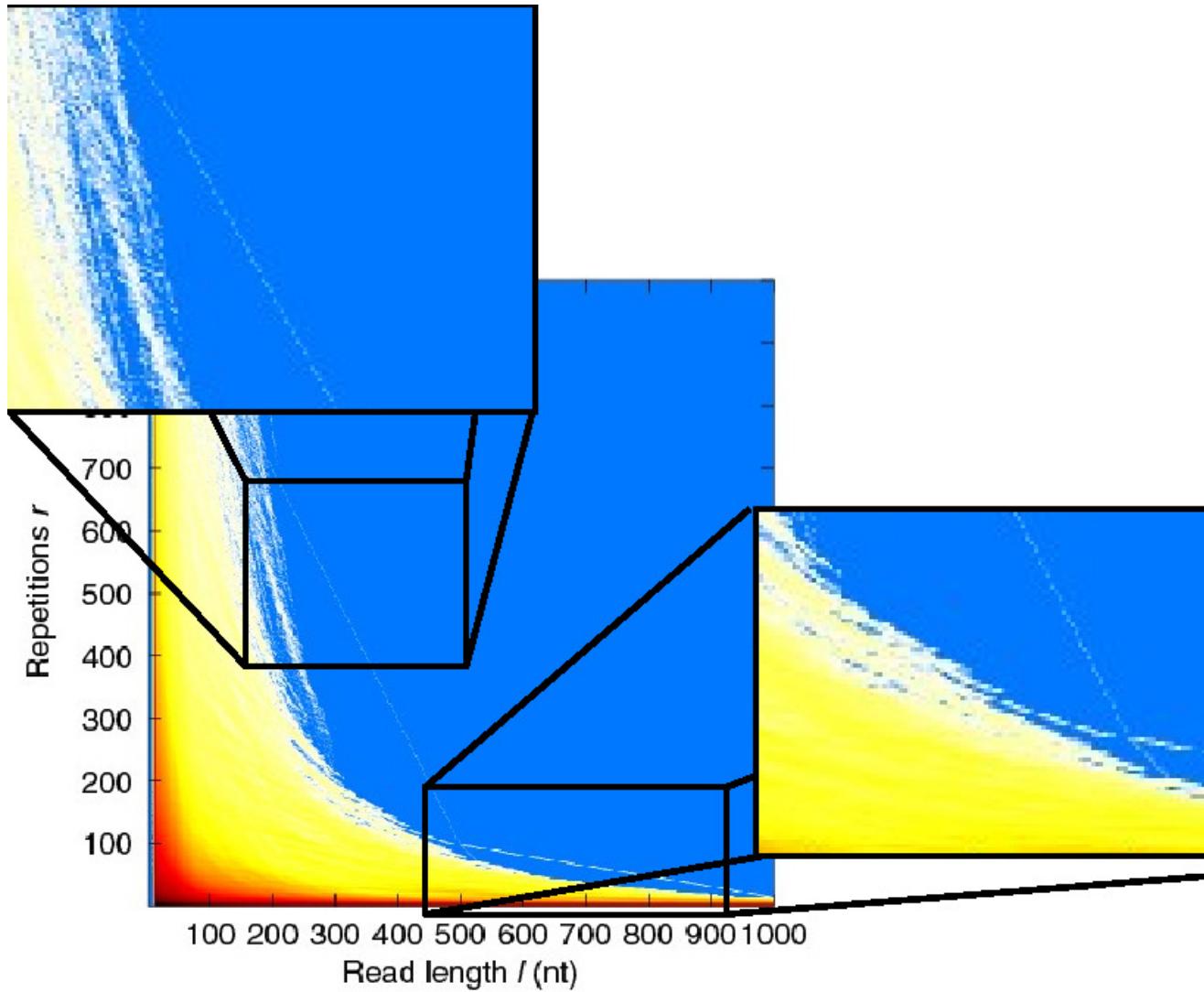
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Repeats in Human Genome



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
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- 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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