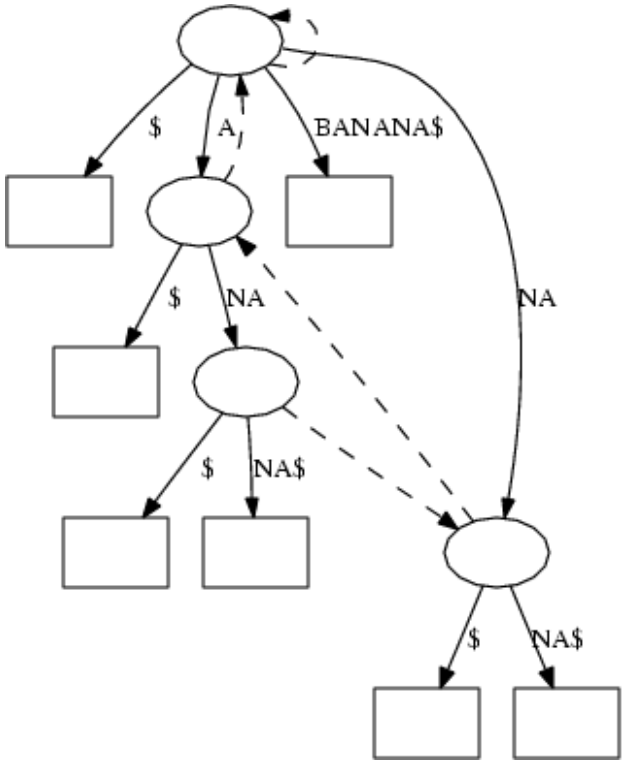
Algorithms and Analysis

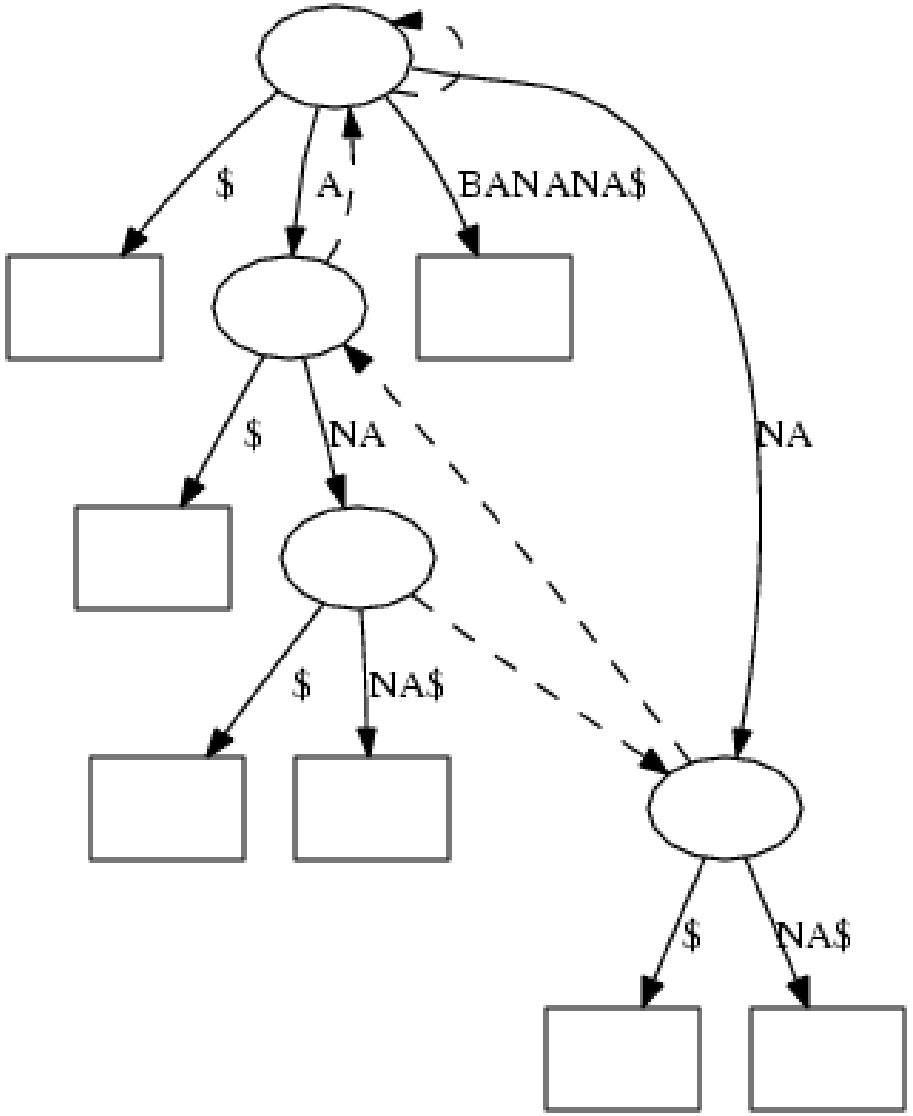
Lesson 1: *Use Data Structures and Algorithms!*



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



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- Taught by Dr Daniela Mihai and me (Adam Prügel-Bennett)
- I'm teaching you algorithms
- The analysis is an ability to reason about programming
- Learning C++ will be a joint effort involving $Low\text{-}level\ programming$, me
- My ambition is not only to teach you data structures and algorithms academically

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Course Structure

- 30ish lectures

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- 4 labs (worth 10%)

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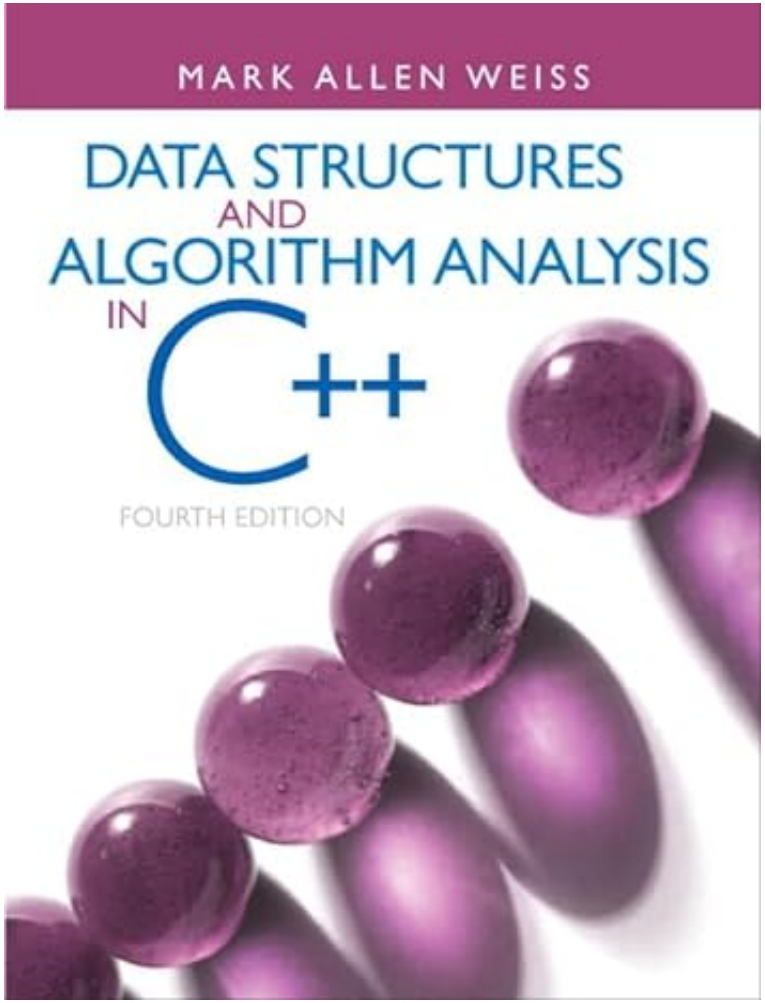

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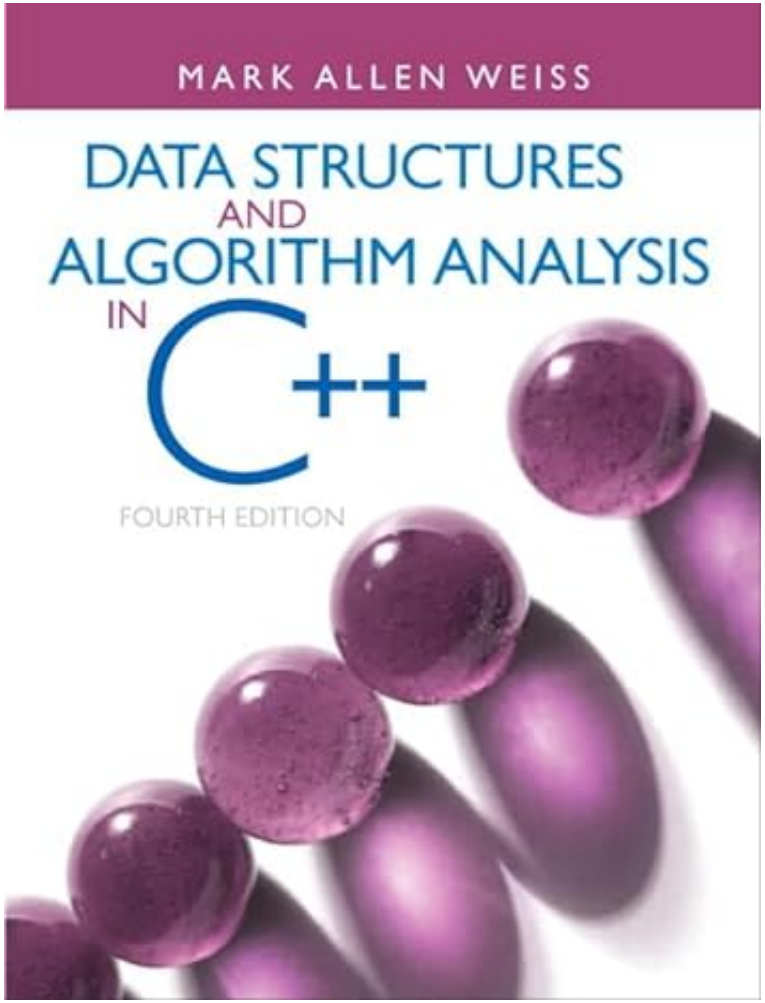

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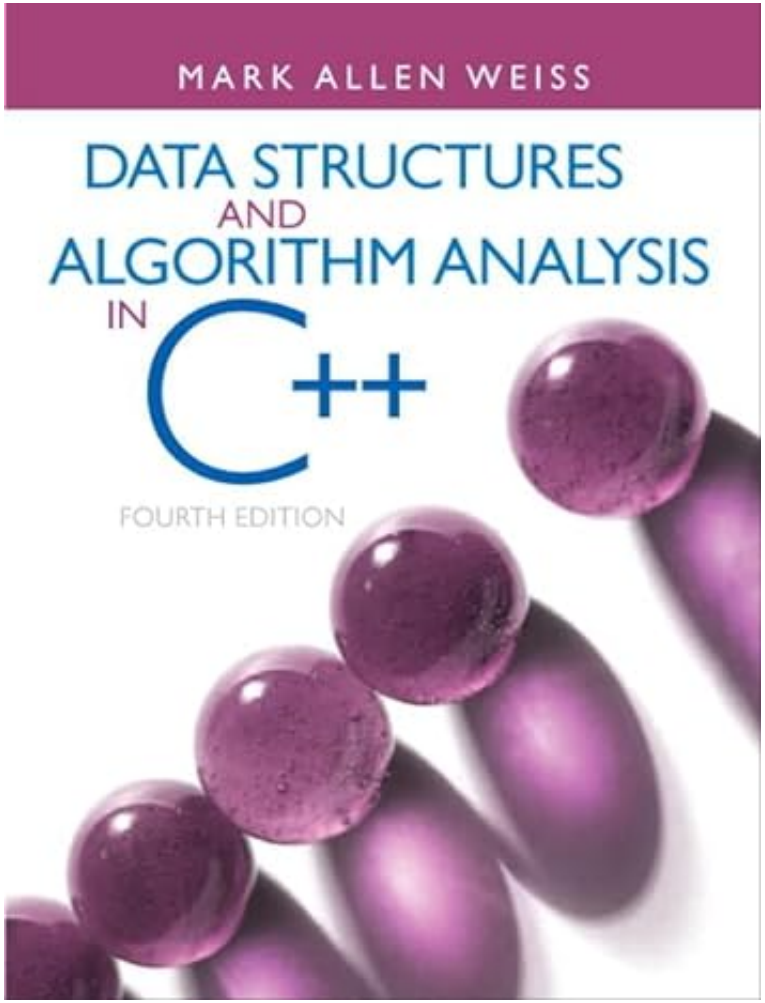

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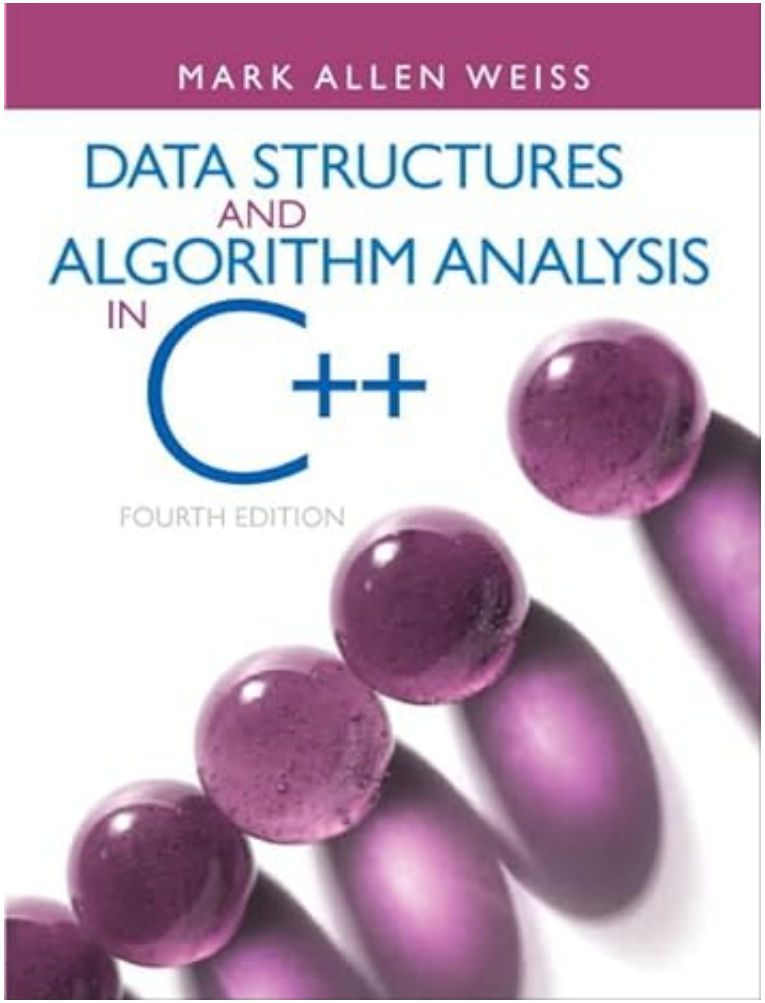

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What is a Data Structure?

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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Thou shall not re-implement common data structures

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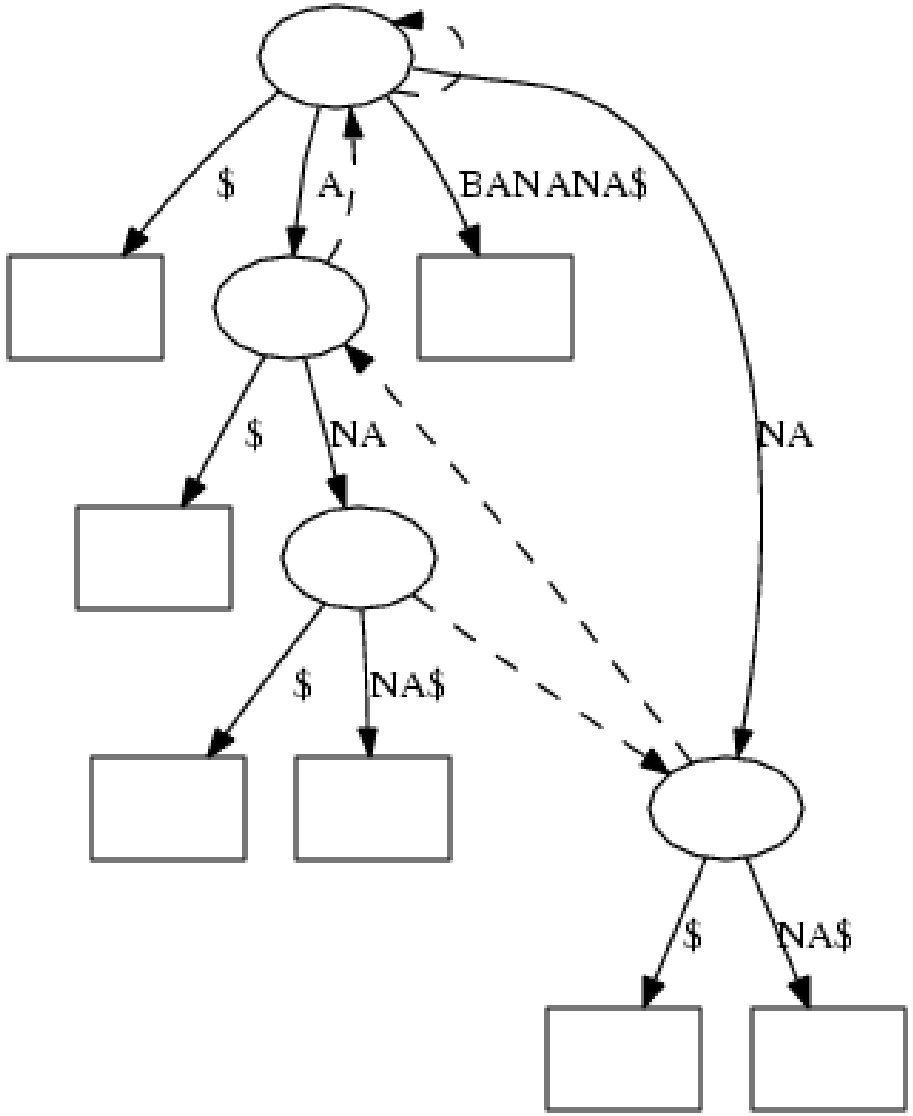

Example: Sort program

- 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
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Data structure version is

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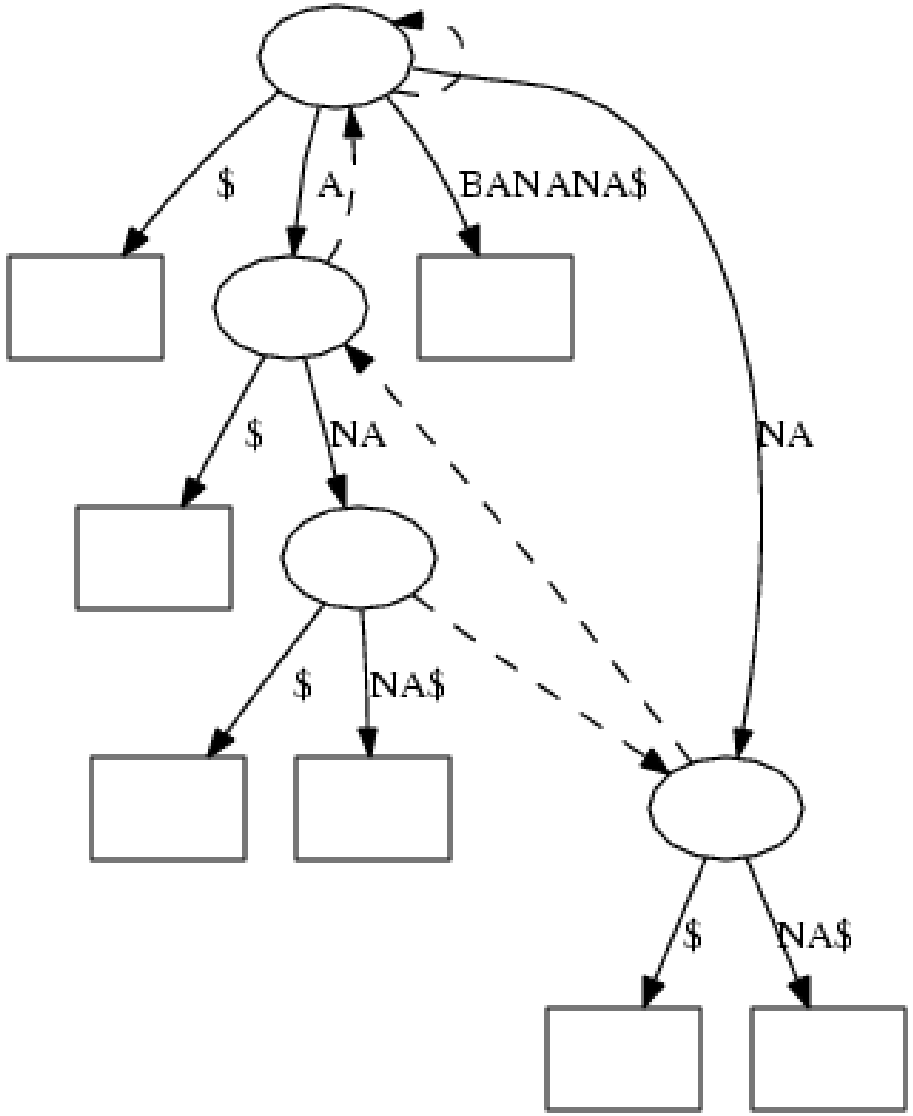

Sophisticated Programs

- 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
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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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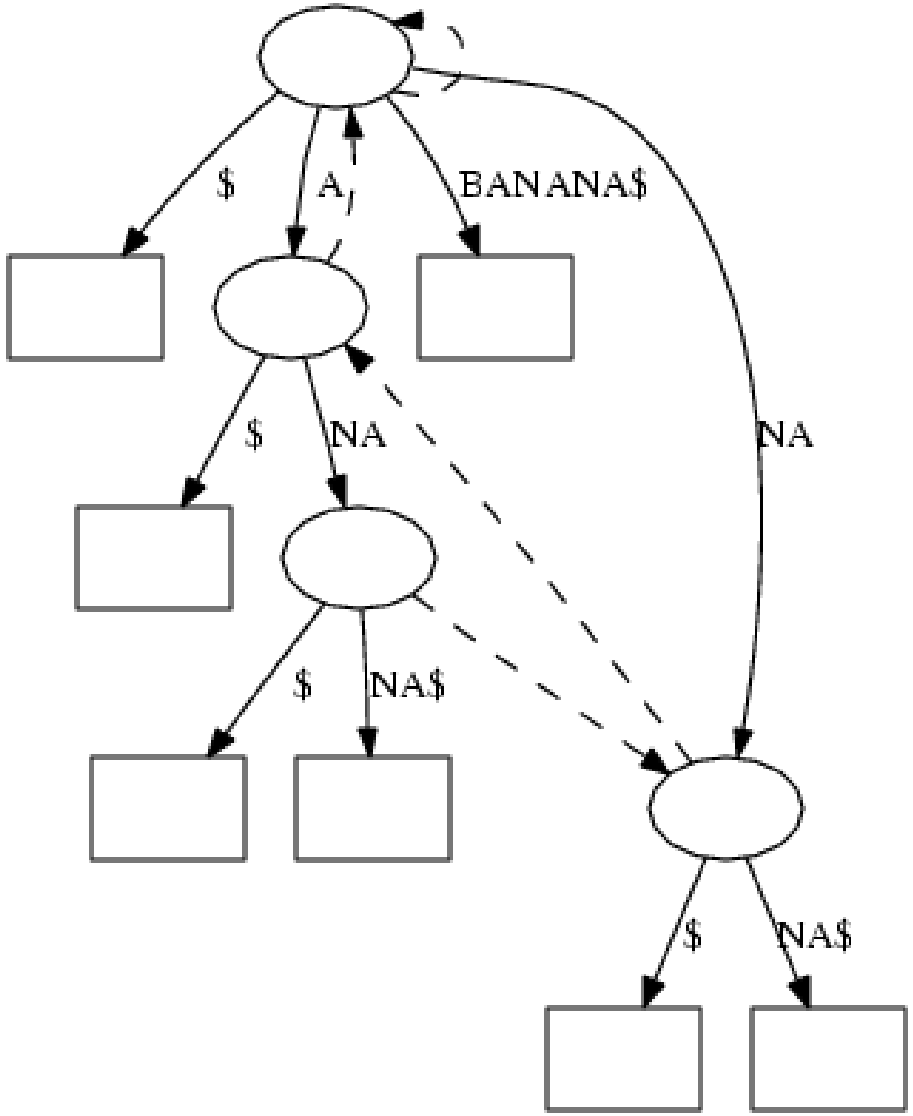

DNA Sequencing

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- The pieces are then read by a sequencing machine
- This reads short sections (around 1000) bases
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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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AAAGA

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

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

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCAT
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
TACTG	GTACG	TAGTA	GAGGT	TATAG	ATAGT
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AA AGA GGTGC

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCAT
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AA AGA GG TGC AT

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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AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCAT
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
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TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
ATAGT	AAAGA	ACTGT	AGTAG	AGAGG	TGCAT
TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
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TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AAAGAGGTGCATATAGTAG TACTGT

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
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TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AAAGAGGTGCATATAGTAG TACTGTACGGA

AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
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TGCAT	GGATT	ATATA	ACGGA	TACTG	GAGGT
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AGAGG	AAAGA	ACTGT	GAGGT	TTAAC	GGTGC
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AAAAGAGGTGCATATAGTAG TACTGTACGGATT

AGAGG AAAGA ACTGT GAGGT TTAAC GGTGC

ATAGT AAAGA ACTGT AGTAG AGAGG TGCAT

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AAAAGAGGTGCATATAGTAG TACTGTACGGATTTAAC

AGAGG AAAGA ACTGT GAGGT TTAAC GGTGC

ATAGT AAAGA ACTGT AGTAG AGAGG TGCAT

TGCAT GGATT ATATA ACGGA TACTG GAGGT

TACTG GTACG TAGTA GAGGT TATAG ATAGT

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New Generation Sequencers

- The estimated cost of sequencing the human genome in 2005 was $\$10\,000\,000$
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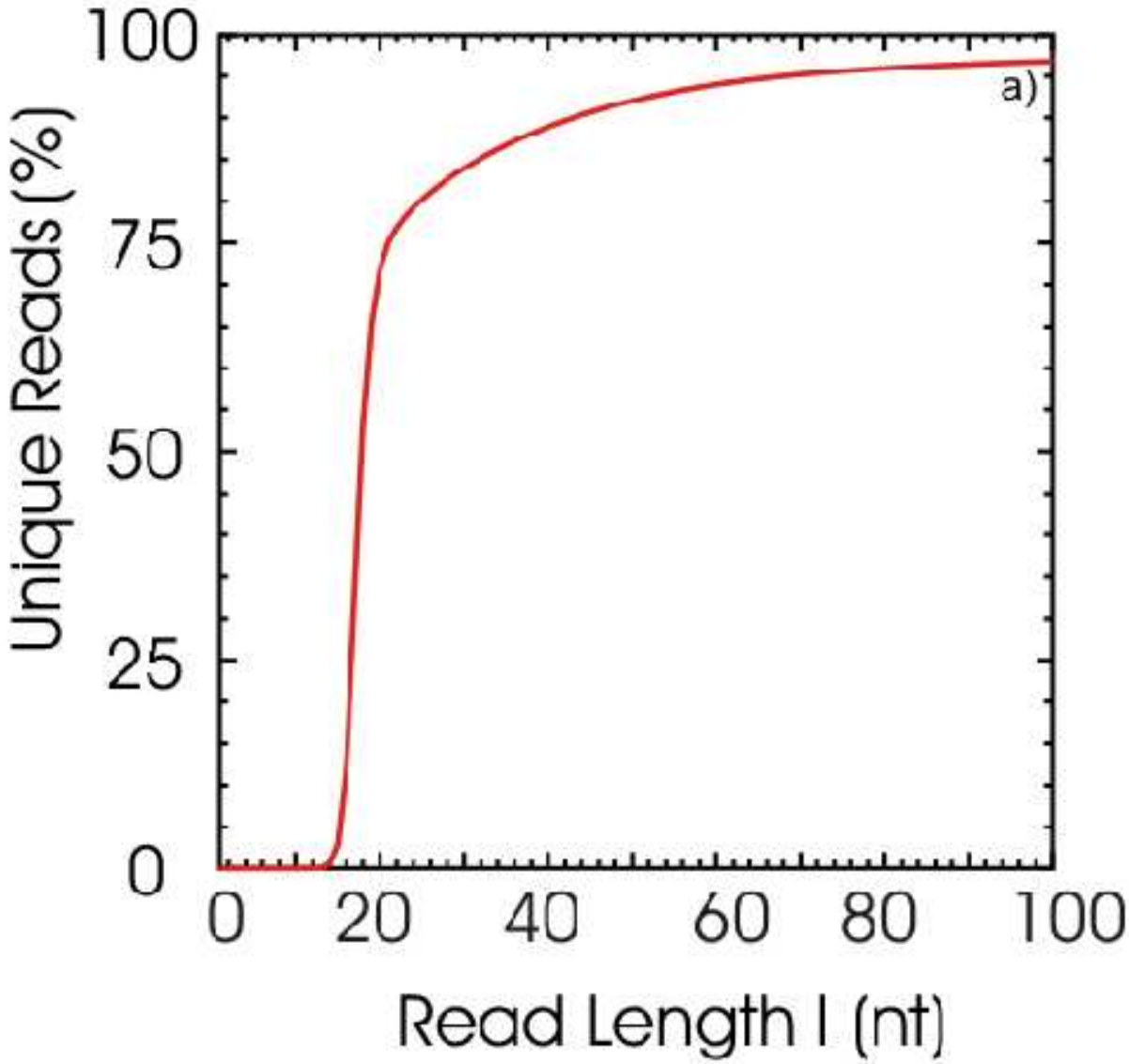
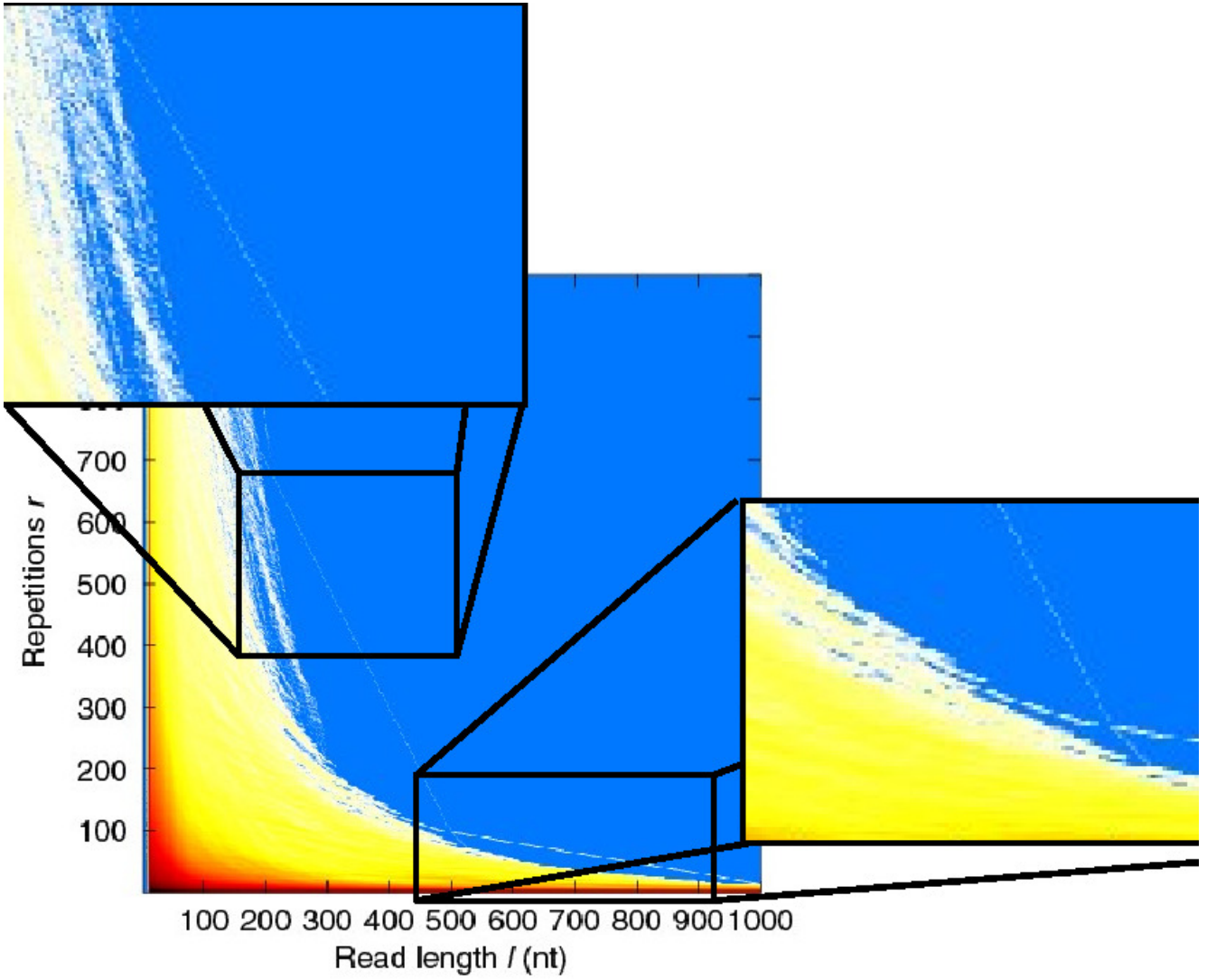
Repeats in Human Genome



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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- 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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