Genome 540 Discussion

January 30th, 2024

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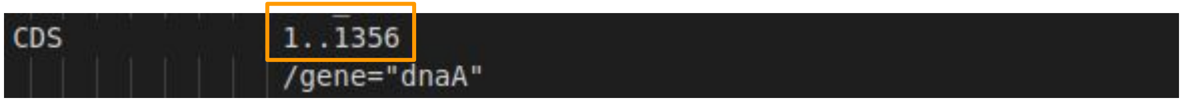
Agenda

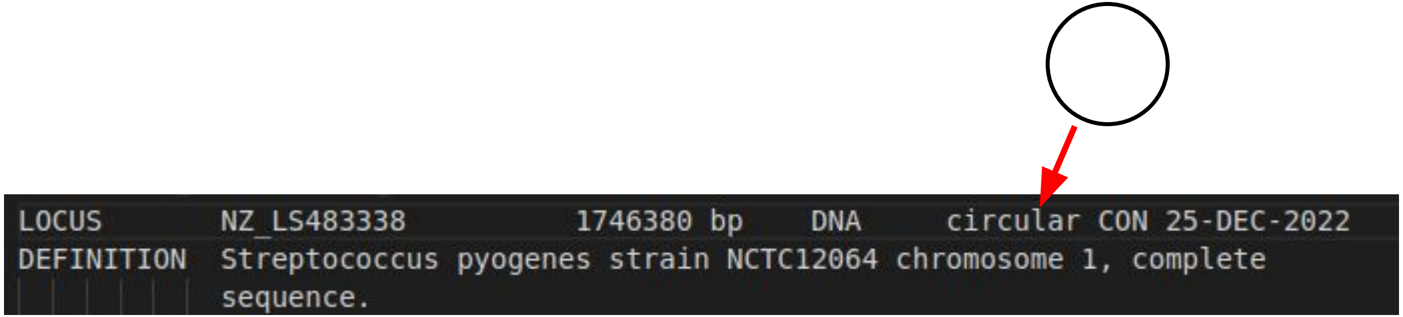
- Assignment 3 Wrap Up
- Assignment 4

Assignment 3 Wrap Up

Edge Case



```
CDS             1..1356
                /gene="dnaA"
```



```
LOCUS       NZ_LS483338          1746380 bp    DNA     circular CON 25-DEC-2022
DEFINITION  Streptococcus pyogenes strain NCTC12064 chromosome 1, complete
            sequence.
```

Any questions?

1. Parse a genbank file (.gbff) and...
    a. Extract all CDS features
    b. Read in the sequence
2. Build a site model for translation start sites (TSS)
    a. Use CDS features to get nucleotide frequencies +/- 10bp around all TSS (21bp total including TSS)
    b. Use sequence to get nucleotide frequencies throughout the genome *on both strands*
    c. Compute the weights using the log2 ratios of the frequencies
3. Use the site model to compute scores at
    a. Every annotated TSS
    b. The entire genome (21bp window) on both strands

Assignment 4

Overview

Part 1: Write a program to find the highest-weight path in a directed acyclic graph using dynamic programming

Part 2: Run your program on a linked list created from DNA sequence

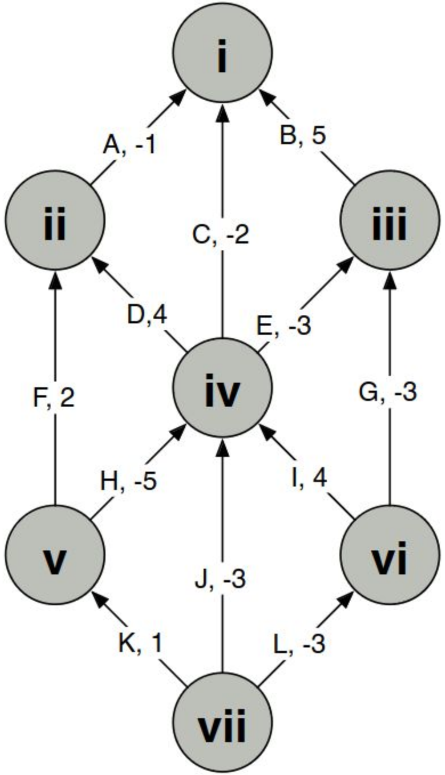
Program 1: Highest weight path

1. Convert graph to text file of **vertices** and **edges** by hand
2. Use dynamic programming to find the max weight path through the graph (Lectures 7/8)
   a. Overall
   b. With constraints (START/END)
3. Output
   a. Path Score
   b. The start/end vertex on the path
   c. Labels for all the edges on path (in order)

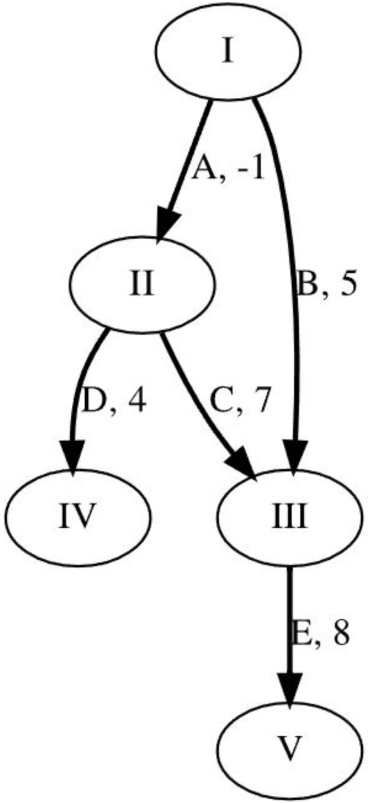
Example:
V vii START
V vi
V v
…
E A ii i -1
E B iii i 5

Part 1
Score: 8.0
Begin: vi
End: ii
Path: ID

Part 2
Score: 4.0
Begin: vii
End: i
Path: LIDA



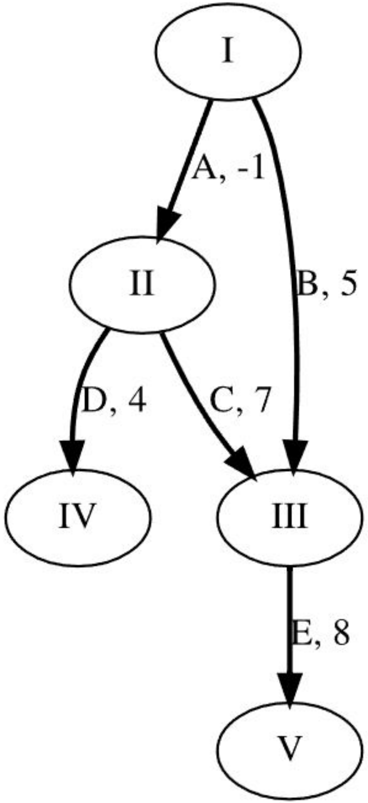
Example - Unconstrained



my_graph.txt:

```
V I
V II
V III
V IV
V V
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```

Example - Unconstrained

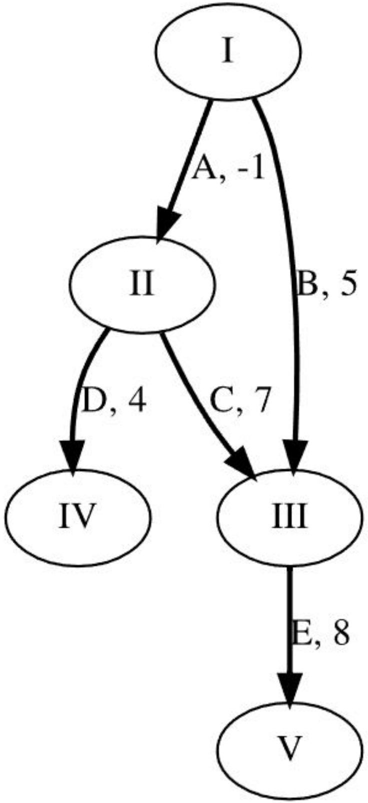


my_graph.txt:

```
V I
V II
V III
V IV
V V
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```

Score: 15
Begin: II
End: V
Path: CE

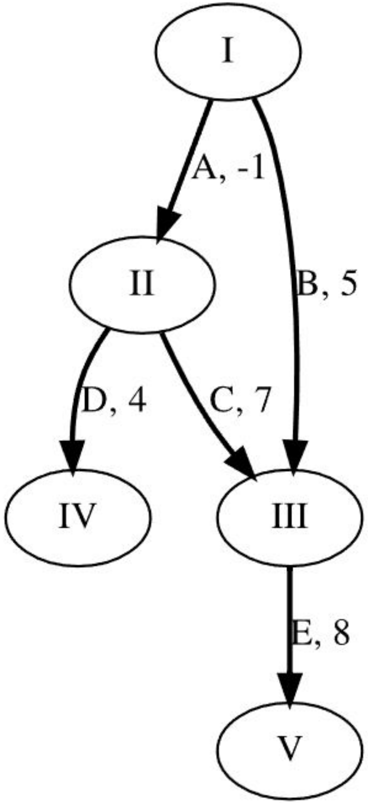
Example - Constrained



my_graph_constrained.txt:

```
V I START
V II
V III
V IV
V V END
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```

Example - Constrained



my_graph_constrained.txt:

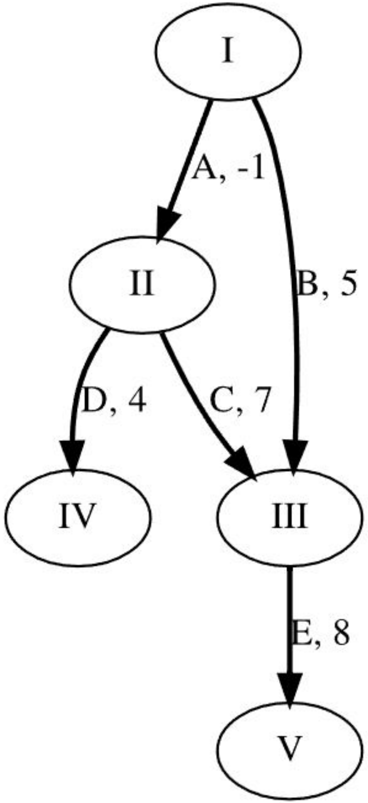
```
V I START
V II
V III
V IV
V V END
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```

Score: 14
Begin: I
End: V
Path: ACE

Example - Dynamic Programming

my_graph.txt:

```
V I
V II
V III
V IV
V V
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```



- Assume that graph file is depth ordered
- Vertex I has no parents so points to itself

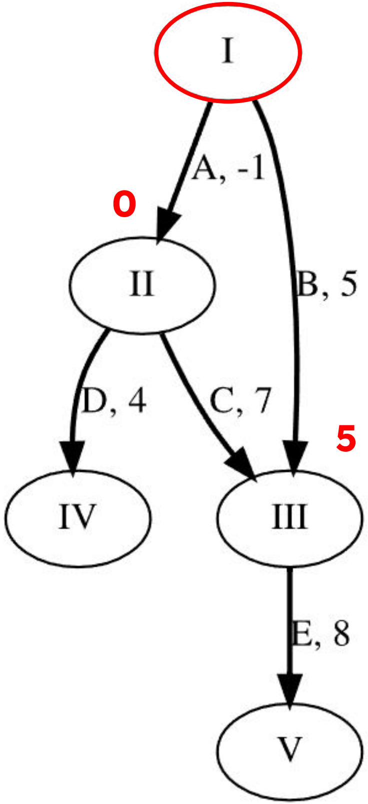
Vertex	I	II	III	IV	V
Highest Weight Parent	I	II	III	IV	V
w(v) (Vertex weight)	0	0	0	0	0

Best Path Start I

Example - Dynamic Programming

my_graph.txt:

```
V I
V II
V III
V IV
V V
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```



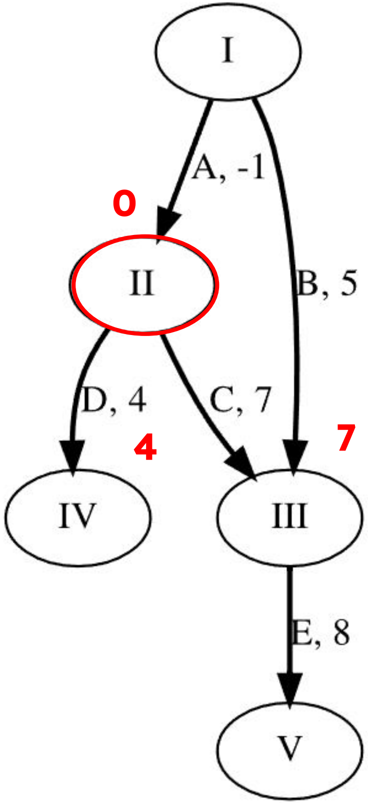
Vertex	I	II	III	IV	V
Highest Weight Parent	I	II	I	IV	V
w(v) (Vertex weight)	0	0	5	0	0

Best Path Start	III

Example - Dynamic Programming

my_graph.txt:

```
V I
V II
V III
V IV
V V
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```



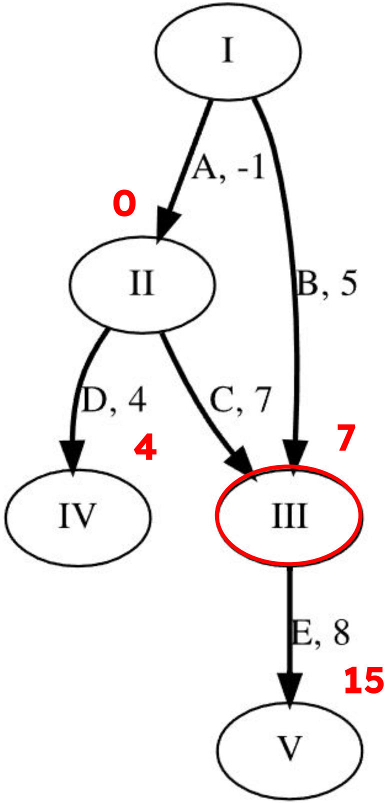
Vertex	I	II	III	IV	V
Highest Weight Parent	I	II	II	II	V
w(v) (Vertex weight)	0	0	7	4	0

Best Path Start III

Example - Dynamic Programming

my_graph.txt:

```
V I
V II
V III
V IV
V V
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```



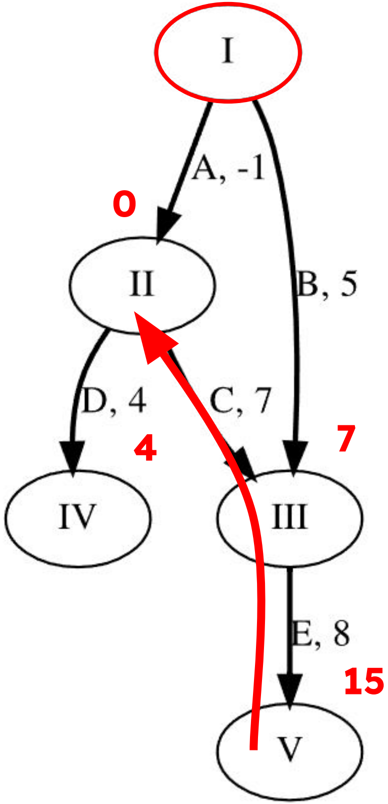
Vertex	I	II	III	IV	V
Highest Weight Parent	I	II	II	II	III
w(v) (Vertex weight)	0	0	7	4	15

Best Path Start V

Example - Dynamic Programming

my_graph.txt:

```
V I
V II
V III
V IV
V V
E A I II -1
E B I III 5
E C II III 7
E D II IV 4
E E III V 8
```



Vertex	I	II	III	IV	V
Highest Weight Parent	I	II	II	II	III
w(v) (Vertex weight)	0	0	7	4	15

Best Path Start V

- Now traceback to find highest weight path

Program 2: DNA Linked List

1. Create a linked list from a DNA sequence and a scoring scheme
   a. Positions are vertices
   b. Bases are edges
2. Run your program from part 1 on the graph

Example:

Scores

A = -1.49

T = -1.49

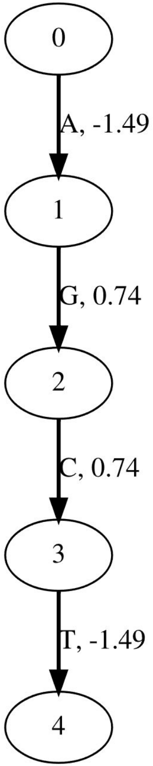
G = .74

C = .74

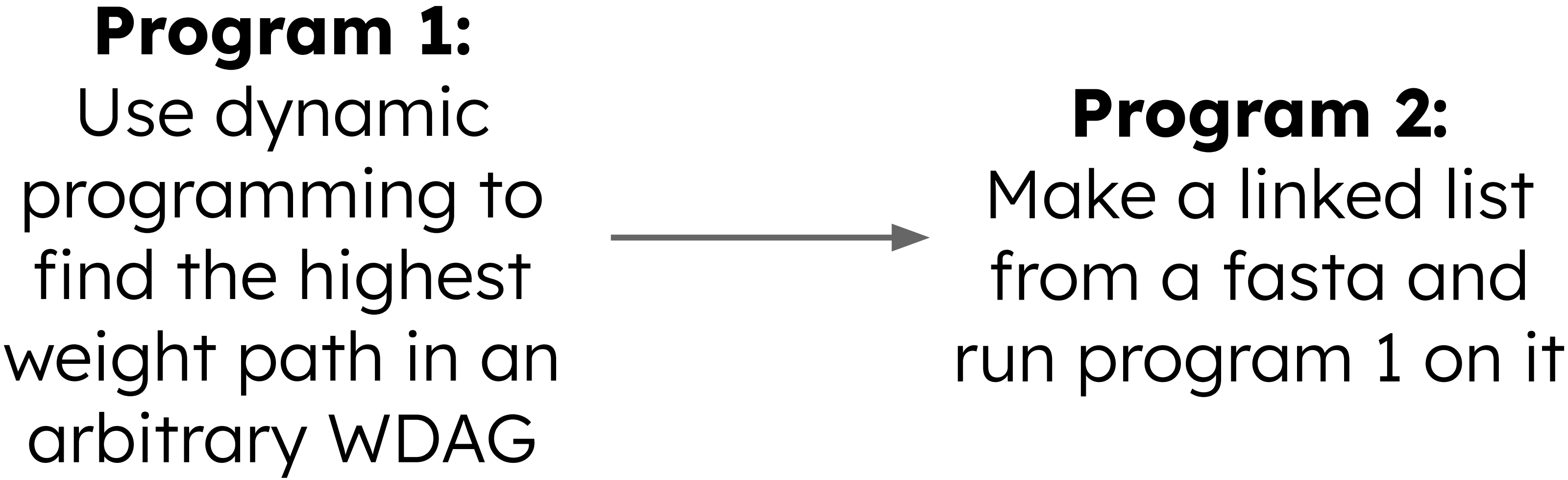
Sequence: AGCT

Graph:

```
V 0
V 1
V 2
V 3
V 4
E A -1.49
E G .74
E C .74
E T -1.49
```



HW4 Summary



Program 1:
Use dynamic programming to find the highest weight path in an arbitrary WDAG

Program 2:
Make a linked list from a fasta and run program 1 on it

Reminders

- HW4 due this Sunday, 11:59pm
- Please have your name in the filename of your homework assignment and match the template