# Hashing and Sequence Assembly

# Pre/Suffixes are nodes; reads are edges

- Each node will stand for either a prefix or a suffix.
  - Prefixes and suffixes are the same length, so each node will be used to represent both.



 Each edge will stand for a read, which connects a prefix to a suffix



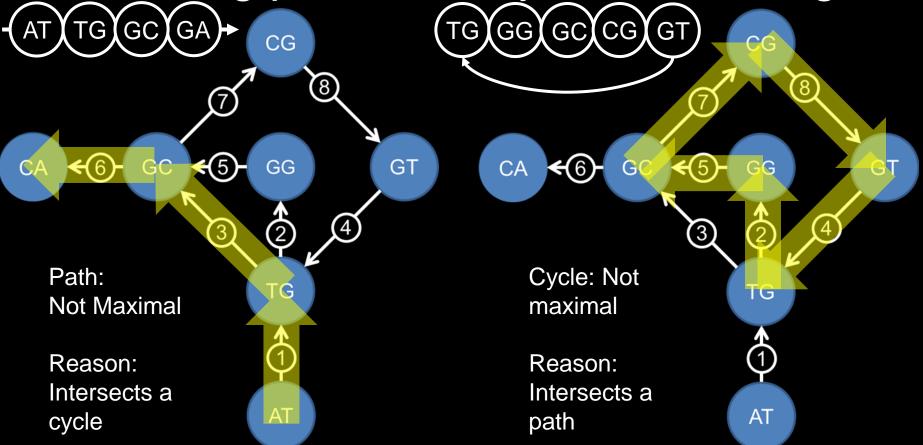
# Paths connect reads into longer sequences



- Paths indicate which reads connect and how
  - based on prefixes and suffixes
- Prefixes and Suffixes always the same length
- Contigs are maximal (longest possible) paths

- How do you know a contig is maximal?
  - It does not intersect any unused cycles
  - Its end nodes cannot be extended over any unused edges (backwards or forwards)

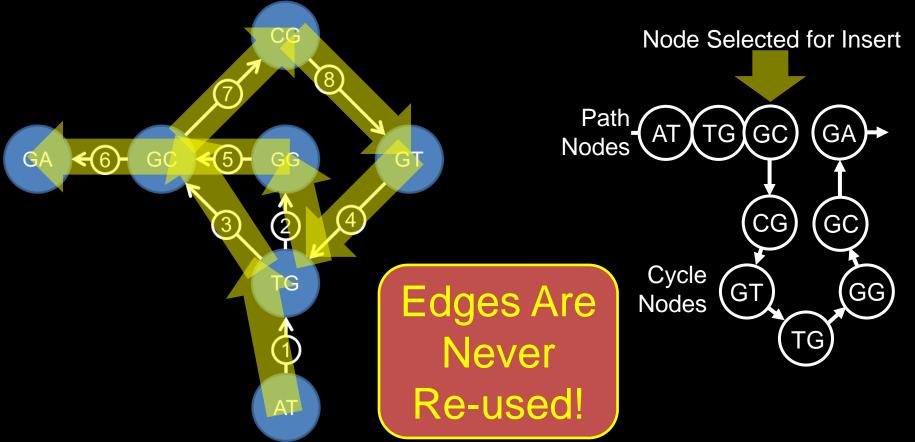
Assembling paths and cycles for contigs



- Cycles can intersect paths and other cycles at nodes, but they CANNOT share edges.
- As you generate paths and cycles, mark edges used, so that they don't accidentally get reused

# Assembling paths and cycles for contigs

- Inserting cycles into paths and other cycles happens at exactly one node
  - Even if the cycle intersects the path at multiple nodes, pick a node. Any node.



# Cycles create ambiguity in final assemblies

- Cycles can intersect a path or other cycles at multiple points
- One point must be chosen for insertion
- The fact that there is a choice means that there are multiple possibilities for the final outcome.
- We will talk about ways to fully deal with this ambiguity later

## Representing large graphs in memory

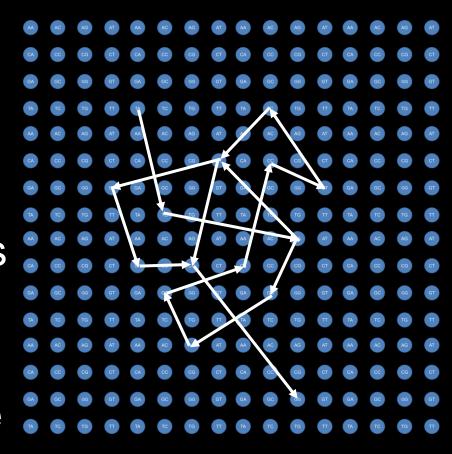
- The exponential space of nodes:
  - -1,073,741,824
  - In larger assembly efforts (e.g. mammalian genomes, etc) this can be 4<sup>31</sup>
- The space of edges is the number of reads:
  - -60,000

It is hard to represent nodes in memory.

Fortunately, you don't have to.

### Lets look at the space of nodes

- There are many more nodes than edges.
- This is because we are numbering nodes that we will never use:
- Lets number only the nodes that we use



### How do we number only nodes we use?

- First, we need a nonredundant index for every node
- Remember first that a node is a prefix or suffix with 15 nucleotides in it:

$$n_0 \, n_1 \, n_2 \, n_3 \, n_4 \, n_5 \, n_6 \, n_7 \, n_8 \, n_9 \, n_{10} \, n_{11} \, n_{12} \, n_{13} \, n_{14}$$

- Where n<sub>0</sub> is either A,C,G, or T
- Let A=0, C=1, G=2, T=3, and the expression:

$$V = n_0(4^0) + n_1(4^1) + ... + n_{13}(4^{13}) + n_{14}(4^{14})$$

- Stand for the whole prefix/suffix
- This ensures that one integer stands for every possible node. We'll call this a node index.

## Some possible nodes and their indices

Example 1:

### AAAAAAAAAAAA

Read

Index

0

$$V = n_0(4^0) + n_1(4^1) + ... + n_{13}(4^{13}) + n_{14}(4^{14})$$

$$V = 0(4^0) + 0(4^1) + ... + 0(4^{13}) + 0(4^{14}) = 0$$

Example 2:

#### Read

Index

#### ACAAAAAAAAAAA

$$V = n_0(4^0) + n_1(4^1) + ... + n_{13}(4^{13}) + n_{14}(4^{14})$$
  

$$V = 0(4^0) + 1(4^1) + ... + 0(4^{13}) + 0(4^{14}) = 4$$

Example 3:

Index

#### GCAAAAAAAAAAAA

6

$$V = n_0(4^0) + n_1(4^1) + ... + n_{13}(4^{13}) + n_{14}(4^{14})$$
  

$$V = 2(4^0) + 1(4^1) + ... + 0(4^{13}) + 0(4^{14}) = 4$$

Example 4:

#### AAAAAAAAAAAAG

Read

Index

536,870,912

 $(40) \cdot 7 \cdot (41) \cdot 7 \cdot (413) \cdot 7 \cdot (414)$ 

$$V = n_0(4^0) + n_1(4^1) + ... + n_{13}(4^{13}) + n_{14}(4^{14})$$

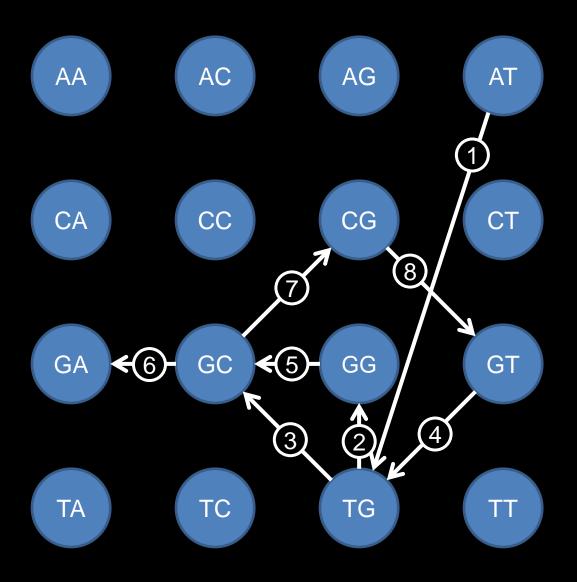
$$V = 0(4^0) + 0(4^1) + ... + 0(4^{13}) + 2(4^{14}) = 536,870,912$$

## Hashing the indices to save space

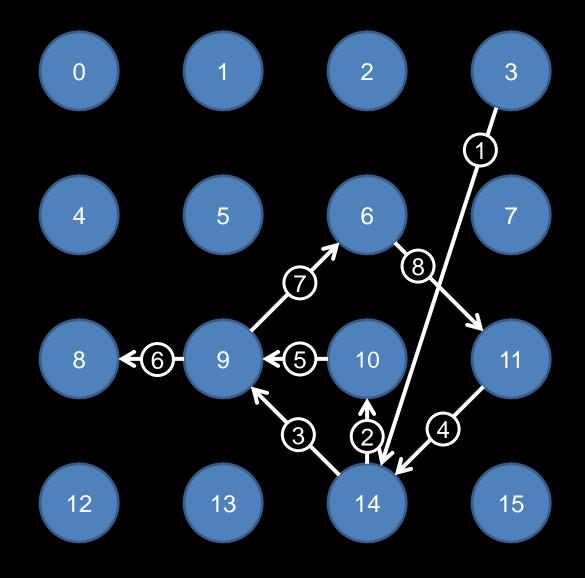
- Suppose we just wanted to make a (nonredundant) list of the nodes that were used in each of our reads
- We could just make a list of the indices
- But we don't care about the indices of nodes that are not touched by any read
- So why not just use their position on the list, instead of the index?



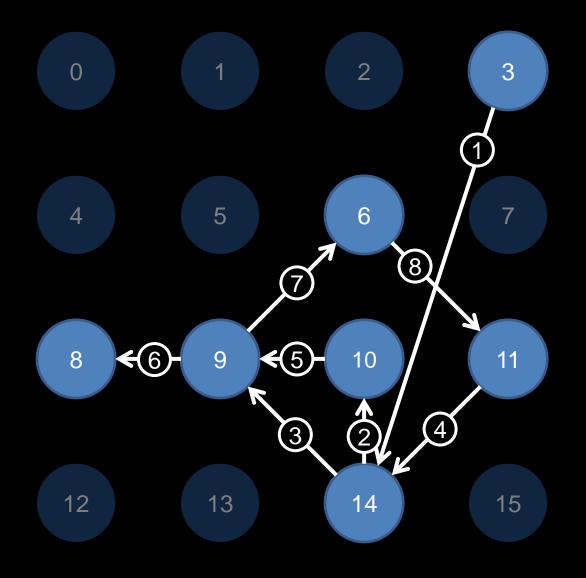
# The graph we built before



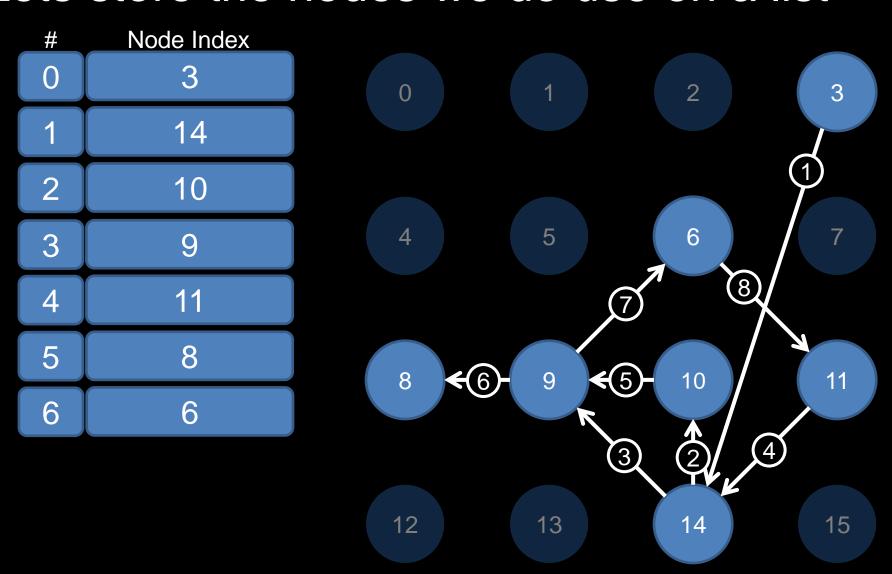
# The graph, substituted with Node Indices



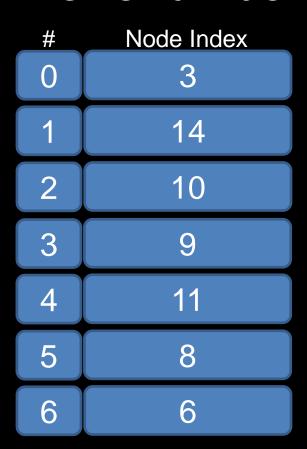
## Grey out the nodes we don't use

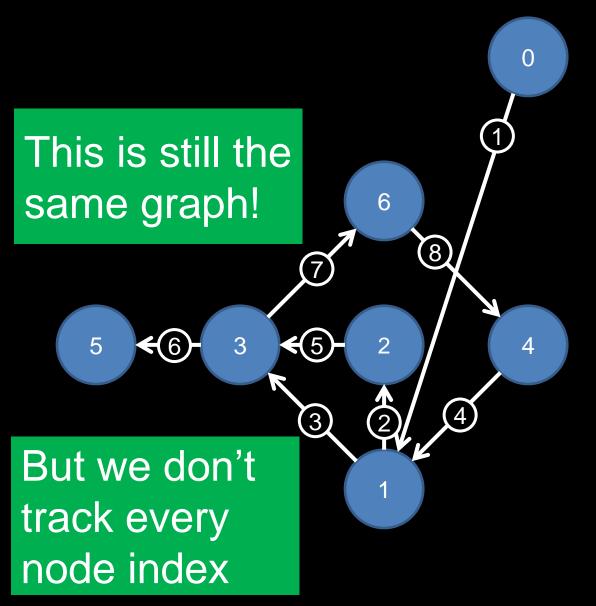


## Lets store the nodes we do use on a list



### If we renumbered the nodes with the list #





## This isn't the whole story yet

- What we've seen so far:
  - We can renumber the nodes in the graph that we use so that we don't have to track all the nodes in the graph

- What we haven't seen so far:
  - How do we store the graph structure in a useful way without having to remember lots of things?

 To do this, we need to know what a hash table does

### Hash Table

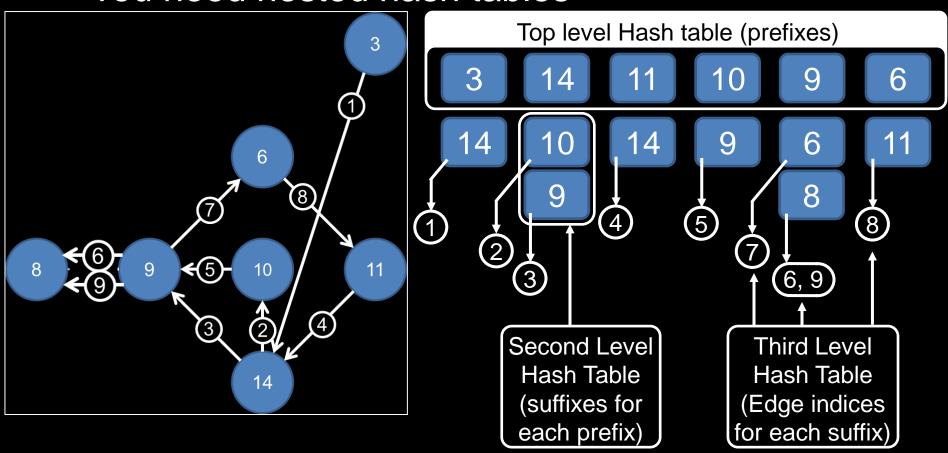
- A hash table is a list that holds "hash keys" in separate buckets. In this case, one key per bucket.
- You can add and remove things from the table
- It can tell you if it is holding a particular key without looking through the whole list



 If I wanted to store the node indices in a hash table, each node index would be a hash key.

# Using the hash table to store edges

- An edge is two nodes:
  - the prefix node and the suffix node
  - You need nested hash tables



A hash table you can use for this purpose /proj/cse308/Project1/setDemo set\_t

A Dynamic Hash Table implemented in C

```
set_t mySet = alloc_set(0);
set_t mySet = alloc_set(SP_MAP);
```

- Sets are allocated in the C style
  - "0" to hold integers
  - "SP\_MAP to hold pointers (Objects, other sets)
- A demonstration is implemented in setDemo cd /proj/cse308/Project1/setDemo;
   ./example -set

# Build the Edge Table with set\_t

First, instantiate the set. Lets call it "outerSet"

```
set_t outerSet = alloc_set(SP_MAP);
```

 Now we are going to go through the reads, and insert them into the edgeSet.

```
for(i = 0; i<numReads; i++) {...}</pre>
```

- We have not instantiated any of the internal hash tables yet because right now because we have not gone through the reads yet
  - We will instantiate the internal hash tables only as we need them.

# Building the table with set\_t

0 1 2 3

4 5 6 7

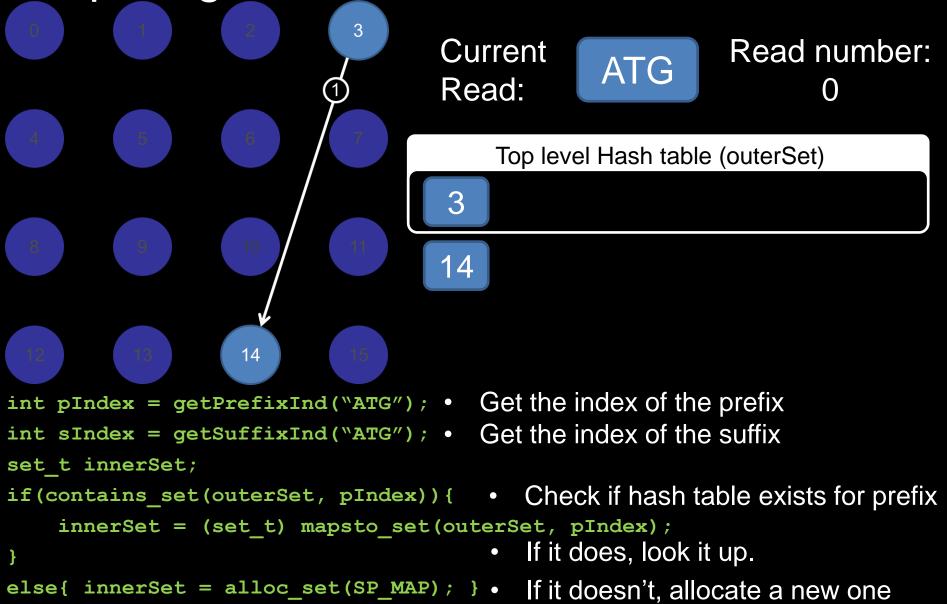
Top level Hash table (outerSet)

8 9 10 11

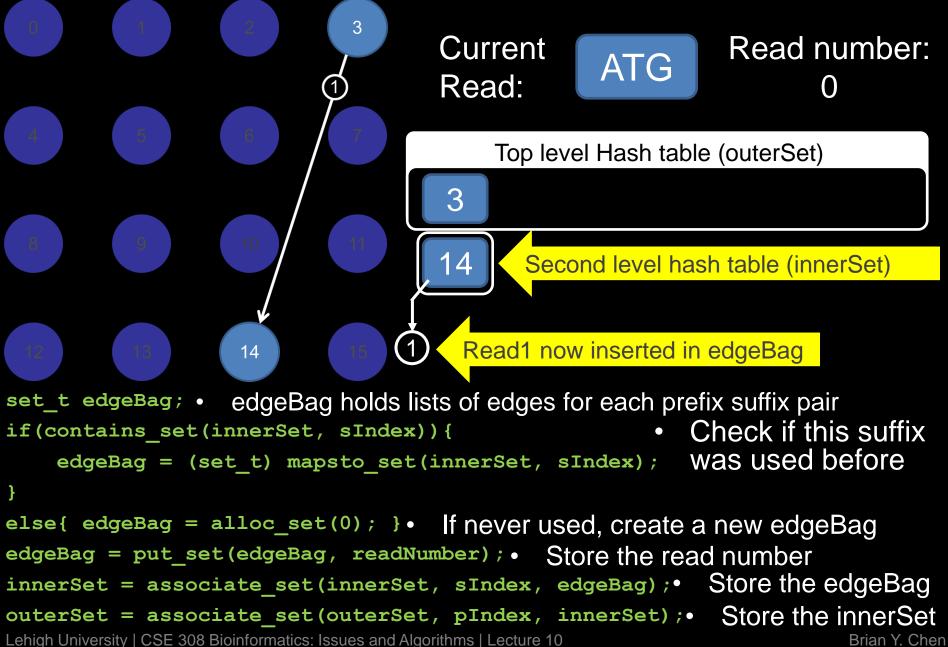
12 13 14 15

set\_t outerSet = alloc\_set(SP\_MAP);
 First, instantiate the set.
 Lets call it "outer"

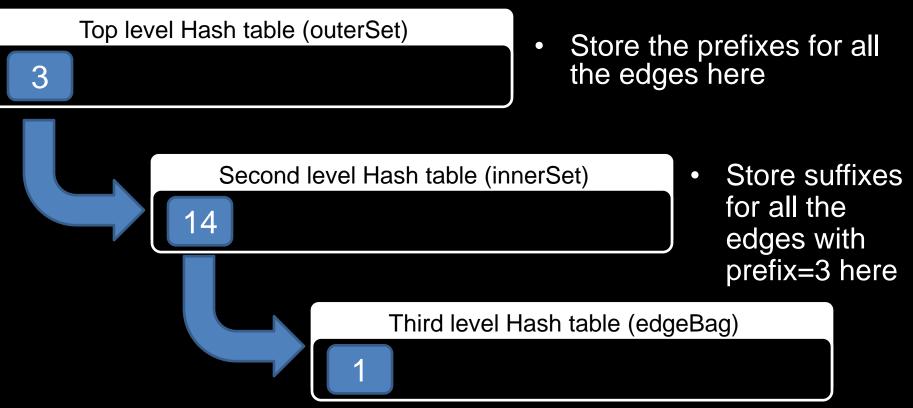
## Preparing to insert a read into outerSet



# Inserting the read into the edgeSet



## What did we just do?



 Multiple reads can have the same prefix and suffix. Store the index of the read (this was the first one) here

### The whole shebang

```
set t outerSet = alloc set(SP MAP);
for( all reads r ) {
 int pIndex = getPrefixInd(r); //this is the actual index
 int sIndex = getSuffixInd(r);
 set t innerSet;
 if( contains set(outerSet, pIndex) ){
    innerSet = (set t) mapsto set(outerSet, pIndex);
 else{ innerSet = alloc set(SP MAP); }
  set t edgeBag;
  if( contains set(innerSet, sIndex) ){
    edgeBag = (set t) mapsto set(innerSet, sIndex);
  else{ edgeBag = alloc set(0); }
  edgeBag = put set(edgeBag, readNumber);
  innerSet = associate set(innerSet, sIndex, edgeBag);
  outerSet = associate set(outerSet, pIndex, innerSet);
```

### Now that we've built an edgeset....

- Now we want to find a path
- We will start somewhere and walk from edge to edge
- We cannot reuse an edge, so we must keep track

```
set_t usedEdges = alloc_set(0);
```

- This set does not contain objects, it just contains edge indices.
- Each time we use an edge, we insert it here:

```
usedEdges = put_set(usedEdges, thisEdge);
```

### Where to start?

- We need to start the path at a node with outdegree > indegree
- How do we calculate outdegree and indegree?
- Outdegree: easy. Make a function for this:
  - Each prefix corresponds to a hash table stored in outerSet. Get it out.

```
innerSet = (set_t) mapsto_set(outerSet, prefixIndex);
```

Each suffix corresponds to an edgeBag. Get it out.

```
edgeBag = (set_t) mapsto_set(innerSet, suffixIndex);
```

– The outdegree is the sum of the number of members in each edgeBag in the innerSet:

```
OutDegree += size_set(edgeBag);
```

### Indegree: slightly harder.

- Each indegree of a node corresponds to one read where this node was a suffix.
- Search through every innerSet in the outerSet.
- Each time an innerSet contains the suffixIndex:
  - Get out the corresponding edgeBag
  - Get the size of the edgeBag
  - Add that size to the total indegree of this node.

### An easier way to get indegree/outdegree

Record this information as you go through the reads:

```
set_t indegrees = alloc_set(SP_MAP);
set_t outdegrees = alloc_set(SP_MAP);
```

 Each time you get an edge, get its prefixIndex and suffixIndex, and store it in the sets:

```
int * counter;
if ( contains_set(indegrees, sufIndex ) {
   counter = (int *) mapsto_set(indegrees, sufIndex);
}
else{   counter = new int[1]; counter[0] = 0; }
counter[0] += 1;
indegrees = associate set(indegrees, sufIndex, counter);
```

 Each time you get an edge, get its prefixIndex, suffixIndex, store it in outdegrees or indegrees

## Walking along a path of edges

- Find a node with outdegree > indegree
  - This has a specific prefix index.
- Find an edge leaving the node.

- Add that edge to the used edges,
- Add the suffixIndex to a list of nodes in your path.
  - Think carefully how you represent your paths/cycles

# Completing paths and cycles

- If you come back to a node you have visited before, it is a cycle.
  - You don't have to stop unless you are out of unused edges. Keep going – a longer path is more useful
- If there are no more unused edges from the node you are on, then it is the end of your path.
- Keep a separate list of all your paths and cycles.

# Detect if your paths and cycles intersect

- You can do this if you store your paths and cycles in sets.
- Just call the contains\_set() function to tell if a node you are on is in another set.
- Be careful how you store paths and cycles in a set.
  - Sets of integers are STRICTLY non-redundant. If you insert an integer that is already in the set, nothing will happen: repeating lists like cycles are bad.
  - While a set might be good for recording what nodes are used in your set, it is bad for storing repeating elements
  - If you only store nodes, then you don't know which edges you are storing. This could be a problem!

# A really important point

- We are only looking at reads that overlap by exactly 15 nucleotides.
- Your test, overlap(read1, read2, 15) should return true only if the 15 nucleotides in the suffix are equal to the 15 nucleotides in the prefix.
  - You don't care if the overlap is of a different length
- There is likely to be more than one read starting at every nucleotide.
- That means that if a read R lines up at a shorter or longer overlap, another read will line up with R at exactly 15.

## You have many resources around you

- Don't work in isolation
  - Consult the other members of the class if you have questions about the project you are working on
  - Consult the other members of your group if you have questions about your report
    - Reports are intentionally cross disciplinary

- Get started now if you have not already started.
- You only have about two weeks left.

# Questions