CS267 Assignment 3:

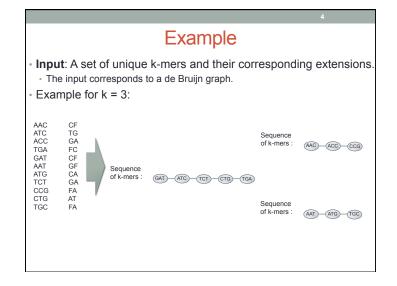
Parallelize Graph Algorithms for de Novo Genome Assembly

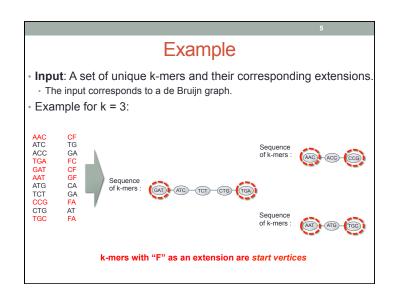
Spring 2015

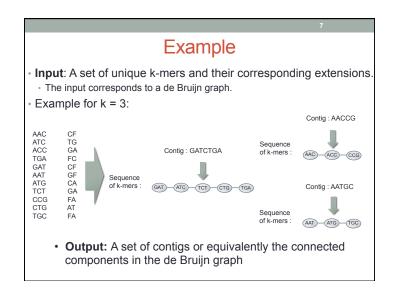
Problem statement

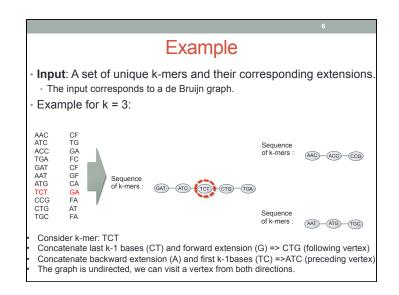
- Input: A set of unique k-mers and their corresponding extensions.
- · k-mers are sequences of length k (alphabet is A/C/G/T).
- · An extension is a simple symbol (A/C/G/T/F).
- The input k-mers form a de Bruijn graph, a special graph that is used to represent overlaps between sequences of symbols.
- Output: A set of contigs, i.e. connected components in the input de Bruijn graph.

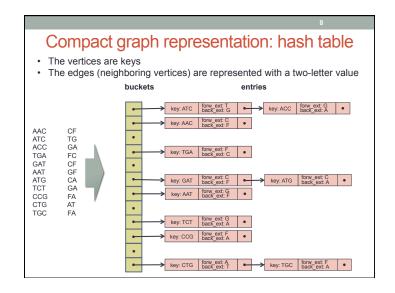
Example **Input**: A set of unique k-mers and their corresponding extensions. Example for k = 3: Format: k-mer forward extension . backward extension CF AAC ATC TG ACC GΑ TGA FC CF GAT AAT GF **ATG** CA TCT GΑ CCG FA CTG TGC FΑ

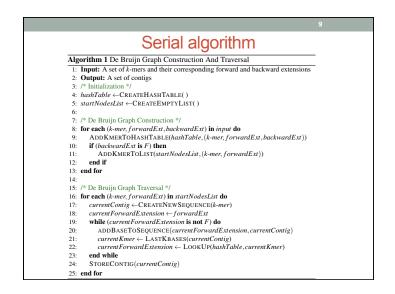


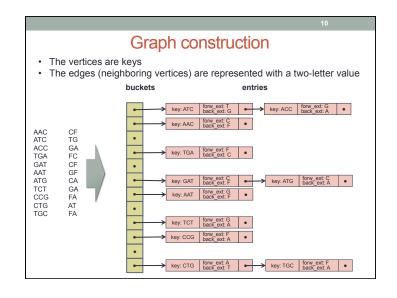


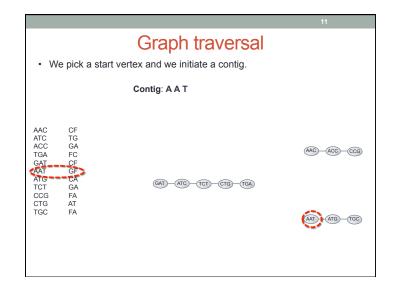


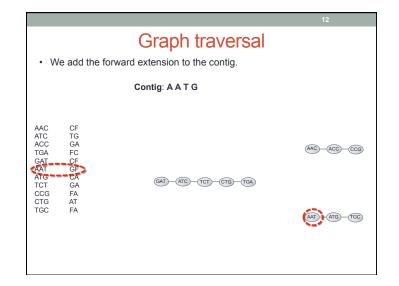


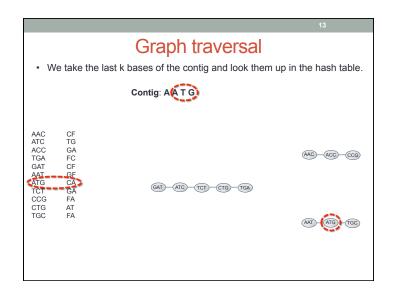


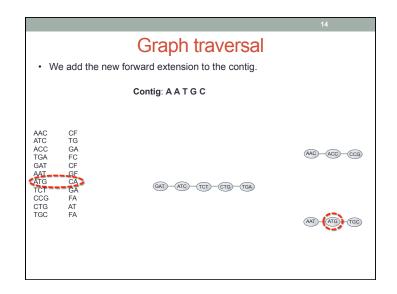


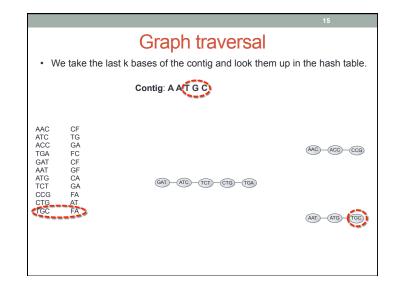


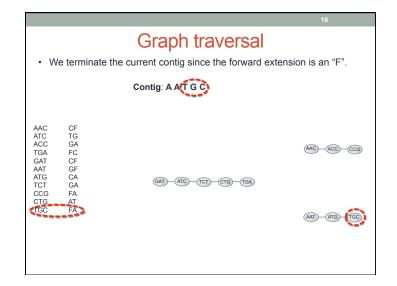


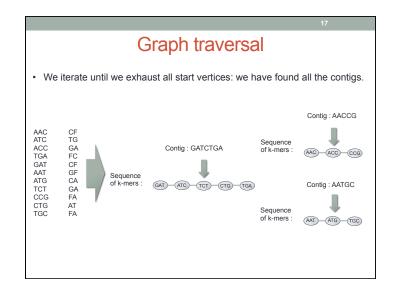












Parallelization hints

- 1. Distribute the hash table among the processors.
 - UPC is convenient: Store the hash table in the shared address space.
 - You may want to use upc_all_alloc().
- 2. Each processor stores part of the input in the distributed hash table.
 - · What happens if two processors try to write the same bucket at the same time?
 - We need to avoid race conditions (UPC provides locks and global atomics).
- 3. We want to traverse the graph in parallel.
 - · Can we determine independent traversals by examining the input?
 - · How can we distribute the work among processors?