CS-240

 $\bullet \bullet \bullet$

1st Programming Project

Project Outline & Entities

- ✤ Simulate human species evolution
- Different species
- Each species consists of different populations
- ***** Each population resides in a **continent**

Species

- Species are stored in a *double-linked* list
- ✤ Sorted on species' ID
- ✤ struct Species
 - ➤ int sid; // species' ID
 - struct Species *next;
 - struct Species *prev;
 - struct Population *head;
 - ➤ struct Population *tail;

Species Double-linked List



Populations

- Populations are stored in a single-linked list
- ✤ Sorted on population's ID
- struct Population
 - ➤ int gid; // population ID
 - ➤ int sid; // species' ID
 - ➤ int cid; // continent's ID
 - ➤ struct Population *next;
 - struct Population *next_species;

Species Double-linked List & Populations



Continents

- Continents are described by an array of size 5
- Each element is a pointer to a *struct ContinentList*, containing the information
- ✤ The lists are *unsorted* and have a *sentinel* node
- struct ContinentPopulation
 - int gid; // population's ID
 - struct ContinentPopulation *next;

Continent's Array



Homo Sapiens

- All species eventually evolve (or contribute) to *Homo Sapiens*
- The evolution is described by a *single-linked list*, *sorted* on the species' ID
- Each node is of type *struct Population*
- Each species' 1st node points to the 1st population of the next species (*next_species* pointer)

Homo Sapiens List



Events

- ♦ S <sid> (new species)
 - Insert new species node in species DLL
- ♦ G <gid> <sid> <cid> (new population)
 - ➤ Traverse species list and locate <sid>
 - Insert new node in its population list
- ♦ M <sid1> <sid2> <sid3> (merge species)
 - Traverse species list and locate **<sidl>** and **<sid2>**
 - ➤ Insert new species with <sid3>
 - Transfer <sid1> and <sid2> populations, in <sid3> (complexity O(n+m))
 - > New population list should still be sorted on the populations' ID
 - Delete <sid1> and <sid2>

More events

D (distribute)

- > Traverse **whole** population list for each species
- ▶ For each population, insert a new node (*struct ContinentPopulation*) in its continent's list
- ➤ Use the population's *<cid>* field to locate the correct continent

✤ K <gid> <sid> (delete population)

- Traverse species list and locate <sid>
- Delete population <gid>
- Delete population from it continent as well

More events

- ♦ F <sid> (species extinction)
 - > Traverse species list in **descending** order
 - Locate and delete species <sid>
 - ➤ Delete all of its populations
 - Delete each population from the continent's array as well

✤ E (evolution)

- ➤ Traverse species list
- > **Transfer** each population list **as-is** to the evolution list
- \succ Update the **next_species** pointer of a species' 1st population to point to the 1st of the next one
- \rightarrow **O(n)** : **n** is the number of species

More events

✤ N (species statistics)

- > Traverse the **homo Sapiens** list and count all species
- \blacktriangleright **O(n)** : **n** is the number of species

✤ J <sid> (population statistics)

- Traverse homo Sapiens list and locate the first population of <sid>
- > Traverse that specific species' population list and count its populations
- ➤ O(n+m) : n is the number of species; m is the number of populations that belong to <sid>

Print events

- **P**: Print species list, **without** their population lists
- **X**: Print species list, **with** population lists
- **C**: Print continent's array and each continent's population list
- ◆ W: Print homo Sapiens list

General Info

✤ Your project should:

- > Contain everything it needs to compile
- ➤ Compile & run in CSD's UNIX machines
- For any questions, contact the TAs using the course's e-mail or mailing list
 - ➢ hy240a@csd.uoc.gr
 - ➢ hy240a-list@csd.uoc.gr