Genome 540 Discussion

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Genome Sciences
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About Me

Background
- from San Diego, CA
- Undergrad: biochemistry
- Gap years:
  - academia: in situ sequencing dev
  - industry: ReadCoor, Inc. startup ^
- UWGS: 4th year with Brian Beliveau

Wet lab
- In situ “omics” tech dev
- Multiplexed FISH tech dev

Dry lab
- Design / analysis pipelines
- Specific probe design
- DNA library design

For fun
- Programming, web dev
- Sailing, skiing

Choosing a programming language

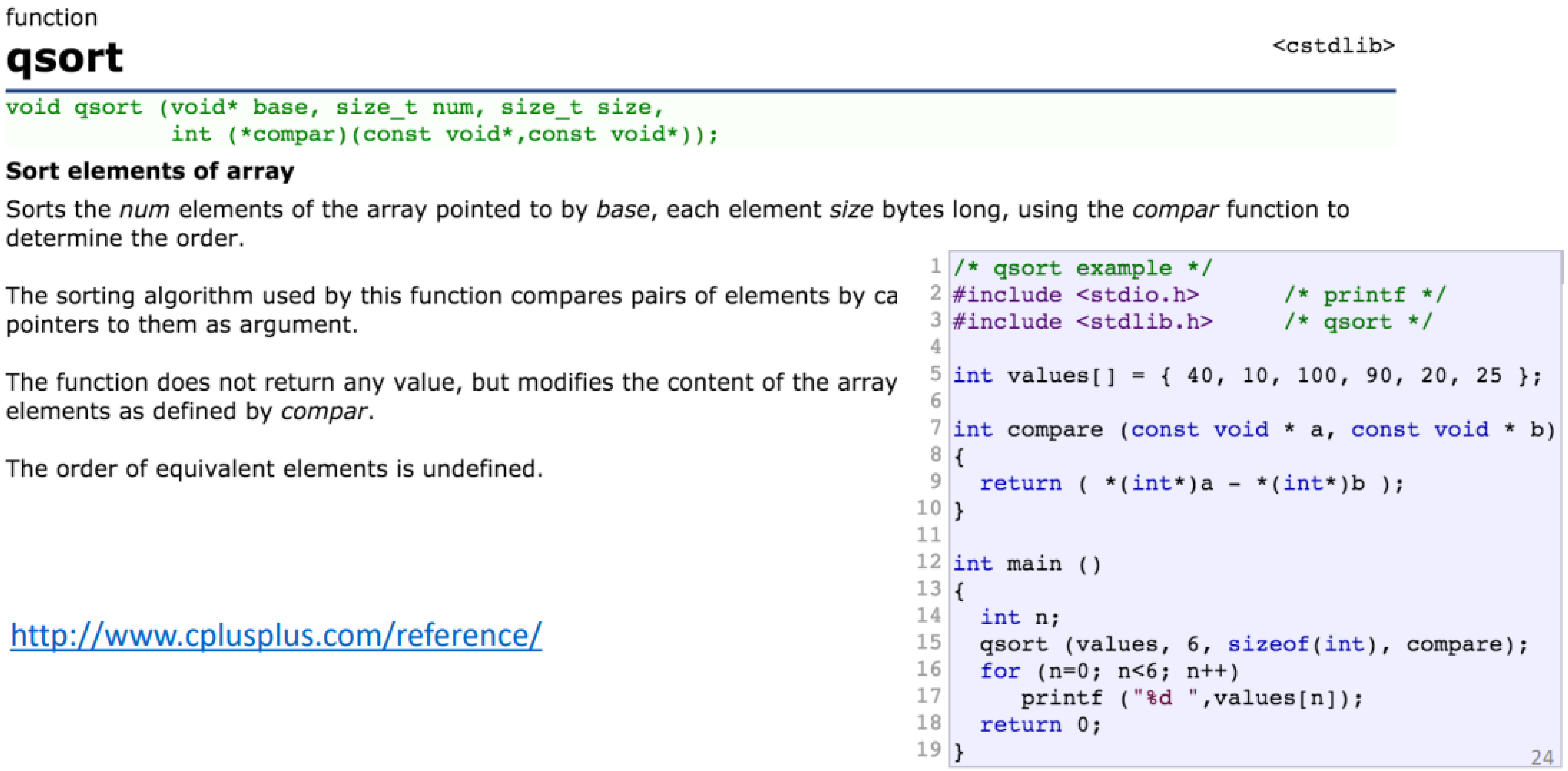
Python
- "interpreted"
- dynamic-typed
- data type is not required while declaring variable

```
A = 5
B = "x"
C = ['x', 'y', 'z']
```

C/C++
- "compiled"
- statically typed
- data type is required while declaring variable
- *debugging is challenging*

```
int A = 5;
char B = 'x';
char C[3] = {'x', 'y', 'z'};
```

Utilizing existing helper functions in C++



function

qsort

<cstdlib>

```
void qsort (void* base, size_t num, size_t size,
            int (*compar)(const void*,const void*));
```

Sort elements of array

Sorts the *num* elements of the array pointed to by *base*, each element *size* bytes long, using the *compar* function to determine the order.

The sorting algorithm used by this function compares pairs of elements by ca
pointers to them as argument.

The function does not return any value, but modifies the content of the array
elements as defined by *compar*.

The order of equivalent elements is undefined.

```
/* qsort example */
#include <stdio.h>      /* printf */
#include <stdlib.h>     /* qsort */

int values[] = { 40, 10, 100, 90, 20, 25 };

int compare (const void * a, const void * b)
{
  return ( *(int*)a - *(int*)b );
}

int main ()
{
  int n;
  qsort (values, 6, sizeof(int), compare);
  for (n=0; n<6; n++)
     printf ("%d ",values[n]);
  return 0;
}
```

http://www.cplusplus.com/reference/

Programming Style

- The more readable your code is
  - The more I'll be able to help you if something's wrong
  - The more useful it will be to you later
  - Try to use Github (version control and easy sharing)

- Tips for readability
  - Intuitive variable/function names, (a, b, c vs. seq_name, seq_length)
  - Comments
    - Outlining general structure of program/key points of implemented algorithm
    - Clarifying any tricky/unintuitive lines of code
  - Simplicity over performance optimization (until it becomes necessary)
  - Write more functions
  - Write less "for" loops

General tips for homework

- C/C++ or Java for some homework are necessary
- Python works for most homework
- R and MATLAB are not suitable

- It is important to understand biological questions
- “Gap” between understanding the algorithm and writing it out
- Your program might work on the test data but not work on the real data (much bigger and some unexpected issues)

- Print intermediate output
- It’s not necessary to write every basic function (for example, sort)
- Please make an effort to match the template!

General tips for homework

- Start with pseudocode
- Start writing and then improve the details
- C++ is much faster than Python (at least for HW1)
- Get comfortable with pointers
- Output to template directly
    - Programmatically generate homework output to turn in
    - Format will be checked programmatically

General tips for homework

My personal experience of each pset:

- [study the spec] What (exactly) are the high level goal(s)?
- [brainstorm] In general, how would I achieve those goals?
    - [review] (do I understand the algorithm/concepts from lectures?)
- [brainstorm] What is a reasonable first step to accomplish?
    - [brainstorm] How do I do that step in <language>?
- [dev] implement the step
- [brainstorm] how can I be sure that I did this step correctly?
    - [brainstorm] what would be a good test to pick up on this?
- [dev] implement some basic testing (e.g. print statements)
- [dev] test the code
- This step works, start thinking of the next step
- [...]

Takeaways:

- Critical to understand lecture material well
    - review and discuss as needed
- Critical to leave enough time
    - Start on psets early!
- Different stages in understanding, planning, implementing, testing
    - Different types of thinking

Programming tips - testing

- Create small, easily-verified test cases
- Edge cases
- Print intermediate output
- Write incrementally, test as you go
    - Assertion statements
- Check against expectations

Programming tips - efficiency

- Remove unnecessary stuff from loops
- Avoid slow comparison routines when sorting
- Profiling tools
  - line_profiler (python)
  - gprof, valgrind (C/C++) [valgrind also identifies memory leaks]
  - dprofpp (Perl)

Topics for future discussion sections?

- Scalable and reproducible bioinformatics pipelines (Snakemake)
- Parallel computing: threading, multiprocessing, cluster computing
- General programming tips, languages (Python, C++, Unix tools)
- Version Control / Github
- Jupyter Notebooks / JupyterLab
- Recent DNA sequence algorithms from literature
- Virtual environments: how and why
- Relational database design