Compiling Cytosim on cluster

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The Linux environment of the cluster login nodes is missing several libraries and packages that are key to Cytosim. They cannot be installed without root privileges (probably for the best), so I found a workaround which involves using an Anaconda environment.

The procedure described below is quite "hacky," so if you are a C++ purist, avert your eyes.

Set up an Anaconda environment

First, load Anaconda with

```
1 module load anaconda3
```

Then, create and activate an environment for Cytosim and load the necessary packages:

```
conda create -n cytosim-env
conda activate cytosim-env

conda install -n cytosim-env python=3.7 numpy scipy matplotlib jupyter jupyterlab
vtk pip

conda install -n cytosim-env -c conda-forge libblas lapack xorg-libxt freeglut
zlib

conda install -n cytosim-env -c anaconda make cmake libpng

conda install -n cytosim-env -c psi4 gcc-5

conda install -n cytosim-env -c menpo glew

-n: --name
, name of the environment to which the package should be installed
```

-c: --channel, channel from which package should be fetched

Modify makefile.inc

There are several modifications that need to be made to makefile.inc for compilation to run successfully. The modifications are in the same order that they appear in the file.

Compiler configuration

Copy the GL directory with *.h files from the glew (or was it freeglut ?) conda package directory to new directory cytosim/src/extras and add an include flag in the makefile.inc file under the gcc section of the compiler settings:

```
1 CXX := ... -Isrc/extras
```

Enable PNG export by changing the HAS_PNG variable:

```
1 HAS_PNG := 1
```

Linux-specific settings

Make sure to make the following edits in the Linux section of makefile.inc

Specify \$BLASDIR in makefile.inc:

```
BLASDIR := /home/alexandral/.conda/pkgs/libblas*/lib/libblas.*
```

Change **GRAFIX** variable to

```
1 GRAFIX := -L$(LIBDIR) -lglut -lGL -lGLU -lXt -lX11
/home/alexandral/.conda/pkgs/glew-2.0.0-0/lib/libGLEW.so
```

For some reason, midway does not have GLEW, so this is a BYOGLEW kind of party.

```
Link to libpng.a of libpng package and to libz.a of zlib package in makefile.inc
LIB_PNG := /home/alexandral/.conda/pkgs/libpng-1.6.37-hbc83047_0/lib/libpng.a
/home/alexandral/.conda/pkgs/zlib-1.2.11-h516909a_1006/lib/libz.a
```

Edit the LD_RUN_PATH environment variable

Run the following command in the shell:

```
1 export LD_RUN_PATH="/home/alexandral/.conda/pkgs/glew-2.0.0-0/lib/"
```

As specified in the GRAFIX variable, the compiler relies on a GLEW shared object in a non-standard location (standard location is /urs/lib/). Therefore, we need to indicate where the executable should look for libGLEW.so whenever it is run. Adding the location of libGLEW.so to LD_RUN_PATH will compile the Cytosim executables with information on where to find the file.

(See https://homepages.inf.ed.ac.uk/imurray2/compnotes/library_linking.txt for more in-depth information about dynamic linking.)



If previously attempted to run make command in cytosim directory, first run

```
1 make clean
```

then

```
1 make alldim
```

The above command will compile executables for 1-, 2-, and 3D (to be found in bin1, bin2, and bin3, respectively). Though the executables are in different directories, they will have the same name. To add the executables to \$PATH, create new bin directory and copy executables into it as sim1, play1, report1, etc. to have dedicated executables for each dimension which can be called from anywhere.