

# Instructor Guide

Two scientific applications are demonstrated to show the problem of why parallelization is eventually needed for large problems.

The codes are included and ready to compile/run. Encourage students to run both of these and to try varying the command-line arguments.

## Drug Design

To compile: `g++ -o dd_serial dd_serial.cpp`

To run: `./dd_serial`

Optional command line arguments (in this order):

- 1) maximum length of the randomly generated ligand strings
- 2) number of ligands generated
- 3) protein string to which ligands will be compared

Try a combination of small and large values to show that as the problem grows, the computational needs grow very quickly.

## Pandemic

To compile: `make clean then make` in the root directory

To run: `./pandemic_serial`

Optional command line arguments:

- n the number of people in the model
- i the number of initially infected people
- w the width of the environment
- h the height of the environment
- t the number of time days in the model
- T the duration of the disease (in days)
- c the contagiousness factor of the disease
- d the infection radius of the disease
- D the deadliness factor of the disease

-m the number of microseconds in between days in the model (used to speed up or slow down the animation)

Try a combination of small and large values to show that as the problem grows, the computational needs grow very quickly.