Hybrid multi-scale Agent-based model (HABM)

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The is a C++ package for Predicting the impact of combined therapies on myeloma cell growth. The HABM combines an ODE system and Agent-based model (ABM). The ODEs was used for modeling the dynamic changes of intracellular signal transductions and ABM for modeling the cell-cell interactions between stromal cells, tumor, and immune components in the bone marrow.

ODEmodel.c and ODEmodel2.c represent two intracellular pathways of MIC and BMSC, respectively. The ODE systems will be solved by a package in libf77. Please create a new fold under the root called "libf77".

The main function of ABM model is SolveMain.cpp

run_main_N.sh was used to compile the whole C++ package as run_main.o

Command: bash run_main_N.sh run_main

After compile, you can directly run run_main to get the results of ABM model one time.

Command: run_main -h (see the main menu of input parameters)

Command: run_main -s 1000 -t 300 -I 1 -D 1 -C 1 -T 1 -b 1 -l 1 -n 1

It means the model will run to 300 time points, and four types of cell populations present in the simulated 3D space. -b,-l,-n were 1, which means the dose for each drug used. The range of each drug in our model is from 1-10 (0 mans no drug).

Due to the HABM is a stochastic model, the reasonable results can be obtained after repeat running the model over hundreds times. The file Helloworld.c will parallel to call run_main and implement the HABM model many times.

For each condition, a set of input parameters of ABM were given in Helloworld.c, and it will repeat 200 times. Therefore, Helloworld.c should be complied each time when you update the input parameters. **Command**: mpicc –o Helloworld Helloworld.c

After compiled the Helloworld.c, myJob.sh is used to submit a job of parallel computing to server.

You can call: sbatch myJob.sh