

Diffusion equation in TCLB solver

In this workshop we will cover basic conceptions related to TCLB solver. We will not dive into detail of TCLB compilation or model development - it's out of scope of this tutorial and is covered in other materials.

The d2q9_reaction_diffusion_system_XXXX models

This TCLB model is a collection of Reaction-Diffusion Partial/Ordinary differential equations systems. Basically, the model is build to solve systems in form:

$$\begin{aligned}\frac{\partial \mathbf{DRE}_i(x,t)}{\partial t} &= \text{Diffusivity_DRE}_i \nabla \mathbf{DRE}_i(x,t) + R_i(\text{RHS}) \\ \frac{\partial \mathbf{DRE}_i(x,t)}{\partial t} &= \text{Diffusivity_DRE}_i \nabla \mathbf{DRE}_i(x,t) + R_i(\text{RHS}) \\ \frac{d\mathbf{ODE}_i(x,t)}{dt} &= F_i(\text{RHS}) \\ \frac{d\mathbf{ODE}_i(x,t)}{dt} &= F_i(\text{RHS})\end{aligned}$$

Where $\mathbf{DRE}_i(x,t)$ is spatially variable field, solution of first Diffusion-Reaction equation, and $\mathbf{ODE}_i(x,t)$ is solution of Ordinary Differential Equation at point x . Both equations are solved using second order, implicit midpoint scheme. Spatial discretisation of DRE is performed using LBM method - details could be found in [X]. The right hand side vector is equal:

$$\text{RHS} = [\mathbf{DRE}_i(x,t), \mathbf{ODE}_i(x,t)]$$

Most of the models have meaningful names for \mathbf{DRE}_i variables and params, provided below.

At point of writing, supported model are:

d2q9_reaction_diffusion_system_SimpleDiffusion

$$\frac{\partial \mathbf{PHI}(x,t)}{\partial t} = \text{Diffusivity_PHI} \nabla \mathbf{PHI}(x,t)$$

or

$$\frac{\partial \phi(x,t)}{\partial t} = \nu \nabla^2 \phi(x,t)$$

d2q9_reaction_diffusion_system_AllenCahn

$$\frac{\partial \mathbf{PHI}(x,t)}{\partial t} = \text{Diffusivity_PHI} \nabla \mathbf{PHI}(x,t) + \text{Lambda} * \mathbf{PHI}(x,t) * (1 - \mathbf{PHI}(x,t))$$

or

$$\begin{aligned}\frac{\partial \phi(x,t)}{\partial t} &= \nu \nabla^2 \phi(x,t) + C \phi(1 - \phi) \\ \frac{\partial I}{\partial t} &= \beta \frac{S}{N} I - \gamma I + \nu_I \nabla I \\ \frac{\partial R}{\partial t} &= \gamma I + \nu_R \nabla R\end{aligned}$$

for $N = 1$

d2q9_reaction_diffusion_system_SIR_ModifiedPeng

or the WSIR model, already referenced in this workshop

$$\begin{aligned}\frac{\partial \mathbf{W}}{\partial t} \mathbf{W} &= \text{Beta}_w * ((\mathbf{I} - \mathbf{W}) + \text{Diffusivity_W} \nabla \mathbf{W}) \\ \frac{\partial \mathbf{S}}{\partial t} \mathbf{S} &= -\text{Beta}_s * \frac{\mathbf{S} * \mathbf{W}}{\mathbf{N}} * \\ \frac{\partial \mathbf{I}}{\partial t} \mathbf{I} &= \text{Beta}_s * \frac{\mathbf{S} * \mathbf{W}}{\mathbf{N}} - \text{Gamma} * \mathbf{I} \\ \frac{\partial \mathbf{R}}{\partial t} \mathbf{R} &= \text{Gamma} * \mathbf{I}\end{aligned}$$

or

$$\begin{aligned}\frac{\partial W}{\partial t} W &= \beta_W \left[\frac{r^2}{8} W + (I - W) \right] \\ \frac{\partial S}{\partial t} S &= -\beta \frac{S}{N} W \\ \frac{\partial I}{\partial t} I &= \beta \frac{S}{N} W - \gamma I \\ \frac{\partial R}{\partial t} R &= \gamma I\end{aligned}$$

Keep in mind that for consistency, it's recommended to set

$$\text{Diffusivity_W} = \text{Beta}_w * \frac{r^2}{8}$$

Additionally, list of models could be extracted via:

```
In [1]:
! tcblmake d2q9_reaction_diffusion_system/list

TCLB_PATH=/home/mdzik/.TCLB/TCLB

d2q9_reaction_diffusion_system_AllenCahn          X
d2q9_reaction_diffusion_system_SIR_ModifiedPeng  -
d2q9_reaction_diffusion_system_SIR_SimpleLaplace -
d2q9_reaction_diffusion_system_SimpleDiffusion   -
d2q9_reaction_diffusion_system_SimpleDiffusion   SIR_SimpleLaplace
d2q9_reaction_diffusion_system_AllenCahn         -
d2q9_reaction_diffusion_system_SIR_ModifiedPeng  -
d2q9_reaction_diffusion_system_SIR_SimpleLaplace -
d2q9_reaction_diffusion_system_SimpleDiffusion   X

d2q9_reaction_diffusion_system_AllenCahn         SimpleDiffusion
d2q9_reaction_diffusion_system_SIR_ModifiedPeng  -
d2q9_reaction_diffusion_system_SIR_SimpleLaplace -
d2q9_reaction_diffusion_system_SimpleDiffusion   X
```

What is included in this environment

To run TCLB model us ipython shell binding:

```
! tcbl ModelName ConfigurationFile.xml

This will effectively run (in the current working directory)

TCLB_PATH/CLB/ModelName/main ConfigurationFile.xml
```

in your Jupyter/Binder. We will use

```
! tcbl ModelName ConfigurationFile.xml > /dev/null && echo "DONE!"

to suppress output in most cases.
```

TCLB solver

As you might noticed TCLB is a set of models (like d2q9). TCLB uses XML as source of configuration plus limited numbr of command line options which will be covered later. There is a python library that helps you build XML on-the-fly if you like.

```
In [2]:
import h5py
import numpy as np
import matplotlib.pyplot as plt
from display_xml import XML

! tcbl d2q9_reaction_diffusion_system_SimpleDiffusion SimpleDiffusion.xml
```

```
MEMO: TCLB: local:0/1 work:0/1 --- connected to:
[ ] -----
[ ] - CLB version: v6.5.0-71-g35292921 -
[ ] Model: d2q9_reaction_diffusion_system_SimpleDiffusion
[ ] -----
[ ] Setting output path to: SimpleDiffusion
[ ] Discarding 1 comments
[ ] Running on CPU
[ ] (0) Ignoring "Unit" element in config file
[ ] [ Global lattice size: 100x100x1
[ ] [ Mesh region size: 1000x1000x1000, Overhead: 0%
[ ] [ Local lattice size: 100x100x1
Hello allocator!
Threading:
[ ] 1x1 | Primal, NoGlobals, InitFromExternal
[ ] 1x1 | Optimize, NoGlobals, InitFromExternal
[ ] 1x1 | SteadyAdjoint, NoGlobals, InitFromExternal
[ ] 1x1 | Primal, IntegratedGlobals, InitFromExternal
[ ] 1x1 | Tangent, IntegratedGlobals, InitFromExternal
[ ] 1x1 | Optimize, IntegratedGlobals, InitFromExternal
[ ] 1x1 | SteadyAdjoint, IntegratedGlobals, InitFromExternal
[ ] 1x1 | Primal, OnlyObjective, InitFromExternal
[ ] 1x1 | Tangent, OnlyObjective, InitFromExternal
[ ] 1x1 | Optimize, OnlyObjective, InitFromExternal
[ ] 1x1 | SteadyAdjoint, OnlyObjective, InitFromExternal
[ ] 1x1 | Primal, NoGlobals, BaseIteration
[ ] 1x1 | Tangent, NoGlobals, BaseIteration
[ ] 1x1 | Optimize, NoGlobals, BaseIteration
[ ] 1x1 | SteadyAdjoint, NoGlobals, BaseIteration
[ ] 1x1 | Primal, IntegratedGlobals, BaseIteration
[ ] 1x1 | Tangent, IntegratedGlobals, BaseIteration
[ ] 1x1 | Optimize, IntegratedGlobals, BaseIteration
[ ] 1x1 | SteadyAdjoint, IntegratedGlobals, BaseIteration
[ ] 1x1 | Primal, OnlyObjective, BaseIteration
[ ] 1x1 | Tangent, OnlyObjective, BaseIteration
[ ] 1x1 | Optimize, OnlyObjective, BaseIteration
[ ] 1x1 | SteadyAdjoint, OnlyObjective, BaseIteration
[ ] 1x1 | Primal, NoGlobals, BaseInit
[ ] 1x1 | Tangent, NoGlobals, BaseInit
[ ] 1x1 | Optimize, NoGlobals, BaseInit
[ ] 1x1 | SteadyAdjoint, NoGlobals, BaseInit
[ ] 1x1 | Primal, IntegratedGlobals, BaseInit
[ ] 1x1 | Tangent, IntegratedGlobals, BaseInit
[ ] 1x1 | Optimize, IntegratedGlobals, BaseInit
[ ] 1x1 | SteadyAdjoint, IntegratedGlobals, BaseInit
[ ] 1x1 | Primal, OnlyObjective, BaseInit
[ ] 1x1 | Tangent, OnlyObjective, BaseInit
[ ] 1x1 | Optimize, OnlyObjective, BaseInit
[ ] 1x1 | SteadyAdjoint, OnlyObjective, BaseInit
[ ] [0] Cumulative allocation of 1619520 B (1.6 MB)
[ ] Creating geom size:10000
[ ] Setting output path to: SimpleDiffusion
[ ] Setting output path to: output/SimpleDiffusion/SimpleDiffusion
[ ] loading geometry ...
[ ] Setting number of zones to 2
[ ] Setting Diffusivity_PHI to 0.1666 (0.166600)
[ ] [0] Settings (Diffusivity For PHI) to 0.166600
[ ] Setting Init_PHI in zone (1) to 0.5 (0.500000)
[ ] Setting Init_PHI in zone (1) to 0.5 (0.500000)
[ ] Initializing lattice ...
[ ] Callback HDF5 with no iterations attribute=-1 2373h 2m
[ ] Negotiated HDF5 chunks: 1x100x100[kB]
[ ] 0 it waiting hdf5
[ ] Setting action Solve at 200.000000 iterations
[ ] Setting callback HDF5 at 10.000000 iterations
[ ] Negotiated HDF5 chunks: 1x100x100[kB]
[ ] Adding HDF5 to the solver hands
[ ] 53.0 MB/sps 5.88 GB/s [=====]2m
[ ] 10 it waiting hdf5
[ ] 53.9 MB/sps 8.74 GB/s [=====]
[ ] 20 it waiting hdf5
[ ] 17.8 MB/sps 2.89 GB/s [=====]
[ ] 30 it waiting hdf5
[ ] 17.7 MB/sps 2.86 GB/s [=====]
[ ] 40 it waiting hdf5
[ ] 17.8 MB/sps 2.88 GB/s [=====]
[ ] 50 it waiting hdf5
[ ] 17.5 MB/sps 2.84 GB/s [=====]
[ ] 60 it waiting hdf5
[ ] 17.4 MB/sps 2.83 GB/s [=====]
[ ] 70 it waiting hdf5
[ ] 16.2 MB/sps 2.82 GB/s [=====]
[ ] 80 it waiting hdf5
[ ] 18.5 MB/sps 2.84 GB/s [=====]
[ ] 90 it waiting hdf5
[ ] 7.4 MB/sps 1.20 GB/s [=====]
[ ] 100 it waiting hdf5
[ ] 16.9 MB/sps 2.72 GB/s [=====]
[ ] 110 it waiting hdf5
[ ] 18.0 MB/sps 2.92 GB/s [=====]
[ ] 120 it waiting hdf5
[ ] 18.1 MB/sps 2.93 GB/s [=====]
[ ] 130 it waiting hdf5
[ ] 18.2 MB/sps 2.95 GB/s [=====]
[ ] 140 it waiting hdf5
[ ] 18.8 MB/sps 3.05 GB/s [=====]
[ ] 150 it waiting hdf5
[ ] 18.8 MB/sps 3.05 GB/s [=====]
[ ] 160 it waiting hdf5
[ ] 8.3 MB/sps 1.35 GB/s [=====]
[ ] 170 it waiting hdf5
[ ] 18.5 MB/sps 2.99 GB/s [=====]
[ ] 180 it waiting hdf5
[ ] 17.8 MB/sps 2.88 GB/s [=====]
[ ] 190 it waiting hdf5
[ ] 18.4 MB/sps 2.98 GB/s [=====]
[ ] 200 it waiting hdf5
[ ] Total duration: 1.161041 s = 0.019351 min = 0.000323 h
```

```
In [4]:
TimeSteps = list()
for i in range(0,200,10):
    f = h5py.File('..output/SimpleDiffusion/SimpleDiffusion_HDF5_008d.h5','a')
    TimeSteps.append(f['PHI'][0,1,:])

TimeSteps = np.array(TimeSteps)

plt.figure(figsize=(8,8))
plt.plot(TimeSteps[5,25,:],T,'o-');
plt.grid(which='both');
plt.xlabel('X');
plt.ylabel(r'$\Phi$');


```

We could also extract 1D image

```
In [5]:
plt.imshow(TimeSteps[5])

Out[5]:
<matplotlib.image.AxesImage at 0x7fde46a9f40>


```

Using TCLBConfig writer class

Now, we are going to generate same XML file using XML library. A nice thing is that we could use it to do some parametric studies. It also does limited "syntax" check.

```
In [6]:
import CLB.CLBXMLWriter as CLBXML

In [7]:
CLBc = CLBXML.CLBConfigWriter()

CLBc.addGeomParam('nx', 100)
CLBc.addGeomParam('ny', 100)

CLBc.addNone(name='city')
CLBc.addBox(dx=35, nx=35)

params = {
    'Diffusivity_PHI':0.1666,
    'Init_PHI':0.5
}

CLBc.addModelParams(params)

params = {
    'Init_PHI':0.5
}

CLBc.addHDF5()
CLBc.addModelParams(params, zone='city')
solve = CLBc.addSolve(iterations=200)
CLBc.addHDF5(iterations=10, parent=solve)

CLBc.write('SimpleDiffusionWithCLBXMLWriter.xml')
```

Apart from float representation, the resulting file is identical

```
In [8]:
f = open('SimpleDiffusionWithCLBXMLWriter.xml', 'r')
XML(''.join(f.readlines()))

Out[8]:
<CLBConfig version="2.0" output="output"/>
<!-- Created using CLBConfigWriter -->
<Geometry predef="none" model="MRT" nx="100.000000000000000000" ny="100.000000000000000000" />
<None name="city" />
<Box dx="35" nx="35" />
</None>
</Geometry>
<Param name="Diffusivity_PHI" value="0.166600000000000000" />
<Param name="Init_PHI" value="0.500000000000000000" />
<Geometry_in_matrix, last_index_in_matrix=1 />
<Beta_FD # backward FD
<Model>
<HDF5>
<Solve Iterations="200">
<HDF5 Iterations="10"/>
</Solve>
</CLBConfig>

In [9]:
! tcbl d2q9_reaction_diffusion_system_SimpleDiffusion SimpleDiffusionWithCLBXMLWriter.xml > /dev/null && echo "DONE!"

Hello allocator!
DONE!
```

```
In [10]:
TimeSteps2 = list()

for i in range(0,200,10):
    f = h5py.File('..output/SimpleDiffusionWithCLBXMLWriter_HDF5_008d.h5','a')
    TimeSteps2.append(f['PHI'][0,1,:])

TimeSteps2 = np.array(TimeSteps2)

plt.figure(figsize=(8,8))
plt.plot(TimeSteps2[5,25,:],T,'o-');
plt.grid(which='both');
plt.xlabel('X');
plt.ylabel(r'$\Phi$');


```

RInside: periodic IC and comparison with Finite Difference

Let's create initial condition, we will start in python

R inside block is build as

```
CLBc.addRunR(eval\
'''
some < r_code
''')

which will result in XML as:
```

```
<RunR>
<![CDATA[
]]>
</RunR>
```

Notice, that < in some cases got converted into <. This is XML character escaping. Keep the CDATA element and all be OK.)

Outmost usable part of R-TCLB integration are accessors to internal Fields:

```
Solver.Fields.FIELDNAME[] = SAMESHAPEVARIABLE;
```

and Actions/Stages:

```
Solver.Actions.InitFromExternalAction();
```

You could also call standard R functions inside (Full R should be available - it's embedded interpreter, see RInside upstream documentation for details/limitations if you need):

```
init = read.table("initial.csv", header = FALSE, sep = ",", dec = ".");
```

Let's create initial "data file"

```
In [11]:
u_ic = np.zeros(200)
u_ic[75:75] = 1
plt.plot(u_ic)
np.savetxt("initial.csv", u_ic, delimiter=',')


```

Now the XML configuration

```
In [12]:
CLBc = CLBXML.CLBConfigWriter()

CLBc.addGeomParam('nx', 200)
CLBc.addGeomParam('ny', 100)

CLBc.addRunR(eval\
'''
init = read.table("initial.csv", header = FALSE, sep = ",", dec = ".");
Solver.Fields.Init_PHI_External[] = init[1,:];
Solver$Actions$InitFromExternalAction();
''')

params = {
    'Diffusivity_PHI':0.1666,
    'Init_PHI':0.5
}

CLBc.addModelParams(params)

CLBc.addHDF5()
solve = CLBc.addSolve(iterations=200)
CLBc.addHDF5(iterations=10, parent=solve)

CLBc.write('SimpleDiffusionWithRInside.xml')
```

f = open('SimpleDiffusionWithRInside.xml', 'r')
XML(''.join(f.readlines()))

```
Out[18]:
<matplotlib.figure.Figure at 0x7fde46a98460>


```

The CLBc object could be reused (something could be appended to it after save, parameters could be overwritten)

XML for diffusion of the example image will look like that:

```
In [19]:
solve = CLBc.addSolve(iterations=200)
CLBc.addHDF5(iterations=10, parent=solve)
CLBc.write('SimpleDiffusionOfDromader_withIterations.xml')
f = open('SimpleDiffusionOfDromader_withIterations.xml', 'r')
XML(''.join(f.readlines()))
```



```
Out [19]: <CLBConfig version="2.0" output="output/">
<!-- Created using CLBConfigWriter-->
<Geometry predef="none" model="MRT" nx="640.0000000000000000" ny="480.0000000000000000"/>
<Model>
<Param name="Diffusivity_PHI" value="0.1666666666666666"/>
<Param name="Init_PHI" value="-0.5000000000000000"/>
</Model>
<RunR>
library('jpeg', lib="r_packages")

myurl &lt;!-- "https://upload.wikimedia.org/wikipedia/commons/thumb/a/a5/M-18A_Dromader_CALM.jpg/640px-M-18A_Dromader_CALM.jpg"
2 &lt;!-- Tempfile)
download.file(myurl,z,mode="wb", quiet=TRUE);
pic &lt;!-- readJPEG(z);
file.remove(z) # cleanup

SolversFields$Init_PHI_External[] = t(pic[,,1]);
SolversActions$InitFromExternalAction();
</RunR>
<HDF5>
<Solve iterations="200">
<HDF5 iterations="10"/>
</Solve>
</CLBConfig>
```

```
In [20]: ! tcib d2q9_reaction_diffusion_system_SimpleDiffusion SimpleDiffusionOfDromader_withIterations.xml > /dev/null

Hello allocator!
DONE
```

```
In [21]: for i in range(0,200,50):
plt.figure()
f = h5py.File('./output/SimpleDiffusionOfDromader_withIterations_HDF5_%.08d.h5'%i)
plt.imshow(f['PHI'][:i,:])
```

