General Agent Based Modeling in LAMMPS

Andrew Jewett
LAMMPS workshop
August 15th, 2019
Definition: Molecular cellular automaton

A hybrid simulation method:
   a) run ordinary molecular dynamics for a short time,
   b) make decisions that modify “atom” and “bond” properties
   c) $\textbf{goto} \rightarrow \text{a)}$ (repeat…)
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Decisions are made *locally*

a) At each iteration, atom types (and bond types) are modified

b) Each new atom type depends on the old atom type, and the atom types of its bonded neighbors according to arbitrary rules which the user can specify.
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Example Uses in Biology:

- membrane trafficking
- cytoskeletal filament growth dynamics
- transcriptional stalling
Background: cell membranes

Example: Flippase mediated membrane curvature
Flippase are motors which pull lipids (or proteins from one side of the membrane to the other)
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CYCLE REPEATS...
Example: Flippase mediated membrane curvature

# Capture a lipid when it's "Head" bead strays to close to the "A" bead:
if atoms @atom:A   @atom:H   and  distance <= 1.35   and  prob 0.1
then atoms @atom:At @atom:Ht  and  bond @bond:Capture

# Inform the bead at the other end of the flippase of the captured lipid:
if   atoms @atom:At @atom:B   and  bond @bond:AB
then atoms @atom:At @atom:Bt

# Create a bond that will pull the captured lipid's head to Bt:
if   atoms @atom:Bt @atom:Ht  and  distance <= 5.5
then atoms @atom:BT @atom:Ht  and  bond @bond:Pull

# Let the original atom ("A") know it's safe to release the lipid:
# First change the type back to "A".
if   atoms @atom:At @atom:BT
then atoms @atom:AT @atom:BT

# Then break the bond connecting "A" to the lipid's "Head" bead:
if   atoms @atom:AT @atom:Ht
then atoms @atom:AT @atom:H  and  bond BREAK

# When the lipids head group arrives at the other side
# break the bond connecting it to the Flippase bead ("B"):
if   atoms @atom:BT @atom:H  and  distance <= 1.3
then atoms @atom:B  @atom:H  and  bond BREAK

# Finally change the first bead back to the "A" state,
# enabling it to accept new lipids in the future:
if   atoms @atom:AT @atom:B
then atoms @atom:A   @atom:B
Example: Flippase mediated membrane curvature

# Capture a lipid when it's "Head" bead strays to close to the "A" bead:
if atoms @atom:A  @atom:H and distance <= 1.35 and prob 0.1
then atoms @atom:At @atom:Ht and bond @bond:Capture

# Inform the bead at the other end of the flippase of the captured lipid:
if atoms @atom:At @atom:B and bond @bond:AB
then atoms @atom:At @atom:Bt

# Create a bond that will pull the captured lipid's head to Bt:
if atoms @atom:Bt @atom:Ht and distance <= 5.5
then atoms @atom:BT @atom:Ht and bond @bond:Pull

# Let the original atom ("A") know it's safe to release the lipid:
# First change the type back to "A".
if atoms @atom:At @atom:BT
then atoms @atom:AT @atom:BT

# Then break the bond connecting "A" to the lipid's "Head" bead:
if atoms @atom:AT @atom:Ht
then atoms @atom:AT @atom:H and bond BREAK

# When the lipids head group arrives at the other side
# break the bond connecting it to the Flippase bead ("B"):
if atoms @atom:BT @atom:H and distance <= 1.3
then atoms @atom:B @atom:H and bond BREAK

# Finally change the first bead back to the "A" state,
# enabling it to accept new lipids in the future:
if atoms @atom:AT @atom:B
then atoms @atom:A @atom:B
Example: Flippase mediated membrane curvature
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SEE: https://www.youtube.com/watch?v=0cuEeEcdy0kU
Example: Flippase mediated membrane curvature
Example: Dynamic Instability of ParM

Example: Dynamic Instability of ParM

if atoms @atom:TF @atom:TF
   and distance <= 7.1 and prob 0.1
-> atoms @atom:TE @atom:TE and bond @bond:P

if atoms @atom:TE @atom:TE and prob 0.9
-> atoms @atom:TF @atom:TF and bond BREAK

if atoms @atom:TE @atom:TF
   and distance <= 7.1 and prob 0.25 &
-> atoms @atom:TB @atom:TE and bond @bond:P
   and angle @atom:S

if atom @atom:TB and prob 0.0015 -> atom @atom:DB

if atom @atom:TE and prob 0.0015 -> atom @atom:DE

if atoms @atom:DB @atom:DE
-> atoms @atom:DE @atom:DF and bond BREAK

if atoms @atom:DE @atom:DE
-> atoms @atom:DF @atom:DF and bond BREAK

if atom @atom:DF and prob 0.0007 -> atom @atom:TF

Example: Dynamic Instability of ParM

```plaintext
if atoms @atom:TF @atom:TF
    and distance <= 7.1 and prob 0.1
-> atoms @atom:TE @atom:TE and bond @bond:P

if atoms @atom:TE @atom:TE and prob 0.9
-> atoms @atom:TF @atom:TF and bond BREAK

if atoms @atom:TE @atom:TF
    and distance <= 7.1 and prob 0.25 &
-> atoms @atom:TB @atom:TE and bond @bond:P
    and angle @atom:S

if atom @atom:TB and prob 0.0015 -> atom @atom:DB

if atom @atom:TE and prob 0.0015 -> atom @atom:DE

if atoms @atom:DB @atom:DE
-> atoms @atom:DE @atom:DF and bond BREAK

if atoms @atom:DE @atom:DE
-> atoms @atom:DF @atom:DF and bond BREAK

if atom @atom:DF and prob 0.0007 -> atom @atom:TF
```


Note: Syntax may change in the future...
Example 2: Dynamic Instability of ParM

Example: Dynamic Instability of ParM

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Example: Walking along a polymer

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if atoms @atom:At @atom:B and bond @bond:R and prob 0.2
then atoms @atom:A @atom:Bt

if atoms @atom:Bt @atom:A and bond @bond:L
then atoms @atom:B @atom:AT

if atoms @atom:W @atom:AT and distance <= 1.5
then atoms @atom:Wt @atom:At and bond @bond:V and angle @angle:Ra @atom:B @atom:Aw @atom:W

if atoms @atom:Wt @atom:A and bond @bond:V
then atoms @atom:W @atom:A and bond BREAK
Example: Walking along a polymer

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if atoms @atom:W @atom:AT and distance <= 1.5
then atoms @atom:Wt @atom:At and bond @bond:V
and angle @angle:Ra @atom:B @atom:Aw @atom:W

if atoms @atom:Wt @atom:A and bond @bond:V
then atoms @atom:W @atom:A and bond BREAK

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Example: Walking along a polymer

if atoms @atom:At @atom:B and bond @bond:R
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then atoms @atom:A @atom:Bt

if atoms @atom:Bt @atom:A
then atoms @atom:B @atom:AT

if atoms @atom:W @atom:AT
then atoms @atom:Wt @atom:At
and angle @angle:Ra @atom:A

if atoms @atom:Wt @atom:A
then atoms @atom:W @atom:A

(DNA version with supercoiling)
Example: DNA supercoiling during transcription
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Example: Loop Extrusion and Genome Folding
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How does DNA fold? The loop extrusion model
Example: Loop Extrusion and Genome Folding

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Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes


Proceedings of the National Academy of Sciences
October 2015
Definition: cellular automaton

MCA can simulate “Cellular Automata”
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- Cellular Automata can simulate Turing Machines
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Example: Conway’s Game of Life
Conway’s Game of Life

1) Any live cell with fewer than two live neighbours dies (underpopulation)
2) Any live cell with two or three live neighbours lives
3) Any live cell with more than three live neighbours dies (overpopulation)
4) Any dead cell with exactly three live neighbours becomes a live cell (reproduction)
Conway’s Game of Life

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Cellular Automata can simulate Turing Machines
Conway's Game of Life in LAMMPS

if atoms @atom:C0 @atom:Live and bond @bond:NeighborUnread
then atoms @atom:C1 @atom:Dead and bond @bond:NeighborRead

if atoms @atom:C1 @atom:Live and bond @bond:NeighborUnread
then atoms @atom:C2 @atom:Dead and bond @bond:NeighborRead

if atoms @atom:C2 @atom:Live and bond @bond:NeighborUnread
then atoms @atom:C3 @atom:Dead and bond @bond:NeighborRead

if atoms @atom:C3 @atom:Live and bond @bond:NeighborUnread
then atoms @atom:C4 @atom:Dead and bond @bond:NeighborRead

if bond @bond:NeighborRead
then bond @bond:NeighborUnread

if atoms @atom:Live @{atom:C0}@{atom:C1} and bond @bond:SendTotal
then atoms @atom:Dead SAME

# Overpopulation: Any live cell with 4 living neighbors dies
if atoms @atom:Live @atom:C4 and bond @bond:SendTotal
then atoms @atom:Dead SAME

# Birth: Any dead cell with exactly 3 living neighbors lives
if atoms @atom:Dead @atom:C3 and bond @bond:SendTotal
then atoms @atom:Live SAME

# Reset counters:
if atom *
then atom @atom:C0

Note: Syntax may change in the future...
1) LAMMPS (now) can simulate cellular automata.

2) Cellular automata (such as Conway’s game of life), can be used to simulate a (universal) Turing machine

3) A Turing machine can simulate anything going on in a living cell (ignoring quantum mechanics).

→ LAMMPS can now simulate the machinery of life.
1) LAMMPS (now) can simulate cellular automata.

2) Cellular automata (such as Conway’s game of life), can be used to simulate a (universal) Turing machine.

3) A Turing machine can simulate anything going on in a living cell (ignoring quantum mechanics).

Moreover, it typically only takes a few of these LAMMPS commands to simulate processes in the cell that biologist care about. See earlier examples.
## Comparison with *fix bond/react*

<table>
<thead>
<tr>
<th><strong>fix bond/react</strong></th>
<th><strong>fix bond/modify</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>consider atoms an arbitrary number of bonds from the central atom</td>
<td>considers only atoms directly bonded to the central atom</td>
</tr>
<tr>
<td>can modify <strong>multiple bonds</strong> in a single reaction step</td>
<td>can modify <strong>only one bond</strong> at a time</td>
</tr>
<tr>
<td>requires creating separate molecule <strong>template files</strong> for each reaction step.</td>
<td>Each step is a <strong>single line command</strong>.</td>
</tr>
<tr>
<td>applies optional <strong>relaxation</strong> (minimization) to nearby atoms for numeric stability</td>
<td><strong>This feature is currently planned.</strong></td>
</tr>
<tr>
<td>does not (yet) consider bond types. <em>(Easy feature to add.)</em></td>
<td>considers bonded types as well as atom types when deciding.</td>
</tr>
</tbody>
</table>

**Both are equivalent. Both are Turing-complete.**
Comparison: *fix bond/react*

This is a single step using *fix bond/react*

(fix bond/modify requires 3 steps to modify 3 bonds)
Comparison: *fix bond/modify*

(Multiple steps are required with *fix bond/modify* to accomplish the same thing)
Comparison: *fix bond/modify*

(Multiple steps are required with *fix bond/modify* to accomplish the same thing)
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*(Multiple steps are required with fix bond/modify to accomplish the same thing)*
Comparison: \textit{fix bond/modify}

\textit{(Multiple steps are required with fix bond/modify to accomplish the same thing)}