BeadWeaver: A Swift and Versatile Tool to Parameterize Coarse Grained Structures

Alejandro Dagnino[1], Jahmal Ennis[1], Grace Brannigan[1, 2]
[1]Center for Computational and Integrative Biology and [2]Department of Physics, Rutgers University, Camden, NJ

Background

Coarse Grained and All-Atomistic

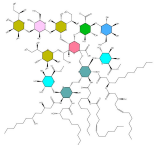
- Molecular Dynamics (MD) simulations are used to study the movements of both atoms and molecules over a specific time scale.
- Coarse Grained (CG) simulations are run on the order of nanosecond to microsecond timescale while all-atomistic (AA) simulations are run on the order of picosecond to nanosecond scale.

BeadWeaver

- BeadWeaver (BW) was created as a way build CG structures by taking pre-existing parameterized pieces of other CG structures and stitching them together in any desired orientation and combination.

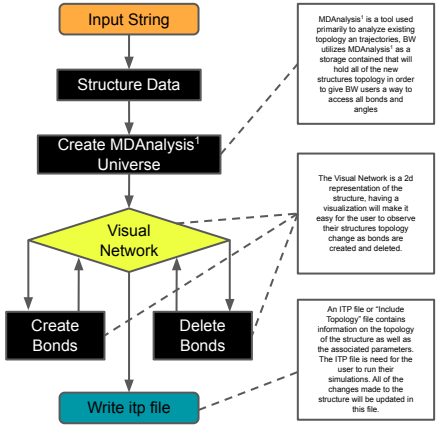
Challenges With Complex Structures

-Tools such as PyCG[3], CG Builder[4], or GROMACS[5] can create CG structures but not without an atomistic step.
- When building systems containing lipopolysaccharides (LPS), which are primarily found in gram-negative bacteria, existing tools do not have the capabilities to create these lipids much less easily editing the pieces of these lipids. BW's flexibility allows complicated structures to be assembled without limitation of size or components.
- To test BW's abilities an already existing model of Escherichia coli's (E.coli) rough lipopolysaccharide (rLPS) was used in order to create Caulobacter Crescentus (C.crescentus) rLPS as they both have very similar structures.



C.crescentus rLPS
Chemical structure

Workflow



Codebase

Topology and Parameters

```
;5-1-2
;  | /
;  3
;  |
;  4

[ KDO ]
        ;Atom
        BeadNum:5
        Bead Type:['SC1', 'P2', 'SN0', 'P4', 'Qa']
        Bead:['S', 'S', 'S', 'S', 'S']
        Charge:[0, 0, 0, 0, -1]
        Mass:[0, 0, 0, 0, 0]

        ;Bonds
        BondCon:['1-2', '1-3', '2-3', '3-4', '1-5']
        BondNum:[.20, .25, .25, .25, .20]
        BondFC:[1200, 44000, 64000, 5500, 37000]

        ;Angle
        AngleCon:['1-2-3', '1-3-2', '2-1-3', '1-3-4', '2-3-4', '3-1-5']
        AngleNum:[50, 60, 70, 164, 104, 315]
        AngleFC:[6, 6, 8, 11, 10, 10]
```

Here the CG parameters and topology of 2-keto-3-deoxyoctulosonate (KDO) are taken from a CG E.Coli structure then written down in BW's format.

Input String

"0KDO3-2KDO1-1(2(3KDO1"

- Bonds bead 3 on KDO #1 to bead 2 on KDO #2
- Decides what bead will bond with KDO #2
- Decides which KDO it will bond to
- Which bead on KDO #3 KDO #2 will bond to

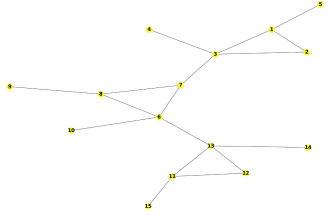
Sample sting input that will bond 3 KDO rings together, BW allows the user to have full control of how the beads are bonded between each piece.

MDAnalysis[1] Universe

<AtomGroup [<Atom 1: S01 of type SP1 resid 1>, <Atom 2: S02 of type P1 resid 1>, <Atom 3: S03 of type P4 resid 1>, ..., <Atom 69: C2F of type C1 resid 1>, <Atom 70: PO of type Qa resid 1>, <Atom 71: PO of type Qa resid 1>]>

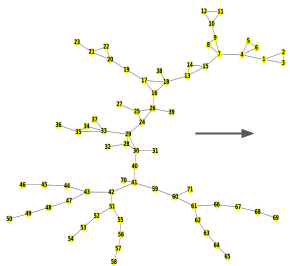
An MDAnalysis[1] universe is created to contain all bead information including bead type, name, mass, and charge.

Visual Network



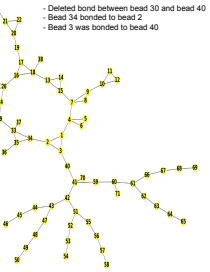
The visual network shows 3 KDO rings bonded together to create a simple structure.

Visual Network



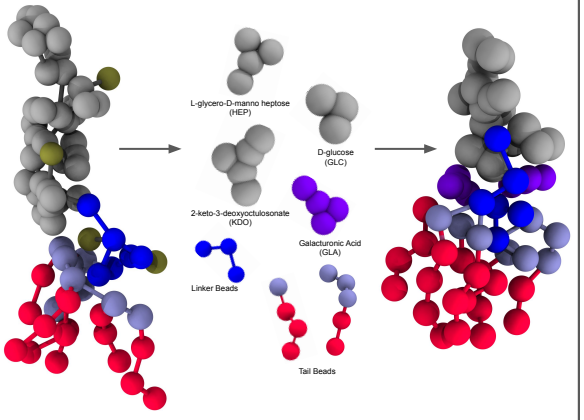
2d Visualization of an E.coli's rLPS made using BW.

- Deleted bond between bead 30 and bead 40
- Bead 34 bonded to bead 2
- Bead 3 was bonded to bead 40



While bonds can be be pre defined by the input string when running BW, the tool has ability to dynamically create and delete bonds.

Creating rLPS

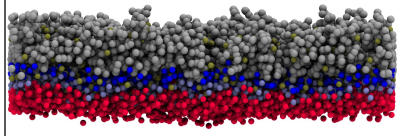


E.coli's rLPS made using BW

Pieces of E.coli's rLPS were deconstructed, and a using a parameterized CG GLA structure, the original pieces from the E.coli were used to create C.crescentus rLPS.

C.crescentus rLPS made from E.coli's rLPS

Membrane



Working along with a modified version MARTINI's insane[2] this membrane was made using BW's model of E.coli's rLPS. A simulation of this membrane was run for 25 ns.

Moving Forward

New Features

- BW's 2d visual will color each individual piece with different color in order for user's to have an easier time when defining bonds between pieces.
- Have BW generate coordinates for each piece of a structure in order to make it easier to work in conjunction with insane[2] as well as give BW the ability to generate a 3d visualization.
- BW's goal is to eventually have a GUI that will make it much easier to create new bonds between pieces as well being able to visualize the structure as it is being built.

Testing

- Unit Testing will be used in order to make sure every function within BW is correctly working.
- End-to-End testing will will ensure the input will always match the expected output. GROMACS[5] will be run to test accuracy of ITP files output by BW.

References

1. N. Michaud-Agrawal, E. J. Denning, T. B. Woolf, and O. Beckstein. MDAnalysis: A Toolkit for the Analysis of Molecular Dynamics Simulations. J. Comput. Chem. 32 (2011)
2. Tsjerk A. Wassenaar, Helgi I. Ingólfsson, Rainer A. Böckmann, D. Peter Tieleman, and Siewert J. Marrink Journal of Chemical Theory and Computation (2015)
3. James A. Graham, Jonathan W. Essex, and Syma Khalid Journal of Chemical Information and Modeling (2017)
4. Yihi Qi, Xi Cheng, Wei Han, Sunhwan Jo, Klaus Schulten, and Wonpil Im Journal of Chemical Information and Modeling (2014)
5. Abraham, M., Alekseenko, A., Basov, V., Bergh, C., Briand, E., Brown, A., Doijade, M., Fiorin, G., Fleischmann, S., Gorelov, S., Gouaillardet, G., Grey, A., Irrgang,M. E., Jalalypour, F., Jordan, J., Kutzner, C., Lemkul, J. A., Lundborg, M., Merz, P., ... Lindahl, E. (2024)

Acknowledgments

- Rutgers Office of Research and Computing (OARC)
- NSF Award 2224195