Diffusion Rates of Flame Retardants in Polyurethane Foam

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Polyurethane

- Product of step-growth polymerization between a monomer with at least two isocyanate functional groups and another monomer with at least two hydroxyl or alcohol groups in the presence of a catalyst
- Different monomers and additives determine physical properties of material
- Used in insulation foam, suspension bushings, adhesives, print rollers and many other applications

Linear polyurethane

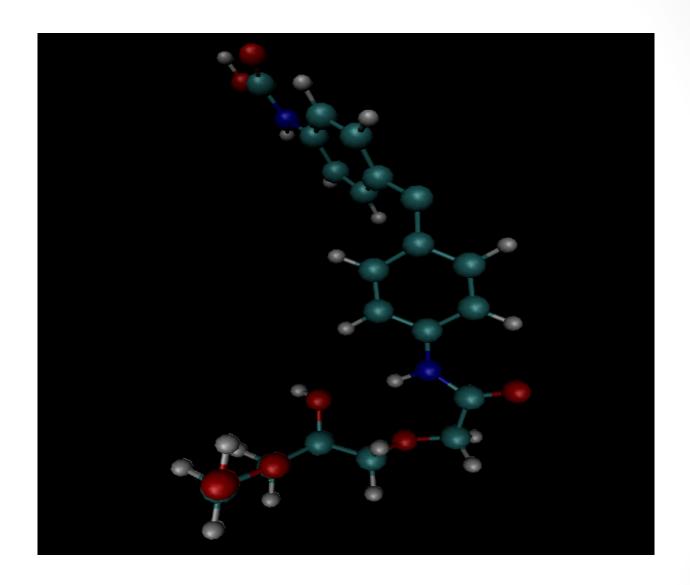
- Synthesized by reacting polymeric MDI with a polyol followed by crosslinking with butane diol to create a polyurethane thermoset
- Most commonly used in automotive seat cushioning and furniture

Research Goal

- Polyurethane is highly flammable in its raw state
- Production companies must introduce flame retardant molecules in the form of powders and liquids to make the polymer more stable
- Must know the best temperature and density of the materials for optimal diffusion of the flame retardant

Simulation Methods

- Polyurethane molecule and flame retardant molecules built in Molden
- Structures optimized on Louisiana Optical Network Initiative (LONI) supercomputers
- Script written for Large Atomic/Molecular Massively Parallel Simulator (LAMMPS) of single molecules
- Fortran code using Monte Carlo algorithm to replicate polyurethane molecule and generate environment for flame retardant diffusion tests
- LAMMPS output can then be visualized in VMD



Optimized polyurethane molecule

```
parro@qb1:~/lammps/Polyurethane
                                                                             - - X
                 real
atom_style molecular bond_style harmonic
pair_style lj/cut 7.0
angle_style harmonic
dihedral style hybrid opls charmm
boundary p p p
read data
                 data.poly
        log.poly
log
velocity all create 375.0 97658764
group ***
                 all nve
thermo style custom step etotal pe ke epair
thermo ***
                                                                    2,0-1
                                                                                   Top
```

Input script for polyurethane molecule

```
parro@qb1:~/lammps/Polyurethane
                                                                          do k1=1, nmol
         dx=delss*(unirand(ix)-0.5d0)
         dy=delss*(unirand(iy)-0.
         dz=delss*(unirand(iz)-0.5d0)
         call potcalc(k1,e0)
         do i1=1, natoms
         r(1, i1, k1) = r(1, i1, k1) + dx
         r(2,i1,k1)=r(2,i1,k1)+dy
          r(3,i1,k1)=r(3,i1,k1)+dz
         enddo
         call potcalc(k1,e1)
         trans=-(e1-e0)/temp
         rn=log(unirand(ia))
         if(trans .lt. log(unirand(ia))) then
          n1=n1+1
          do i1=1, natoms
          r(1,i1,k1)=r(1,i1,k1)-dx
           r(2, i1, k1) = r(2, i1, k1) - dy
           r(3,i1,k1)=r(3,i1,k1)-dz
          enddo
         endif
                                                                 242,1
```

Monte Carlo code for creating environment

```
jparro@qb1:~/lammps/Polyurethane
                                                                      - - X
Reading data file ...
 orthogonal box = (-9.44326 - 9.44326 - 9.44326) to (9.44326 9.44326) 9.44326
 2 by 2 by 2 processor grid
 256 atoms
Setting up run ...
Memory usage per processor = 1.54811 Mbytes
Step Elapsed Temp Press PotEng KinEng TotEng
                             1 0.037851562
                                                       0 1.4941406
                                                                         1.49414
06
                             1 0.037851562
     100
              100
                                                           1.4941406
                                                                         1.49414
06
     200
              200
                             1 0.037851562
                                                       0
                                                           1.4941406
                                                                         1.49414
06
     300
              300
                             1 0.037851562
                                                           1.4941406
                                                                         1.49414
06
     400
              400
                             1 0.037851562
                                                           1.4941406
                                                                         1.49414
06
              500
                             1 0.037851562
                                                                         1.49414
     500
                                                           1.4941406
06
                                                                         1.49414
     600
              600
                            1 0.037851562
                                                           1.4941406
06
     700
              700
                             1 0.037851562
                                                           1.4941406
                                                                         1.49414
06
                                                             26,21
                                                                            15%
```

Output file for simulation

Acknowledgements

- LA-SiGMA, funded by the National Science Foundation (NSF) award number #EPS-1003897
- Dr. Randall Hall, Chemistry Dept., LSU
- Louisiana Optical Network Initiative (LONI)
- Large Atomic/Molecular Massively Parallel Simulator (LAMMPS)
- Humphrey, W., Dalke, A. and Schulten, K., "VMD Visual Molecular Dynamics", J. Molec. Graphics, 1996, vol. 14, pp. 33-38. (VMD)
- G.Schaftenaar and J.H. Noordik, "Molden: a pre- and postprocessing program for molecular and electronic structures",
 J. Comput.-Aided Mol. Design, 14 (2000) 123-134 (Molden)