

A reactive molecular dynamics study of phenol and phenolic polymers in extreme environments

PRESENTED BY

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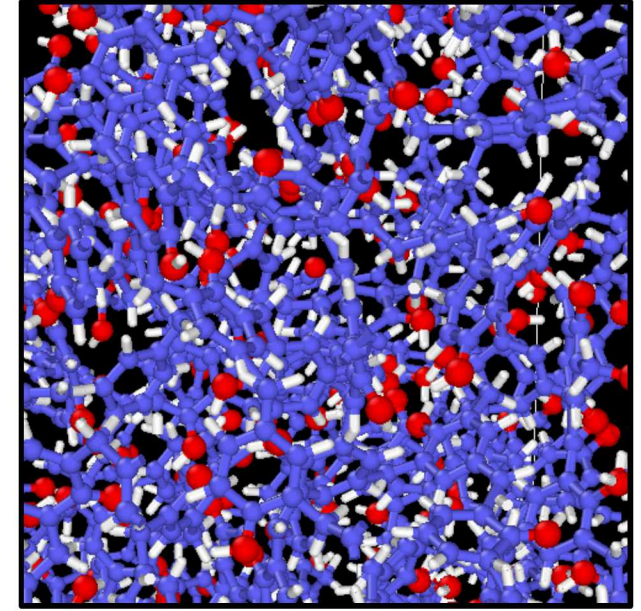
Intro/Rationale

Phenolic polymers

- Commonly used in extreme environments.
- Can vary greatly, depending on curing conditions, in crosslink extent, initial density, stoichiometry, molecular structure.

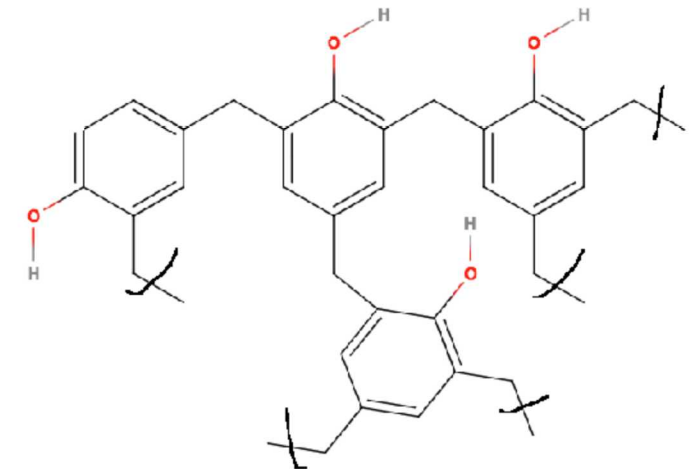
Reactive molecular dynamics (MD) can provide insight into

- Processes that occur during heating and shock.
- The relationship between molecular structure and density, shock response, and pyrolytic breakdown.



Questions

- 1.) Which reax parametrization is the most appropriate for modeling chemistry during pyrolysis and high pressure shock (yields the most accurate activation energies and reaction energies)?
- 2.) Which is the most appropriate for phenolic shock (most accurately represents the intermolecular interactions of phenolics)?



3 Reax parametrizations

ReaxFF - Bond order MD potential that handles chemistry.

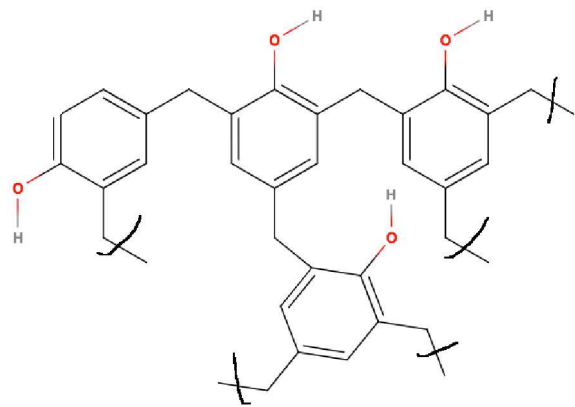
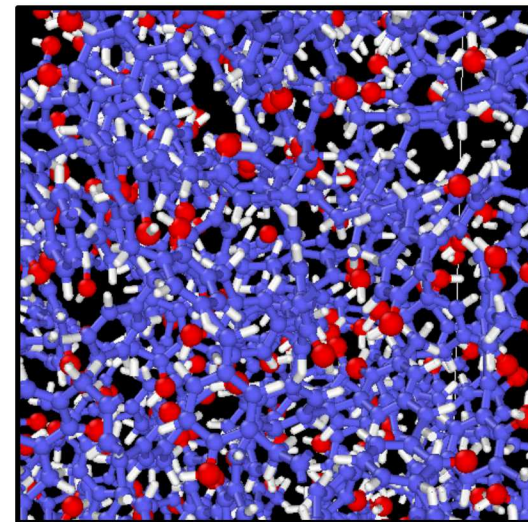
Various parametrizations for different combinations of atoms under different conditions.

Parametrizations for H/C/O containing systems:

1.) CHO - commonly used for hydrocarbon reactivity.

2.) Mattsson - Past success simulating polymers under chemistry-inducing shock (up to 60 GPa). Well tested for systems containing H and C.

3.) Hydrogen Bond Augmented 2018 (HBA18) - Mattsson parametrization utilizing the O-H...O hydrogen bonding parameters from CHO. New hybrid parametrization - introduced to capitalize on the the strengths of the other two.



S. Plimpton *J. Comp. Phys.* **117**, 1-19 (1995).

A. C.T. van Duin et al. *J. Phys. Chem.* **105**, 9396-9409 (2001).

K. Chenoweth et al. *J. Phys. Chem. A* **112**, 1040-1053 (2008).

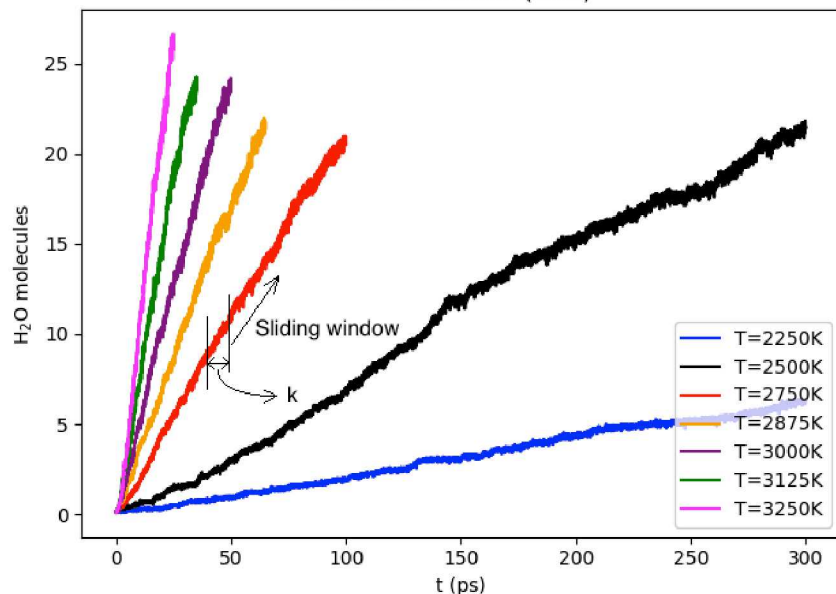
A. Harpale et al. *Carbon* **130**, 315-324 (2018).

T.R. Mattsson et al. *Phys. Rev. B* **81**, 054103 (2010).

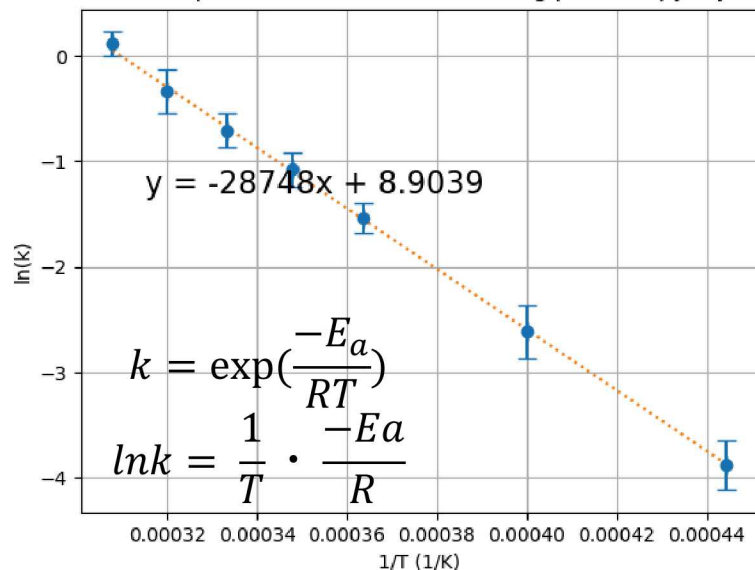
J. Matthew D. Lane and N.W. Moore *J. Phys. Chem. A* **122**, 3962-3970 (2018).

Phenolic pyrolysis activation energies

Water formation (CHO)



Arrhenius plot for water formation during phenolic pyrolysis



Water

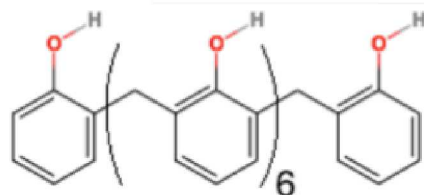
- Abundant phenolic pyrolysis byproduct
- Formation kinetics studied with MD in the past.

”Global”

- Mass of all volatilizable species as a function of time
- Closer proxy to experimentally determined activation energies based on thermogravimetric analysis (TGA).
- Mass cutoff(s) based on heaviest gaseous products observed experimentally.

Methodology

- 1.) 16 linear chains - 15 instances.
- 2.) Water formation rates determined at various temperatures.
- 3.) Activation energies (E_a) extracted using the Arrhenius equation:



- D. Jiang et al. *J. Phys. Chem. A* **113**, 6891-6894 (2009).
 T. G. Desai et al. *Polymer* **52**, 577-585 (2011).
 K.A. Trick et al. *Carbon* **33**(11), 1509-1515 (1995).
 K.A. Lincoln *AIAA Journal* **21**(8), 1204 (1983).

Phenolic pyrolysis activation energies

NVT ensemble
 1776 atoms - 16 linear phenolic chains
 Periodic boundary conditions
 15 instances
 7-10 temperatures ranging from 2000 - 3250 K.
 10s to 100s of ps per simulation
 0.25 fs timestep



| $\rho = 1.25 \text{ g/cc}$ | $E_a \text{ (H}_2\text{O)}$ (kJ/mol) | $E_a \text{ (Global)}$ (kJ/mol) | Source of variation |
|----------------------------|---|------------------------------------|---------------------------------------|
| Exp, Jiang | ----- | 223-305 | Temperature region and heating rates |
| Exp, Trick | ----- | 74-198 | Temperature region and heating rates |
| Exp, Freidman | ----- | 192 - 293 | Heating rate, method of determination |
| MD, Jiang | 332 +/- 64 | ----- | |
| MD, Desai | 286 +/- 46 | ----- | |
| This work, CHO | 246 +/- 23 | 301 +/- 32 | |
| This work, HBA18 | 135 +/- 5 | 210 +/- 12 | |
| This work, Mattsson | 130 +/- 6 | 191 +/- 13 | |

All reax parametrizations agree with experiment - variation too great to constrain MD results, which vary.

CHO 3250 K volatile evolution

H. Jiang et al. *Carbon* **48**, 352-358 (2010).

K.A.Trick et al. *Carbon* **35**(3), 393-401 (1997).

H. L. Freidman *J. Polym. Sci. C* **6**(1), 183-195 (1964).

6 Crystalline phenol

Experimental crystal structure of phenol

-Characterized by hydrogen-bonded chains of molecules aligned parallel to crystallographic b axis, where the molecules are arranged in approximate threefold helices.

Phenol crystal - re-equilibrated with each parametrization

- NPT ensemble
- 123 K – ambient pressure
- 0.1 fs timestep
- 150 – 200 ps equilibration

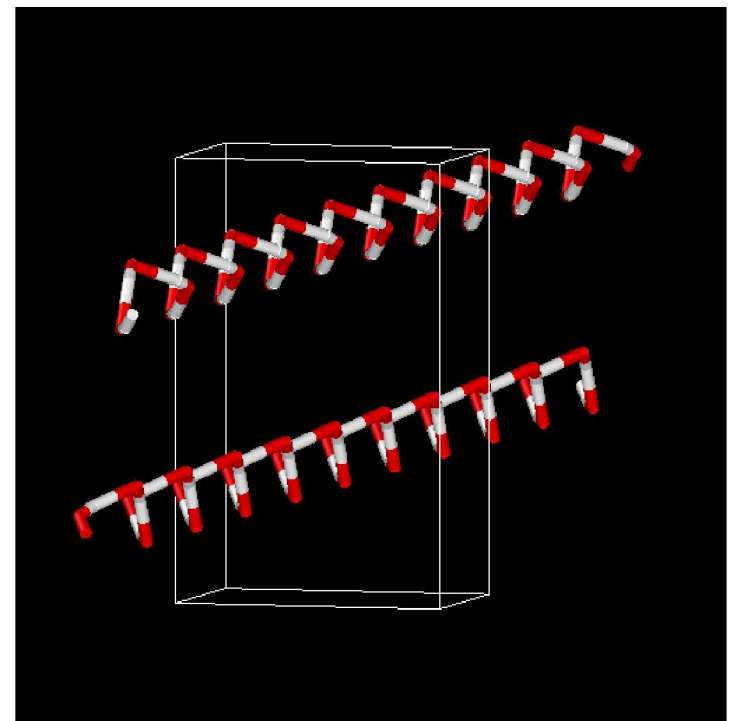
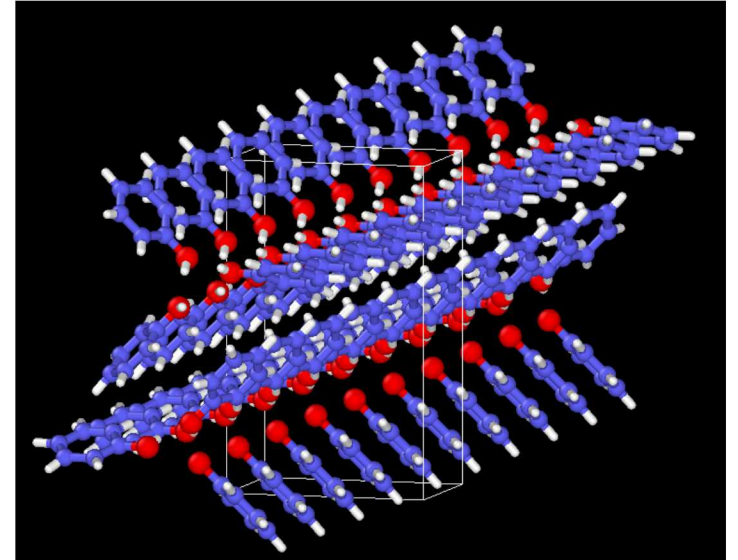
Density evaluated and compared with experiment.

Crystallinity evaluated based on

- Qualitative assessment of 3-fold helix retention
- Diffusion coefficient

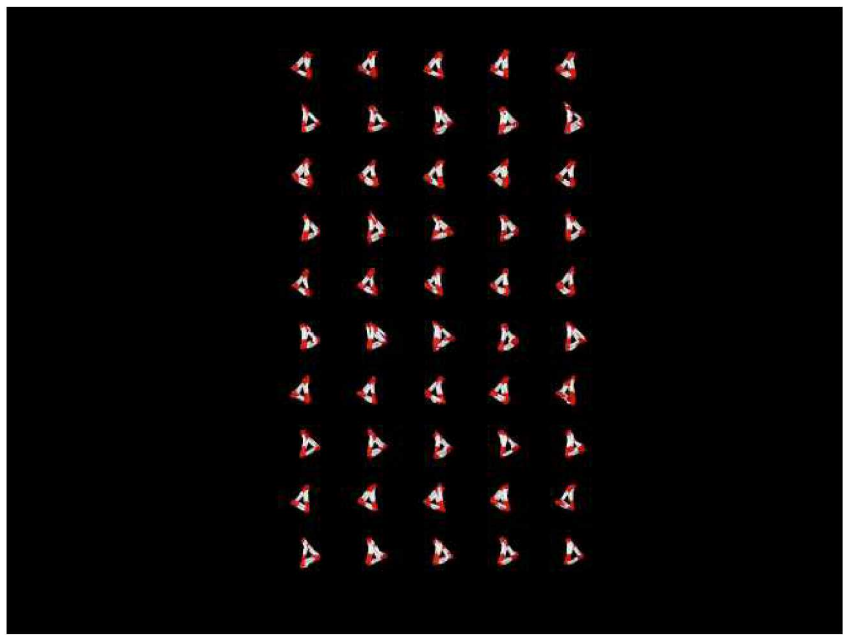
V. E. Zavodnik et al. *Zh. Strukt. Khim.* **28**, 175 (1987).

David R. Allan et al. *Acta Cryst.* **B58**, 1018-1024 (2002).

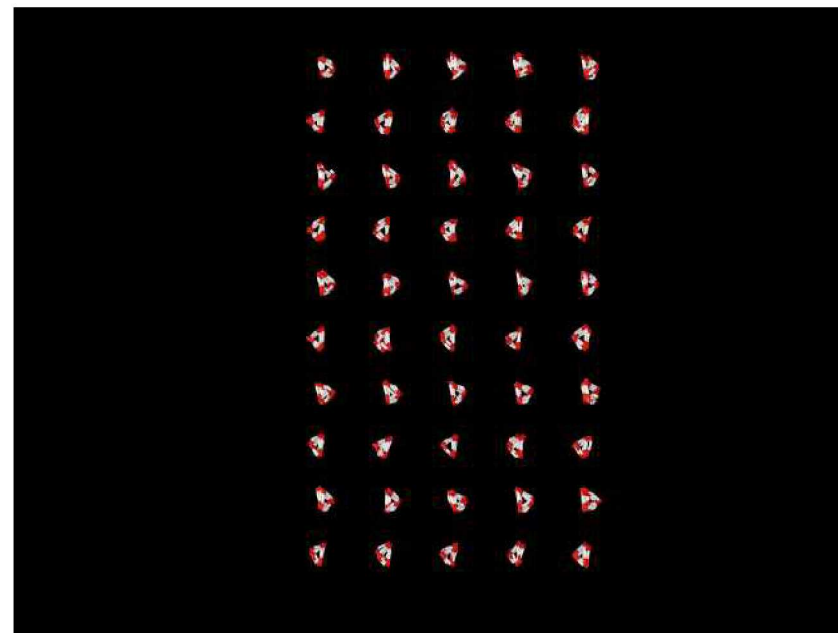


7 Crystalline phenol

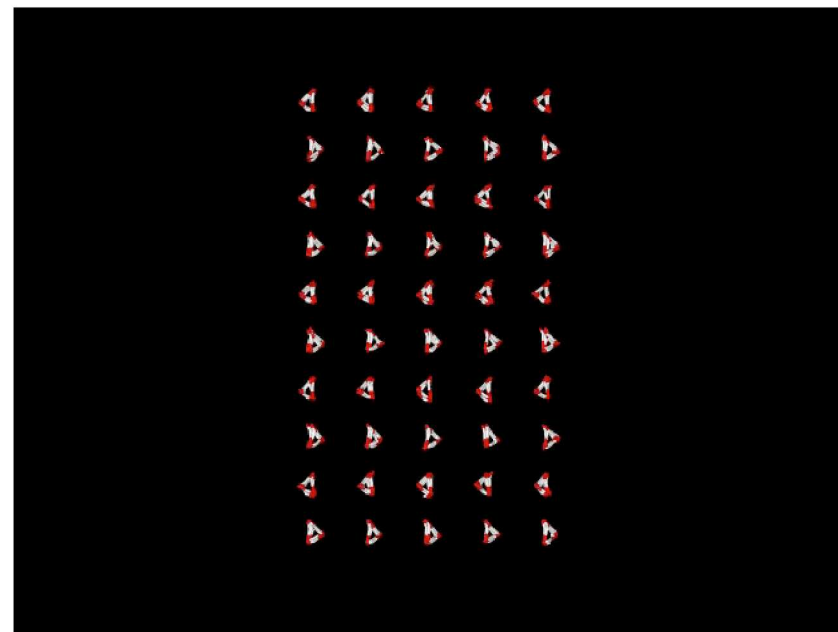
| Reax parametrization | Diffusion coefficient ($\text{\AA}^2/\text{ps}$) | Density (g/cc) |
|----------------------|--|-------------------|
| CHO | $2.3 \pm 3.3 \times 10^{-4}$ | 1.432 ± 0.003 |
| HBA18 | $9.3 \pm 2.5 \times 10^{-4}$ | 1.200 ± 0.003 |
| Mattsson | $9.8 \pm 0.4 \times 10^{-3}$ | 1.180 ± 0.002 |
| Zavodnik, Exp | ----- | 1.19 |



Mattsson



CHO

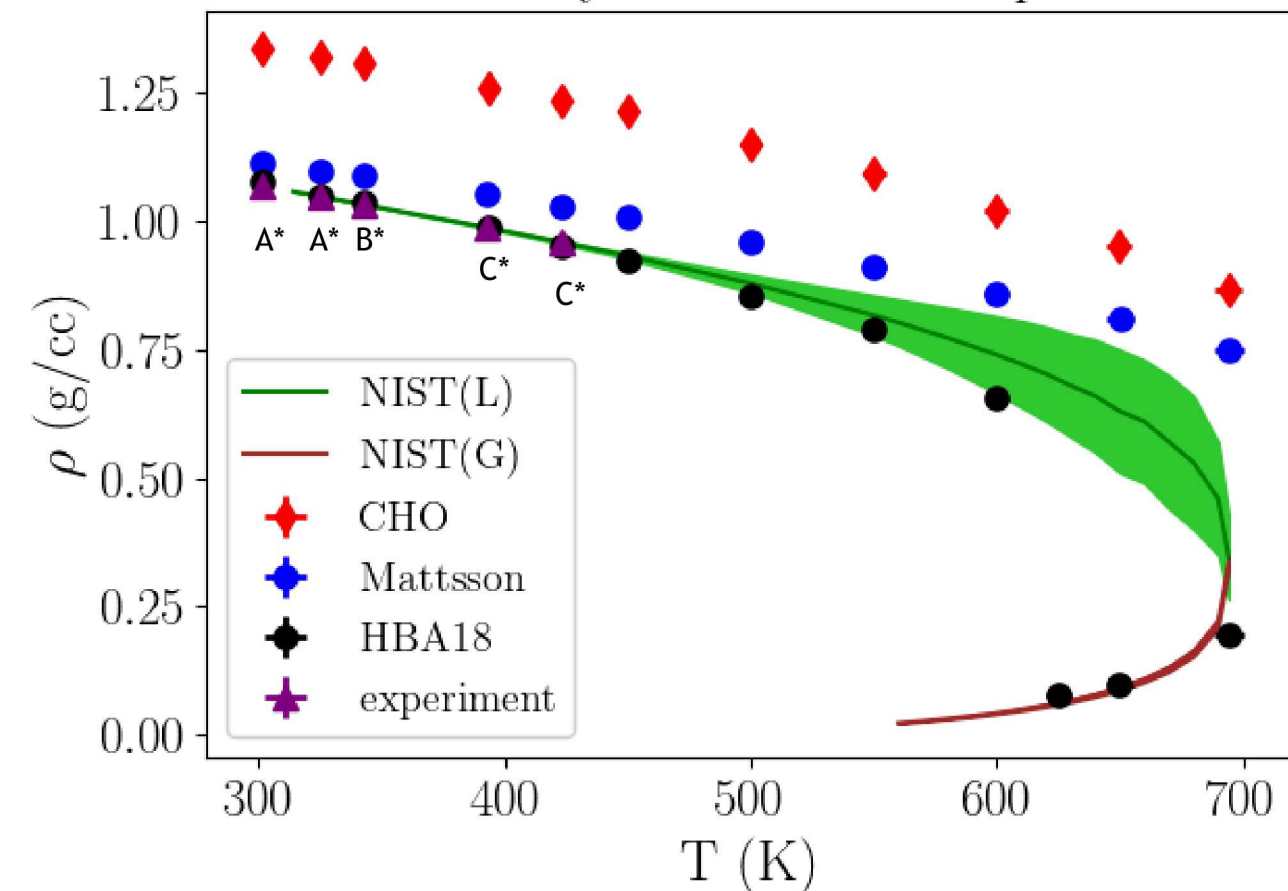


HBA18

HBA18 captures H-bonding interactions from CHO to retain crystallinity. Density maintained due to Mattsson parameters.

Phenol density at various temperatures

Phenol density as a function of temperature



Phenol equilibration - various points in P,T space along L/G coexistence curve.

Phenol data extracted from NIST web thermo data tables – derived from ThermoData Engine.

HBA18 agrees with experiment and the NIST model to a greater degree than the parametrizations from which it was derived.

A* R. B. Badachhape et al. *J. Chem. And Eng. Data* **10**, 143 (1965).
 B* D. L. Cunha et al. *J. Chem. Eng. Data*. **58**, 2925-2931 (2013).
 C* C.A. Buehler et al. *J. Am. Chem. Soc.* **54**(6), 2398-2405 (1932).
 E.W. Lemmon et al. 2018 <https://dx.doi.org/10.18434/T4JS3C>
J. Chem. Inf. Model. **45**, 816-838 (2005).
J. Chem. Inf. Model. **47**, 1713-1754 (2007).
J. Chem. Inf. Model. **49**, 503-517 (2009).
J. Chem. Inf. Model. **49**, 2883-2896 (2009).

Conclusions

- 1.) All three MD parametrizations can accurately model phenolic pyrolysis based on activation energies.
- 2.) HBA18 is the most ideal reaxFF parametrization for studying shock:
 - Accurately models crystalline phenol.
 - Accurately models phenol across a range of temperatures relevant for shock.

Future work

Quantify energies associated with common product formation pathways for all three parametrizations and compare with quantum chemical calculations.



Acknowledgements

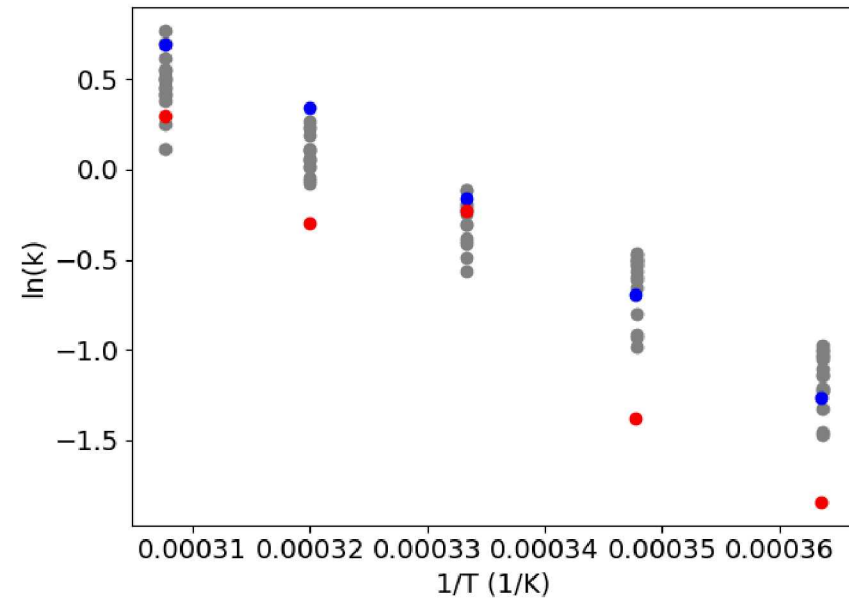
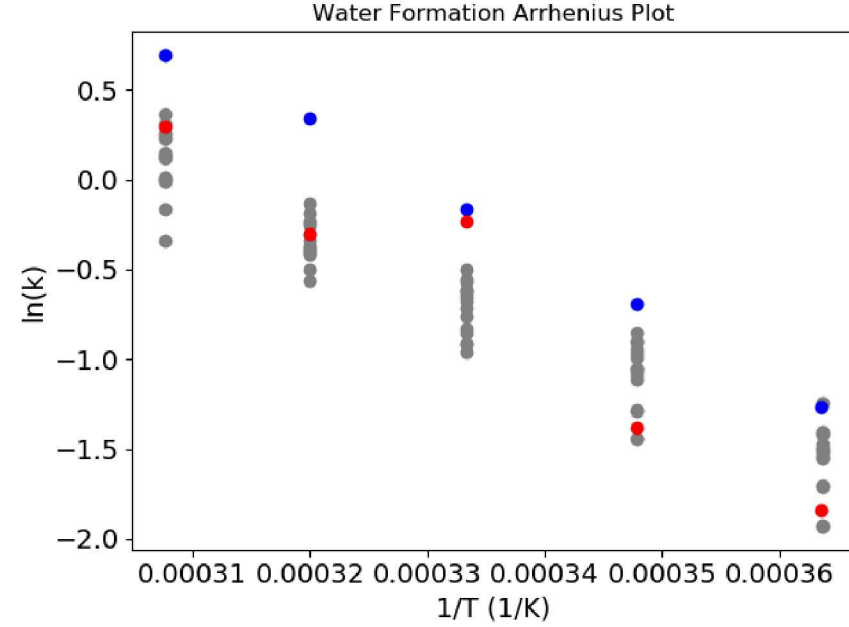
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High Performance Computers

NIST

Dr. Kenneth Kronlein

Bonus slides



- D. Jiang et al. *J. Phys. Chem. A* **113**, 6891-6894 (2009).
- T. G. Desai et al. *Polymer* **52**, 577-585 (2011).