

# 1 Supplementary Material: “Molecular Modeling and Simulations of AOT–water Reverse Micelles in Iso–octane: Structural and Dynamic Properties” by Stéphane Abel, Fabio Sterpone, Sanjoy Bandyopadhyay and Massimo Marchi

The following will provide potential parameters and topology for di–2–ethylhexylsulfocinate, AOT and isoctane, as described in the paper. The actual files corresponding to the parameter and topology files of the program ORAC can be obtained from one of the authors (Massimo Marchi e-mail: mmarchi@cea.fr). These files can be easily adapted to run with other MD packages. For extensive information on the parameter and topology format of ORAC see its documentation on the web site <http://www.chim.unifi.it/orac/>.

## 1.1 Potential Parameters

The potential parameters given in this supplementary material refers to the potential function in Eq. 1 of the article, namely to:

$$\begin{aligned} V(\vec{R}) = & \sum_{\text{stre.}} k_b(b - b_0)^2 + \sum_{\text{bend.}} k_\theta(\theta - \theta_o)^2 \\ & + \sum_{\text{tors.}} k_\phi(1 + \cos(n_\phi\phi + \delta)) + \sum_{\text{impr.}} k_\omega(\omega - \omega_o)^2 \\ & + \sum_{i,j} 4\epsilon_{ij}\left[\left(\frac{\sigma_{ij}}{r_{ij}}\right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}}\right)^6\right] + \sum_{i,j} \frac{q_i q_j}{r_{ij}}. \end{aligned} \quad (1)$$

In the following parameter set, the units are used:

- Force constants ( $K_b, K_\theta, K_\phi, K_\omega$ ) are in Kcal/mol
- Equilibrium distances ( $b_o$ ) are in Å.
- Angles ( $\theta_o, \delta, \omega_o$ ) are in degrees
- $R_{ij}^*$  are in Å with  $R^* = \sigma\sqrt[6]{2}$  with  $\sigma$  the Lennard–Jones diameter.
- $\epsilon_{ij}$  is in Kcal/mol.
- 1-4 interactions are scaled according to CHARMM’s scaling factors: 1.0 for charge–charge interactions and 1.0 for Lennard–Jones.
- CHARMM’s Berthelot mixing rules are used for all parameters.

In the following list, BOND, BINDINGS, TORSION PROPER and TORSION IMPROPER provide bond stretching, angle bending, torsion and improper torsion potential parameters. Following the keyword NONBONDED MIXRULE the Lennard–Jones parameters are given.

## Parameter File

```

#####
# isoctane and the act
#####

ctl1  hal1  309.00   1.111
ctl2  hal2  309.00   1.111
ctl3  hal3  322.00   1.111
ctl1  ct11  222.50   1.500
ctl1  ct12  222.50   1.538
ctl1  ct13  222.50   1.538
ctl2  ct12  222.50   1.530
ctl2  ct13  222.50   1.528

#####
#For TIP3P water model
#####

#ht      ht      0.0      1.5139
ht      ht      450.0     1.5139
ht      ot      450.0     0.9572
END

```

BENDINGS

obl	cl	ct13	70.00	125.00	20.00	2.44200
obl	cl	ct12	70.00	125.00	20.00	2.44200
obl	cl	ct11	70.00	125.00	20.00	2.44200
osl	cl	obl	90.00	125.90	160.00	2.25760
cl	osl	ct11	40.00	109.60	30.00	2.26510
cl	osl	ct12	40.00	109.60	30.00	2.26510
cl	osl	ct13	40.00	109.60	30.00	2.26510
hal2	ct12	cl	33.00	109.50	30.00	2.16300
hal3	ct13	cl	33.00	109.50	30.00	2.16300
ct12	ct12	cl	52.00	108.00		
ct13	ct12	cl	52.00	108.00		
ct12	ct11	cl	52.00	108.00		
ct11	ct12	cl	52.00	108.00		
osl	cl	ct13	55.00	109.00	20.00	2.32600
osl	cl	ct12	55.00	109.00	20.00	2.32600
ohl	cl	obl	50.00	123.00	210.00	2.26200
ocl	cl	ct12	40.00	118.00	50.00	2.38800
ocl	cl	ct13	40.00	118.00	50.00	2.38800
ocl	cl	ocl	100.00	124.00		
ohl	cl	ct13	55.00	110.50		
ohl	cl	ct12	55.00	110.50		
hol	ohl	cl	55.00	115.00		
osl	ct11	ct12	75.70	110.10		
osl	ct11	ct13	75.70	110.10		
osl	ct12	ct11	75.70	110.10		
osl	ct12	ct12	75.70	110.10		
osl	ct12	ct13	75.70	110.10		
hal2	ct12	hal2	35.50	109.00	5.40	1.80200
hal3	ct13	hal3	35.50	108.40	5.40	1.80200
hal1	ct11	osl	60.00	109.50		
hal2	ct12	osl	60.00	109.50		
hal3	ct13	osl	60.00	109.50		
ct12	osl	pl	20.00	120.00	35.00	2.33000
ct13	osl	pl	20.00	120.00	35.00	2.33000
hol	ohl	pl	30.00	115.00	40.00	2.30000
osl	pl	os1	80.00	104.30		
osl	pl	o21	98.90	111.60		
osl	pl	ohl	48.10	108.00		
o21	pl	o21	120.00	120.00		
o21	pl	ohl	98.90	108.23		
nt1	ct12	hl	40.00	109.50	27.00	2.13000
nt1	ct15	hl	40.00	109.50	27.00	2.13000
hl	ct12	hl	24.00	109.50	28.00	1.76700
hl	ct15	hl	24.00	109.50	28.00	1.76700
ct15	nt1	ct12	60.00	109.50	26.00	2.46600
ct15	nt1	ct15	60.00	109.50	26.00	2.46600
hl	ct12	ct12	33.43	110.10	22.53	2.17900
hl	ct12	ct13	33.43	110.10	22.53	2.17900
hal1	ct11	ct11	34.50	110.10	22.53	2.17900
hal1	ct11	ct12	34.50	110.10	22.53	2.17900
hal1	ct11	ct13	34.50	110.10	22.53	2.17900
hal2	ct12	ct11	26.50	110.10	22.53	2.17900
hal2	ct12	ct12	26.50	110.10	22.53	2.17900
s1	ct11	hal1	34.50	110.10	22.53	2.17900
s1	ct11	cl	52.00	108.00		
s1	ct11	ct12	58.35	113.50	11.16	2.56100
o21	s1	o21	130.00	109.47	35.00	2.45000
ct11	cl	osl	55.00	109.00	20.00	2.32600
o21	s1	ct11	85.00	98.00		
#####						
#						
#For tetraedr carbon of isoctan						
#						
######						
hal1	ct11	cl	33.00	109.50	30.00	2.16300
ct12	ct11	ct12	58.350	113.50	11.16	2.56100
ct11	ct12	ct13	58.350	113.50	11.16	2.56100
ct11	ct12	ct12	58.350	113.50	11.16	2.56100
ct13	ct0	ct13	58.350	113.50	11.16	2.56100
hal2	ct12	ct0	26.500	110.10	22.53	2.17900
ct13	ct0	ct12	58.350	113.50	11.16	2.56100
ct0	ct12	hal2	26.500	110.10	22.53	2.17900
hal3	ct13	ct0	33.430	110.10	22.53	2.17900
hal2	ct12	ct0	26.500	110.10	22.53	2.17900
ct0	ct12	ct11	58.350	113.50	11.16	2.56100
ct13	ct11	ct13	58.350	113.50	11.16	2.56100
######						
#						
######						
hal3	ct13	hal3	35.500	109.00		
hal2	ct12	hal2	26.500	110.10		
hal2	ct12	ct13	34.600	110.10		
hal2	ct12	ct12	26.500	110.10		
ct13	ct12	ct12	58.000	115.00		
hal3	ct13	ct12	34.600	110.10		
ct12	ct12	ct12	58.350	113.60		
hal2	ct12	ct13	34.600	110.10		

```
ctl2 ctl3 hal3  34.600  110.10
hal3 ctl3 ctl1  33.430  110.10
ctl1 ctl3 hal3  33.430  110.10
ctl1 ctl2 ctl1  58.350  113.50
ctl2 ctl1 ctl3  58.350  113.50
ht   ot   ht   55.000  104.52
END
```

TORSION PROPER

x	ct11	ohl	x	0.1400	3	0.0
x	ct12	ohl	x	0.1400	3	0.0
x	ct13	ohl	x	0.1400	3	0.0
obl	cl	ct12	hal2	0.0000	6	180.0
obl	cl	ct13	hal3	0.0000	6	180.0
obl	cl	ct11	hal1	0.0000	6	180.0
osl	cl	ct12	hal2	0.0000	6	180.0
osl	cl	ct13	hal3	0.0000	6	180.0
osl	cl	ct11	hal1	0.0000	6	180.0
obl	cl	osl	ct11	0.9650	1	180.0
obl	cl	osl	ct11	3.8500	2	180.0
obl	cl	osl	ct12	0.9650	1	180.0
obl	cl	osl	ct12	3.8500	2	180.0
obl	cl	osl	ct13	0.9650	1	180.0
obl	cl	osl	ct13	3.8500	2	180.0
x	cl	osl	x	2.0500	2	180.0
x	ct12	cl	x	0.0500	6	180.0
x	ct13	cl	x	0.0500	6	180.0
x	ct11	cl	x	0.0500	6	180.0
x	cl	ohl	x	2.0500	2	180.0
hal2	ct12	cl	ohl	0.0000	6	180.0
hal3	ct13	cl	ohl	0.0000	6	180.0
osl	pl	osl	ct12	1.2000	1	180.0
osl	pl	osl	ct12	0.1000	2	180.0
osl	pl	osl	ct12	0.1000	3	180.0
o2l	pl	osl	ct12	0.1000	3	0.0
osl	pl	osl	ct13	1.2000	1	180.0
osl	pl	osl	ct13	0.1000	2	180.0
osl	pl	osl	ct13	0.1000	3	180.0
o2l	pl	osl	ct13	0.1000	3	0.0
ohl	pl	osl	ct12	0.9500	2	0.0
ohl	pl	osl	ct12	0.5000	3	0.0
ohl	pl	osl	ct13	0.9500	2	0.0
ohl	pl	osl	ct13	0.5000	3	0.0
x	ohl	pl	x	0.3000	3	0.0
x	ct11	osl	x	0.0000	3	0.0
x	ct12	osl	x	0.0000	3	0.0
x	ct13	osl	x	0.0000	3	0.0
ct13	ct12	osl	cl	0.7000	1	180.0
ct12	ct12	osl	cl	0.7000	1	180.0
ct13	ct11	osl	cl	0.7000	1	180.0
ct12	ct11	osl	cl	0.7000	1	180.0
sl	ct11	ct12	cl	0.7000	1	180.0
ct11	ct12	cl	osl	0.1500	1	180.0
ct11	ct12	cl	osl	0.1500	1	180.0
ct11	ct12	cl	osl	0.5300	2	180.0
ct12	ct12	cl	osl	0.1500	1	180.0
ct12	ct12	cl	osl	0.1500	1	180.0
ct12	ct12	cl	osl	0.5300	2	180.0
ct12	ct11	cl	osl	0.1500	1	180.0
ct12	ct11	cl	osl	0.1500	1	180.0
ct12	ct11	cl	osl	0.5300	2	180.0
ct12	ct11	cl	osl	0.1500	1	180.0
ct12	ct11	cl	osl	0.1500	1	180.0
ct12	ct11	cl	osl	0.5300	2	180.0
ct13	ct12	cl	osl	0.1500	1	180.0
ct13	ct12	cl	osl	0.5300	2	180.0
sl	ct11	cl	osl	0.1500	1	180.0
sl	ct11	cl	osl	0.1500	1	180.0
sl	ct11	cl	osl	0.5300	2	180.0
x	ct12	nt1	x	0.2600	3	0.0
x	ct15	nt1	x	0.2300	3	0.0
x	ct12	nh31	x	0.1000	3	0.0
nh31	ct12	ct12	ohl	0.7000	1	180.0
nh31	ct12	ct12	osl	0.7000	1	180.0
nt1	ct12	ct12	ohl	4.3000	1	180.0
nt1	ct12	ct12	ohl	0.4000	3	180.0
nt1	ct12	ct12	ohl	0.4000	3	180.0
nt1	ct12	ct12	osl	3.3000	1	180.0
nt1	ct12	ct12	osl	0.4000	3	180.0
nt1	ct12	ct12	osl	0.4000	3	180.0
x	ct11	ct11	x	0.2000	3	0.0
x	ct11	ct12	x	0.2000	3	0.0
x	ct11	ct13	x	0.2000	3	0.0
hal3	ct13	osl	s1	0.0000	3	0.0
ct12	osl	s1	o2l	0.0000	3	0.0
ct13	osl	s1	o2l	0.0000	3	0.0
cl	ct11	s1	o2l	0.0000	3	0.0
hal1	ct11	s1	o2l	0.0000	3	0.0
ct12	ct11	s1	o2l	0.0000	3	0.0
hel1	cell	cell	hell1	1.0000	2	180.0
ct13	cell	cell	hell1	1.0000	2	180.0
x	cell	cell	x	0.1300	1	180.0
x	cell	cell	x	24.0000	2	180.0
x	cel2	cel2	x	4.9000	2	180.0
ct12	cell	cel2	hell2	5.2000	2	180.0
ct13	cell	cel2	hell2	5.2000	2	180.0
hell1	cell	cel2	hell2	5.2000	2	180.0
cell1	cell	ct12	hal2	0.0300	3	0.0
cell1	cell	ct13	hal3	0.0300	3	0.0
cell1	cell	ct12	ct12	0.4000	3	0.0
cel2	cell	ct12	ct12	0.4000	3	0.0

```

cel2 cel1 ct12 ct13    0.4000   3    0.0
cel2 cel1 ct12 hal2   0.1200   3    0.0
cel2 cel1 ct13 hal3   0.0500   3    180.0
hel1 cel1 ct12 ct12   0.1200   3    0.0
hel1 cel1 ct12 ct13   0.1200   3    0.0
hel1 cel1 ct12 hal2   0.8700   3    0.0
hel1 cel1 ct13 hal3   0.3400   3    0.0
x   ct0 ct13   x     0.200   3    0.0
x   ct0 ct12   x     0.200   3    0.0
#####
# For the isoctan and act act too
#
#####
x   ct12 ct12 x     0.1900   3    0.0
x   ct12 ct13 x     0.1600   3    0.0
x   ct13 ct13 x     0.1525   3    0.0
ctl3 ct12 ct12 ct13  0.1000   2    180.0
ctl3 ct12 ct12 ct13  0.1500   4    0.0
ctl3 ct12 ct12 ct13  0.1000   6    180.0
ctl2 ct12 ct12 ct13  0.1000   2    180.0
ctl2 ct12 ct12 ct13  0.1500   4    0.0
ctl2 ct12 ct12 ct13  0.1000   6    180.0
ctl2 ct12 ct12 ct12  0.1000   2    180.0
ctl2 ct12 ct12 ct12  0.1500   4    0.0
ctl2 ct12 ct12 ct12  0.1000   6    180.0
obl x   x   cl     100.00  0.00000
hel2 hel2 cel2 cel2   3.00  0.00000
ocl x   x   cl     96.00  0.00000
END

```

```

NONBONDED MIXRULE
#####
#For isoctan and act molecule too
#####
# s(all) e(all) s(14) e(14) mass
hol 0.22450 -0.04600 0.00000 0.00000 1.00800
hol 0.22450 -0.04600 0.00000 0.00000 1.00800
hl 0.70000 -0.04600 0.00000 0.00000 1.00800
hel1 1.25000 -0.03100 0.00000 0.00000 1.00800
hel2 1.26000 -0.02600 0.00000 0.00000 1.00800
cl 2.00000 -0.07000 0.00000 0.00000 12.01100
ctl1 2.27500 -0.02000 0.00000 0.00000 12.01100
#####
# For decan and act molecule
#####
hal1 1.32000 -0.02200 0.00000 0.00000 1.00800
hal2 1.34000 -0.02800 0.00000 0.00000 1.00800
hal3 1.34000 -0.02400 0.00000 0.00000 1.00800
ctl2 2.01000 -0.05600 0.00000 0.00000 12.01100
ctl3 2.04000 -0.07800 0.00000 0.00000 12.01100
#####
ctl5 2.06000 -0.08000 0.00000 0.00000 12.01100
cel1 2.09000 -0.06800 0.00000 0.00000 12.01100
cel2 2.08000 -0.06400 0.00000 0.00000 12.01100
obl 1.70000 -0.12000 0.00000 0.00000 15.99940
ocl 1.70000 -0.12000 0.00000 0.00000 15.99940
o2l 1.70000 -0.12000 0.00000 0.00000 15.99940
ohl 1.77000 -0.15210 0.00000 0.00000 15.99940
nh3l 1.85000 -0.20000 0.00000 0.00000 14.00700
nt1 1.85000 -0.20000 0.00000 0.00000 14.00700
sl 2.10000 -0.47000 0.00000 0.00000 32.06000
sod 1.36375 -0.04690 0.00000 0.00000 22.98977
osl 1.77000 -0.1521 0.00000 0.00000 15.99940
#####
#
#For tetraedr carbon of isoctan
#
#####
ct0 2.27500 -0.02000 0.00000 0.00000 12.01100
#####
# For the TiP3P water
#####
ht 0.22450 -0.04600 0.00000 0.00000 1.00800
ot 1.76820 -0.15210 0.00000 0.00000 15.99940
#####
END

```

## 1.2 Topology File

The following is the ORAC topology file AOT, residue AOT, and iso-octane, residue ISO. Charges are given as the third field within the keywords atoms and group, while labels and types are given as first and second fields. The keyword bonds contains a list of bonds each defined by two atom labels. The keyword imphd gives a list of improper torsions defined by four (4) labels. termatom is an ORAC internal keyword.

```

h10    hal2    0.0900
group
c8      ct12   -0.1800
h11    hal2    0.0900
h12    hal2    0.0900
group
c9      ct13   -0.2700
h13    hal3    0.0900
h14    hal3    0.0900
h15    hal3    0.0900
group
c10    ct12   -0.1800
h16    hal2    0.0900
h17    hal2    0.0900
group
c11    ct13   -0.2700
h18    hal3    0.0900
h19    hal3    0.0900
h20    hal3    0.0900
group
c12    cl     0.6300
o3      obl    -0.5200
o4      osl    -0.3400
group
c13    ct12   -0.1800
h21    hal2    0.0900
h22    hal2    0.0900
group
c14    ct11   -0.0900
h23    hal1    0.0900
group
c15    ct12   -0.1800
h24    hal2    0.0900
h25    hal2    0.0900
group
c16    ct12   -0.1800
h26    hal2    0.0900
h27    hal2    0.0900
group
c17    ct12   -0.1800
h28    hal2    0.0900
h29    hal2    0.0900
group
c18    ct13   -0.2700
h30    hal3    0.0900
h31    hal3    0.0900
h32    hal3    0.0900
group
c19    ct12   -0.1800
h33    hal2    0.0900
h34    hal2    0.0900
group
c20    ct13   -0.2700
h35    hal3    0.0900
h36    hal3    0.0900
h37    hal3    0.0900
#group
#na    sod    1.0000
end

bonds
s      os1    s      os2    s      os3
s      c1     c1     h1
c1     c3     c3     o1     c3     o2
o2     c4     c4     h4     c4     h5
c4     c5     c5     h6
c5     c6     c6     h7     c6     h8
c6     c7     c7     h9     c7     h10
c7     c8     c8     h11    c8     h12
c8     c9     c9     h13    c9     h14    c9     h15
c5     c10    c10    h16    c10    h17
c10    c11    c11    h18    c11    h19    c11    h20
c1     c2     c2     h2     c2     h3
c2     c12    c12    o3     c12    o4
o4     c13    c13    h21    c13    h22
c13    c14    c14    h23
c14    c15    c15    h24    c15    h25
c15    c16    c16    h26    c16    h27
c16    c17    c17    h28    c17    h29
c17    c18    c18    h30    c18    h31    c18    h32
c14    c19    c19    h33    c19    h34
c19    c20    c20    h35    c20    h36    c20    h37
end

imphd
o1     c1     o2     c3
o3     c2     o4     c12
end

terminator * *
RESIDUE-END

```

```

RESIDUE ISO ( Total Charge = 0.0)
atoms
group
c21 ct13 -0.2700
h38 hal3 0.0900
h39 hal3 0.0900
h40 hal3 0.0900
group
c22 ct0 0.0000
group
c23 ctl2 -0.1800
h41 hal2 0.0900
h42 hal2 0.0900
group
c24 ctl1 -0.0900
h43 hal1 0.0900
group
c25 ct13 -0.2700
h44 hal3 0.0900
h45 hal3 0.0900
h46 hal3 0.0900
# 3 methyl
group
c26 ct13 -0.2700
h47 hal3 0.0900
h48 hal3 0.0900
h49 hal3 0.0900
group
c27 ct13 -0.2700
h50 hal3 0.0900
h51 hal3 0.0900
h52 hal3 0.0900
group
c28 ct13 -0.2700
h53 hal3 0.0900
h54 hal3 0.0900
h55 hal3 0.0900
end

bonds
c21 c22 c22 c23 c23 c24
c24 c25 c22 c26 c22 c27
c24 c28
c21 h38 c21 h39 c21 h40
c23 h41 c23 h42
c24 h43
c25 h44 c25 h45 c25 h46
c26 h47 c26 h48 c26 h49
c27 h50 c27 h51 c27 h52
c28 h53 c28 h54 c28 h55
end

terminator * *
RESIDUE-END

```