Lecture 7 - Topic 2: Force Fields (Molecular Mechanics)  OPLS Force Fields Optimal Potentials for Liquid Simulations Model	
Presented By Arvind R. CSE Department, Stony Brook University	

# OUTLINE

- Introduction & Background
- Results
- Applications
- Summary

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- Introduction & Background
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#### COVERAGE

- Development of the OPLS FF.
- OPLS Concepts
- Force Field Equations

Time: 4 minutes

# COVERAGE OUTLINE • Relative Energies • Introduction & Background Optimized Structures Results • Energetic Results • Molecular Volumes and Densities Applications • Heat Capacities and Compressibilities Summary • Radial Distribution Functions Time: 15 minutes 10/15/2003 CSE Department, SUNY Stony Brook COVERAGE OUTLINE • Crambin Properties • Introduction & Background Potential Functions for Nucleotide Bases • Results and Comparisons Applications Time: 10 minutes Summary 10/15/2003 CSE Department, SUNY Stony Brook COVERAGE OUTLINE • Strengths • Introduction & Background • Weaknesses • Results and Comparisons Applications Time: 1 minute Summary

# Introduction and Background

- Development of the OPLS FF.
- OPLS What is it?
- Force Field Equations
- Computational Methods



## **Development of OPLS**



- Background work for OPLS comes from AMBER and the classical frameworks of Molecular Dynamics (MD) and Monte Carlo (MC) statistical mechanics.
- Laid out by Jorgensen from Yale.
- Has been applied to varied molecules:
  - simple molecules like C2H6 to
  - Complex molecules like proteins, DNA, etc.

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#### OPLS - what is it?



- Stands for Optimized Potentials for Liquid Simulation.
- Optimized various parameters are chosen to calculate...
- Potentials We are interested in calculating the potential energy for each structure.
- Liquid Simulation Framework of Liquids being simulated using the computer to determine various properties of organic chemicals.

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## **OPLS - Types**



- OPLS-UA (United Atom)
  - Sites for non-bonded interactions are placed on all non-hydrogen atoms, and on hydrogen attached to the hetero-atoms or carbons in aromatic rings.
  - The computation time is proportional to the total number of interaction sites squared.

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## **OPLS - Types**



- OPLS AA (All Atom)
  - More flexibility for charge distributions and torsion energetics.
  - Computationally expensive
  - Results are in more accord with the experimental results for
    - Free energies of compounds
    - Torsion Potentials

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#### **Force Field Equations** Energy $E_{bond}(\emptyset)$ Stretching Energy A $E_{angle}(\emptyset)$ Bending Energy E<sub>torsion</sub>(Ø) Torsion Energy Non-bonded Energy $\mathsf{E}_{\mathsf{non-bonded}}(\emptyset)$ stretching Angle Non-Bonded Interactions $E(\emptyset) = E_{bond}(\emptyset) + E_{angle}(\emptyset) + E_{torsion}(\emptyset) + E_{non-bonded}(\emptyset)$ 12

# Specific Parameters for the OPLS Force Field



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$$E_{bond}(\emptyset) = \sum_{r} K_r (r - r_{eq})^2$$

$$E_{angle}(\emptyset) = \sum_{i} K_{\Theta} (\Theta - \Theta_{eq})^2$$

$$E_{\text{non-bonded}} = \sum_{i} \sum_{j} \left[ q_{i} q_{j} e^{2} / r_{ij} + 4 \epsilon_{ij} (\sigma_{ij}^{12} / r_{ij}^{12} - \sigma_{ij}^{6} / r_{ij}^{6}) \right] f_{ij}$$

$$\mathsf{E}_{\mathsf{torsion}} = \sum_{i} \ V_{1}^{i} / 2 \Big[ 1 + \cos(\emptyset_{i} + f_{i} 1) \Big] + V_{2}^{i} / 2 \Big[ 1 - \cos(2\emptyset_{i} + f_{i} 2) \Big] + \mathsf{E}_{\mathsf{torsion}} \Big] + \mathsf{E}_{\mathsf{torsion}} \Big[ - \mathsf{E}_{\mathsf{torsion}} \Big] + \mathsf{E}_{\mathsf{torsion}$$

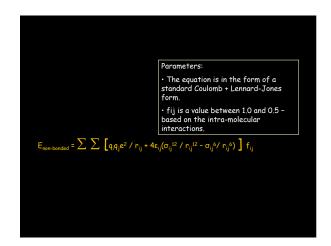
 $V_3^i/2[1+\cos(3\emptyset_i+f_i3)]$ 

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Parameters:  $E_{bond}(\emptyset) = \sum_{r} K_r (r - r_{eq})^2$ Req and Kr refer to values taken from AMBER force field. Kr refers to the spring constant between the two atoms.



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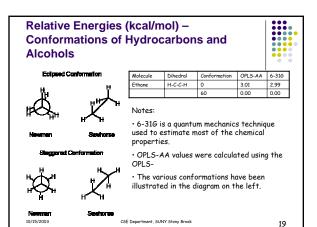
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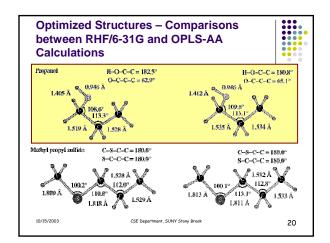
• Øi is the dihedral angle.

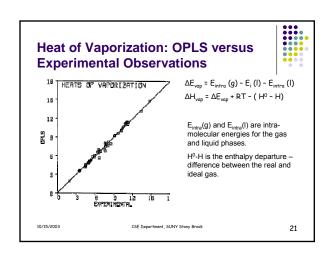
• V1, V2, V3 are coefficients in the Fourier series.

• f1, f2, f3 are phase angles.  $E_{torsion} = \sum_{i=1}^{n} V_1^{i}/2 \left[1 + \cos(\emptyset_i + f_i 1)\right] + V_2^{i}/2 \left[1 - \cos(2\emptyset_i + f_i 2)\right] + V_3^{i}/2 \left[1 + \cos(3\emptyset_i + f_i 3)\right]$ 

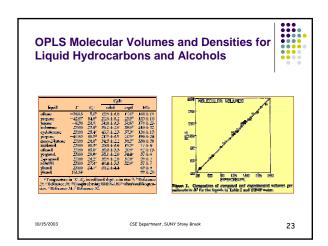
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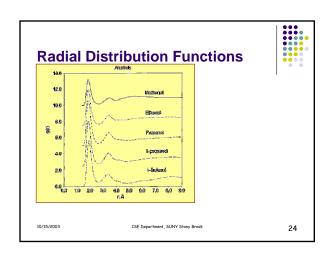






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					Att.	_
liquid	T	-2000(4)	Energy	Emp(I)	calcu	expel
£36.566	5.96	5.49 ± 0.02	615±0.01	5.UF-0.01	6.03 ± 6.02	5.87
CHECKERH	25.00	625 ± 0.02	6.78 ± 0.03	$0.87 \pm 0.00$	6.79 ± 6.64	6.38
CHECKETHAN	25.80	7.45 ± 0.05	ID 21:±:0.04	10.35 ± 0.02	7.88 ±0.85	75.00
CHOCHS.	25.88	6.40 ± 0.00	$10.08 \pm 0.02$	10.08 ± 0.01	7.05 ± 0.07	6.04
EIGEIESCIG.	25.88	7.35 ± 0.91	9.77 ± 0.04	9.80 ± 9.62.	7.97 ± 0.86	7.03
E366SEEL	25.88	$6.39 \pm 9.93$	$9.12 \pm 0.03$	D. 15° ± 0.02.	8.85 ± 0.89	9.0
personance:	221.15	12.45 ± 0.85	$-30.74 \pm 0.03$	-21.02.4: 0.05	15.71 ± 0.07	13.49
personance:	100.00	14.95±0.84	$-32.93 \pm 0.03$	$-25.08 \pm 0.02$	15.55 ± 0.07	
1633-2	108,89	12.00 ±0.85	$-6.05 \pm 0.05$	-0.35 ± 0.02.	13.55 ± 0.05	13.30
NAME OF	25.89	15.85 ± 0.85	$\pm 2.77 \pm 0.04$	-5.07 ± 0.03	15.85 ±0.05	15.5
DWA	25.88	11.45 ± 9.83	$8.72 \pm 0.06$	$8.79 \pm 0.02$	11.99 ± 0.67	11.75
DSHE	-34.60	464±082	8.14 ± 0.01	8.45 ± 0.61	2.15 ± 6.65	5.14
E40E	7.38	5.35 ± 0.03	SQL±0.02	5.09 ± 0.05	5.97 ± 0.64	5.60
DEE	25.99	6.09 ± 0.02	$9.16 \pm 0.01$	S.25 ± 0.02.	6.80 ± 0.05	6.50
THE	25.88	6.83 ± 0.83	$27.92 \pm 0.01$	$27.98 \pm 0.02$	$7.49 \pm 0.81$	7.5
DB343	25.88	637 ±085	9.51 ± 0.01	5.男子000	7.45 ±0.85	6.90
1,3 dienologe	25.88	6.47 ± 0.83	$29.13 \pm 0.01$	$26.81 \pm 0.03$	8.74 ± 6.64	8.50
away sead	2589	12.69 ± 081	$-44.99 \pm 0.01$	-15.12.4:0.6t	$12.51 \pm 0.65$	0.49
program pend.	100.00	10.70 ± 081	$-0.78 \pm 0.01$	$-15.93 \pm 0.02$	10.44 ± 0.05	11.30
erence.	25.99	5.67 ± 682	-0.37 ± 0.02	$-0.32.\pm0.02$	6.22.±6.63	6.24
proposal	25.88	7.05 ± 0.85	6.19 ± 0.04	$5.22 \pm 0.03$	7.51 ±0.85	7.00
proposone	25.88	871±085	$-3.22 \pm 0.02$	-3.45 ± 0.6.63	$7.24 \pm 0.05$	7.4
rutanone:	25.88	SEL 1-085	$2.15 \pm 0.05$	$2.07 \pm 0.02$	9.55 ± 8.64	9.25
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# **Applications of OPLS**

- Protein Properties
- Nucleotides Properties



#### **Crambin Protein**

- 46 Residues 326 Nonhydrogen atoms.
- 15 different residues with Cys(6), Thr(6), Ala(5), Tle(5), Gly(4), Pro(4), Asn(3), Ser(3), Arg(2), Val(2), Tyr(2), Asp(1), Glu(1), Leu(1), Phe(1).
- Secondary structure 2 regions of α-helix and a small anti-parallel β-sheet



<u>Crambin Protein Structure</u>

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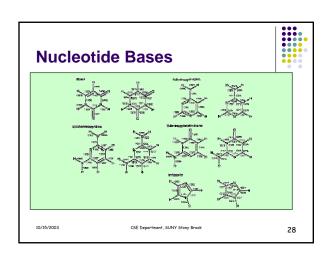
#### **Crambin Structure**

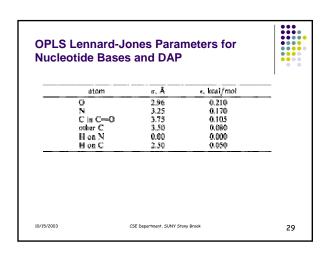


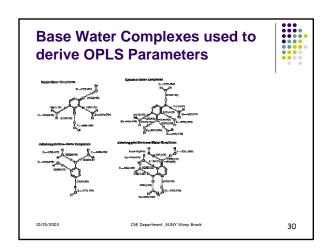
Table XIV. Results of Energy Minimizations for the Crambin Crystal

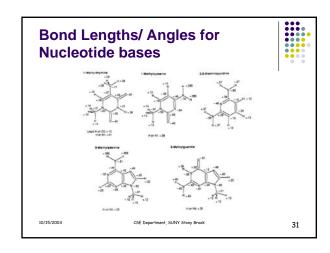
	force field		
property	AMBER	AMBER/OPLS	
final energy, kcal/mol	-6516.1	-9015.1	
rms—protein, Å rms—backbone, Å rms—side chains, Å	0.22 0.19 0.25	0.17 0.14 0.20	
rms— $\Phi$ , deg rms— $\psi$ , deg rms— $\omega$ , deg	7.2 7.9 4.1	6.1 5.6 4.6	

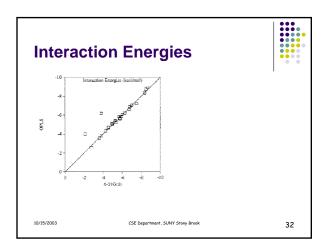
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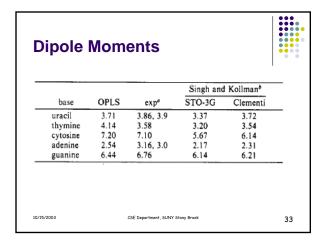


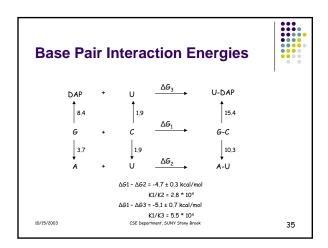


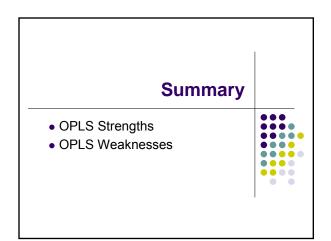












# **Strengths**



- Applied to different molecules with varied sizes
- Can simulate molecular interactions with certain accuracy.

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#### Weaknesses



- Parameter tweaking is a specialized "art as well as science" which have been done to "fit" molecular modeling.
- Each molecule requires a different parameter setting, and hence finding and adjusting parameters is a manual process.

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# **THANK YOU!**

