Coarse-graining

"reducing the irrelevant degrees of freedom"



Orginal size – 2.4 Mb



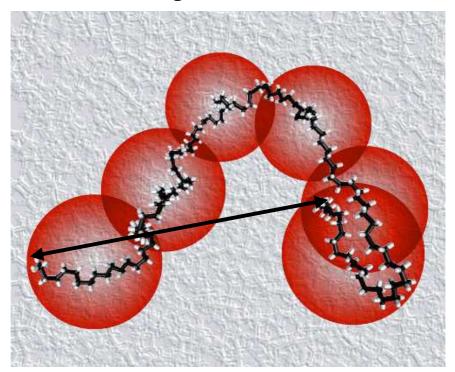
Compressed to 24Kb

The 'coarse-grained' picture is poor resolution. Yet, the sea, rock, trees and clouds is still recognizable. In fact, on 5 m distance from the screen it is hard to tell the difference between the two pictures.

Goal of Coarse-Graining (CG)

Goal: Scale up the size and time-scale of a fine-grained system of interest via the reduction of irrelevant degrees of freedom.

Coarse-grained simulations are commonly used for studying polymers, granular mater, colloids and biological materials!



Example: How does the end-to-end distance of a polymer in solution changes with polymer length?

Problem: Fine-grained (atomistic) simulations can only yield

limited data points.

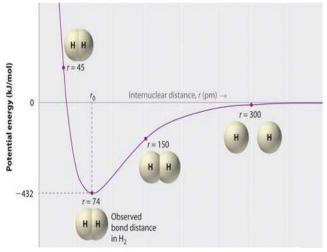
Solution: Construct a coarse-grained model.

Coarse-graining

"reducing the irrelevant degrees of freedom"

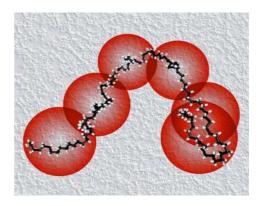
'Classic' atomic description:

bead size = van der Waals radius

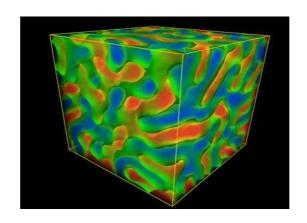


$$U_{AA} = 4\varepsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \alpha \left(\frac{\sigma}{r} \right)^{6} \right]$$

Coarse-grained description:

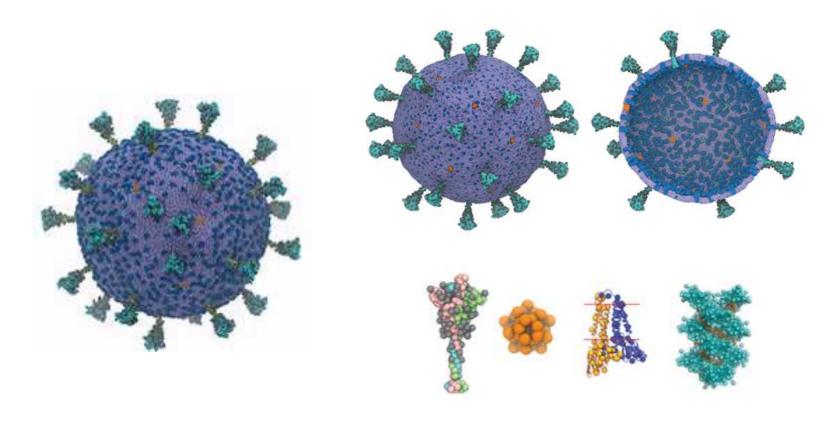


- particle based description
- allows larger ∆t, results in faster diffusion (irrelevant degrees → friction)



- density based description
- diffusion equations

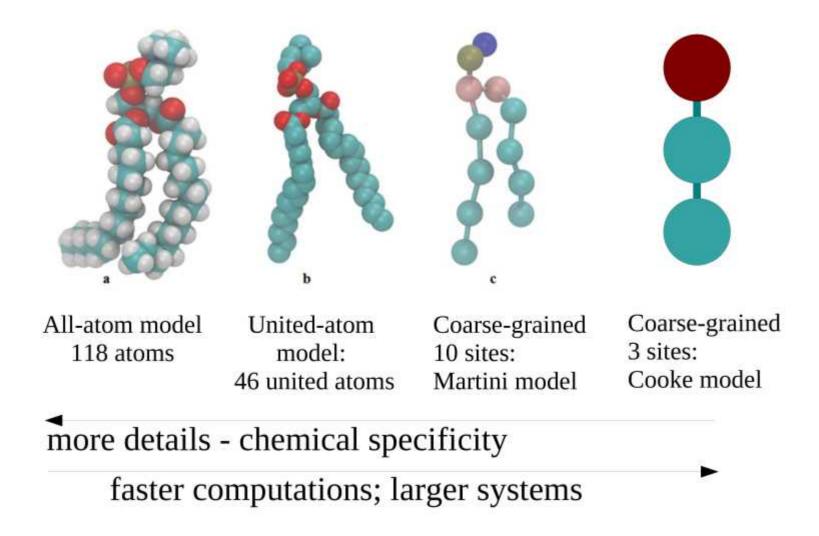
Coarse-graining: SARS-COV2 virus



Voth group, Uchicago CG method: force matching



Coarse-graining: A lipid



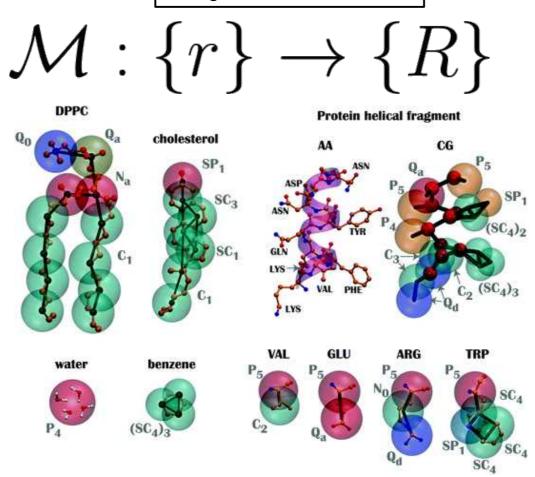


{} indicate a single specific configuration

$$\mathcal{M}: \{r\} \to \{R\}$$

Goarse-graining: Example of a mapping scheme (the Martini model)

{} indicate a single specific configuration



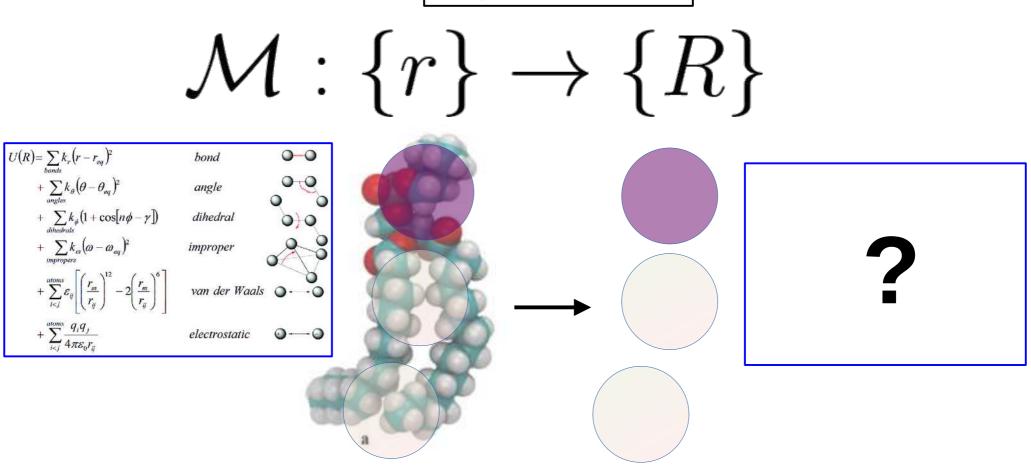
Marrink, Risselada,..,Mark, J. Phys. Chem. B, 2007

The mapping is predefined or better user-defined!



Goarse-graining: What to solve...

{} indicate a single specific configuration

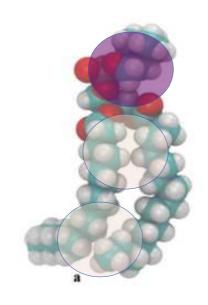


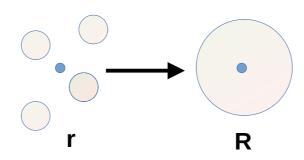
• Given the defined mapping **M**, how would the corresponding CG force-field or Hamiltonian looks like?



Coarse-graining: Fundamentals

• For each coarse-grained configuration $\bf R$ there exists a sub-ensemble of fine-grained configurations $\bf r$. Therefore, only the mapping from $\bf r$ to $\bf R$ is well-defined!





The mapping operation M only acts on the configuration space.

$$\mathcal{M}: \{r\} \to \{R\}$$

• The goal of coarse-graining is to reproduce the configurational part of the fine-grained partition function Z₀ for all relevant degrees of freedom while omitting all irrelevant degrees of freedom:

$$Z_0=\int d\{r\}e^{-eta H_0}$$

 The coarse-grained partition function can be expressed in terms of the original fine-grained Hamiltonian :

$$Z_{CG} = \int d\{R\} e^{-eta H_{CG}} = \int d\{R\} \int d\{r\} \delta(R-\mathcal{M}(r)) e^{-eta H_0(\{r\})}$$

$$Z_{CG} = \int d\{r\} e^{-eta H_0(\{r\})} = Z_0$$

Constructing all coarse-grained configurations from all fine-grained configurations:

$$\Omega(\{R\}) o \int d\{r\} \delta(R-\mathcal{M}(\{r\}))$$



.....not possible.....but Boltzmann weighted!!

• Coarse-graining poses an inverse problem: We can construct all the configurations R from the fine-grained trajectory r, since we know the mapping M. Therefore, we can in principle reconstruct H_{CG} since H_0 is known.

$$Z_{CG}=\int d\{R\}e^{-eta H_{CG}}=\int d\{R\}\int d\{r\}\delta(R-\mathcal{M}(r))e^{-eta H_0(\{r\})}$$
 unknown!

• **Disclaimer:** U_{CG} is only solved for a particular thermodynamic state point corresponding to the fine-grained ensemble/trajectory (temperature and pressure). The solution for U_{CG} is therefore not generally transferable to other state points!

Goarse-graining: Henderson theorem

Formulate structure based on correlation functions:

$$\rho$$
1(r1) density

All we use! \rightarrow ρ 2(r1,r2) pair correlation, RDF or g(r)

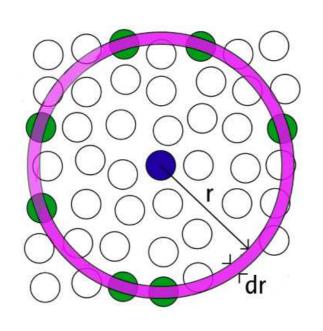
 ρ 3(r1,r2,r3) 3-body correlation

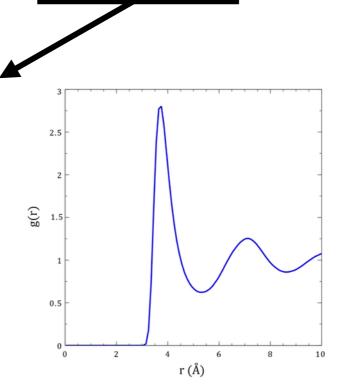
.....

Henderson theorem: "For each set of RDFs there is an unique set of pair potentials reproducing this set of RDFs" (R.L.Henderson, Phys. Lett. A., 1974). In essence, this theorem is analogous to the Kirkwood superposition approximation (!) stating that multibody correlations can be effectively decomposed into pair correlations (RISM integral theory).



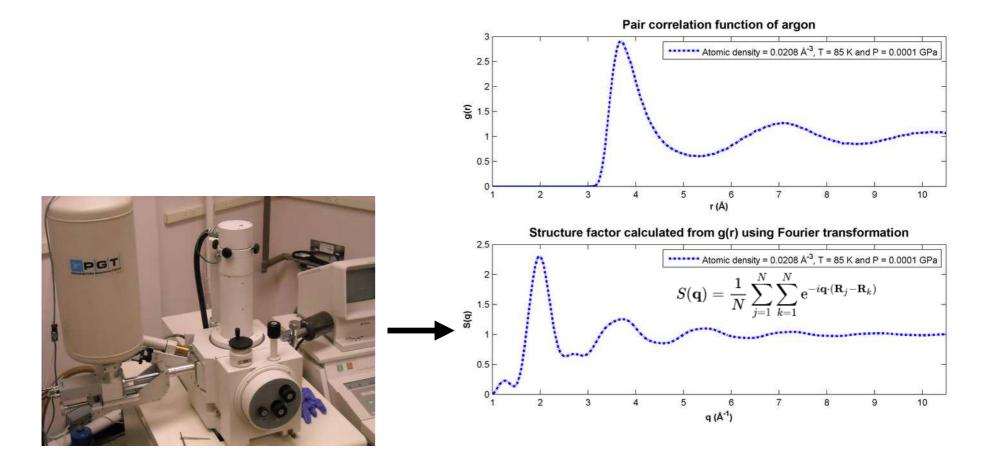
$$Z_{CG} = \int d\{R\} e^{-eta H_{CG}} = \int d\{R\} \int d\{r\} \underline{\delta(R-\mathcal{M}(r))} e^{-eta H_0(\{r\})}$$





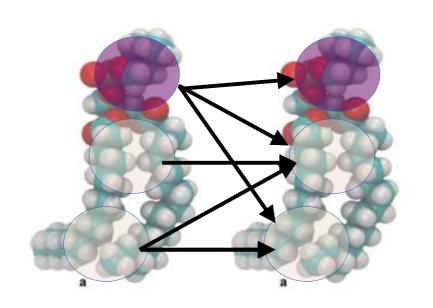
$$g(r) = \frac{V}{4\pi r^2 N^2} \langle \sum_{i} \sum_{j \neq i} \delta(r - r_{ij}) \rangle$$

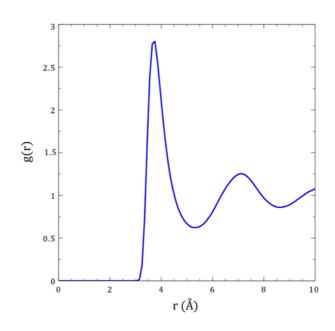




• The fourier transform of g(r) – the structure factor S(q) – can be experimentally resolved by Xray and neutron scattering.

$$Z_{CG} = \int d\{R\} e^{-eta H_{CG}} = \int d\{R\} \int d\{r\} \delta(R-\mathcal{M}(r)) e^{-eta H_0(\{r\})}$$





- If there are n unique bead types, then n! different g(r) must be reproduced for the non-bonded interactions!
- For the bonded interactions bond length and angle distributions must be (simultaneously) reproduced!

$$Z_{CG} = \int d\{R\}e^{-\beta H_{CG}} = \int d\{R\}\int d\{r\} \underline{\delta(R-\mathcal{M}(r))}e^{-\beta H_0(\{r\})}$$

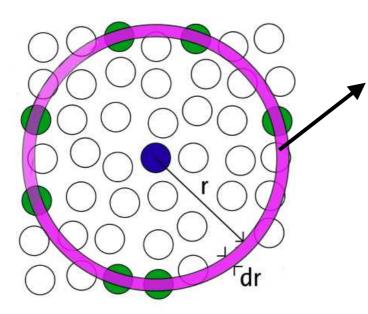
 Solve!

Two main approaches for structured-based systematic coarsegraining:

- 1) Inverse Monte-Carlo.
- 2) Inverse Boltzman.
- Both IMC and IB rely on iterative adaptation/fitting of a tabulated trial potential to reproduce g*(r).

$$Z_{CG} = \int d\{R\}e^{-\beta H_{CG}} = \int d\{R\}\int d\{r\} \delta(R-\mathcal{M}(r))e^{-\beta H_0(\{r\})}$$

 Solve!

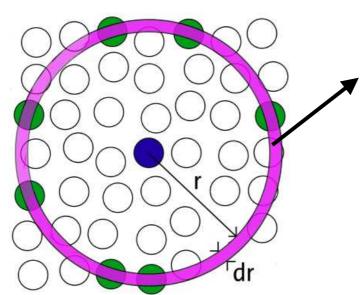


 s_{lpha} The number of interaction pairs in the shell lpha (7 in this example).

The total energy is thus given by:

$$H=\sum_{lpha}V_{lpha}S_{lpha}$$
 unknown!





 S_{lpha} The number of interaction pairs in the shell lpha (7 in this example).

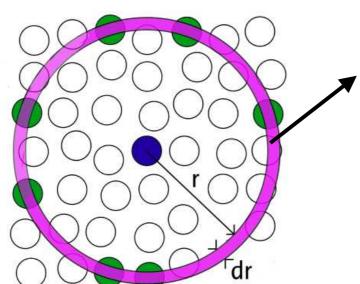
The total energy is thus given by:

$$H=\sum_{lpha}V_{lpha}S_{lpha}$$
 unknown!

Main idea: Construct a relationship between V and $\langle S \rangle$ or better its fluctuation $\Delta \langle S \rangle$:

$$\Delta < S_{lpha}> = \sum_{\gamma} rac{\partial < S_{lpha}>}{\partial V_{\gamma}} \Delta V_{\gamma} + \mathcal{O}\left(\Delta V^2
ight)$$





 s_{lpha} The number of interaction pairs in the shell lpha (7 in this example).

The total energy is thus given by:

$$H = \sum_{lpha} V_{lpha} S_{lpha}$$
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$$\Delta < S_{lpha}> = \sum_{\gamma} rac{\partial < S_{lpha}>}{\partial V_{\gamma}} \Delta V_{\gamma} + \mathcal{O}\left(\Delta V^2
ight)$$
 coupling with in other shells!



Main idea: Construct a relationship between V and <S> or better its fluctuation $\Delta <$ S>:

$$\Delta < S_{lpha}> = \sum_{\gamma} \left(rac{\partial < S_{lpha}}{\partial V_{\gamma}}
ight) \Delta V_{\gamma} + \mathcal{O}\left(\Delta V^2
ight)$$
 ensemble averaging

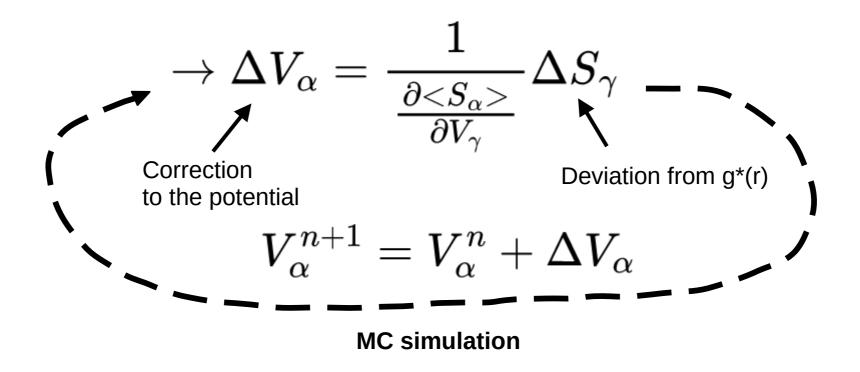
Accumulation yields ΔV at α . Subsequent accumulation of $\Delta V(\alpha)$ yields $V(\alpha)$

$$rac{\partial < S_lpha >}{\partial V_\gamma} = - \underline{eta(< S_lpha S_\gamma > - < S_lpha > < S_\gamma >)}$$
 ensemble averaging

• Note that $V(\alpha)$ is a discreet potential! Forces are thus not well-defined! This is why Monte-Carlo is used rather than molecular dynamics to sample configurations.



$$rac{\partial < S_{lpha}>}{\partial V_{\gamma}} = - \underline{eta(< S_{lpha}S_{\gamma}> - < S_{lpha}> < S_{\gamma}>})$$
 ensemble averaging





Lyubartsev AP, Laaksonen A. *Calculation of effective interaction potentials* from radial distribution functions: A reverse Monte Carlo approach. Phys Rev E Stat Phys Plasmas Fluids Relat Interdiscip Topics. 1995

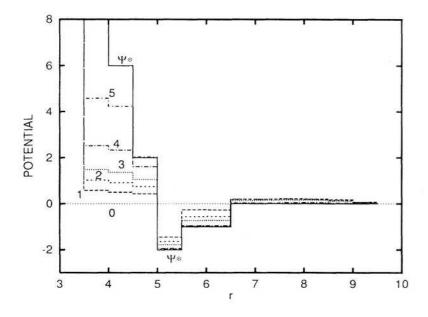
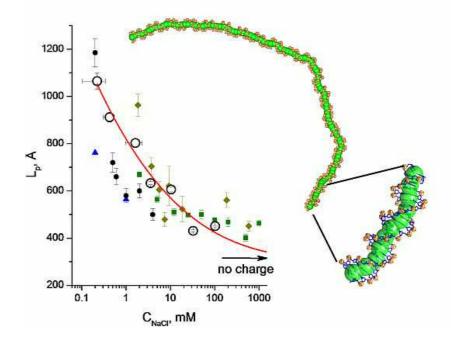


FIG. 2. An example of the convergent iterative procedure starting from zero potential with a damping parameter $\lambda=0.5$; notations as in Fig. 1.

Korolev, N., Luo, D., Lyubartsev, A. P., & Nordenskiöld, L. (2014). A Coarse-Grained DNA Model Parameterized from Atomistic Simulations by Inverse Monte Carlo. Polymers, 6(6), 1655-1675



 Potentials resolved with the Inverse Monte-Carlo method can be fitted to cubic splines and used for molecular simulations.



Systematic coarse-graining: Inverse Boltzmann

Update V(r) using a simple iterative scheme in MD simulations:

$$\Delta V^n(r) = k_B T ln(g^n(r)/g^*(r))$$

The value of the potential V(r) at r is obtained via accumulation of all ΔVs upto r:

$$V(r) = \Delta V(\alpha) + \Delta V(\beta)...$$

Schommers, Phys. Rev. A, 28, 3599 (1983)
D. Reith et al., J. Chomp. Chem. 24(13), 1624 (2003)
A. Lyubartsev et al., Phys. Rev. E. 52 (4), 3730 (1995)

- V(r) must be fitted to cubic splines after each iteration n if based on MD!
- May yield a different result than IMC.
- May not completely convert in case of multicomponents (multi-objectives).

Systematic coarse-graining: Inverse Boltzmann

$$\Delta V^n(r) = k_B T ln(g^n(r)/g^*(r))$$

Initial 'guess' : g(r)=1

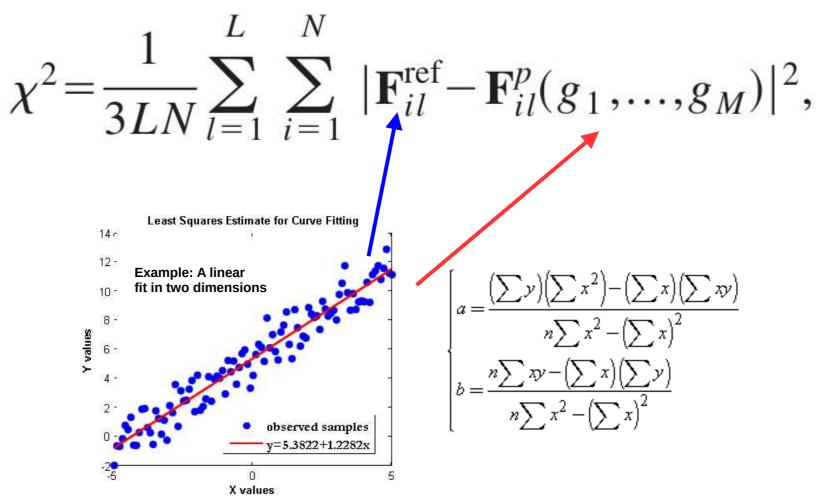
$$\Delta V^0(r) = -k_BTln(g^*(r))$$

• V^o also provides a reasonable first potential for IMC



Systematic coarse-graining: Force matching

Main idea: Project the many-body potentials on the function provided by the force-field using a variational principle (least square fit)



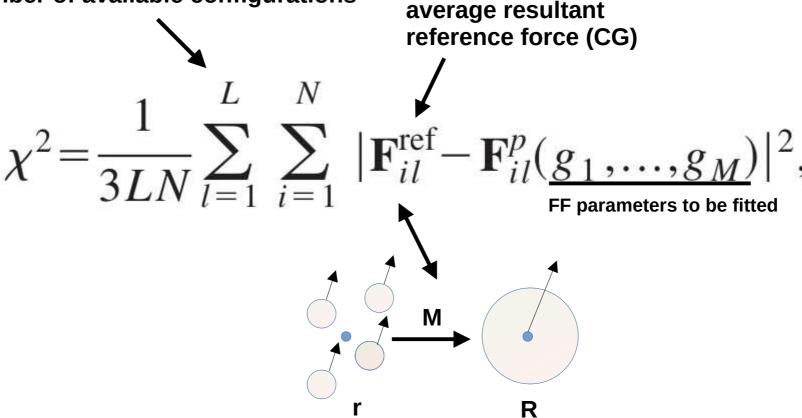
https://mathworld.wolfram.com/LeastSquaresFittingPolynomial.html



Systematic coarse-graining: Force matching

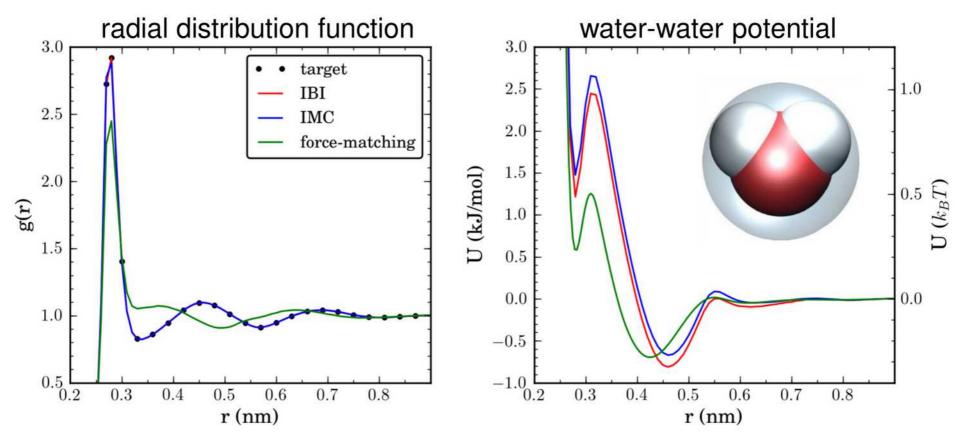
Main idea: Project the many-body potentials on the function provided by the force-field using a variational principle (least square fit)

L is number of available configurations



- The Force-field is constructed via a "rerun" over an equilibrated fine-grained trajectory consisting of **L** snapshots.
- Requires knowledge of (mapped) reference forces.
- Pair-wise interactions are introduced explicitly via the rule on how $g_1,...,g_M$ determines \mathbf{F}^p

Systematic coarse-graining: Comparison for water molecules



Votca Package, Kremer group, Mainz



Systematic (top-down) coarse-graining

Systematic or top-down coarse-graining:

Pro:

• All one needs is a long equilibrium trajectory of the fine-grained target system to either obtain the RDFs or use it for force-matching.

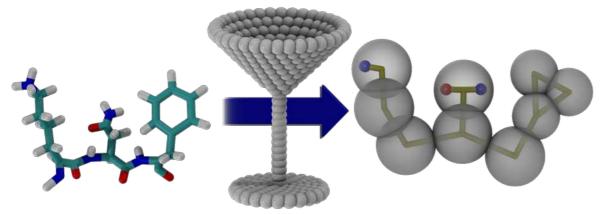
Con:

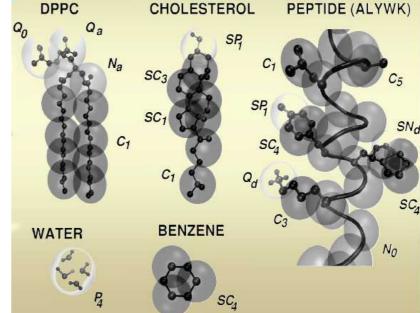
- The potentials are tuned to describe the system at equilibrium for a particular thermodynamic state point.
- The obtained potentials are 'case' dependent and typically not transverable, i.e., adding additional components may require complete reparametrisation which also implies generating new fine-grained trajectories.

The alternative: Construct highly transferable coarse-grained force-fields from first principles (bottom-up). This is labor intensive and not trivial!

Examples of bottom-up coarse-grained force-field: Martini & Spica







Standard (!) Lennard-Jones potential:

$$U_{\text{AA}} = 4\varepsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \alpha \left(\frac{\sigma}{r} \right)^{6} \right]$$
 GROMACS fast, flexible & free

The 'superatom' approach: several atoms modeled as a single 'atom'.

The gain: $\Delta t \times 10 \& N/4 \& Diffusion \times 4 => 160x speed up!$

SJ Marrink, *HJ Risselada*,...., AE Mark, J. Phys. Chem. B,7812-7824,2007

Main idea: Construct universally compatible interaction types for functional chemical groups commonly found within biomolecules. Then build new molecules like building with "lego" blocks.

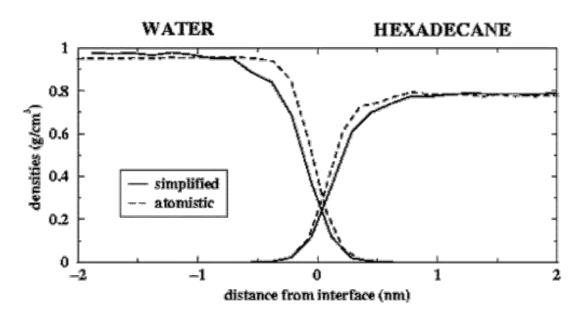
Chose ε and σ such that thermodynamic properties are reproduced

TABLE 2: Properties of Water and Alkanes with the CG Model Compared to Experimental Values^a

$U_{\rm AA} = 4\varepsilon$	$\left(\frac{\sigma}{r}\right)^{12}$	$\alpha \left(\frac{\sigma}{r}\right)^6$

system	CG model	density, ^b g cm ⁻³	compressibility, c 10^{-5} bar^{-1}	diffusion, ^{d} 10^{-5} cm ^{2} s ^{-1}
water	P	0.99 (0.99)	6 (4.5)	2.0 (2.3)
butane	C	0.68 (0.58)	28 (> 17)	1.9 (>5)
hexane	C-C	0.58 (0.66)	14 (17)	0.7(4)
octane	C-C	0.77 (0.70)	14 (13)	0.6(2)
decane	C-C-C	0.67 (0.73)	12 (11)	0.35(1)
dodecane	C-C-C	0.80(0.75)	12 (10)	0.3(-)
tetradecane	C-C-C-C	0.71 (0.76)	12 (9)	0.25(-)
hexadecane	C-C-C-C	0.81 (0.77)	12 (9)	0.2(-)
octadecane	C-C-C-C-C	0.74 (0.78)	11 (-)	0.2(0.3)
eicosane	C-C-C-C-C	0.82 (0.79)	11 (-)	0.15 (-)

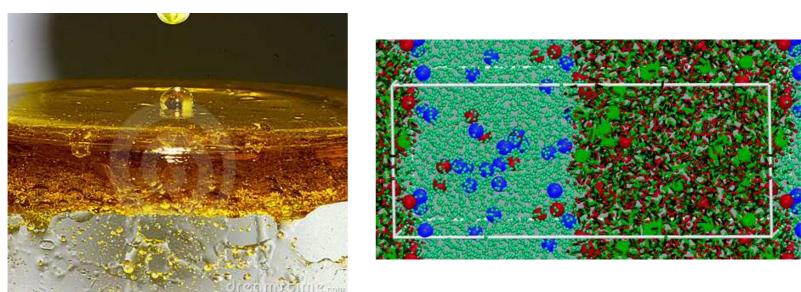
^a Properties at 300 K, unless specified. Experimental properties are given in parentheses. ^b Experimental densities at 293 K.²⁰ ^c Experimental isothermal compressibilities from ref 20. The values from simulations are computed from the volume fluctuations in an NPT ensemble. ^d Diffusion rates were obtained from the slope of the mean squared displacement (MSD) curve in the long time limit. Experimental values extrapolated from temperature-dependent data.²¹



Lorentz-Berthelot rules:

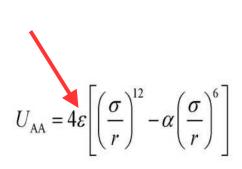
$$\sigma_{ij} = rac{\sigma_{ii} + \sigma_{jj}}{2}$$

$$\epsilon_{ij} = \sqrt{\epsilon_{ii}\epsilon_{jj}}$$



Martini force-field does not reproduce surface tensions because its usage of a LJ12-6 potential!

Example: Note that sigma is 0.47, mass is 72 u, and only ϵ differs between the 5 different interactions types



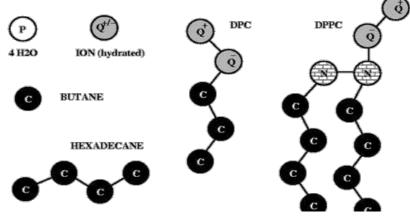
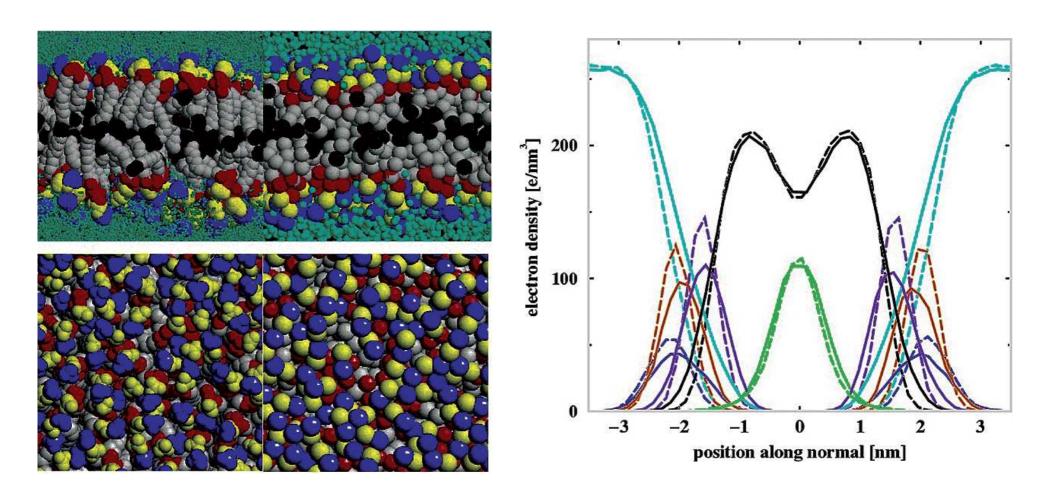


TABLE 1: Interaction Matrix^a

group	subtype	P	N			\mathbf{C}	Q				
			0	d	a	da		0	d	a	da
P		Ι	IV	Ш	III	II	V	1	I	I	I
N	O	IV	III	III	III	III	III	III	III	III	Ш
	d	Ш	III	II	II	II	IV	Ш	III	II	II
	a	III	III	II	II	\mathbf{II}	IV	III	II	III	\mathbf{II}
	da	II	III	II	II	I	V	Ш	II	II	I
C		V	III	IV	IV	V	Ш	V	V	V	V
Q	0	I	III	Ш	III	Ш	V	Ш	Ш	III	Π
	d	I	III	III	II	II	V	III	III	II	I
	a	I	III	П	Ш	II	V	Ш	II	III	I
	da	I	III	II	II	I	V	II	I	I	I

^a Level of interaction I (attractive), II (semiattractive), III (intermediate), IV (semirepulsive) or V (repulsive). Four different groups are considered: polar (P), nonpolar (N), apolar (C), and charged (Q). Both groups N and Q have four subtypes: 0 for no hydrogen bonding capabilities present, d for groups acting as hydrogen bond donor, a for groups acting as hydrogen bond acceptor, and da for groups with both donor and acceptor options.

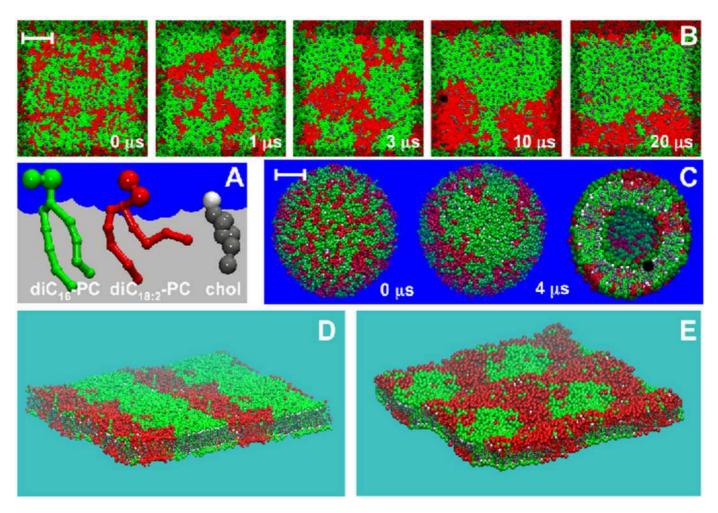
The goal is to minimize the number of interaction types required to describe all possible molecules!



SJ Marrink, HJ Risselada,...., AE Mark, J. Phys. Chem. B,7812-7824,2007



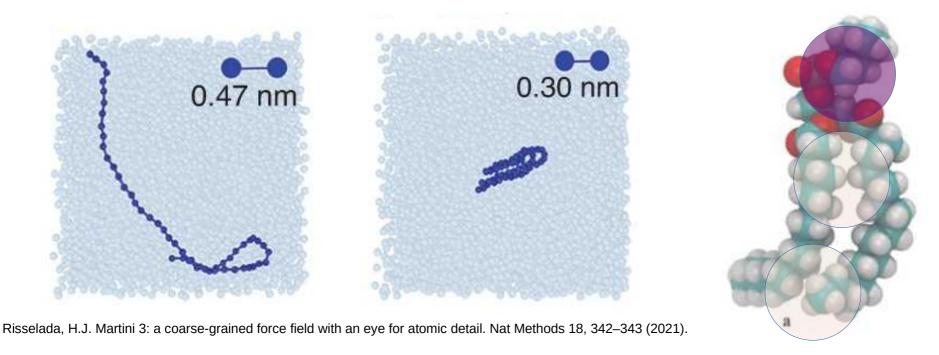
Simulation of the liquid ordered/disorder phase separation in ternary mixtures



HJ Risselada, SJ Marrink, PNAS, 17367-17372, 2008

Bottom-up coarse-graining: A general challenge

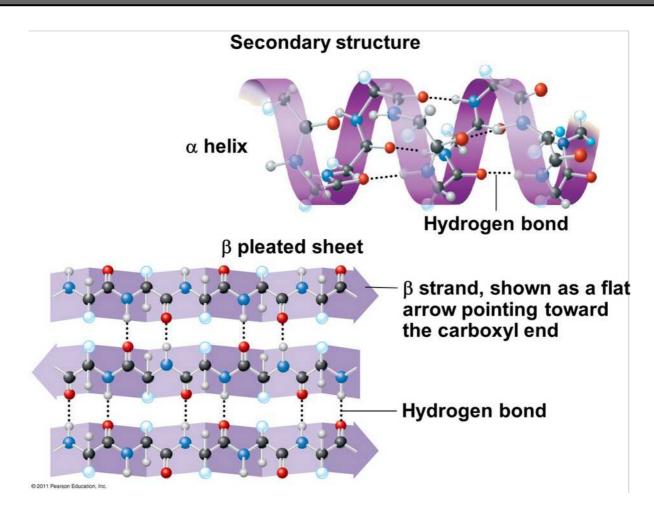
Bonded and non-bonded interactions are not independent!



- The bond length between CG beads is not uniquely defined.
- Bonded and non-bonded interactions must be optimized/parametrized simultaneously!
- Labor intensive & independent people work on dependent parameters.



Bottom-up coarse-graining: A general challenge

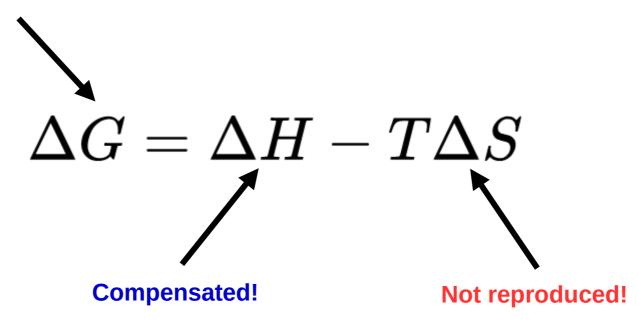


• Irrelevant degrees of freedom are not always irrelevant!



Bottom-up coarse-graining: A general challenge

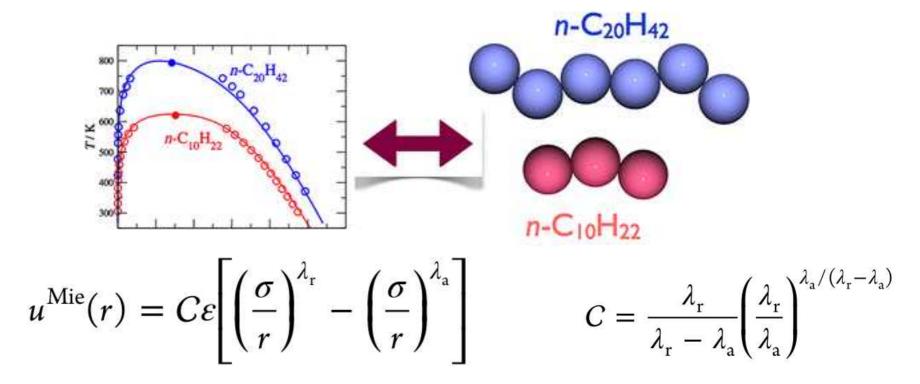
Reproduced!



The prediction of phase behavior in bottom-up force-fields like Martini is only "accurate" when the phase transition temperature lies close to the temperature of parametrization (room temperature).



Top-down coarse-graining over a large temperature range: the statistical associating fluid theory (SAFT-gamma)

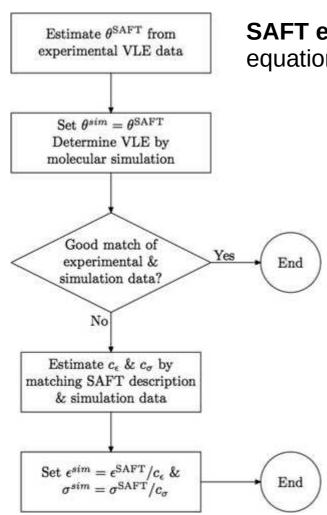


Avendano, C., Lafitte, T., Galindo, A., Adjiman, C. S., Jackson, G., & Müller, E. A. (2011). SAFT-y force field for the simulation of molecular fluids. 1. A single-site coarse grained model of carbon dioxide. The Journal of Physical Chemistry B, 115(38), 11154-11169.

Avendaño, C., Lafitte, T., Adjiman, C. S., Galindo, A., Müller, E. A., & Jackson, G. (2013). SAFT-y force field for the simulation of molecular fluids: 2. Coarse-grained models of greenhouse gases, refrigerants, and long alkanes. The Journal of Physical Chemistry B, 117(9), 2717-2733

• Use the vapor (saturation) pressure and saturated-liquid density data over a wide range of temperatures as target properties

Top-down coarse-graining: SAFT Force-Field



SAFT equations: Analytical relationships between the equations of state (g(r)) and the pair-wise interaction parameters.

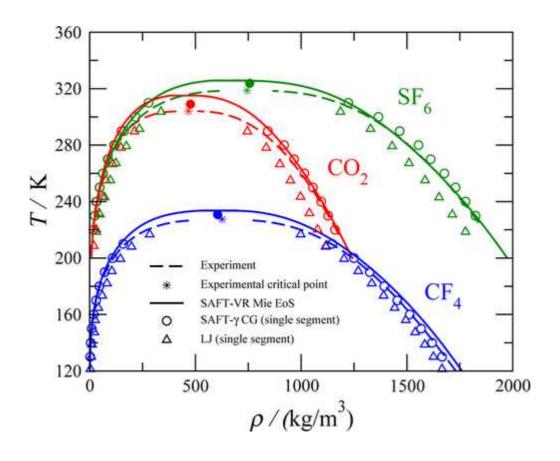
$$\min_{\sigma, \varepsilon, \lambda_{r}, \lambda_{a}, m_{s}} F_{\text{obj,exp}}(\sigma, \varepsilon, \lambda_{r}, \lambda_{a}, m_{s})$$

$$= \min_{\sigma, \varepsilon, \lambda_{r}, \lambda_{a}, m_{s}} \left\{ \sum_{i=1}^{N_{p}} \left(\frac{P_{v}^{\text{SAFT}}(T_{i}; \sigma, \varepsilon, \lambda_{r}, \lambda_{a}, m_{s}) - P_{v}^{\text{exp}}(T_{i})}{P_{v}^{\text{exp}}(T_{i})} \right)^{2} + \sum_{j=1}^{N_{p}} \left(\frac{\rho_{l}^{\text{SAFT}}(T_{j}; \sigma, \varepsilon, \lambda_{r}, \lambda_{a}, m_{s}) - \rho_{l}^{\text{exp}}(T_{j})}{\rho_{l}^{\text{exp}}(T_{j})} \right)^{2} \right\}$$

$$+ \sum_{j=1}^{N_{p}} \left(\frac{\rho_{l}^{\text{SAFT}}(T_{j}; \sigma, \varepsilon, \lambda_{r}, \lambda_{a}, m_{s}) - \rho_{l}^{\text{exp}}(T_{j})}{\rho_{l}^{\text{exp}}(T_{j})} \right)^{2} \right\}$$
(3)



Top-down coarse-graining:SAFT Force-Field



Avendaño, C., Lafitte, T., Adjiman, C. S., Galindo, A., Müller, E. A., & Jackson, G. (2013). SAFT-y force field for the simulation of molecular fluids: 2. Coarse-grained models of greenhouse gases, refrigerants, and long alkanes. The Journal of Physical Chemistry B, 117(9), 2717-2733



Done.....



