

Isabela Quintela Matos

**Partition Coefficient Calculations of
Molecules Mimicking Asphaltenes Through
Molecular Simulation Using The
Coarse-Grained SAFT- γ Mie Force Field**

Rio de Janeiro

2018

Isabela Quintela Matos

**Partition Coefficient Calculations of Molecules
Mimicking Asphaltenes Through Molecular Simulation
Using The Coarse-Grained SAFT- γ Mie Force Field**

Dissertação de Mestrado apresentada ao
Programa de Pós-Graduação em Tecnologia de Processos Químicos e Bioquímicos,
Escola de Química, Universidade Federal
do Rio de Janeiro, como requisitos parcial à
obtenção do título de Mestre em Engenharia
Química.

Universidade Federal do Rio de Janeiro

Escola de Química

Programa de Pós-Graduação em Tecnologia de Processos Químicos e Bioquímicos

Supervisor: Charlles Rubber de Almeida Abreu

Co-supervisor: Papa Matar Ndiaye

Rio de Janeiro

2018

Isabela Quintela Matos

Partition Coefficient Calculations of Molecules Mimicking Asphaltenes Through Molecular Simulation Using The Coarse-Grained SAFT- γ Mie Force Field/ Isabela Quintela Matos. – Rio de Janeiro, 2018-

34 p. : il. (algumas color.) ; 30 cm.

Supervisor: Charlles Rubber de Almeida Abreu

Dissertação (Mestrado) – Universidade Federal do Rio de Janeiro

Escola de Química

Programa de Pós-Graduação em Tecnologia de Processos Químicos e Bioquímicos, 2018.

1. Palavra-chave1. 2. Palavra-chave2. 2. Palavra-chave3. I. Orientador. II. Universidade xxx. III. Faculdade de xxx. IV. Título

Errata sheet

Elemento opcional da [ABNT](#) (2011, 4.2.1.2). Exemplo:

FERRIGNO, C. R. A. **Tratamento de neoplasias ósseas apendiculares com reimplantação de enxerto ósseo autólogo autoclavado associado ao plasma rico em plaquetas**: estudo crítico na cirurgia de preservação de membro em cães. 2011. 128 f. Tese (Livre-Docência) - Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, 2011.

Folha	Linha	Onde se lê	Leia-se
1	10	auto-conclavo	autoconclavo

Isabela Quintela Matos

Partition Coefficient Calculations of Molecules Mimicking Asphaltenes Through Molecular Simulation Using The Coarse-Grained SAFT- γ Mie Force Field

Dissertação de Mestrado apresentada ao
Programa de Pós-Graduação em Tecnologia de Processos Químicos e Bioquímicos,
Escola de Química, Universidade Federal
do Rio de Janeiro, como requisitos parcial à
obtenção do título de Mestre em Engenharia
Química.

Trabalho aprovado. Rio de Janeiro, 24 de novembro de 2012:

Charles Rubber de Almeida Abreu
Orientador

Professor
Convidado 1

Professor
Convidado 2

Rio de Janeiro
2018

*Este trabalho é dedicado às crianças adultas que,
quando pequenas, sonharam em se tornar cientistas.*

Acknowledgements

Os agradecimentos principais são direcionados à Gerald Weber, Miguel Frasson, Leslie H. Watter, Bruno Parente Lima, Flávio de Vasconcellos Corrêa, Otavio Real Salvador, Renato Machnievscz¹ e todos aqueles que contribuíram para que a produção de trabalhos acadêmicos conforme as normas ABNT com L^AT_EX fosse possível.

Agradecimentos especiais são direcionados ao Centro de Pesquisa em Arquitetura da Informação² da Universidade de Brasília (CPAI), ao grupo de usuários *latex-br*³ e aos novos voluntários do grupo *abnT_EX2*⁴ que contribuíram e que ainda contribuirão para a evolução do *abnT_EX2*.

¹ Os nomes dos integrantes do primeiro projeto *abnT_EX* foram extraídos de <http://codigolivres.org.br/projects/abntex/>

² <http://www.cpai.unb.br/>

³ <http://groups.google.com/group/latex-br>

⁴ <http://groups.google.com/group/abntex2> e <http://www.abntex.net.br/>

*“Não vos amoldeis às estruturas deste mundo,
mas transformai-vos pela renovação da mente,
a fim de distinguir qual é a vontade de Deus:
o que é bom, o que Lhe é agradável, o que é perfeito.
(Bíblia Sagrada, Romanos 12, 2)*

Abstract

Segundo a [ABNT \(2003, 3.1-3.2\)](#), o resumo deve ressaltar o objetivo, o método, os resultados e as conclusões do documento. A ordem e a extensão destes itens dependem do tipo de resumo (informativo ou indicativo) e do tratamento que cada item recebe no documento original. O resumo deve ser precedido da referência do documento, com exceção do resumo inserido no próprio documento. (...) As palavras-chave devem figurar logo abaixo do resumo, antecidas da expressão Palavras-chave:, separadas entre si por ponto e finalizadas também por ponto.

Palavras-chave: latex. abntex. editoração de texto.

Abstract

This is the english abstract.

Keywords: latex. abntex. text editoration.

List of Figures

Figure 2.1.1—Values for parameter χ according to the ring geometry (MÜLLER; MEJÍA, 2017)	19
--	----

List of Tables

List of symbols

Γ	Letra grega Gama
Λ	Lambda
ζ	Letra grega minúscula zeta
\in	Pertence

Contents

1	LITERATURE REVIEW	14
1.1	Coarse Grained Force Fields	14
1.2	Solvation Free Energy	16
2	SAFT-γ MIE FORCE FIELD	17
2.1	SAFT-VR Mie EoS	17
2.1.1	Ideal Contribution	17
2.1.2	Monomer Contribution	17
2.1.3	Chain Contribution	18
2.1.4	Ring Contribution	19
2.1.5	Combining rules for the intermolecular potential parameters	20
2.2	Parameter Estimation for the SAFT-γ Mie Force Field	20
	BIBLIOGRAPHY	24
	APPENDIX	28
	APPENDIX A – QUISQUE LIBERO JUSTO	29
	APPENDIX B – NULLAM ELEMENTUM URNA VEL IMPERDIET SODALES ELIT IPSUM PHARETRA LIGULA AC PRETIUM ANTE JUSTO A NULLA CURABITUR TRISTIQUE ARCU EU METUS	30
	ANNEX	31
	ANNEX A – MORBI ULTRICES RUTRUM LOREM.	32
	ANNEX B – CRAS NON URNA SED FEUGIAT CUM SOCIIS NA- TOQUE PENATIBUS ET MAGNIS DIS PARTURIENT MONTES NASCETUR RIDICULUS MUS	33
	ANNEX C – FUSCE FACILISIS LACINIA DUI	34

1 Literature Review

1.1 Coarse Grained Force Fields

Molecular simulations can be carried out at different levels of descriptions. The detailed atomistic level or *ab initio* level is described by the laws of quantum mechanics. The system consists of a set of subatomic particulars in which Schrodinger's equation is solved for all of them. The next level is the atomistic description. It considers that the system is made up of atoms following the laws of statistical mechanics. Force fields at this level are based on pair potentials with Coulombic charged sites, which account for the molecular interactions. The contributions due to intramolecular interactions like bond-stretching, angle-bending and torsion are also usually accounted by these kind of force fields. When the scale of the simulations needs to be increased and the atomistic simulations become too computationally expensive, the coarse-grained (CG) description is more suited. It considers that the system is made up of pseudo atoms or beads that contain multiple atoms.

There is a obvious loss of information in grouping atoms, hence it is necessary to assure that the process of eliminating unnecessary or unimportant information ('coarse graining') doesn't affect the system's physical behavior. The coarse grained force fields based on this description are developed by mapping the atomistic model to define the pseudo atoms. This mapping is normally done by grouping similar functional groups. The level of coarse-graining also needs to be defined, up to 6 heavy atoms (non-hydrogen atoms) per bead in order to not loose much detail and maintain isotropic representations of the beads (SHINODA; DEVANE; KLEIN, 2007; MARRINK et al., 2007; HADLEY; MCCABE, 2012). The CG force field can be parametrized following two different approaches: bottoms up and top down. The bottoms up approach uses information of a more detailed scale such as the *ab initio* description or the atomistic description to obtain the information necessary to the parametrization. This method depends highly of the quality of the detailed model to succeed. Meanwhile, the top down methodology obtains the parameters from one larger scales. This information at larger scales could be experimentally observed data like thermodynamic properties or native-structure based properties.

One of the first applications of coarse grained models is the study of protein folding (LEVITT; WARSHE, 1975; LEVITT, 1976). These earlier protein CG models were based on the structure of the molecule and they contributed for the knowledge of the physicochemical forces associated with protein folding and protein interactions (KOGA; TAKADA, 2001). More recent models focused on retaining the protein's chemical speci-

ficity. The Bereau and Deresmo model (BEREAU; DESERNO, 2009) has a up to four-bead representation and was used in studies of protein folding and aggregation. However, this model still needs tuning to improve stability of proteins (BEREAU; BACHMANN; DESERNO, 2010). The OPEP (Optimized Potential for Efficient Protein Structure Prediction) model (STERPONE et al., 2014; STERPONE; DERREUMAUX; MELCHIONNA, 2015) has up to six-bead representation. It was used to investigate a variety of phenomena, ranging from protein folding to *ab initio* peptide structure prediction (BARDUCCI; BONOMI; DERREUMAUX, 2011; CHEBARO et al., 2009b; CHEBARO et al., 2009a). Other CG protein models used in the literature are the Scorpion (solvated coarse-grained protein interaction) (BASDEVANT; BORGIS; HA-DUONG, 2013), the UNRES (united residue) (ADAM et al., 2014) and the MARTINI model (LARS et al., 2013). The later one is the most popular model for the CG modeling of membrane proteins (MARRINK; TIELEMAN, 2013). The MARTINI model is also extensively used as CG model for water. This model represents four water molecules as one bead using a shifted Lennard Jones potential for the non bonded interactions. Though its extensive use, the MARTINI water model doesn't properly represent properties as interfacial tension and compressibility (HE et al., 2010) and can freeze at room temperature (WINGER et al., 2009; MARRINK et al., 2007), what makes necessary the use of anti-freeze agents during the simulations. This behavior can be explained by the high level of coarse graining (4:1), the lack of explicit charges and the use of the 12-6 potential. With the idea of improving the MARTINI model, Chiu, Scott e Jakobsson (2010) used the Morse Potential, which is softer than the LJ potential. Meanwhile, Shinoda, Devane e Klein (2007) used different forms of the Mie potential. They concluded that a 12-4 Mie Potential was ideal for the all water cross interactions and a 9-6 Mie Potential was suited for all the solute-solute interactions.

Outside of the Martini framework, He et al. (2010) studied different levels of coarse-graining for water ranging for one to 4 molecules per bead using different Mie and Morse potentials. Other works also assessed the use of Soft-core potentials to study aqueous solutions of surfactants (SHINODA; DEVANE; KLEIN, 2007), ionic liquids (BHARGAVA; KLEIN, 2009), lipids (SHINODA; DEVANE; KLEIN, 2010) and membranes (PANTANO; KLEIN, 2009). Other CG force field for water based on the Mie Potential is the SAFT- γ Mie (LOBANOVA et al., 2015). In this model, the water molecule can be represented by two different one isotropic bead interacting via a 8-6 Mie Potential models. The CGW1-vle model was parametrized using saturated-liquid density and vapor pressure data, and should be used for simulations of aqueous systems' fluid-phase equilibria at high temperatures and pressures. This model still suffers from premature freezing with a triple point at 343 K. The other model, CGW1-ift, was parametrized using saturated-liquid density and vapor-liquid interfacial tension, hence it is best suited for interfacial properties calculations. Both models have temperature-dependent size and energy parameters and performed well for these properties over the entire

temperature range of the liquid. The SAFT- γ Mie force field have also been applied to other compounds with satisfactory results. Müller e Mejía (2017) parametrized the force field for aromatic compounds and tested it with simulations of fluid phase equilibrium. Herdes, Totton e Müller (2015) carried out simulations of alkanes and light gases with this force fields. Binary and ternary mixtures of water, carbon-dioxide and water (LOBANOVA et al., 2016), thermodynamic and transport properties of carbon dioxide and methane (AIMOLI; MAGINN; ABREU, 2014a; AIMOLI; MAGINN; ABREU, 2014b) and water/oil interfacial tension (HERDES et al., 2017) were also studied with this force field.

1.2 Solvation Free Energy

2 SAFT- γ Mie Force Field

2.1 SAFT-VR Mie EoS

The SAFT-VR Mie equation of state (LAFITTE et al., 2013) is the basis for the SAFT- γ Mie coarse grained force field (AVENDAÑO et al., 2011). This EoS was initially developed to describe chain molecule formed from fused Mie segments using the Mie attractive and repulsive potential. The Mie potential is a type of generalized Lennard-Jones potential that can be used to describe explicitly repulsive interactions of different hardness/softness and attractive interactions of different ranges, and is given by:

$$U_{Mie}(r) = \epsilon \frac{\lambda_r}{\lambda_r - \lambda_a} \left(\frac{\lambda_r}{\lambda_a} \right)^{\left(\frac{\lambda_a}{\lambda_r - \lambda_a} \right)} \left[\left(\frac{\sigma}{r} \right)^{\lambda_r} - \left(\frac{\sigma}{r} \right)^{\lambda_a} \right] \quad (2.1)$$

where ϵ is the potential well depth, σ is the segment diameter, r is the distance between the spherical segments, λ_r is the repulsive exponent and λ_a is the attractive exponent. This equation uses the Barker e Henderson (1976) high perturbation expansion of the Helmholtz free energy up to third order and an improved expression for the radial distribution function (RDF) of Mie monomers at contact to obtain a equation able to give an accurate theoretical description of the vapor-liquid equilibria and second derivative properties (LAFITTE et al., 2013). For a non-associating fluid, the Helmholtz free energy is:

$$\frac{A}{N\kappa_b T} = a = a^{IDEAL} + a^{MONO} + a^{CHAIN} \quad (2.2)$$

2.1.1 Ideal Contribution

The ideal contribution for a mixture is given by:

$$a^{IDEAL} = \sum_{i=1}^{N_c} x_i \ln (\rho_i \Lambda_i^3) - 1 \quad (2.3)$$

where $x_i = N_i/N$ is the molar fraction of component i , $\rho_i = N_i/V$ is the number density, N_i is the number of molecules of each component and Λ_i^3 is de Broglie wavelength.

2.1.2 Monomer Contribution

The monomer contribution describes the interactions between Mie segments and can be expressed for a mixture as:

$$a^{MONO} = \left(\sum_{i=1}^{N_c} x_i m_{s,i} \right) a^M \quad (2.4)$$

In the equation above, $m_{s,i}$ is the number of spherical segments making up the molecule i and a^M is the monomer dimensionless Helmholtz free energy and it is expressed as a third order perturbation expansion in the inverse temperature (BARKER; HENDERSON, 1976):

$$a^M = a^{HS} + \beta a_1 + \beta a_2^2 + \beta a_3^3 \quad (2.5)$$

where $\beta = \kappa_b T$ and a^{HS} is the hard-sphere dimensionless Helmholtz free energy for a mixture :

$$a^{HS} = \frac{6}{\pi \rho_s} \left[\left(\frac{\zeta_2^3}{\zeta_3^2} - \zeta_0 \right) \ln(1 - \zeta_3) + \frac{3\zeta_1\zeta_2}{1 - \zeta_3} + \frac{\zeta_2^3}{\zeta_3(1 - \zeta_3)^2} \right] \quad (2.6)$$

The variable $\rho_s = \rho \sum_i^{N_c} x_i m_{s,i}$ is the total number density of spherical segments and ζ_l are the moments of the number density:

$$\zeta_l = \frac{\pi \rho_s}{6} \left(\sum_{i=1}^{N_c} x_{s,i} d_{ii}^l \right), l = 0, 1, 2, 3 \quad (2.7)$$

where $x_{s,i}$ is the mole fraction of the segments and is related through the mole fraction of component i (x_i) by:

$$x_{s,i} = \frac{m_{s,i} x_i}{\sum_{k=1}^{N_c} m_{s,k} x_k} \quad (2.8)$$

The effective hard-sphere diameter d_{ii} for the segments is:

$$d_{ii} = \int_0^{\sigma_{ii}} (1 - \exp(-\beta U_{ii}^{Mie}(r))) dr \quad (2.9)$$

The integral in Eq. (2.9) is normally obtained by means of Gauss-Legendre with a 5-point quadrature (PAPAIIOANNOU et al., 2014). The detailing of the terms of Eq. (2.4) can be found in Lafitte et al. (2013).

2.1.3 Chain Contribution

The chain formation of m_s tangentially bonded Mie segments contribution is based on the first-order perturbation theory (TPT1) (PAPAIIOANNOU et al., 2014) and can be expressed as:

$$a^{CHAIN} = - \sum_{i=1}^{N_c} x_i (m_{s,i} - 1) \ln(g_{ii}^{Mie}(\sigma_{ii})) \quad (2.10)$$

The $g_{ij}^{Mie}(\sigma_{ij})$ term correspond to the value of the radial distribution function (RDF) of the hypothetical Mie system evaluated at the effective diameter and can be obtained with the perturbation expansion:

$$g_{ij}^{Mie}(\sigma_{ij}) = g_{d,ij}^{HS}(\sigma_{ij}) \exp[\beta \epsilon g_{1,ij}(\sigma_{ij}) / g_{d,ij}^{HS}(\sigma_{ij}) + (\beta \epsilon)^2 g_{2,ij}(\sigma_{ij}) / g_{d,ij}^{HS}(\sigma_{ij})] \quad (2.11)$$

The other terms in the equations above are explicitly exposed in the original article (LAFITTE et al., 2013).

2.1.4 Ring Contribution

There are two forms for the Helmholtz free energy for rings formed from m_s tangentially bonded segments in the literature. The first one (LAFITTE et al., 2012) considered that the difference between a chain and a ring molecule is that the latter one has one more bond that is connecting the first segment to the last. With this assumption, the Eq. (2.10) can be adapted to rings by:

$$a^{RING} = - \sum_{i=1}^{N_c} x_i m_{s,i} \ln(g_{ii}^{Mie}(\sigma_{ii})) \quad (2.12)$$

According to Lafitte et al. (2012), Eq. (2.12) needs an additional parametrization with molecular simulation data so the EoS can be used in molecular simulations, but this procedure is not the necessary for chain molecules. Recently Müller e Mejía (2017) tried to correct this inconsistency by means of developing the ring free energy based on the work of Müller e Gubbins (1993) who obtained rigorous expressions for molecular geometries of rings of $m_s = 3$ for hard fluids. The final expression developed for the ring dimensionless Helmholtz free energy is:

$$a^{RING} = - \sum_{i=1}^{N_c} x_i (m_{s,i} - 1 + \chi_i \eta_i) \ln(g_{ii}^{Mie}(\sigma_{ii})) \quad (2.13)$$

$\eta_i = m_{s,i} \rho_i \sigma_{ii}^3 / 6$ is the packing fraction and χ_i is a parameter which depends on $m_{s,i}$ and on the geometry of the ring of each component i . For a value of $\chi = 0$ Eq. (2.13) is equal to Eq. (2.10) and the system corresponds to a hard sphere system of triangles when $\chi = 1.3827$. Müller e Mejía (2017) also calculated values of ζ for values of $m_s = 3, m_s = 4, m_s = 5, m_s = 7$ with pseudo-experimental data from molecular dynamics (MD) for a defined pure fluid. The values of χ for each geometry estimated can be seen in the figure below:

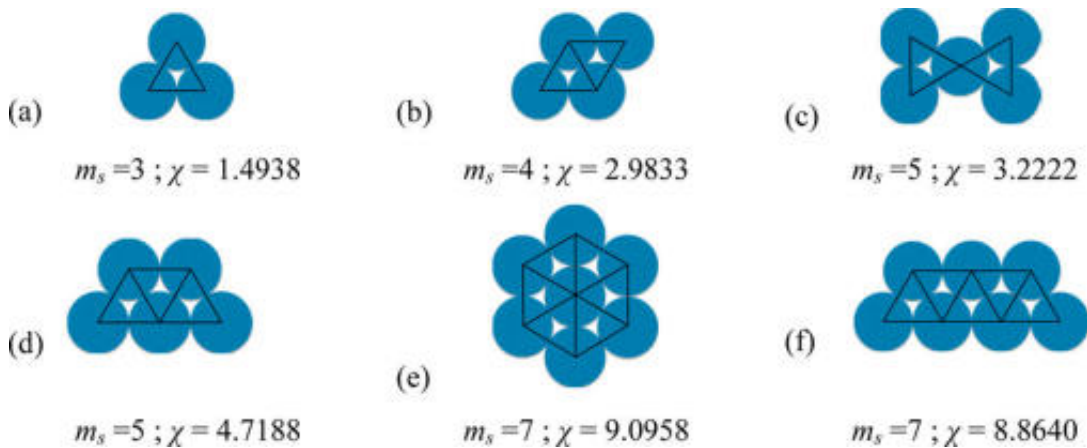


Figure 2.1.1 – Values for parameter χ according to the ring geometry (MÜLLER; MEJÍA, 2017)

2.1.5 Combining rules for the intermolecular potential parameters

Lafitte et al. (2013) also suggested mixing rules for the potential parameters based on Lorentz-Berthelot combining rules (ROWLINSON; SWINTON, 1982):

$$\sigma_{ij} = \frac{\sigma_{ii} + \sigma_{jj}}{2} \quad (2.14)$$

$$\lambda_{k,ij} - 3 = \sqrt{(\lambda_{k,ii} - 3)(\lambda_{k,jj} - 3)}, k = r, a \quad (2.15)$$

$$\epsilon_{ij} = (1 - k_{ij}) \frac{\sqrt{\sigma_{ii}^3 \sigma_{jj}^3}}{\sigma_{ij}^3} \sqrt{\epsilon_{ii} \epsilon_{jj}} \quad (2.16)$$

The k_{ij} is a binary interaction parameter to correct the deviations of the Lorentz-Berthelot rule for chemically distinct compounds. This parameter can also be fitted to experimental data or pseudo experimental data.

2.2 Parameter Estimation for the SAFT- γ Mie Force Field

The SAFT- γ Mie is a force field that uses a coarse graining top down methodology in its parameterization. This methodology aims to obtain the intermolecular parameters from macroscopic experimental data like fluid-phase equilibrium or superficial tension data. The idea is that the force field's parameters estimated with the equation of state can be used on molecular simulations since both the SAFT-VR Mie EoS and the force field use the same explicit intermolecular potential model (Mie potential). This correspondence between models has already been seen for a variety of fluids in which this force field was parameterized and this success in the representation of the properties of real fluids can be imputed to the degrees of freedom of Mie Potential (HERDES; TOTTON; MÜLLER, 2015). This flexibility also provides an exploration of a very large parameter space without using a iterative simulation scheme (AVENDAÑO et al., 2011).

Each substance has initially five parameters to be estimated ($m_s, \sigma, \epsilon, \lambda_r$ and λ_a) according to Eq. (2.1). The number of segments are usually fixed in an integer value so it can be used in the coarse grained simulations. The attractive parameter can also be fixed since there is a high correlation between the attractive and repulsive parameter. Usually, the parameter is fixed in the London value of 6, which is expected to be a good representation of the dispersion scale of most simple fluids that don't have strong polar interactions (RAMRATTAN et al., 2015; HERDES; TOTTON; MÜLLER, 2015). There are two strategies to obtain the parameters of each substance: one is by fitting the Saft-Vr Mie EoS to experimental data as vapor pressure and liquid density and the

other is using correspondent state parametrization. The first one, generally, minimizes the following unweighted least-squares objective function:

$$\min_{\sigma, \epsilon, \lambda_r} F_{obj}(\sigma, \epsilon, \lambda_r) = \sum_{i=1}^{N_p} \left(\frac{P_v^{SAFT}(T_i, \sigma, \epsilon, \lambda_r) - P_v^{exp}(T_i)}{P_v^{exp}(T_i)} \right)^2 + \sum_{i=1}^{N_p} \left(\frac{\rho_l^{SAFT}(T_i, \sigma, \epsilon, \lambda_r) - \rho_l^{exp}(T_i)}{\rho_l^{exp}(T_i)} \right)^2 \quad (2.17)$$

where N_p is the number of experimental points, P_v is the vapor pressure and ρ_l is the saturated liquid density. The minimized properties can also change and other possible properties as superficial tension and speed of sound can also be taken into account. These multiple parameters make it necessary the use of a wide range of experimental data since multiple solutions can be found for the fit. So one need to be careful in deciding the level of coarse graining (i.e. the parameter m_s) and subsequent parameter space that will not result in some physical inconsistencies like a fluid with premature freezing.

Lafitte et al. (2012) suggested that the two corrections factors (c_σ and c_ϵ) should be estimated with simulation data when using Eq. (2.12) for the ring contribution. They are related to the EoS parameters by scaled parameters:

$$\sigma^{scaled} = c_\sigma \sigma^{SAFT} \quad (2.18)$$

$$\epsilon^{scaled} = c_\epsilon \epsilon^{SAFT} \quad (2.19)$$

According to Lafitte et al. (2012), these corrections are necessary because the approximations employed in the EoS theory generate discrepancies between molecular simulations and the EoS results for ring molecules modeled with Eq. (2.12). The objective function for this second estimation is given by:

$$\min_{c_\sigma, c_\epsilon} F_{obj}(c_\sigma, c_\epsilon) = \sum_{i=1}^{N_p} \left(\frac{P_v^{sim}(T_i, \sigma^{SAFT}, \epsilon^{SAFT}) - P_v^{SAFT}(T_i, \sigma^{scaled}, \epsilon^{scaled})}{P_v^{sim}(T_i, \sigma^{SAFT}, \epsilon^{SAFT})} \right)^2 + \sum_{i=1}^{N_p} \left(\frac{\rho_{liq}^{sim}(T_i, \sigma^{SAFT}, \epsilon^{SAFT}) - \rho_{liq}^{SAFT}(T_i, \sigma^{scaled}, \epsilon^{scaled})}{\rho_{liq}^{sim}(T_i, \sigma^{SAFT}, \epsilon^{SAFT})} \right)^2 \quad (2.20)$$

The repulsive parameter is maintained in the value found on the minimization of Eq. (2.17), so the refined values for the force field are:

$$\sigma^{sim} = \sigma^{SAFT} / c_\sigma \quad (2.21)$$

$$\epsilon^{scaled} = \epsilon^{SAFT} / c_\epsilon \quad (2.22)$$

It is interesting to point out that this new parametrization is not necessary when using Eq. (2.13) as the ring contribution. The other method to obtain the force field parameters is the correspondent state parametrization for the EoS SAFT-VR Mie (MEJÍA; HERDES; MÜLLER, 2014). This method considers that the unweighted volume average of the attractive contribution to the Mie intermolecular potential, a_1 , can be given a mean field approximation:

$$a_1 = 2\pi\rho\sigma^3\epsilon\alpha \quad (2.23)$$

The van der Waals constant, α , considering $\lambda_a = 6$ is related by the Mie exponents by:

$$\alpha = \frac{1}{\epsilon\sigma^3} \int_{\sigma}^{\infty} \phi(r)r^2 dr = \frac{\lambda_r}{3(\lambda_r - 3)} \left(\frac{\lambda_r}{6} \right)^{6/(\lambda_r - 6)} \quad (2.24)$$

The parametrization in this method starts by using the experimental acentric factor, ω , for each molecule with a fixed value of m_s to obtain the value of the repulsive exponent with the following Padé series:

$$\lambda_r = \frac{\sum_{i=0} a_i \omega^i}{1 + \sum_{i=1} b_i \omega^i} \quad (2.25)$$

a_i and b_i are dependent parameters of the number of segments and a table with its values is presented in the original paper (MEJÍA; HERDES; MÜLLER, 2014). Substituting λ_r into Eq. (2.24), the van der Waals constant can be found. The reduced critical potential T_c^* can also be related to α by a Padé series:

$$T_c^* = \frac{\sum_{i=0} c_i \alpha^i}{1 + \sum_{i=1} d_i \alpha^i} \quad (2.26)$$

The values of c_i and d_i are also available in the original paper. The reduced temperature of the equation above is used in conjunction with the experimental critical temperature, T_c , to find the energy parameter with the relation below:

$$T_c^* = \frac{\kappa_b T_c}{\epsilon} \quad (2.27)$$

The diameter parameter, however, is not obtained with the critical properties, but with the reduced liquid density, $\rho_{T_r=0.7}$, at the reduced temperature, T_r , of 0.7. This

density is also obtained with a Padé series using parameters obtained by [Mejía, Herdes e Müller \(2014\)](#):

$$\rho_{T_r=0.7}^* = \frac{\sum_{i=0} j_i \alpha^i}{1 + \sum_{i=1} k_i \alpha^i} \quad (2.28)$$

The relation among the equation above, σ and the experimental density is given by:

$$\rho_{T_r=0.7}^* = \rho_{T_r=0.7} \sigma^3 N_{av} \quad (2.29)$$

where N_{av} is The Avogadro number. This correspondent state method has the advantage of only requiring critical data, that it is available for a great range of fluids, and one liquid density point. In addition to that, there is an available online parameter database obtained with this strategy ([ERVIK; MEJÍA; MÜLLER, 2016](#)).

The binary interaction parameter k_{ij} of Eq. (2.16) is necessary to adjust the mixture behaviour of chemically distinct components. Normally, it is fitted to experimental binary vapor liquid equilibrium or superficial tension data with the SAFT-VR Mie EoS ([MÜLLER; MEJÍA, 2017](#); [LOBANOVA et al., 2016](#)). However, [Ervik et al. \(2016\)](#) used molecular simulation results to fit the parameter to the superficial tension data of the mixture water-toluene. The strategy followed by them was to do simulations in three values of k_{ij} and then refine the parameter value until a value in good agreement with the experimental data was found.

Bibliography

ADAM, L.; MACIEJ, B.; CEZARY, C.; EWA, G.; YI, H.; DAWID, J.; PAWEL, K.; MACIEJ, M.; MARIUSZ, M.; A, M. M.; ANDREI, N.; STANISLAW, O.; A, S. H.; K, S. A.; RAFAL, S.; TOMASZ, W.; YANPING, Y.; BARTLOMIEJ, Z. A unified coarse-grained model of biological macromolecules based on mean-field multipole-multipole interactions. *Journal of molecular modeling*, v. 20, p. 2306, 2014.

AIMOLI, C. G.; MAGINN, E. J.; ABREU, C. R. Force field comparison and thermodynamic property calculation of supercritical CO_2 and CH_4 using molecular dynamics simulations. *Fluid Phase Equilib.*, v. 368, p. 80–90, 2014.

AIMOLI, C. G.; MAGINN, E. J.; ABREU, C. R. Transport properties of carbon dioxide and methane from molecular dynamics simulations. *THE JOURNAL OF CHEMICAL PHYSICS*, v. 141, p. 134101, 2014.

ASSOCIAÇÃO BRASILEIRA DE NORMAS TÉCNICAS. NBR 6028: Resumo - apresentação. Rio de Janeiro, 2003. 2 p.

ASSOCIAÇÃO BRASILEIRA DE NORMAS TÉCNICAS. NBR 14724: Informação e documentação — trabalhos acadêmicos — apresentação. Rio de Janeiro, 2005. 9 p.

ASSOCIAÇÃO BRASILEIRA DE NORMAS TÉCNICAS. NBR 14724: Informação e documentação — trabalhos acadêmicos — apresentação. Rio de Janeiro, 2011. 15 p. Substitui a Ref. [ABNT \(2005\)](#).

AVENDAÑO, C.; LAFITTE, T.; GALINDO, A.; ADJIMAN, C. S.; JACKSON, G.; MULLER, E. A. Saft- γ force field for the simulation of molecular fluids.1. a single-site coarse grained model of carbon dioxide. *The Journal of Physical Chemistry B*, v. 115, p. 11154–11169, 2011.

BARDUCCI, A.; BONOMI, M.; DERREUMAUX, P. Assessing the quality of the opep coarse-grained force field. *Journal of Chemical Theory and Computation*, v. 7, p. 1928– 1934, 2011.

BARKER, J. A.; HENDERSON, D. What is "liquid"? understanding the states of matter. *Review of Modern Physics*, v. 48, p. 587–671, 1976.

BASDEVANT, N.; BORGIS, D.; HA-DUONG, T. Modeling protein-protein recognition in solution using the coarse-grained force field scorpion. *Journal of Chemical Theory and Computation*, v. 9, p. 803–813, 2013.

BEREAU, T.; BACHMANN, M.; DESERNO, M. Interplay between secondary and tertiary structure formation in protein folding cooperativity. *Journal of the American Chemical Society*, v. 132, p. 13129– 13131, 2010.

BEREAU, T.; DESERNO, M. Generic coarse-grained model for protein folding and aggregation. *Journal of Chemical Physics*, v. 130, p. 235106, 2009.

BHARGAVA, B.; KLEIN, M. L. Formation of micelles in aqueous solutions of a room temperature ionic liquid: a study using coarse grained molecular dynamics. *Molecular Simulation*, v. 107, p. 393–401, 2009.

CHEBARO, Y.; DONG, X.; LAGHAEI, R.; DERREUMAUX, P.; MOUSSEAU, N. Pep-fold: an online resource for de novo peptide structure prediction. *Nucleic Acids Research*, v. 37, p. 498–503, 2009.

CHEBARO, Y.; DONG, X.; LAGHAEI, R.; DERREUMAUX, P.; MOUSSEAU, N. Replica exchange molecular dynamics simulations of coarse-grained proteins in implicit solvent. *Journal of Physical Chemistry B*, v. 113, p. 267–274, 2009.

CHIU, S.; SCOTT, H.; JAKOBSSON, E. A coarse-grained model based on morse potential for water and n-alkanes. *Journal of Chemical Theory and Computation*, v. 6, p. 851–863, 2010.

ERVIK, A.; LYSGAARD, M. O.; HERDES, C.; JIMÉNEZ-SERRATOS, G.; MÜLLER, E. A.; MUNKEJORD, S. T.; MÜLLER, B. A multiscale method for simulating fluid interfaces covered with large molecules such as asphaltenes. *Journal of Computational Physics*, v. 327, p. 576–611, 2016.

ERVIK, A.; MEJÍA, A.; MÜLLER, E. A. Bottled saft: A web app providing saft- γ mie force field parameters for thousands of molecular fluids. *Journal of Chemical Information and Modeling*, v. 56, p. 1609–1614, 2016.

HADLEY, K. R.; MCCABE, C. Coarse-grained molecular models of water: a review. *Molecular Simulation*, v. 38, p. 671–681, 2012.

HE, X.; SHINODA, W.; DEVANE, R.; KLEIN, M. L. Exploring the utility of coarse-grained water models for computational studies of interfacial systems. *Molecular Simulation*, v. 108, p. 2007–2020, 2010.

HERDES, C.; ERVIK, A.; MEJÍA, A.; MÜLLER, E. A. Prediction of the water/oil interfacial tension from molecular simulations using the coarse-grained saft- γ mie force field. *Fluid Phase Equilib.*, 2017.

HERDES, C.; TOTTON, T. S.; MÜLLER, E. A. Coarse grained force field for the molecular simulation of natural gases and condensates. *Fluid Phase Equilibria*, v. 406, p. 91–100, 2015.

KOGA, N.; TAKADA, S. Roles of native topology and chain-length scaling in protein folding: a simulation study with a go-like model. *Journal of Molecular Biology*, v. 331, p. 171–180, 2001.

LAFITTE, T.; APOSTOLAKOU, A.; AVENDANO, C.; GALINDO, A.; ADJIMAN, C. S.; MULLER, E. A.; JACKSON, G. Accurate statistical associating fluid theory for chain molecules formed from mie segments. *The Journal of Chemical Physics*, v. 139, p. 154504, 2013.

LAFITTE, T.; AVENDAÑO, C.; PAPAIOANNOU, V.; GALINDO, A.; ADJIMAN, C. S.; JACKSON, G.; MÜLLER, E. A. Saft- γ force field for the simulation of molecular fluids: 3. coarse-grained models of benzene and hetero-group models of n-decylbenzene. *Molecular Physics*, v. 110, p. 1189–1203, 2012.

LARS, V.; PERIOLE, X.; TIELEMAN, D. P.; MARRINK, S. J. Improved parameters for the martini coarse-grained protein force field. *Journal of Chemical Theory and Computation*, v. 9, p. 687–697, 2013.

LEVITT, M. A simplified representation of protein conformations for rapid simulation of protein folding. *Journal of Molecular Biology*, v. 104, p. 59–107, 1976.

LEVITT, M.; WARSHE, A. Computer-simulation of protein folding. *Nature*, v. 253, p. 694–698, 1975.

LOBANOVA, O.; AVENDAÑO, C.; LAFITTE, T.; MÜLLER, E. A.; JACKSON, G. Saft- γ force field for the simulation of molecular fluids: 4. a single-site coarse-grained model of water applicable over a wide temperature range. *Mol. Phys.*, v. 113, p. 1228–1249, 2015.

LOBANOVA, O.; MEJÍA, A.; JACKSON, G.; MÜLLER, E. A. Saft- γ force field for the simulation of molecular fluids 6: Binary and ternary mixtures comprising water, carbon dioxide, and n-alkanes. *The Journal of Chemical Thermodynamics*, v. 93, p. 320–336, 2016.

MARRINK, S. J.; RISSELADA, H. J.; YEFIMOV, S.; TIELEMAN, D. P.; VRIES, A. H. de. The martini force field: Coarse grained model for biomolecular simulations. *Journal of Physical Chemistry B*, v. 111, p. 7812–7824, 2007.

MARRINK, S. J.; TIELEMAN, D. P. Perspective on the martini model. *Chemical Society Reviews*, v. 42, p. 6801–6822, 2013.

MEJÍA, A.; HERDES, C.; MÜLLER, E. A. Force fields for coarse-grained molecular simulations from a corresponding states correlation. *Industrial and Chemical Engineering Research*, v. 53, p. 4131–4141, 2014.

MÜLLER, E. A.; GUBBINS, K. E. Simulation of hard triatomic and tetratomic molecules. a test of associating fluid theory. *Molecular Physics*, v. 80, p. 957–976, 1993.

MÜLLER, E. A.; MEJÍA, A. Extension of the saft-vr mie eos to model homonuclear rings and its parametrization based on the principle of corresponding states. *Langmuir*, -, p. A–L, 2017.

PANTANO, D.; KLEIN, M. L. Characterization of membrane-protein interactions for the leucine transporter from aquifex aeolicus by molecular dynamics calculations. *Journal of Physical Chemistry B*, v. 113, p. 13715–13722, 2009.

PAPAIIOANNOU, V.; LAFITTE, T.; AVENDAÑO, C.; ADJIMAN, C. S.; JACKSON, G.; MÜLLER, E. A.; GALINDO, A. Group contribution methodology based on the statistical associating fluid theory for heteronuclear molecules formed from mie segments. *The Journal of Chemical Physics*, v. 140, p. 054107, 2014.

RAMRATTAN, N.; AVENDAÑO, C.; MÜLLER, E.; GALINDO, A. A corresponding-states framework for the description of the mie family of intermolecular potentials. *Molecular Physics*, v. 113, p. 1–16, 2015.

ROWLINSON, J. S.; SWINTON, F. L. *Liquid and Liquid Mixtures*. 3. ed. London: Butterworth Scientific, 1982.

SHINODA, W.; DEVANE, R.; KLEIN, M. L. Multi-property fitting and parameterization of a coarse grained model for aqueous surfactants. *Molecular Simulation*, v. 33, p. 27–36, 2007.

SHINODA, W.; DEVANE, R.; KLEIN, M. L. Zwitterionic lipid assemblies: molecular dynamics studies of monolayers, bilayers, and vesicles using a new coarse grain force field. *Journal of Physical Chemistry B*, v. 114, p. 6836–6849, 2010.

STERPONE, F.; DERREUMAUX, P.; MELCHIONNA, S. Protein simulations in fluids: Coupling the opep coarse-grained force field with hydrodynamics. *Journal of Chemical Theory and Computation*, v. 11, p. 1843– 1853, 2015.

STERPONE, F.; MELCHIONNA, S.; TUFFERY, P.; PASQUALI, S.; MOUSSEAU, N.; CRAGNOLINI, T.; CHEBARO, Y.; ST-PIERRE, J.-F.; KALIMERI, M.; BARDUCCI, A.; LAURIN, Y.; TEK, A.; BAADEN, M.; NGUYEN, P. H.; DERREUMAUX, P. The opep protein model: from single molecules, amyloid formation, crowding and hydrodynamics to dna/rna systems. *Chemical Society Reviews*, v. 43, p. 4871– 4893, 2014.

WINGER, M.; TRZESNIAK, D.; BARON, R.; GUNSTEREN, W. van. On using a too large integration time step in molecular dynamics simulations of coarse-grained molecular models. *Physical Chemistry Chemical Physics*, v. 11, p. 1934, 2009.

Appendix

APPENDIX A – Quisque libero justo

Quisque facilisis auctor sapien. Pellentesque gravida hendrerit lectus. Mauris rutrum sodales sapien. Fusce hendrerit sem vel lorem. Integer pellentesque massa vel augue. Integer elit tortor, feugiat quis, sagittis et, ornare non, lacus. Vestibulum posuere pellentesque eros. Quisque venenatis ipsum dictum nulla. Aliquam quis quam non metus eleifend interdum. Nam eget sapien ac mauris malesuada adipiscing. Etiam eleifend neque sed quam. Nulla facilisi. Proin a ligula. Sed id dui eu nibh egestas tincidunt. Suspendisse arcu.

APPENDIX B – Nullam elementum urna vel imperdiet sodales elit ipsum pharetra ligula ac pretium ante justo a nulla curabitur tristique arcu eu metus

Nunc velit. Nullam elit sapien, eleifend eu, commodo nec, semper sit amet, elit. Nulla lectus risus, condimentum ut, laoreet eget, viverra nec, odio. Proin lobortis. Curabitur dictum arcu vel wisi. Cras id nulla venenatis tortor congue ultrices. Pellentesque eget pede. Sed eleifend sagittis elit. Nam sed tellus sit amet lectus ullamcorper tristique. Mauris enim sem, tristique eu, accumsan at, scelerisque vulputate, neque. Quisque lacus. Donec et ipsum sit amet elit nonummy aliquet. Sed viverra nisl at sem. Nam diam. Mauris ut dolor. Curabitur ornare tortor cursus velit.

Morbi tincidunt posuere arcu. Cras venenatis est vitae dolor. Vivamus scelerisque semper mi. Donec ipsum arcu, consequat scelerisque, viverra id, dictum at, metus. Lorem ipsum dolor sit amet, consectetur adipiscing elit. Ut pede sem, tempus ut, porttitor bibendum, molestie eu, elit. Suspendisse potenti. Sed id lectus sit amet purus faucibus vehicula. Praesent sed sem non dui pharetra interdum. Nam viverra ultrices magna.

Aenean laoreet aliquam orci. Nunc interdum elementum urna. Quisque erat. Nullam tempor neque. Maecenas velit nibh, scelerisque a, consequat ut, viverra in, enim. Duis magna. Donec odio neque, tristique et, tincidunt eu, rhoncus ac, nunc. Mauris malesuada malesuada elit. Etiam lacus mauris, pretium vel, blandit in, ultricies id, libero. Phasellus bibendum erat ut diam. In congue imperdiet lectus.

Annex

ANNEX A – Morbi ultrices rutrum lorem.

Sed mattis, erat sit amet gravida malesuada, elit augue egestas diam, tempus scelerisque nunc nisl vitae libero. Sed consequat feugiat massa. Nunc porta, eros in eleifend varius, erat leo rutrum dui, non convallis lectus orci ut nibh. Sed lorem massa, nonummy quis, egestas id, condimentum at, nisl. Maecenas at nibh. Aliquam et augue at nunc pellentesque ullamcorper. Duis nisl nibh, laoreet suscipit, convallis ut, rutrum id, enim. Phasellus odio. Nulla nulla elit, molestie non, scelerisque at, vestibulum eu, nulla. Ut odio nisl, facilisis id, mollis et, scelerisque nec, enim. Aenean sem leo, pellentesque sit amet, scelerisque sit amet, vehicula pellentesque, sapien.

ANNEX B – Cras non urna sed feugiat cum sociis natoque penatibus et magnis dis parturient montes nascetur ridiculus mus

Sed consequat tellus et tortor. Ut tempor laoreet quam. Nullam id wisi a libero tristique semper. Nullam nisl massa, rutrum ut, egestas semper, mollis id, leo. Nulla ac massa eu risus blandit mattis. Mauris ut nunc. In hac habitasse platea dictumst. Aliquam eget tortor. Quisque dapibus pede in erat. Nunc enim. In dui nulla, commodo at, consectetur nec, malesuada nec, elit. Aliquam ornare tellus eu urna. Sed nec metus. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas.

ANNEX C – Fusce facilisis lacinia dui

Phasellus id magna. Duis malesuada interdum arcu. Integer metus. Morbi pulvinar pellentesque mi. Suspendisse sed est eu magna molestie egestas. Quisque mi lorem, pulvinar eget, egestas quis, luctus at, ante. Proin auctor vehicula purus. Fusce ac nisl aliquam ante hendrerit pellentesque. Class aptent taciti sociosqu ad litora torquent per conubia nostra, per inceptos hymenaeos. Morbi wisi. Etiam arcu mauris, facilisis sed, eleifend non, nonummy ut, pede. Cras ut lacus tempor metus mollis placerat. Vivamus eu tortor vel metus interdum malesuada.