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Dear Prof. Lipson:

Thank you for finding three excellent reviewers for our manuscript "Coarse-grained Molecular Dynamics Simulation of Polyethylene Terephthalate (PET)". All three reviewers made numerous suggestions that have improved the quality and readability of our manuscript. These suggestions have now been addressed in the revised manuscript.

Below, we provide our itemized response to the reviewers' comments. The reviewers' comments are written in italics, and our responses are written in normal font. We have noted the page numbers where we have made the corrections and additions to the manuscript.

In conclusion, we believe that we have adequately addressed the reviewers' comments and concerns, and are resubmitting a revised manuscript that is suitable for publication in *Macromolecules*.

Sincerely,

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Itemized Response to Reviewers

Reviewers comments are italicized. Our responses are in normal font. Page numbers indicating the locations of changes correspond to the revised manuscript.

Reviewer (1)

The authors present a coarse grained model for PET obtained using distribution functions from atomistic simulations together with an integral equation approach to obtain the CG nonbonded interactions. The approach seems interesting and the work leads to new simulation data for dynamics of PET melts.

I cannot assess the quality of the integral equation approach – here the editor will have to rely on an alternative reviewer.

Comments/questions:

1) Line 10: "though" should read "through"

Correction made.

2) Page 2, line 43: "by Hossein and Florian" should be removed (these are the first names of the authors in reference 12)

Correction made.

3) Page 2, line 48: "resources, it beyond" should read "resources, it is beyond"

Correction made.

4) Page 3, line 41: The authors mention two methods to obtain nonbonded CG potentials. Here, the authors should include a recently published single-chain coarse graining method by Fritz et al. (Macromolecules (2009) 42, 7579-7588). In this method, the effective pair potential, which describes the interaction between two CG super-atoms, is obtained by calculating the free energy expended to introduce atomistic interactions between all atoms contained by the two CG super-atoms as a function of their center of mass separation distance. This effective pair potential is obtained from atomistic simulations of two oligomers in vacuum which are computationally very cheap. The resulting model provides the melt density and structure (pair correlation functions) as model predictions (unlike iterative Boltzmann inversion and the method reported by the authors of the present work).

We thank the reviewer for pointing this reference out. Obviously, we miss this recently published paper. To make the review of methods comprehensive, we add the following paragraph on page 4.

"Alternative methods are being developed recently to improve computational accuracy and efficiency of the CG procedure. Fritz *et al.*[24] recently present a new approach that obtains both the bonded and nonbonded interactions of the CG model of PS from the sampling of isolated atomistic chains and pairs of oligomers in vacuum. The method is computationally inexpensive. The CG model of PS using the calculated CG potentials reproduces the melt packing, the density and local chain conformations of atactic as well as stereoregular PS."

5) Page 4, line 23: "On the other hand, it is simple and fast compared to the current methods of comparable accuracy". The same holds for the single-chain coarse graining method mentioned in my previous point.

We address this comment by adding one paragraph on page 4, see last comment.

6) The time scaling factors are quite small. The authors should point out that this is due to the choice of their "atomistic" model, which, in fact, already is an intermediately coarse grained united atom model. In this context the authors should also discuss how the dynamic properties obtained with the "atomistic" model compare to what is known experimentally. Very often, united atom models explore conformation space faster in comparison to all-atom models, hence the speed up factors would have been significantly larger if the CG model had been parameterized based on an all-atom polymer model (see Ref 18).

We agree with the reviewer on this point. Our atomistic model is actually a united-atom model in that the hydrogen atoms bound to the carbon are not explicitly considered. Were these hydrogen atoms explicitly considered, the atomistic simulations would take longer and the speed-up factors would be greater.

We add a sentence on page 8.
"Note here that in our atomistic simulations, a united-atom model was used for hydrogen bound to carbon, already eliminating some degrees of freedom. The speed up factor would be larger if the hydrogens were explicitly accounted for in the atomistic simulation."

To discuss how the dynamic properties obtained with the "atomistic" model compare with what is known experimentally, we add a sentence on page 10.

"In the sections below, our discussion is largely confined to comparison between the atomistic MD and CGMD simulations, as well as comparison of the observed results with the Rouse and reptation theories. Comparison of the results of the atomistic simulations with experimental measurements, which was in general quantitative, is available elsewhere.[5]"

7) The authors do not discuss why they have chosen the particular CG mapping scheme shown in figure 1. Although they mention on p.11 that ideally all CG potentials are independent of each other, they do not show that this is indeed the case with their mapping scheme. To better understand the statistical interdependencies, the authors can e.g. plot a 2D-density map of torsion angles sampled by two adjacent torsions along the polymer backbone (see Fig 7 in the reference mentioned under point 4).

We chose the mapping scheme based on the following considerations: 1) reduction of degree of freedom for computational efficiency so that long time dynamic properties can be studied; 2) keeping sufficient structural detail to capture atomistic chain conformations.). We add the following sentences on page 6 to explain this.

"This mapping scheme contains a reduction in the number of degrees of freedom that enhances computational efficiency making the study of the dynamics of longer-chains tractable, while at the same time keeping sufficient structural details to reproduce the atomistic chain conformations. The validation of this choice of mapping scheme is given in the Results and Discussion section.”

Following the procedure established by Harmandaris, we sought to establish the independence of each bonded mode by reproducing the atomistic distribution functions with the CG potential. The stretching, bending, and torsion distributions match fairly well and validate the assumption of independence.

We agree that the assumption that all the interaction modes are independent of each other can also be studied in a way that is presented in Fritz *et al.*[24] work. As noted above, we were unaware of this recent work until it was mentioned in the review. Consequently, we did not record the necessary information required to generate a statistically reliable 2D density map of torsion angles. This is a good suggestion. We will keep it in mind for the CGMD simulation of other polymers now underway in our lab. We have added a note to the manuscript on page 12 regarding the approach of Fritz *et al.*

“We have validated the assumption of independence of the bonded modes through direct comparison of the distribution from the atomistic and CG simulations. Further understanding of the statistical interdependencies of different interaction modes could be achieved through additional analysis described in the literature.[13, 16, 30]”

8) To validate the CG model in terms of its accuracy in describing the chain structure at local level, the authors should consider presenting the mean square internal distances between CG beads as a function of the number of CG bonds (#bonds) that separate the beads along the chain. For small #bonds this quantity can be compared with the atomistic model. In their manuscript, the authors compare only the end-to-end distances as a limiting case.

We understand the reviewer’s concern on the local structure’s mapping since it can be used to judge whether the model is capable of reproducing atomistic level structure at all length scales. We show a direct comparison of the atomistic and CG results for the stretching distribution. This corresponds to beads separated by 1 bond. Similarly, we show the same comparison for bending and torsion, which correspond respectively to beads separated by 2 and 3 bonds. In the OZPY inverse procedure, we work strictly in terms of radial PDFs and the bending and stretching distributions are recorded in terms of separation, rather than bending or dihedral bond angles. These distributions are reported in terms of angles in the manuscript since that is the conventional approach. Finally, we also have a direct comparison of the end-to-end distance for the decamer, which has 20 bonds in it. Therefore, we have good reproduction of separation between beads for 1, 2, 3 ,and 20 bonds.

9) The authors systematically use the abbreviation PCF (Pair Correlation Function) for various types of distributions. This is very confusing and needs to be revised (“probability distribution function (PDF)” would be a better choice) because the relevant distribution functions go beyond pair correlations. A “bonded PCF” (p. 11), which involves angles or torsions, is determined by intramolecular correlations that are 3-body or 4-body. Related to this, equation (1) is confusing: it defines a potential based on the PCF (r) αβ ϕ *g (r) αβ , which one immediately associates with a radial distribution function. Since the variable r is a distance (between sites α and β), the potential must describe a nonbonded interaction or a coarse grained bond. Nonbonded interactions however cannot be obtained by application of eq (1) and are calculated by other means.*

The only difference between a pair correlation functions (PCF) and a probability distribution functions (PDF) is a normalization constant. PCFs for a simple fluid like argon implicitly capture 3-body effects. If this were not the case, then equation (1) could be used to generate non-bonded potentials. The purpose of the Ornstein-Zernike equation is to capture (at least to the Percus-Yevick approximation in this work) the effect of both the direct (2-body) and indirect (greater than 2-body) correlations.

Since it already generated confusions, we change all the bonded pair correlation functions (PCFs) in the manuscript to probability distribution function (PDFs). Also, following Harmandaris, we specifically explain how to make equation (1) applicable for bending and torsion modes. These changes appear on pages 6, 11 and 28.

10) Equation (2) should contain a logarithm in the second term on the rhs.

Correction made

11) The discussion on page 6 (in between eqns 1 and 2) is not very clear. The problem the authors try to address plays no role in the iterative Boltzmann inversion method. It also plays no role in the reversible work method of Fritz et al. (see point 4). Differences between "fragment molecules and target molecules" play no role in the application of Fritz's method to polystyrene, because the phenyl rings are not isolated, but part of an oligomer. Hence, the mutual ring orientations are consistent with the constraints induced by the backbone. The authors correctly point out that these differences ("fragment molecules and target molecules") may play a role in the work discussed in refs 15 and 20. The discussion at this point should however be revised in order to clarify for what the various methods do account and for what they do not account.

We have added the following paragraph on page 6.

"The calculated potentials cannot be used under ambient pressure condition or be applied to study the formation of ordered structures driven by enthalpic interactions.[30] Fritz *et al.*[30] recently developed a new method that addresses these drawbacks. The method derives nonbonded potentials from constraint dynamics with the all–atom model of two trimers (or tetramers) of PS in vacuum. In this way, the atomistic melt properties are not used in the parameterization while the potential can still be used in the condensed melt phase. To some extent, the multibody contributions to the effective potential are taken into account."

12) page 6, line 18: the term "interaction energy" should not be used when referring to a potential of mean force (which is the case here) or to an effective interaction potential in general. Since degrees of freedom are lost by systematic coarse graining, the final model does not (and should not) reproduce the energy.

We agreed that potential of mean force or an effective interaction potential instead of interaction energy should be used here. A corresponding correction is made on page 6. We agree that the CG model does not reproduce the correct energy due to the reduction of degree of freedom by systematic coarse graining. For this reason, we tried to use scaling factors to see whether we could scale the energy to obtain the energy in the atomistic simulation. The results are satisfactory (almost perfect for kinetic energy) and reliable for the potential energy contributions. This is a result of the systematic coarse-graining mapping.

13) Page 14. Scaling factors for potential energies are meaningless (see previous point). I disagree with the last sentence of section 3.1.

Scaling factors for potential energies are no more meaningless than scaling factors for self-diffusivities. Both serve a practical purpose in that they allow one to extract estimates of a property from the "atomistic" system from the CG system. These scaling factors have a practical utility. We have retained them.
We did modify the last sentence of section 3.1 on page 15 to read,

"These scaling factors for the energies allow one to compute thermodynamic properties, such as the internal energy, of the atomistic chain from the CGMD simulation."

*14) Page 15. Mean square displacement (MSD). To observe diffusion, the quantity MSD/6*t should reach a plateau value (the diffusion constant) in the limit 1/t → 0. A figure with MSD/6*t versus 1/t is more convincing than the double logarithmic plot in Fig 10. Figure 10 shows that the maximum displacement of the longer chains (DP=30-50) is significantly smaller than the average radius of gyration (Table 2). This is a concern, because it indicates that the time scales may not yet be sufficiently large to obtain an accurate diffusion constant.*

The reviewer's point is well taken. We too are concerned that we run our simulations long enough to obtain statistically reliable diffusivities. To our knowledge, there is only one criteria for the proper use of the Einstein relation to measure the self-diffusivity and that criterion is that the observation time reach the long-time limit. The way to determine that one has reached the long-time limit is to calculate the exponent relating the observation time to the mean square displacement. In the long time limit, this exponent is unity. We have been extraordinarily meticulous in making sure that our diffusivities satisfy the long-time limit. In Figure 10, we plot the MSD on a log-log axis and report in the legend the exponent, which is either 1.00 or 1.01 for all chains. Therefore, we have strong confidence in these diffusivities despite the relatively short distances traveled. The existence of a second "longer-time" regime that takes place after the Einstein long-time regime has been reached would necessitate the existence of a different diffusional mechanism. To our knowledge, there is no mechanism to support this additional mechanism. We do however accept the reviewers point that the statistical accuracy of the estimate diminishes as the chain length increases due to the fact that we have not been able to simulate for as many relaxation times with the long chains as we did with the short chains. This is already reflected in the uncertainties reported in Table 1 where the standard deviation is 19% for DP=10 and 40% for DP=50. We have added a note to this effect on page 16,

"We acknowledge that it is likely that the statistical accuracy of the estimate diminishes as the chain length increases due to the fact that we have not been able to simulate for as many relaxation times with the long chains as we did with the short chains. This is reflected in the uncertainties reported in Table 1 where the standard deviation is 19% for DP=10 and 40% for DP=50."

15) In the figure captions (p.28), the captions of Figures 5 and 6 are reversed.

Correction made

Reviewer (2)

This paper presents a coarse-grained model for PET, using a new method to obtain the nonbonded coarse-grained potentials. This method does not require iteration and may provide more precise potential functions. The coarse-grained force field is using to study various molecular weights, and the scaling exponents for end-to-end distance, radius of gyration and self-diffusivity are reported. An entanglement analysis is also provided.

The paper is interesting, relevant and well written. I recommend that it be accepted in its current form. The comments below are either trivial or up to the authors to implement.

1. on page 3, the authors list polymers for which coarse-grained models are available. I've also seen models for polyethylene, polyethylene oxide, and polyisoprene, if the authors wish to have a complete listing.

We add additional references to include these models.

2. The A beads in Figure 1 are very dark [un-seeable, really] when the paper is printed in black and white.

We thank the reviewer for pointing this problem out. We intend to have color figures in the paper to avoid this problem.

3. Top of page 11, Figure 3 is referred to when I think the authors meant Figure 4.

Correction made

4. The AA, AB, BB pair distribution functions look almost identical whereas the CG potentials for AA, AB and BB are quite different. This must result due to differing influence of "more than pairwise" interactions. It may be interesting to explore this further.

In general, small changes in the PCF can correspond to huge changes in properties. Alternatively, large changes in the interaction potential correspond to rather modest (at least to the eye) changes in the PCF. This is, we think, how it should be.

5. I wonder if different scaling for various dynamic properties could be resolved by first scaling time [single scaling, perhaps using mean squared displacement] and then calculating the various dynamic properties using scaled time coordinates.

The origin of the time scaling factor is a subject of great interest.

We have added the following comment in response to this point on page 16 of the manuscript,

"At this point, we do not have a complete explanation for the discrepancy. The use of a time scaling constant has only an empirical basis. The different dynamic properties (relaxation time, diffusivity, viscosity) represent mechanisms of entropy generation. Because the entropy of the atomistic and coarse-grained models are different, it may well turn out that the use of a single time-scaling constant gives only a first order approximation of the diverse effects of a more complicated issue."

Review #3

I liked the work presented in the paper by Wang and at. It is a honest and detailed discussion of a novel coarse-grained model for PET. The authors present a detailed study of the properties emerging from a coarse-grained simulation and compare them to the atomistic simulation. I believe this is a very valuable piece of information for two reasons: 1) the novelty of the system investigated (PET), 2) and the care in the presentation and the extended analysis of the data.

It is disappointing that the Rouse regime for diffusion disappears, however it looks like there is a broad transition to entangled dynamics, which covers the Rouse regime and bridges directly to the short chain scaling exponents. I find this information interesting.

We agree that the combination of the scaling exponents and the entanglement analysis indicate a broad transition.

The ballistic regime in the mean-square-displacement should be more extended with respect to the atomistic simulation, and maybe the authors could comment on that as well.

In this work, we have restricted our analysis of the MSDs to the linear regime, from which the the diffusivities can be extracted. We acknowledge that it is an interesting idea that had not occurred to us that the effects that result in the need for time-scaling may also be apparent in the transition from the ballistic regime to the linear regime. We are not prepared to comment on that at this time.

We also suggest a few other comments/changes. The work presented in references 27,28 does not use an "iterative procedure" as stated in page 4 end of first paragraph. Instead given the atomistic description, structural properties and interaction potential are output of the theory. The interaction potential is then used as an input to coarse-grained simulations directly, with no need of an iterative self-consistent procedure (see for example Yatsenko et al. PRL v.93, p.257803 (2004).)

We understand the methods used in reference 27 and 28. We listed reference 27, 28 as typical examples on using IE theory in CG procedure. When talking about "iterative procedure", we mean reference 29 only. We have cleaned this up so that there is no longer any confusion. We cite the work of Yatsenko *et al.* PRL v.93, p.257803 (2004) after reference 28 (reference 35 in the revised manuscript to make the review on current work comprehensive.

Because the analytical coarse-grained potential is available, a first-principle rescaling of the dynamics can be directly calculated as presented in Lyubimov et al. J. Chem. Phys. v.132, p. 2249031 (2010).

We thank the reviewer for bringing this paper to our attention. As we noted in our response to reviewer two, the origin of the time scaling behavior as a function of the resolution of the model is very interesting to us. We have cited this paper on page 3 of the revised manuscript. Perhaps this procedure can be used to explain the different scaling factors obtained for the diffusivity and the viscosity.

Summarizing, this is a very interesting a carefully done piece of research and the paper should be published in Macromolecules after minor corrections.