

## Article

# General-purpose coarse-grained toughened thermoset model for 44DDS/DGEBA/PES

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**Abstract:** The objective of this work is to predict the morphology and material properties of crosslinking polymers used in aerospace applications. We extend the open-source dybond plugin for HOOMD-Blue to implement a new coarse-grained model of reacting epoxy thermosets and use the 44DDS/DGEBA/PES system as a case study for calibration and validation. We parameterize the coarse-grained model from atomistic solubility data, calibrate reaction dynamics against experiments, and check for size-dependent artifacts. We validate model predictions by comparing glass transition temperatures measurements at arbitrary degree of cure, gel-points, and morphology predictions against experiments. We demonstrate for the first time in molecular simulations the cure-path dependence of toughened thermoset morphologies.

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**Keywords:** epoxy; coarse-grained; glass transition; molecular dynamics

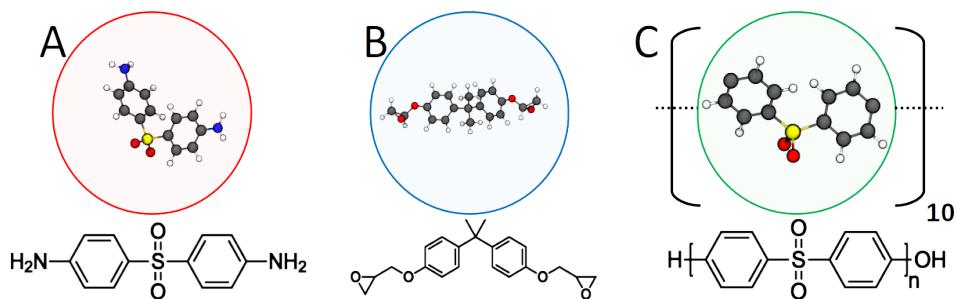
## 1. Introduction

Lightweight composites are increasingly used as alternatives to metal components of aircraft, especially over the last decades. Initially reserved for the most demanding aerospace applications, such as fighter aircraft, composite components are now prevalent in commercial aircraft, including 50% of the weight of the Boeing 787 [1]. This proliferation is enabled by improvements in composite formulations and processing, yet there exist significant opportunities to improve the reliable manufacturing of composite aerospace parts. Specifically, control of the thermoset matrix nanostructure (*morphology*) during the curing is currently underdeveloped and improvements could drastically increase the reliability and reduce the time and energy costs of part fabrication [2–4]. The challenge lies in understanding how morphology depends on the conditions experienced by the part during curing, and which morphologies have sufficient material properties for specific applications. Improved ability to predict properties from morphologies and morphologies from processing will enable:

1. Predicting how deviations from process specifications impact performance.
2. Composite formulations optimized for manufacturing requirements.
3. Temperature schedules (termed *cure profiles*) optimized for speed and reproducibility.

Embedding fibers in a matrix of polymers serves to support the fibers and transfers loads between them, providing the attractive bulk mechanical properties of fiber-based composites. The main chemical components of a thermoset are an epoxy species, an amine species, and sometimes a toughening agent.

31 Here we focus on the epoxy bisphenol A diglycidyl ether (DGEBA), amine 4,4'-diaminodiphenyl  
32 Sulfone (44DDS) mixed with toughener Poly(oxy-1,4-phenylsulfonyl-1,4-phenyl) (PES), a toughened  
33 thermoset found in aerospace applications (Figure 1). Thermoset manufacturers recommended cure  
34 profiles for matrix formulations based on cure requirements of the crosslinked polymer. Recommended  
35 cure profiles are empirically determined and are not necessarily the most efficient paths to sufficiently  
36 cured parts.



**Figure 1.** Coarse-grained representations of 44DDS (A), DGEBA (B), and PES (C) repeat units. The amines (A) can bond to up to four epoxies (B), which can each bond to up to two amines. All toughener molecules are linear 10-mers of C.

37 Temperature deviations away from a desired cure profile increase the probability that the  
38 morphology and material properties of a part are compromised, and these parts must undergo material  
39 review to confirm whether this is the case. Material review involves the creation of a sample volume  
40 cured with the same temperature deviation as the original part, which then undergoes mechanical  
41 testing. Throwing away the deviant part and curing a new one usually costs less time and effort  
42 than replicating the deviation and validating the sample volume, which is wasteful in the cases of  
43 sufficiently strong deviants. Avoiding this waste would be possible if the sensitivity of mechanical  
44 properties to cure profile deviations were more fully understood.

Computer simulations are needed for making sense of cure profile sensitivity because the parameter space combinatorics prohibit experimental enumeration, compounded by the impracticality of obtaining atomic-level detail of each cured morphology. Formulating a thermoset includes choosing the chemistry and proportions of epoxy, crosslinker, toughener, and additives compounds, resulting in combinatorial explosion of candidate formulations. Further, each formulation can result in a wide range of morphologies that depend upon cure profile, the number of which adds another factor to the intractability of enumeration. Models for thermoset curing implemented in computer simulations provide a proxy for part fabrication that are faster and less expensive to perform, and can provide insight into how atomic-level structure evolves and impacts properties. Further, modern GPU hardware enables sensitivity analysis and optimizing cure profiles for desired morphologies because screenings of independent formulations and cure profiles can be performed in parallel.

Computationally predicting morphology requires models that faithfully capture the thermodynamics and kinetics of the crosslinking reaction between amine and epoxy molecules, and resulting phase separation of any tougheners present. Doing so is challenging because reactions dynamics occur at fast ( $1 \times 10^{-12}$  s) and small ( $1 \times 10^{-10}$  m) scales, while morphology evolution occurs at slow ( $1 \times 10^2$  s) and large ( $1 \times 10^{-6}$  m) scales. Accurately simulating the cross-linking of the epoxy and amine species is crucial when modeling these systems as the bonding network influences the properties of the thermoset [5,6], in particular the relationship between the glass transition temperature  $T_g$  and cure fraction  $\alpha$  described by the DiBenedetto equation [5,7–13]. Atomistic molecular dynamics (MD) simulations with temperature-independent bonding models have been successfully deployed to generate crosslinked nanostructures and glass transition temperatures  $T_g$ , but are limited to simulation volumes around ( $13 \text{ nm}^3$ ) [14–18]. The work of Li, Strachan, and coworkers [14,15] demonstrates atomistic simulations of DGEBA reacted with 44DDS, 33DDS, and other crosslinkers to predict mechanical properties including  $T_g$ , density, modulus, and expansion coefficients. In the case of

69  $T_g$  for 44DDS/DGEBA, the atomistic simulations performed overpredict  $T_{g,sim} = 525$  K compared  
 70 to DSC experiments  $T_{g,exp} = 450$  K at 92% cure, though no empirical fitting is performed and  
 71 cooling-rate-dependent corrections help explain the discrepancy [14,15]. Khare and Phelan investigate  
 72 similar, untoughened DGEBA (2-mers) and 44DDS and predict 489 K  $\leq T_{g,sim}(\alpha = 100\%) \leq 556$  K,  
 73 depending on cooling rate [18].

74 Coarse-grained approaches demonstrate the ability to access substantially larger simulation  
 75 volumes and time scales than atomistic approaches, and mapping atomistic degrees of freedom  
 76 into crosslinked networks enables calculation of material properties [19–22]. In both Refs. [20]  
 77 and [22], one-site dissipative particle dynamics (DPD) models are used to represent reacting monomers  
 78 of 44DDS/DGEBA and DGEBA/DETA, respectively. In both cases, experimentally reasonable  
 79  $T_g$  are calculated after backmapping, and the case is made for large system sizes for observing  
 80 toughener microstructure [20] and sufficient structural relaxation [22]. Langeloth *et al.* develop  
 81 a coarse-grained model of intermediate resolution to study toughened DGEBA/DETA and show  
 82 significant discrepancies in  $T_g(\alpha)_{CG} < T_g(\alpha)_{AA}$ . Earlier this year Pervaje *et al.* develop another  
 83 intermediate-resolution coarse-grained model of reacting thermosets parameterized by SAFT- $\gamma$  Mie  
 84 calculations, which includes temperature-dependent reactions and a novel bonding algorithm [23].  
 85 Applied to polyester-polyol resins,  $T_g$  predictions from the coarse model are in agreement with  
 86 experiments [23]. While the exact details and experimental validations depend on the thermoset  
 87 formulation and the force fields used, multiscale approaches that use coarse models to access long  
 88 times, large volumes, and high cure fractions  $0.9 < \alpha < 0.95$  and atomistic simulations for mechanical  
 89 property calculations have begun spanning the 12 orders of magnitude between reaction dynamics  
 90 and phase separation.

91 However, to predict how thermoset microstructure depends on cure profiles,  
 92 temperature-dependent reaction models are necessary. In our prior work developing *epoxy* [24], we  
 93 implemented such a reaction model with DPD coarse-grained simulations. Here, we extend *epoxy* and  
 94 focus on simulation workflows for parameterizing, validating, and exploring materials behaviors  
 95 of reacting thermosets with 44DDS/DGEBA toughened with PES as a case study. While prior  
 96 studies [14,15,18,20–23,25,26] have included or implemented (1) Reaction rates calibrated against  
 97 experimentally observed reaction models, (2) Microphase separation of toughener, or (3)  $T_g(\alpha)$   
 98 validated against experiments, this work is distinguished by the inclusion of all three simultaneously,  
 99 and crucially (4) We demonstrate for the first time structural sensitivity to cure profile.

## 100 2. Model

Spherical simulation elements (“beads”) are used to represent monomers of amine 44DDS (A),  
 epoxy DGEBA (B), and each repeat unit of PES (C) 10-mers (Figure 1). Non-bonded interactions are  
 modeled with the 12-6 Lennard-Jones (LJ) potential

$$V_{LJ}(r) = 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \quad r < r_{cut} \\ = 0 \quad \quad \quad r \geq r_{cut}$$

where the parameters  $\sigma$  represent “size” of simulation elements and  $\epsilon$  sets the magnitude of the  
 potential energy minimum between two simulation elements. Throughout this work  $\sigma$  is used as the  
 dimensionless length scale and  $\sigma_A = \sigma_B = \sigma_C = \sigma = 1$  nm. We note that the relatively hard-core repulsion  
 of the LJ potential prevents chain crossing that is commonplace in DPD simulations, with impacts on  
 network structure and  $T_g$  calculations. Energy scales  $\epsilon$  calculated from cohesive energy calculations  
 described in Section 4.1.1 and are summarized in Table 1. Interactions between dissimilar simulation  
 elements (“cross” interactions) are obtained using Lorentz-Berthelot (LB) mixing rules applied in prior  
 DGEBA studies [27–29], where

$$\epsilon_{AB} = \sqrt{\epsilon_A \epsilon_B} \quad (1)$$

and

$$\sigma_{AB} = \frac{\sigma_A + \sigma_B}{2}. \quad (2)$$

101 Harmonic potentials are used to model bond stretching between pairs of bonded simulations elements.  
 102 Harmonic angle potentials are used to model bending among triplets of bonded PES (type C) simulation  
 103 elements, but no angle potentials are used for epoxy-amine triplets. No dihedral or improper  
 104 constraints are implemented here.

**Table 1.** Interaction strengths ( $\varepsilon_{ij}$ ) determined by cohesive energy calculations.

	(A) 44DDS	(B) DGEBA	(C) PES
(A) 44DDS	0.9216	0.9600	0.9026
(B) DGEBA		1.0000	0.9402
(C) PES			0.8840

Bond formation between amine and epoxy simulation elements is modeled through the stochastic creation of harmonic bonds between A and B beads that are sufficiently close by an activated process with probability of bond formation

$$p = e^{-\frac{E_a Y}{k_B T}}, \quad (3)$$

105 where  $E_a$  is activation energy and bond-order factor  $Y = 1.0$  if the bond being proposed is the first  
 106 bond to form for either bead and  $Y = 1.2$  otherwise.

107 By design, the energy scale for modeling pairwise interactions is distinct from the energy scale for  
 108 modeling bond formation, which are both distinct from the energy scale for modeling vitrification.  
 109 This modeling choice facilitates the empirical bridging of timescales that is the focus of the present  
 110 work through exploitation of temperature-time superposition [6]. We report dimensionless simulation  
 111 temperatures  $T = \frac{k_B T^K}{\epsilon}$  throughout this work, where  $k_B$  is Boltzmann's constant,  $T^K$  is temperature in  
 112 Kelvin, and  $\epsilon$  is an energy unit for either pairwise interactions, bonding reactions, or vitrification. These  
 113 energy scales span about three orders of magnitude, with  $\epsilon_{pair} = \epsilon = 2.1 \times 10^{-22}$  J,  $\epsilon_{rxn} = 1.78 \times 10^{-19}$   
 114 J, and  $\epsilon_{vit} = 6.63 \times 10^{-21}$  J. The pairwise energy scale is derived from cohesive energy described in  
 115 Section 4.1.1, the reaction energy scale is set from experimental measurements of activation energy [30],  
 116 and the vitrification energy scale is set by equating the dimensionless  $T_g^{sim}(\alpha = 1)$  to an experimental  
 117 measurement of  $T_g^{exp}(\alpha = 1) = 480$  K [31].

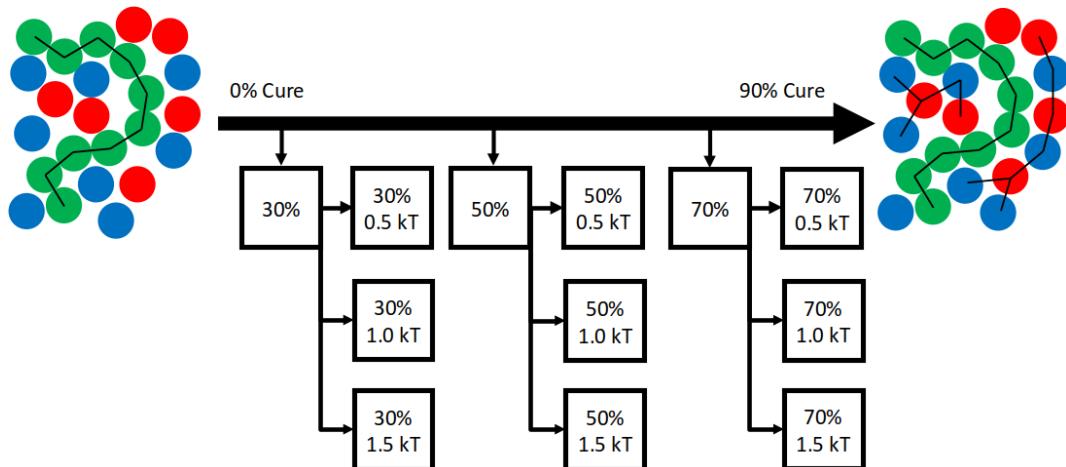
### 118 3. Methods

119 Simulations of curing epoxy thermosets (with and without toughener) are implemented with  
 120 the open source dynamic bonding plugin "dybond" [32] written for the HOOMD-blue [33] molecular  
 121 dynamics engine. Data storage, retrieval, and job submission is done with the signac [34,35] framework.  
 122 System initialization is performed with mBuild [36]. Plots are created using matplotlib [37] and all  
 123 scripts used for job submission and data analysis are available at this repository [38]. We use the  
 124 bonding algorithm as outlined in our previous work [24]. Briefly, every  $\tau_B$  molecular dynamics  
 125 steps we attempt to form  $n_B$  possible bonds where center-to-center distance between an epoxy and  
 126 amine simulation element is  $r \leq 1.0\sigma$  and with probability as in Eqn. 3. Here,  $n_B = 0.005n_T$ , where  
 127  $n_T$  is the total number of bonds that can be formed, equal to four times the number of A beads for  
 128 the stoichiometric mixtures of A and B. Simulation element positions and velocities are integrated  
 129 forward in time according to Langevin equations of motion with drag coefficient  $\gamma = 4.5$  and step size  
 130  $\delta t = 0.01$ . Random initial configurations are used for each independent simulation run. We calculate  
 131 the toughener (PES-PES, C-C) structure factor  $S(q)$  for simulation snapshots using the "diffract" utility  
 132 described in Ref. [39], enabling identification of any periodic domain features that could indicate  
 133 phase separation. Unless otherwise noted, simulation parameters summarized in Table 2 are used  
 134 throughout.

**Table 2.** Fiducial simulation parameters. Note that in the present CG model, monomer% and volume% are equivalent but are not identical to corresponding experimental fractions.

Parameter	Value
Bond equilibrium (A-B,C-C) ( $r_o$ )	$1.0 \sigma$
Bond force constant (A-B,C-C) ( $k$ )	$100 \frac{\epsilon_{pair}}{\sigma^2}$
Angle equilibrium (C-C-C) ( $\theta_0$ )	$109.5^\circ$
Angle force constant (C-C-C) ( $k_{angle}$ )	$25 \frac{\epsilon_{pair}}{\sigma^2}$
Non-bonded interaction cutoff $r_{cut}$	$2.5 \sigma$
Number density ( $\rho_n = N/V$ )	1.0
Activation Energy ( $E_A$ )	$3.0 \epsilon_{rxn}$
Bonding distance maximum	$1.0 \sigma$
Secondary bond weight (Y)	1.2
Enthalpy of Reaction ( $\Delta T_{rxn}$ )	0.0
Bond Period ( $\tau_B$ )	1.0
Maximum attempted bonds ( $n_b$ )	$0.005n_T$
Langevin drag ( $\gamma$ )	4.5
%monomers 44DDS:DGEBA:PES	20:40:40
Cure temperature ( $T$ )	3.0
Step size ( $\delta t$ )	0.01

135 Glass transition temperatures are calculated directly from coarse-grained simulation volumes as  
 136 described in section 4.3.3 of Ref. [40]. Briefly, snapshots of simulations that have reached a specified  
 137 degree of cure  $\alpha$  are used to initialize new simulations that are instantaneously quenched across a  
 138 range of temperatures to identify  $T_g$ , below which the self-diffusion coefficient  $\mathcal{D}$  vanishes (Figure 2).



**Figure 2.**  $T_g$  prediction workflow: Snapshots at specified  $\alpha$  are copied from a curing simulation to initialize instantaneous quenches across candidate low temperatures to identify where the self-diffusion coefficient  $\mathcal{D}$  vanishes.

Diffusion coefficients  $\mathcal{D} = \frac{d\text{MSD}}{6\delta t}$  are measured directly from quenched trajectories, where MSD is the mean-squared displacement averaged over “B” (DGEBA) simulation elements. We employ piecewise regression to identify the discontinuity in  $\mathcal{D}(T)$ . Calculations of  $T_g(\alpha)$  are validated against theory by measuring the R-squared fit of the DiBenedetto equation [41] modified by Pascault and Williams [13]

$$T_g(\alpha) = \frac{\lambda\alpha(T_{g1} - T_{g0})}{1 - \alpha(1 - \lambda)} + T_{g0}, \quad (4)$$

139 where  $\lambda$  is chemistry specific and represents the non-linear relationship between  $T_g$  and degree of cure  
 140 and varies from 0 to 1 [13],  $T_{g0}$  is the glass transition temperature at zero percent cure, and  $T_{g1}$  is the

141 glass transition temperature at one hundred percent cure ( $\alpha = 1$ ). We set  $\lambda = 0.5$  for its quality of fit  
 142 here, and note it is larger than  $\lambda$  from prior work on 44DDS/DGEBA (0.34 [42]—0.38 [43]).

## 143 4. Results

144 The 6064 independent MD simulations performed in this work fall into three categories:

- 145 1. Setup
- 146 2. Validation
- 147 3. Exploration

148 In total, approximately 15,000 GPU-hours of simulation time are performed over about three months.

149 Descriptions of analysis and simulation methods specific to each type of simulation are included in the  
 150 appropriate subsections that follow.

### 151 4.1. Setup simulations

152 We perform 33 all-atom simulations to determine coarse-grained forcefield parameters, 4480  
 153 coarse-grained simulations to calibrate reaction kinetics, and 1448 coarse-grained simulations check  
 154 for finite-size effects before performing validation and exploration studies.

#### 155 4.1.1. Forcefield parameterization

We perform 33 all-atom MD simulations to calculate cohesive energies  $e_{coh}$  of amine 44DDS (A),  
 epoxide DGEBA (B), and toughener PES (C) moieties to parameterize their non-bonded interactions of  
 their coarse-grained simulation elements  $\varepsilon_i$ . In liquids,  $e_{coh}$  represents the energy required to separate  
 molecules from the liquid state into isolated molecules in the vapor phase

$$e_{coh} = E_{bulk} - E_{isolated} \quad (5)$$

156 and is calculated from the difference in average molar potential energies  $E$  between bulk and isolated  
 157 molecules [24,44]. Cohesive energies have been used to estimate macroscopic miscibility [45] and  
 158 parameterize coarse LJ models [44] and we do the same in the present work. We use the OPLS-2005  
 159 force field and NPT simulations at  $P = 1$  atm, and simulate 11 temperatures equally spaced over  
 160  $T \in [273, 600]$  K. Each simulation volume is initialized with 500 molecules (monomers of DGEBA  
 161 and 44DDS, 10-mers of PES) at a density of 1 g/cm<sup>3</sup>. After equilibration, densities in agreement  
 162 with experiments of 0.8–1.14 g/cm<sup>3</sup> (DGEBA), 1.3–1.1 g/cm<sup>3</sup> (44DDS), and 1.3–1.2 g/cm<sup>3</sup> (PES) are  
 163 observed. Averaging over temperatures, we calculate  $e_{coh}$  for DGEBA, 44DDS and PES monomers  
 164 as 30.36 kcal/mol, 27.98 kcal/mol and 26.84 kcal/mol respectively. We de-dimensionlizes pairwise  
 165 interactions in the coarse-grained models by normalizing by the DGEBA cohesive energy, resulting in  
 166 the interaction potentials of Table 1.

#### 167 4.1.2. Reaction kinetics calibration

168 Two parameters are tuned to calibrate reaction kinetics: The maximum number of bonds attempted  
 169 per bonding step  $n_B$  and the number of time steps between bonding steps  $\tau_B$ . Reaction calibration  
 170 is important for two primary reasons: First, the higher the ratio of  $n_B/\tau_B$ , the faster simulations can  
 171 cure to higher  $\alpha$ , which saves time. Therefore, the largest  $n_B/\tau_B$  that replicates experimental reaction  
 172 dynamics optimizes computational throughput. Second, validating first-order reaction dynamics lays  
 173 the foundation for exploratory simulations with self-accelerated reactions. We perform 20 independent  
 174 coarse-grained simulations of 44DDS/DGEBA/PES at each of 224 combinations of  $(n_B, \tau_B, T)$  to  
 175 identify the combinations that best fit a first-order reaction model from experimental data [30]. Each  
 176 simulation has  $N = 50000$  (10000 A, 20000 B, and 2000 10-mer chains of C) coarse simulation elements  
 177 and is cured isothermally at  $T \in \{0.2, 0.5, 1.0, 2, 3, 4, 5, 6\}$ . Reaction parameters are sampled over the  
 178 sets  $n_B \in \{2.5 \times 10^{-5}, 5 \times 10^{-5}, 1 \times 10^{-4}, 1 \times 10^{-2}\} \times n_T$  (where  $n_T$  is the total number of bonds that can be

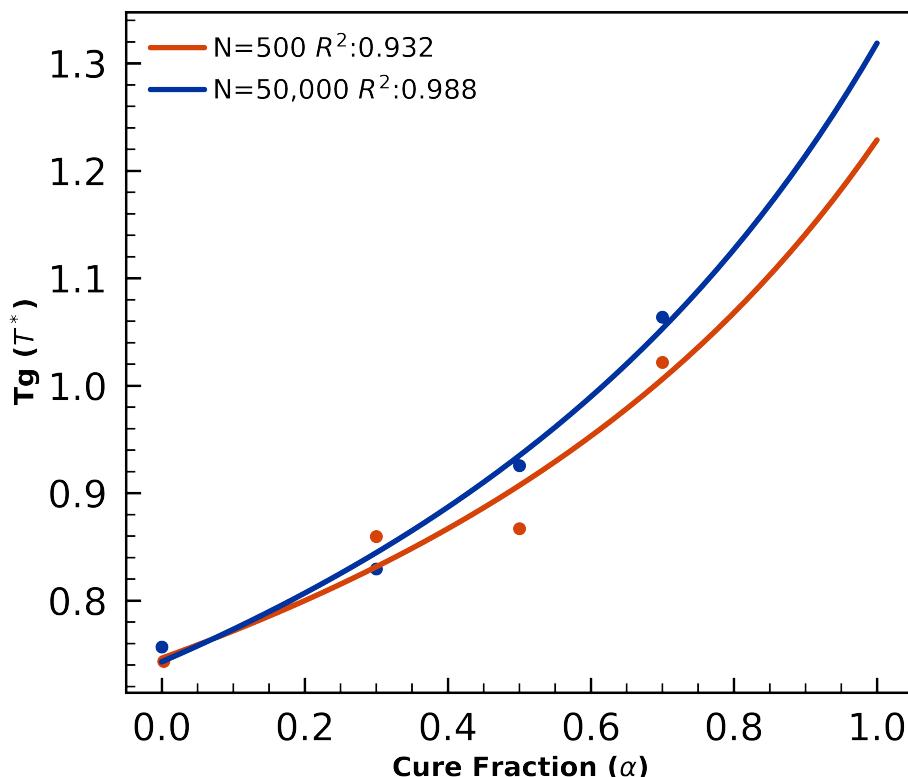
179 formed, 40,000 here) and  $\tau_B \in \{1, 2, 10, 20, 40, 80, 100\}$ . We find  $n_B = 2.5 \times 10^{-5} n_T = 1.0$  and  $\tau_B = 1.0$  here,  
 180 and use  $n_B = 2.5 \times 10^{-5} n_T$  for other system sizes.

181 4.1.3. Finite Size Effects

182 Here we investigate the effect of small system sizes on the prediction of glass transition  
 183 temperatures and morphology.

184 4.1.4. Glass Transition - small systems

185 We perform curing simulations and  $T_g(\alpha)$  calculations of small  $N = 500$  volumes and find  
 186 deviations relative to  $N = 50,000$  predictions of  $T_g(\alpha)$ . For each  $N = 500$  and  $N = 50,000$ ,  
 187 DGEBA/44DD/PES blends are cured isothermally at  $T = 3$ . Simulation snapshots at intervals  $\alpha \in$   
 188  $\{0, 0.3, 0.5, 0.7\}$  are used to initialize new trajectories that are quenched to  $T = \{0.05, 0.15, \dots, 2.95, 3.0\}$ .  
 189 Three independent quenches are performed for each of the 60 quench temperatures.  $T_g$  calculated  
 from the quenches and the DiBenedetto fits are presented in Figure 3. While the smaller systems



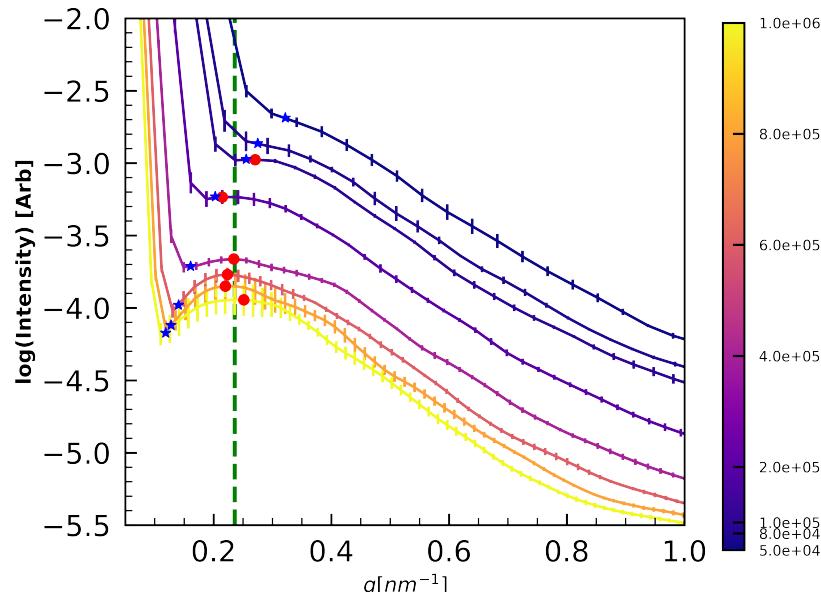
190  
 191 **Figure 3.**  $T_g(\alpha)$  calculations and DiBenedetto fits for  $N = 500$  (orange) and  $N = 50,000$  volumes of  
 192 coarse-grained 44DDS/DGEBA/PES show the smaller system sizes result in noisier  $T_g$  predictions.

193 are noisier, the qualitative trend in  $T_g(\alpha)$  is not without value, as these predictions can be used for  
 194 estimates bounds of  $T_g$  that will lower the computational cost of measuring the glass transition in  
 195 larger systems.

196 4.1.5. Morphology - small systems

197 We next apply our model to study the domain sizes of PES toughener that evolve over the  
 198 course of curing. We use the PES-PES structure factor to quantify the domain size of the PES  
 199 toughener. We expect sufficiently large system sizes to demonstrate PES domain sizes independent  
 of simulation volume, but to find volumes below which microphase separation cannot be resolved.  
 Three replicates of system sizes with  $N \in \{5 \times 10^4, 8 \times 10^4, 1 \times 10^5, 2 \times 10^5, 4 \times 10^5, 6 \times 10^5, 8 \times 10^5, 1 \times 10^6\}$

200 are cured isothermally to 90% with fiducial parameters shown in Table 2 and simulations were run  
 201 for  $1 \times 10^7 \Delta t$ . The resulting structure factors  $S(q)$  are summarized in Figure 4 and local maxima in  
 202  $S(q)$  (red dots) indicate PES domains with a characteristic spacing of  $26 \pm 2$  nm emerge in  $N \geq 2 \times 10^5$   
 systems. Importantly, cubic simulation volumes below  $N = 2 \times 10^5$  are too small to resolve these 26



**Figure 4.** Finite size effects: PES-PES structure factor in  $\alpha = 0.9$  simulations shows emergence of a  $0.236 \pm 0.019 \text{ nm}^{-1}$  ( $26 \pm 2$  nm) feature (dashed green line), too large to resolve in simulations where  $N \leq 2 \times 10^5$ . The color bar indicate system size ( $N$ ). The blue star indicate half of the box length.

203 nm PES features, as the half-box-length (blue stars) for these volumes are smaller than 26 nm (recall  
 204 conversion factor  $l = \frac{2\pi}{q}$  between lengths  $l$  and wavenumbers  $q$ ). Note that in the too-small volumes,  
 205 no local maxima (red dots) are observed, and  $S(q)$  appears to diverge at low  $q$ . Therefore, for studies  
 206 of microphase separation in 44DDS/DGEBA/PES, system sizes of at least  $N = 2 \times 10^5$  are necessary.  
 207 More broadly, microphase separation on length scales larger than half the periodic box length manifest  
 208 as macrophase separation because local maxima in  $S(q)$  cannot be resolved for  $q < \frac{\pi}{L}$  for box length  $L$ .  
 209

#### 210 4.2. Validation simulations

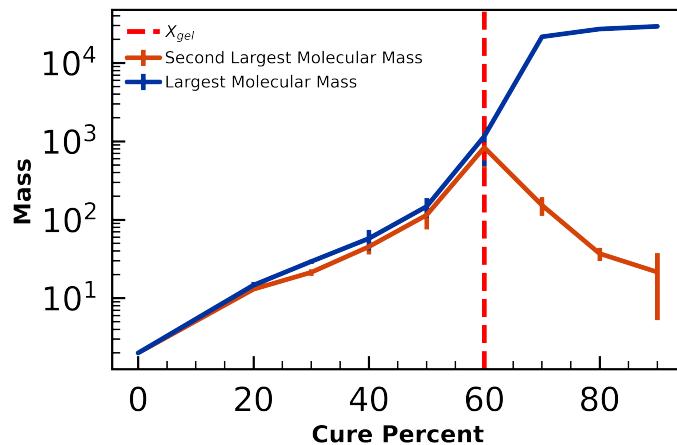
211 Validation simulations comprise 1424 coarse-grained MD simulations for calculating gel points,  
 212 glass transition temperatures, and morphology of toughened 44DDS/DGEBA/PES and untoughened  
 213 44DDS/DGEBA blends.

##### 214 4.2.1. Gel-point validation

215 Isothermal curing simulations of the fiducial  $N = 50,000$  toughened 44DDS/DGEBA/PES  
 216 volumes are performed to predict gelation. The gel-point is dependent on the underlying bonding  
 217 network that forms as the amine and epoxy react, and is therefore a useful metric for validation in  
 218 addition to  $T_g$  and  $S(q)$ . We calculate the gel-point by examining at what degree of cure  $\alpha$  the molecular  
 219 weight of the largest and second largest chain diverge. We use the NetworkX [46] python package to  
 220 measure the size of molecules as curing proceeds.

221 We sample 26 independent isothermally cured ( $T = 3$ ), toughened volumes spanning cure fractions  
 222 from  $\alpha = 0\%$  to  $\alpha = 92.4\%$  and find the gel-point measured by molecular mass at  $\alpha_{gel} = 60\%$  (Figure 5, in  
 223 good agreement with theory and experiments. Flory-Stockmayer theory of gelation [47,48] predicts that  
 224 gelation of 44DDS/DGEBA (a bifunctional monomer and a tetrafunctional monomer) at  $\alpha_{gel} = 58\%$  [49].  
 225 Flory-Stockmayer theory is known to underpredict the cure fraction at gelation, as steric hindrance

226 prevents functional groups reacting with equal probability [50]. Experiments of 44DDS/DGEBA curing  
 227 measure  $\alpha_{gel} > 50\%$  [51] and  $\alpha_{gel} = 60\%$  [52].



**Figure 5.** Divergence of the largest (blue) and second-largest (orange) molecular mass indicates gelation, here calculated at  $\alpha = 60\%$ , in agreement with theory (58%) and experiments (60%). Error bars denote standard deviations of 3 independent samples, except the 90% cure case, which have 2 samples.

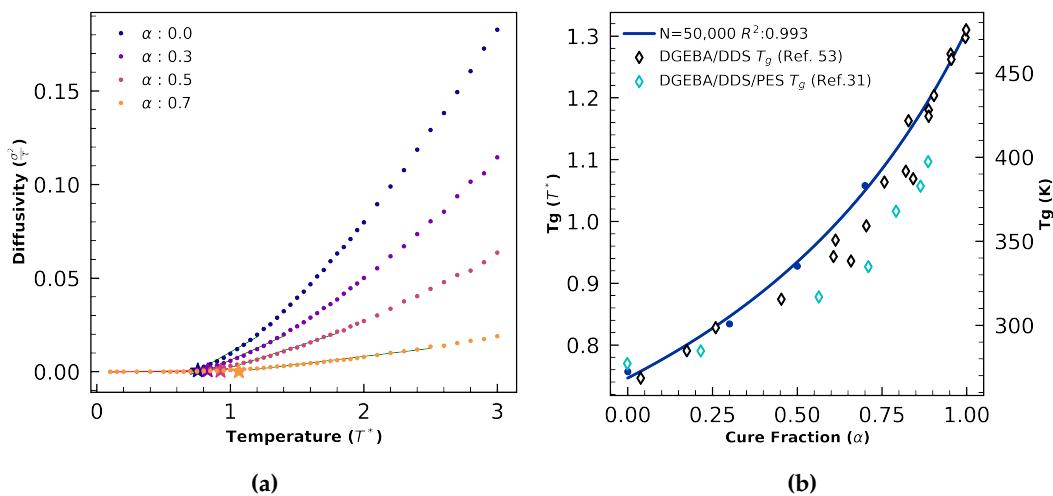
#### 228 4.2.2. Glass Transition Validation

229 A total of 1770 coarse-grained MD simulations are performed to validate predicted  $T_g(\alpha)$  against  
 230 experimental data and theoretical fit to the DiBenedetto equation. First, three independent isothermal  
 231 curing simulations are performed for  $N = 50,000$  systems at the fiducial simulation parameters.  
 232 Independent snapshots from  $\alpha = 0$  to  $\alpha = 0.9$  at intervals of  $d\alpha = 0.1$  are taken from each curing  
 233 simulation to initialize independent quenches (Figure 2.) These 30 independent snapshots representing  
 234 the full range of cure fractions are each quenched in independent simulations to each of the 40  
 235 dimensionless temperatures from 0.05 to 2.0 at intervals of  $dT = 0.05$ , plus each of the 15 temperatures  
 236 from 2.1 to 3.5 in intervals of  $dT = 0.1$ , plus  $T \in \{3.6, 4.0, 4.5, 5.0\}$ . From these simulations we focus on  
 237  $\alpha \in \{0, 0.3, 0.5, 0.7\}$  for determining fits to the DiBenedetto equation, and temperatures  $0.1 < T_{quench} < 2.5$   
 238 for identifying glass transition temperatures.

239 We use piecewise regression to identify  $T_g$  from diffusivity measurements from each of the  
 240 aforementioned simulations (Figure 6a), and fit with the DiBenedetto equation (Figure 6b). We  
 241 validate against experiments of 44DDS/DGEBA by setting the extrapolated dimensionless value  
 242 of  $T_g(\alpha = 1) = 1.32$  equal the experimental measurement 480 K and then checking intermediate  
 243  $\alpha = 0.4$  predictions. Here, our predicted  $T_g(\alpha = 0.4) = 320$  K is 6.7% higher than the experimental  
 244 interpolation of 300 K for PES-toughened 44DDS/DGEBA [31], and 6.5% higher than the experimental  
 245 interpolation of 310 K for the untoughened system [53] (Figure 6b). Several other untoughened epoxy  
 246 systems which have a similar epoxy/amine chemistry also shows a similar trend in the DiBenedetto  
 247 equation where the  $T_g(\alpha = 0.4) \approx 300$  K [49,53,54]. It is also known from experiments that the uncured  
 248 44DDS/DGEBA/PES system is completely miscible and flows at room temperature. Both conditions  
 249 ( $T_g(\alpha = 0) < 293$  K, and  $T_g(\alpha = 0.4) \approx 300$  K) are satisfied by the current model.

#### 250 4.2.3. Morphology validation

251 To validate predictions of microphase separated morphology we first perform 3 independent  
 252 curing simulations at  $T = 3$  of the fiducial simulations (Table 2) at each of 5 system sizes ( $N =$   
 253  $\{4 \times 10^5, 6 \times 10^5, 8 \times 10^5, 1 \times 10^6\}$ ). These sizes are chosen because  $N = 4 \times 10^5$  corresponds to cubic  
 254 simulation volumes with side length  $L = 74$  nm, far larger than needed to measure 26 nm periodic  
 255 features with Fourier-based  $S(q)$  analysis (see Section 4.1.5). As in the simulations for understanding  
 256 minimum simulation sizes, we measure the structure factor  $S(q)$ —specifically the wave number of



**Figure 6.** (a) Diffusivities measured from quenches of 44DDS/DGEBA/PES as a function of cure fraction and temperature. Green lines indicate linear fits of mid- $T$  diffusivities used to calculate  $T_g$ , which are indicated by stars. (b)  $T_g(\alpha)$  (blue symbols) and the DiBenedetto fit (blue curve) from (a). The simulated  $T_g$  at low and high cure fractions shows close agreement with  $T_g$  values measured from an experimental 44DDS/DGEBA system [53] (open black diamonds) and 44DDS/DGEBA/PES [31] (open cyan diamonds).

any local maxima—to quantify microphase separation and when systems reach steady states. A representative time evolution of  $S(q)$  is shown in Figure 7(a) for an  $N = 1 \times 10^6$  system, which reaches steady state after  $7 \times 10^6$  steps. Figure 7(b) shows a representative  $N = 1 \times 10^6$  morphology after achieving steady state. The average PES-PES  $S(q)$  measured for fiducial systems with  $N \geq 4 \times 10^5$  has a local maximum at  $q_{\text{max}} = 0.235 \pm 0.020 \text{ nm}^{-1}$ , corresponding to feature spacings of  $26.6 \pm 2.5 \text{ nm}$ .

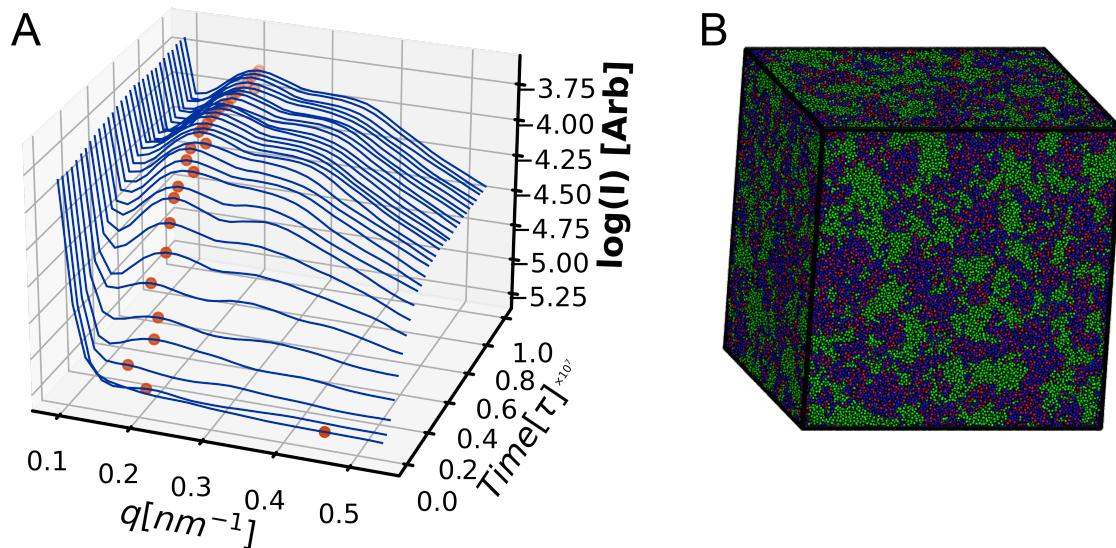
In experiments by Rosetti *et al.* [55], chemically similar DGEBA/44DDS toughened with PES is observed to undergo increasing reaction-induced phase separation that increases with increasing cure temperature. Nonfunctional PES, most similar to the system studied here, remains mixed at a cure temperature of 363 K, phase separates into 250 nm domains when cured at 403 K, and 400 nm domains when cured at 423 K. The length scales of nonfunctional PES phase separation we predict here are smaller than those reported in Ref. [55], but we observe the same qualitative trend of larger domain sizes with higher cure temperatures in the cure-path-dependent simulations forthcoming in Section 4.3.2. Phenoxy-functionalized PES, which can participate in crosslinking, is observed by Rosetti *et al.* that smaller PES nodular domains phase separate (40 nm at 4033 K and 150 nm at 423 K). Smaller PES-rich domains are observed in experiments with a tri-functional epoxy, 44DDS, and functionalized PES, around 20 nm [56]. To fully resolve phase separation of 250 nm domains,  $(500 \text{ nm})^3$  simulation volumes are needed, a factor of 5 larger than the largest volumes cured here. In summary, the simulations presented here demonstrate toughener phase separation on length scales smaller than similar-but-not-equivalent experiments, and  $N = 1 \times 10^6$  systems corresponding to  $(100 \text{ nm})^3$  volumes can routinely be cured to  $\alpha = 0.9$  in one week.

#### 4.3. Exploration simulations

Exploration simulations are performed to measure the effect of including reaction enthalpy (80 simulations) and the dependence of cure profile on final morphologies (23 simulations).

##### 4.3.1. Enthalpy Experiment

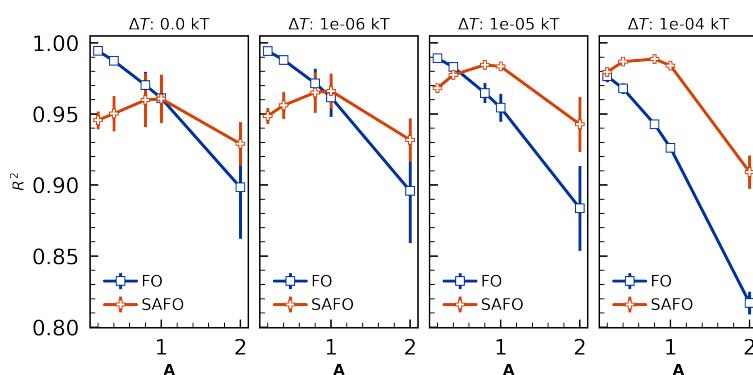
With temperature-dependent reaction rates in the present model, we perform nonisothermal reaction simulations of otherwise fiducial systems to investigate what models of reaction enthalpy are



**Figure 7.** (A) PES-PES structure factor evolution for  $N = 1 \times 10^6$  is used to quantify equilibration. Red symbols indicate the wavenumber  $q_{max}$  of a local maximum in  $S(q)$ .

283 Sufficient for modeling self-accelerated first-order reaction kinetics. In the present case we assume the  
 284 change in energy associated with the crosslinking reaction is instantaneously distributed among all  
 285 simulation degrees of freedom, corresponding to an increase in temperature where  $\Delta H_{rxn} = C_v \Delta T_{rxn}$  for  
 286 heat capacity  $C_v$  in the NVT ensembles studied here. We perform simulations with per-bond  $\Delta T_{rxn} =$   
 287  $0.0, 1 \times 10^{-6}, 1 \times 10^{-5}, 1 \times 10^{-4}$  in addition to the same  $n_B$  and  $\tau_B$  ranges described in Section 4.3.1.

288 Results summarized in Figure 8 validate first-order reaction kinetics are accurately modeled when  
 289  $\Delta T \leq 1 \times 10^{-6}$ , and that  $\Delta T = 1 \times 10^{-4}$  is sufficiently large for self-accelerated first-order kinetics to  
 290 always beat first-order kinetic fits to concentration profiles. Unlike the isothermal simulation cases  
 291 where  $\Delta T = 0$  and reaction kinetics become more accurate as  $A$  is decreased, in the self-accelerated  
 first-order kinetic models there exist optimal  $A \approx 1$ . In sum, the present model permits straightforward



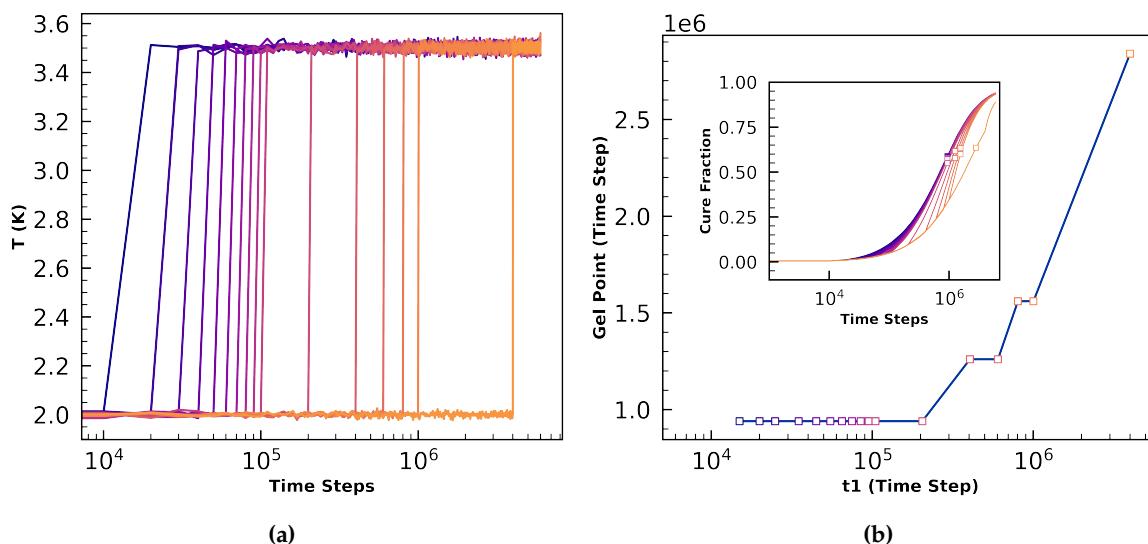
**Figure 8.** Quality of fit for first-order (FO) and self-accelerated first-order (SAFO) reaction models as a function of  $\Delta T_{rxn}$  and  $A = \frac{n_B}{\tau_B}$  validate FO kinetics are most accurate for  $\Delta T = 0$ , and that SAFO kinetics best fit the concentration profiles when  $\Delta T = 1e-4$ . Error bars show standard error in  $R^2$  value averaged across cure temperatures  $T = 0.5, 1.0, 2.0, 4.0, 6.0 \text{ kT}$

292 modeling of self-accelerated reactions through the inclusion of a per-bond change in temperature that  
 293 is validated against kinetic models.

295 4.3.2. Sensitivity to Cure Profile

296 The final studies in this work investigate the dependence on structure of nonisothermal cure  
 297 profiles meant to be representative of industrial temperature schedules. We first perform 17 simulations  
 298 of otherwise fiducial  $N = 5 \times 10^4$  volumes that step up from  $T = 2.0$  to  $T = 3.5$  instantaneously at time  
 299  $t_1$  ranging between  $1.5 \times 10^4$  steps and  $4 \times 10^6$  steps. We next perform 3 replicate simulations of  
 300  $N = 4 \times 10^5$  volumes that each experience two changes in temperature: From  $T_1 = 1.0$  up to  $T_2 = 2.0$   
 301 at  $t_1 = 1 \times 10^5$  steps, followed by a quench down to  $T_3 = 1.2$  at either  $t_2 = 2 \times 10^6$  steps or  $t_2 = 9.5 \times 10^6$   
 302 steps. Except for the instantaneous temperature changes described above, the simulations performed  
 303 in this section are all isothermal. We calculate the time of gelation and  $S(q)$  to quantify structure.

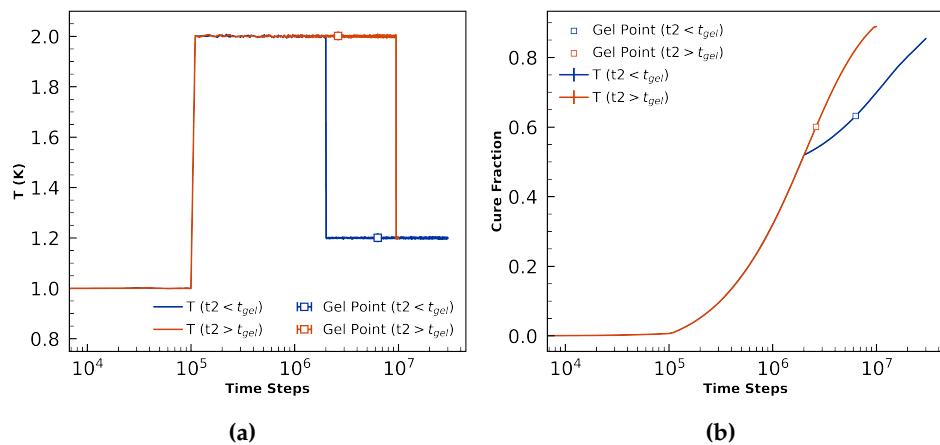
304 Results from the temperature steps from  $T = 2$  to  $T = 3.5$  are summarized in Figure 9, and  
 305 demonstrate that gelation before  $1e6$  steps have elapsed is independent of initial time when  $t_1 < 2 \times 10^5$ .  
 306 Inset in Figure 9b are the cure profiles on semilog axes with open squares indicating gelation times,  
 which are summarized in the main plot. The delay in gelation with longer times at low  $T$  is expected



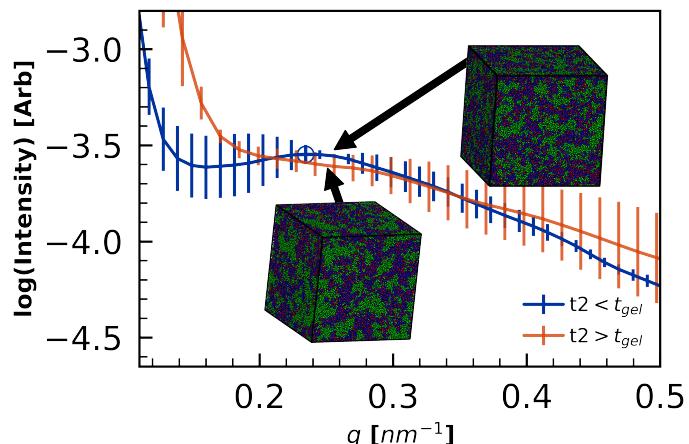
307 **Figure 9.** (a) Temperature profiles where the initial ramp up time ( $t_1$ ) is varied. (b) Time to gelation is  
 308 not affected by  $t_1 < 2 \times 10^5$ .  $t_1$  time denotes the time at which the cure temperature is ramped up  
 309 and held constant.

310 because the more time spent at higher temperature, the faster curing occurs, and the faster gelation  
 311 will occur. Bicontinuous microphase separated morphologies are observed for all simulations here,  
 312 but no measurable differences in periodic length scales are observed. These results demonstrate that  
 313 modifying the cure profile enables control over how quickly systems gel.

314 The final 6 simulations of  $N = 4 \times 10^5$  volumes are cured isothermally at  $T_1 = 1$  for  $1 \times 10^5$  steps  
 315 before being instantaneously heated to  $T_2 = 2$ . Three simulations are quenched to  $T_3 = 1.2$  before  
 316 gelation at  $t_2 = 2 \times 10^6$  steps, and held there until a total of  $3e7$  steps have elapsed. The other three  
 317 simulations are quenched to  $T_3 = 1.2$  after gelation at  $t_2 = 9.5 \times 10^6$  steps, and held there until a total of  
 318  $1e7$  steps have elapsed. Note that  $T_g(\alpha = 0.87) = 1.2$ , so systems with  $\alpha < 0.87$  will be above the glass  
 319 transition temperature at all points during these cure profiles. Temperature schedules, gel points, and  
 320 cure profiles for these pre- and post-gelation quenches are summarized in Figure 10. The temperature  
 321 set points correspond to  $T_1 = 365$  K,  $T_2 = 730$  K, and  $T_3 = 438$  K.  $T_2$  is chosen such that it is much higher  
 322 than  $T_g(\alpha = 1.0) = 480$  K, facilitating diffusion especially before gelation. We analyze morphologies  
 323 with final cure fraction  $\alpha = 0.855$  for both pre-gelation (blue data) and post-gelation (orange) quenches,  
 324 neither of which is ever below its glass transition temperature.



**Figure 10.** Temperatures profiles (a) and curing profiles (b) for  $t_2 < t_{gel}$  ( $t_2 = 2 \times 10^6 \Delta t$ ) and  $t_2 > t_{gel}$  ( $t_2 = 9.5 \times 10^6 \Delta t$ ). The hollow squares show gel point.  $T_2$  is chosen to be higher than and  $T_3$  is chosen to be slightly lower than the  $T_g$  of the fully cured system ( $T_g(\alpha = 1.0) = 480$  K).



**Figure 11.** PES-PES structure factor shows difference in morphology as a result of varying  $t_2$  of the “Step” curing profile. Both simulation volumes are cured to  $\alpha = 0.855$ . Error bars represent standard error from the three replicate simulations. The length scales of microphase separation are much smaller in the pre-gelation quench (blue), whereas  $S(q)$  diverges around  $q_{L/2} = 0.17 \text{ nm}^{-1}$ , indicating a higher degree of phase separation that is apparent in the more distinct clumping of the inset visualizations.

Average  $S(q)$  for the pre- and post-gelation cures are shown in Figure 11. Two features of the  $S(q)$  stand out: First, the length-scales of phase separation are smaller for the pre-gelation quench. Second, there is higher variance in the measured  $S(q)$  in the pre-gelation quenches.

The observations of increased phase separation in the post-gelation quench are consistent with experiments demonstrating increased phase separation with higher cure temperatures [31,53]. These observations are also consistent with two different mechanistic explanations: (1) Higher temperatures increase curing rates, which increase reaction-induced phase separation, and (2) Quenching pre-gelation keeps the morphology from being kinetically arrested, and so the tougheners can more easily mix and distribute in the unvitrified volume if thermodynamically favorable. These results demonstrate that thermoset volumes with identical cure fractions can have significant cure-path-dependent microstructures.

## 5. Conclusions and Outlook

We demonstrate a coarse-grained model of toughened epoxy thermosets that

1. Offers straightforward forcefield parameterization.
2. Can capture first-order and self-accelerated first order reaction dynamics.
3. Is validated against experimental gel points, glass transition temperatures, and morphology for 44DDS/DGEBA/PES blends.
4. Does not require backmapping for  $T_g$  calculation.
5. Can cure million-particle volumes (corresponding to 31-million atoms and  $(100 \text{ nm})^3$  periodic boxes) to  $\alpha = 0.9$  in under one week.
6. Demonstrates for the first time sensitivity of morphology to cure profile.

In sum, the present work represents progress towards efficient prediction of the morphology and properties of realistic toughened thermosets and provides template workflows for calibrating models to specific formulations and cure profiles. These functionalities offer opportunity to develop a deeper understanding of aerospace-grade thermosets and more reliable manufacturing processes.

The main shortcomings of this work are the degree of validation against experimental  $T_g$  and morphology. While the low and high cure fractions matched experimental glass transition temperatures for 44DDS/DGEBA, the curvature of our DiBenedetto fit was smaller than observed in experiments. We expect subsequent work in improved  $T_g$  detection from diffusivity data, calculation of  $T_g$  from back-mapped morphologies to provide better predictions of  $T_g$  across the full spectrum of cure fractions. While we recognize experiments characterizing toughener phase separation on the 10 nm - 50 nm length scales are challenging, additional work in this area would provide key datasets to validate against. Alternatively, applying the workflows presented here to thermoset formulations with small-scale phase separation characterized would be a information-rich extension of this work. Finally, this work sets the stage for investigations that simultaneously calibrate the energy scales of monomer interactions, reaction kinetics, vitrification to experimental curing profiles that measure the degree to which hour-long curing profiles can accurately be predicted by a few billion steps of a coarse-grained model.

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### Abbreviations

The following abbreviations are used in this manuscript:

44DDS	4,4'-Diaminodiphenyl Sulfone
AAMD	All-Atom Molecular Dynamics
DGEBA	Bisphenol A diglycidyl ether
DPD	Dissipative Particle Dynamics
FO	first order
LB	Lorentz-Berthelot
LJ	Lennard-Jones
MD	molecular dynamics
PES	Poly(oxy-1,4-phenylsulfonyl-1,4-phenyl)
PRM	piecewise regression method
SAFO	self-accelerated first order

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