**Palit *et al.* Reply:** The experiments of Le Coeur *et al.* [1] do not truly probe the dilute regime for a simple reason: In the dilute regime, the chain conformations are independent of the concentration. They cannot be in the dilute regime, because their determined chain size still depends on the polymer concentration. Second, a feature of Le Coeur's work that is worrying to us is that the trend $R_g(0,\Phi)$ that they infer from extrapolation to a zero polymer concentration ($c_p = 0$) is the opposite of the trend they observe at finite $c_p$. They have no data below the concentration where their $R_g$'s ostensibly cross over. We, on the other hand, have experimental results (not only diffusion but also SANS) in the regime where all quantities are independent of the concentration. We expand on these two points below.

First, it is worth pointing out that $c^*$ does not characterize a sharp transition point. We cannot say this any better than de Gennes (see Ref. [2], p. 76): "Clearly this threshold is not sharp; it is more properly defined as a region of crossover between (a) and (c)…." In the book, regions (a) and (c) are defined as dilute and concentrated. Plotting $c^*$, obtained from a formula that is invalid in the presence of crowders, is not meaningful in determining the concentration regime where an extrapolation (to $c_p = 0$) is valid. Our definition is more meaningful in the sense that it is a lower limit of the overlap region and, therefore, the upper limit of the dilute region.

Second, our limits are obtained purely experimentally. In crowded systems, it is never clear *a priori* when you are in the dilute limit for a single probe species. This must be determined experimentally. Le Coeur *et al.* do not have SANS data below our definition of $c^*$ and rely on an uncontrolled extrapolation. We do have SANS data in this regime (at $c = 0.001$ g/cm$^3$). We highlight this fact below by replotting Fig. 5(a) in our Letter [3] on a logarithmic concentration scale: the results at four different Ficoll packing fractions are on top of each other and highlighted with a square box in Fig. 1. Linear fits *à la* Le Coeur (dashed lines with stars showing the extrapolated value at $c = 0$), for our data at concentrations $c = 0.005$ g/cm$^3$ and above, do not pass through the data at $c = 0.001$ g/cm$^3$. Our piecewise fit (using the diffusion $c^*$, solid lines) does.

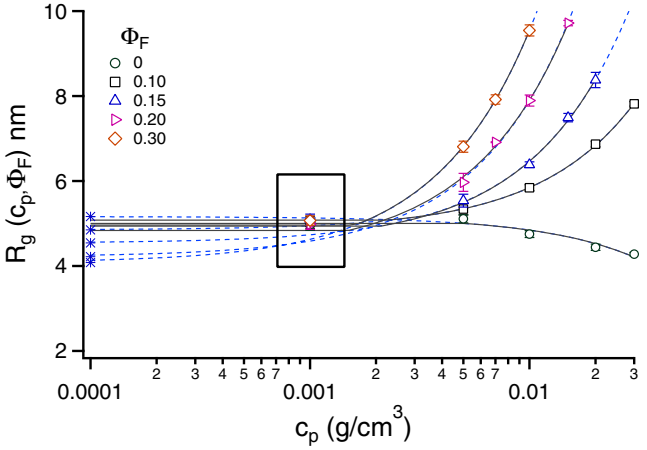


FIG. 1. SANS in the dilute limit: The PEG radius of gyration $R_g(c_p,\Phi_F)$, obtained from SANS measurements for Ficoll volume fractions from $\Phi_F = 0$ to $\Phi_F = 0.30$, is plotted on a logarithmic concentration scale to highlight the concentration $c = 0.001$ g/cm$^3$, which is below the $c*$ obtained from diffusion measurements. $R_g(0.001\ \text{g/cm}^3,\Phi_F)$ shows no dependence on $\Phi_F$, consistent with the piecewise fit using the diffusion $c*$ (solid lines) but not with the linear extrapolation (curved dashed lines on the logarithmic concentration scale).

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