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Supporting information for article:

Supercell refinement: a cautionary tale

Jeffrey Lovelace, Václav Petrícek, Garib Murshudov and Gloria E. O. Borgstahl

In the paper we argued that the $T_0=1/2$ solution will have a shallower error well leading to a broader well that when it combines with the error well for the correct solution (deeper and have steeper sides) will cause refinements starting near the average to favor the $T_0=1/2$ solution.

The error space was approximated by using the initially calculated R values for molecular states that were biased toward one of the two solutions ($T_0=0$ or $T_0=1/2$). Figure S1a shows that $T_0=1/2$ is seems to provide evidence supporting our view about the shape of the error space.

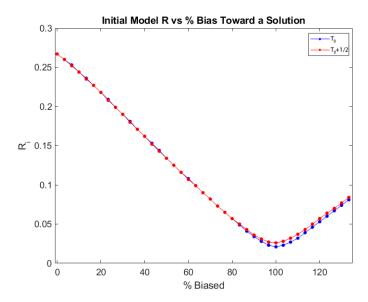


Figure S1(a): Plot of the initial R values as a function of the % bias toward the T_0 =0 or the T_0 =1/2 solutions. The T_0 solution can achieve a lower R value. A bias of 0% is the average structure 100% represents one of the two solutions and >100% represents an overshooting of the rotation.

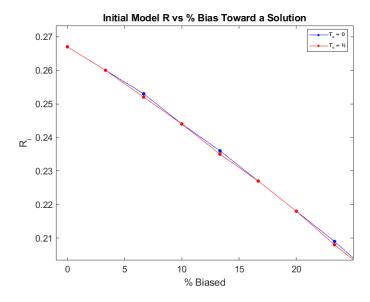


Figure S1(b): Zoomed in region of Fig. S1a near the starting point of refinement. Although T_0 =0 has the lowest final R value, T_0 =1/2 has (slightly) lower R values for states near the average structure which may cause refinement approaches to favor the T_0 =1/2 because of these locally more favorable R values.

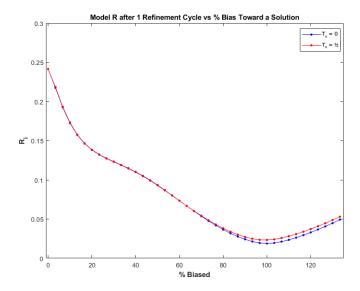


Figure S1(c): Plot of the R values after one cycle of refinement as a function of the % bias toward the T_0 =0 or the T_0 =1/2 solutions. The T_0 =solution can achieve a lower R value. A bias of 0% is the average structure 100% represents one of the two solutions and >100% represents an overshooting of the rotation.

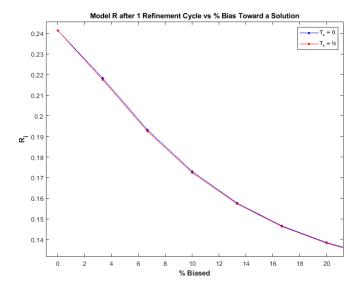


Figure S1(d): Zoomed in region of Fig. S1c near the starting point of refinement. Although T_0 =0 has the lowest R value, T_0 =1/2 has (slightly) lower R values for states near the average structure which may cause refinement approaches to favor the T_0 =1/2 because of these locally more favorable R values.