Supplemental figures for “Do hierarchical structures assemble best via hierarchical pathways?”

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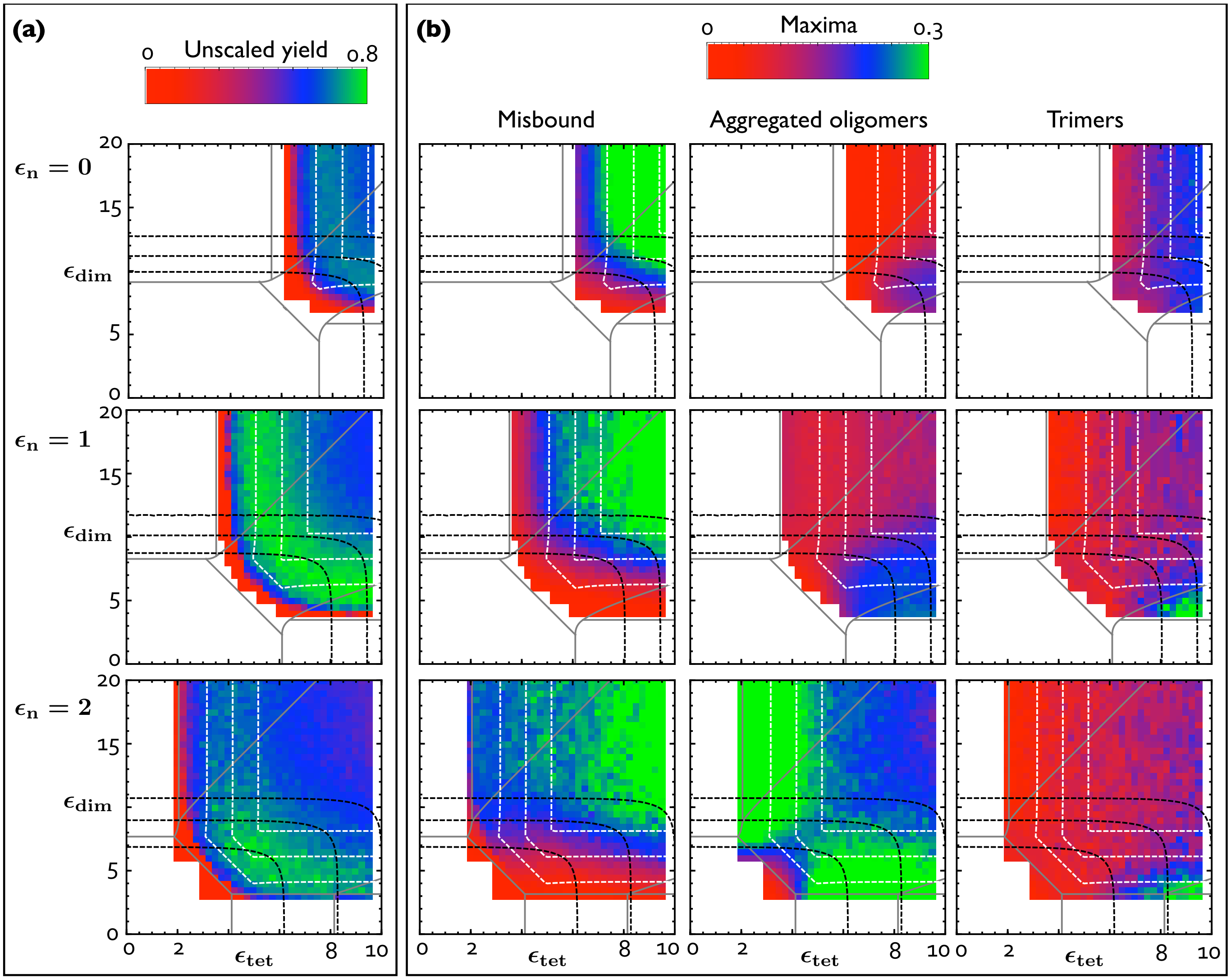

Fig. 1 *Weak nonspecific interaction is generally beneficial, but diminishes the effectiveness of hierarchical pathways relative to the direct one.* **(a)** Phase diagram and *unscaled* yield after 10^7 MC cycles as a function of specific interaction strengths $\varepsilon_{\mathrm{tet}}$ and $\varepsilon_{\mathrm{dim}}$ for three nonspecific interaction strengths and a concentration $\phi = 0.1$. **(b)** As for scaled yield, pathway diagrams illustrate that the regions of high *unscaled* yield are bounded by regions exhibiting three types of kinetic trapping: misbinding, aggregation of oligomers (dimers or tetramers), and the formation of trimers. Weak nonspecific interaction (middle row) facilitates assembly, while stronger nonspecific interaction (bottom row) begins to suppress it. Furthermore, nonspecific modes of binding disfavor hierarchical pathways: moving from top to bottom, strengthening nonspecific interactions first disfavors assembly via tetramers (compare first and second rows), then disfavors assembly via dimers (compare second and third rows).

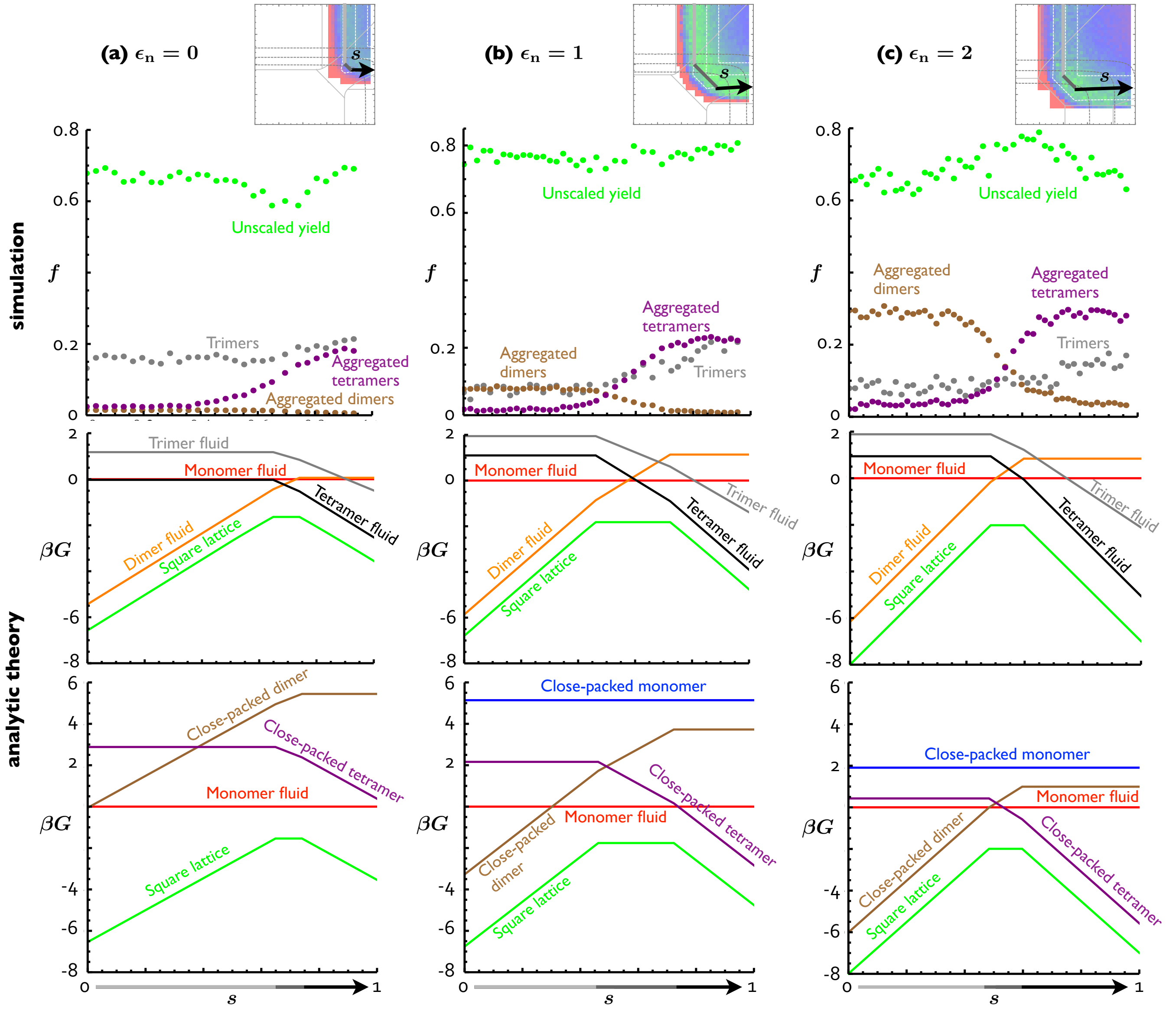

Fig. 2 *Comparison of dynamics and thermodynamics reveals principles of good assembly.* Dynamic quantities (second row) including *unscaled* yield respond to variations in the free energies of bulk phases in free energies (third and fourth rows), along paths, labeled *s*, of constant thermodynamic driving force (top row) through the phase diagrams of Fig. 1. Shown are free energies of pure fluid and crystal phases; the free energies of equilibrium coexisting phases are equal or slightly lower. Hierarchical pathways owe their existence to dimer and tetrameter phases close to or lower than the parent phase in free energy; when these low-lying oligomer phases are close-packed (see right column, bottom panel), dynamic aggregation of oligomers leads to a reduction in yield (see right column, second panel). Non-hierarchical pathways resulting in high yield tend to occur when nothing lies between the monomer fluid and the target crystal in free energy.

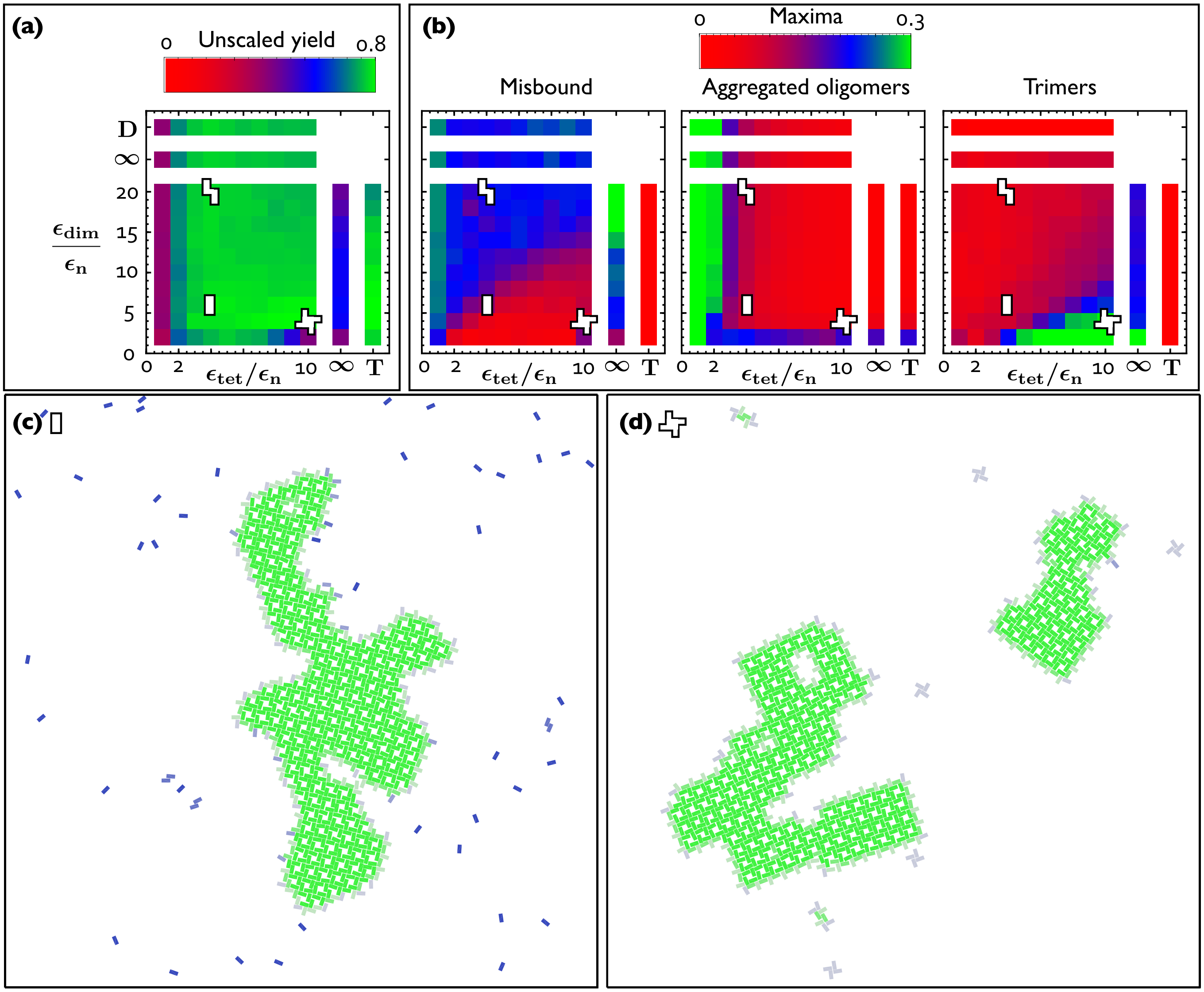

Fig. 3 *Building blocks designed to assemble directly perform better than building blocks designed to assembly hierarchically, even under optimal conditions.* **(a)** 'Pathway design diagram' showing *unscaled* yield after 10^7 MC cycles at $\phi = 0.1$, for a wide range of building block designs defined by different interaction strength ratios $\varepsilon_{\mathrm{tet}}/\varepsilon_{\mathrm{n}}$ and $\varepsilon_{\mathrm{dim}}/\varepsilon_{\mathrm{n}}$. The absolute values of these parameters are chosen, at each point on the diagram, in order to optimize assembly; building blocks identified in this way are therefore the best-designed representatives of certain kinds of pathway. The symbol ∞ denotes unbreakable specific interactions, and the row (resp. column) marked 'D' (resp. 'T') correspond to simulations initialized with dimers (resp. tetramers) bound by unbreakable interactions. Comparison of yield and **(b)** pathways demonstrates that while oligomer aggregation has been largely eliminated, the trimer kinetic trap is always present when strong tetramer-forming bonds exist. Symbols show the points of intersection of this diagram with those shown in panels (c-d) and Fig. 4. In contrast to the analogous Fig. 7 of the main text, the trimer kinetic trap is only associated with reduced *unscaled* yield for strongly tetramer-stabilizing designs, e.g. $\varepsilon_{\mathrm{tet}}/\varepsilon_{\mathrm{n}} = \infty$ but not $\varepsilon_{\mathrm{tet}}/\varepsilon_{\mathrm{n}} \leq 10$. However, comparison of snapshots at 10^7 MC cycles for **(c)** the monomer-stabilizing design that optimizes scaled yield and **(d)** the tetramer-stabilizing design that optimizes unscaled yield suggests that scaled yield is a better order parameter for quantifying the quality and compactness of crystals.

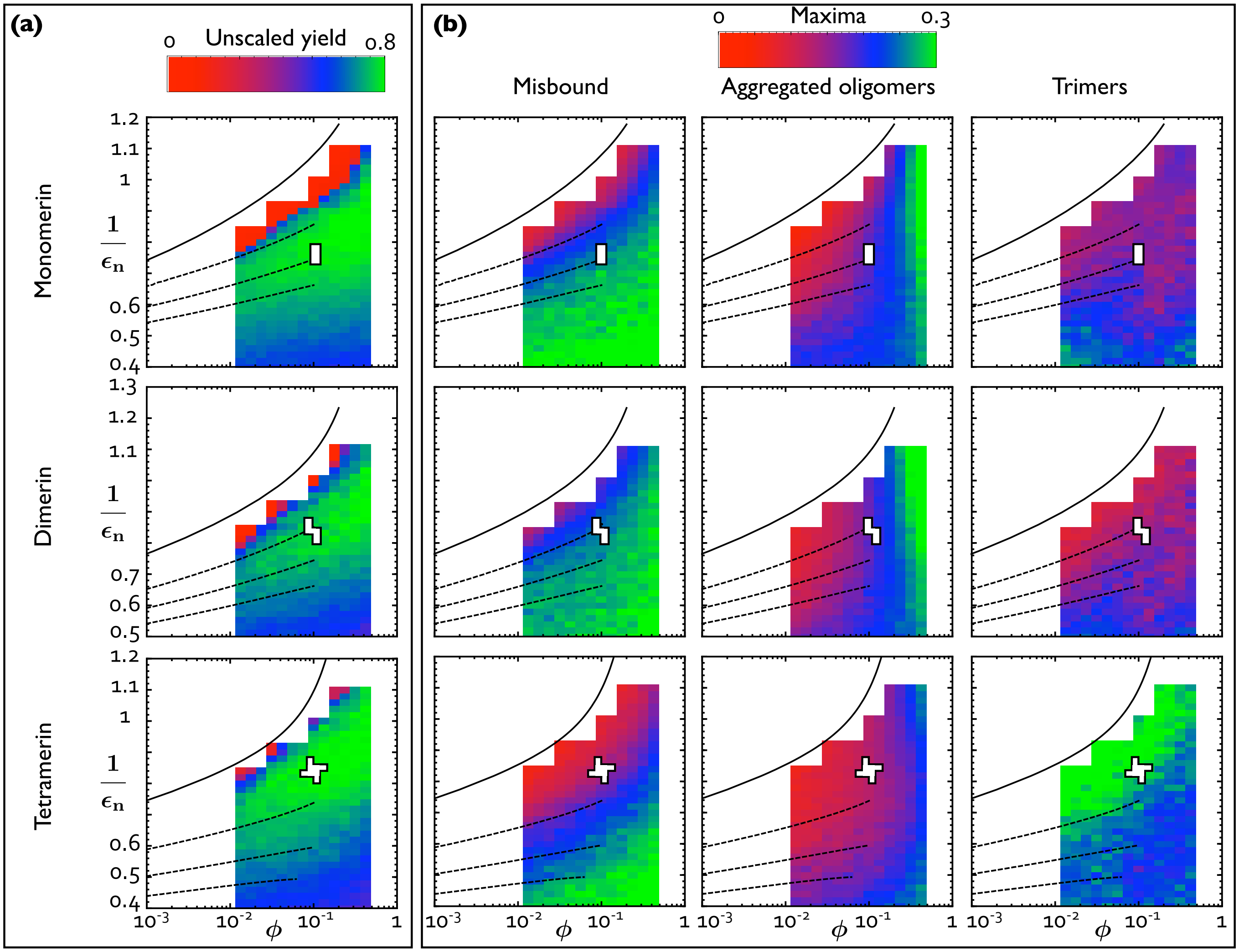

Fig. 4 *Apparently similar temperature-versus-packing fraction phase diagrams can conceal markedly different dynamics.* **(a)** Temperature-packing fraction phase diagrams displaying *unscaled* yield for three building blocks representative of non-hierarchical, dimer-dominated, and tetramer-dominated assembly, from top to bottom. Symbols show the points of intersection of these diagram with that shown in Fig. 3, equivalent to the temperature of peak yield for packing fraction $\phi = 0.1$. The associated **(b)** pathway diagrams show that thermodynamic phase diagrams that look similar in this representation can harbor markedly different dynamics. In particular, tetramerin assembles via a trimer-rich intermediate, which acts as the dominant kinetic trap at high temperature and low packing fraction.