Algorithmic Self-Assembly of DNA Sierpinski Triangles

Supporting Figures

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Figure S1: Representations and tile sets used in simulations. (a) Rectangular rendition of the tiles used in the kTAM simulations. Bond strengths (either 1 or 2) are indicated on output binding domains by the number of pins. (b) Square rendition of the tiles used by the kTAM simulator, xgrow. (c) Error-free Sierpinski triangle growth from a border, shown in the orientation used by xgrow, i.e., rotated 45° counterclockwise from b.