

Algorithmic Self-Assembly of DNA Sierpinski Triangles

Supporting Figures

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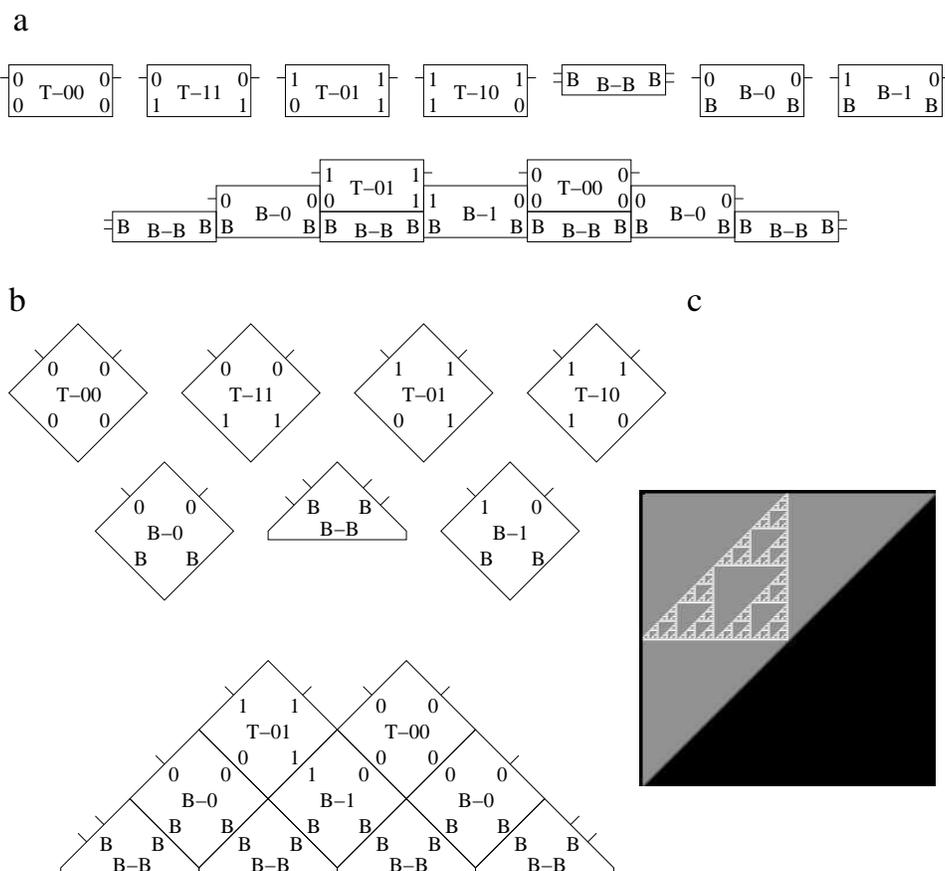


Figure S1: Representations and tile sets used in simulations. **(a)** Rectangular rendition of the tiles used in the kTAM simulations. Bond strengths (either 1 or 2) are indicated on output binding domains by the number of pins. **(b)** Square rendition of the tiles used by the kTAM simulator, *xgrow*.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