A Python library for structural DNA nanotechnology

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Structural DNA nanotechnology is a powerful technique for bottom-up self-assembly of nanoscale structures. Potential applications are vast and only limited by the researchers' imagination. For large and complex structures, the manual or semi-automatic designing process is time-consuming and requires a detailed inspection of the model, leading to user error. We introduce MENDEL, a software library that allows the automatic, extensive, and parametric DNA nanostructures design in this work. MENDEL contains a set of commands that automate the designing process, allow the abstraction of turning sites, compute staples, and parametrize scaling and repetitive features; thus, reducing user error, design complications, and time-to-complete. Running MENDEL through Blender renders a 3D representation of the model. Also, for community convenience, MENDEL generates caDNAno/CanDo compatible files. MENDEL is available as open-source software at https://github.com/SBMI-LAB/MENDEL.

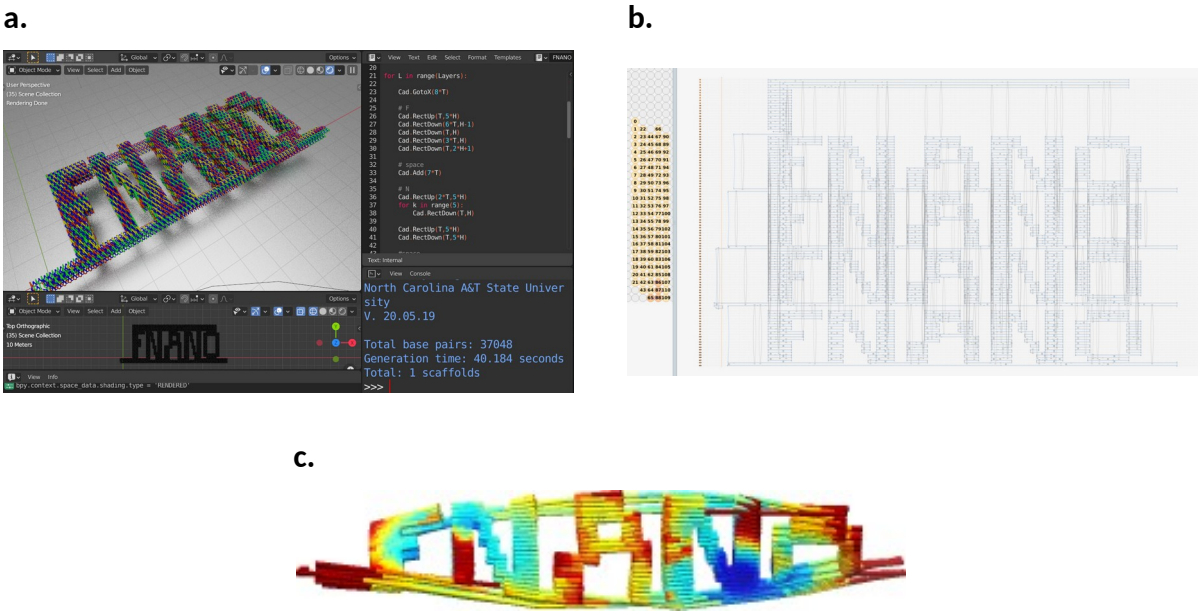

Fig. 1. In under 41 seconds, MENDEL generated a four-layered origami consisting of 37,048 base pairs. (a) Blender interface with scripting window and MENDEL commands, (b) CaDNAno file generated, (c) CANDO geometry prediction.

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