#### Design and conversion to simulation format oxDNA/RNA simulation INPUT OUTPUT FOR MD XYZ **oxDNA** oxDNA atom cadnano full atom Webserver **Tiamat** Python package CanDo - The TacoxDNA webserver<sup>1</sup> provides tools to convert from nanotechnology design tools to the oxDNA format - These files will not have physical geometry and must be relaxed prior to simulation - Also supports conversion to and from PDB for use in other simulation software were not forming as designed.

# Studying unstable paranemic crossovers in RNA tiles

Simulation identified the parts of the structure which

### **Trajectory Analysis** Free energy Free energy of paranemic cohesio Understanding energy barriers between states can inform design choices Mean Structure and Flexibility 4.86 10.03 15.20 20.37 25.54 Singular value decomposition for rigid structures.

Multidimensional scaling for small, flexible structures.

Identify duplexes based 0.08

Quantify flexibility and 20.02

on H-bonds. Calculate 🚖

angle in the plane

vectors.

defined by the duplex

identify metastable

configurations

Interduplex Angles

design

triangular mes square mesh

General-Purpose analysis package for coarse-grained simulations of DNA/RNA nanotechnology

**Arizona State University** Erik Poppleton, Michael Matthies, Shuchi Sharma, Joakim Bohlin, Petr Šulc

<sup>a</sup> Center for Molecular Design and Biomimetics, The Biodesign Institute, Arizona State University, Tempe, AZ, USA <sup>b</sup> Physics Department, University of Oxford, Oxford, UK

## **Unsupervised clustering** 0.00 0.25 0.50 0.75 1.00

Using DBSCAN<sup>2</sup>, an unsupervised machine learning algorithm, to identify structurally distinct subpopulations in a trajectory and exploring differences in bonding and angles

#### Visualization

OxDNA Viewer is a Three.js browser app that reads, edits, and writes oxDNA simulation files. Modify single configurations, create videos from trajectories, and overlay data from other analyses

Download at:

https://github.com/sulcgroup/oxdna-viewer

#### Interstem angle Hydrogen Bonding Interactions between particles, particularly base pairing, is used to identify weak or strained regions **Bond Occupancy** 0.00 0.25 0.50 0.75 1.00

Principal Component Analysis Show the strongest components of overall motion

over the trajectory. Identifies the most dynamic regions, as well as collective motions.

#### The oxDNA/RNA<sup>3,4,5</sup> model

- Coarse-grained models built for nanotechnolgy
- Accurately reproduces structure, thermodynamics, and mechanics of single- and double-stranded DNA/RNA
- Monte-Carlo and Molecular Dynamics methods
- Efficiently sample systems up to 2 million nucleotides

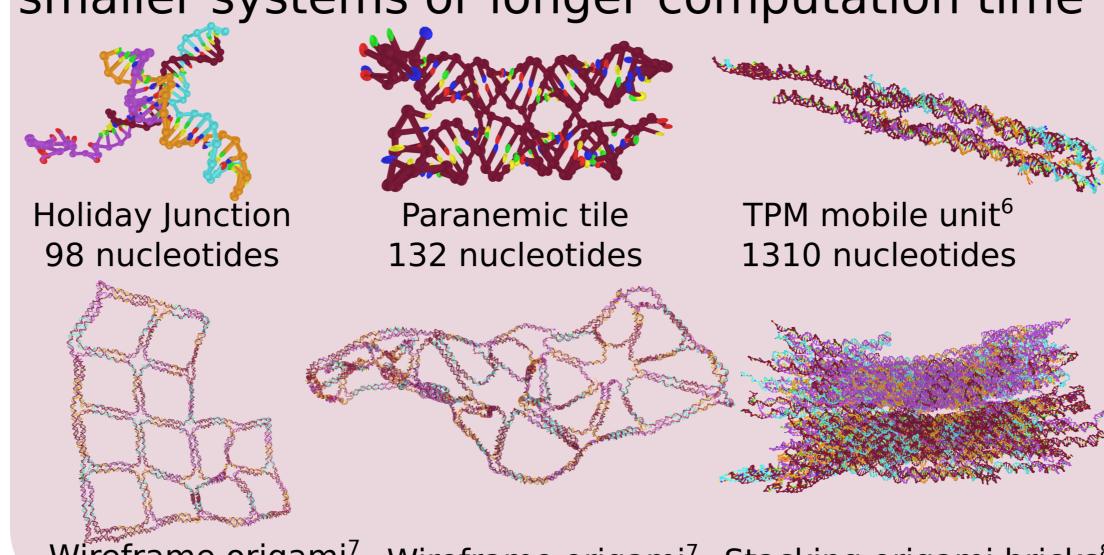
Download: dna.physics.ox.ac.uk

#### Input vectors for DBSCAN

- Clustering can be performed on any vector space that has density differences.
- This example uses each snapshot's representation in principal component space

#### Scale and sampling

- More complete sampling is possible with smaller systems or longer computation time



Wireframe origami<sup>7</sup> Wireframe origami<sup>7</sup> Stacking origami bricks<sup>8</sup> 8694 nucleotides 13763 nucleotides 33694 nucleotides

#### **Code structure**

- These are generic tools for most structures
- Functions like file reading and parallelization are modular for use in custom applications
- Written in Python 3 and TypeScript

#### **Editing in the visualizer**

- One strength of DNA/RNA nanotechnology is the modularity of components.
- oxDNA viewer has basic editing functions - Translation, rotation, nicking, ligation, deletion
- Export, then continue the simulation!



The two bricks, designed in CaDNAno, of the DNA TPM<sup>6</sup> structure before being joined by the teather in oxDNA Viewer

#### References

J. Comput. Chem. jcc.26029 (2019). doi:10.1002/jcc.26029 2. Ester, M., Kriegel, H.-P., Jorg, S. & Xu, X. A Density-Based Clustering Algorithms for Discovering Clusters. KDD-96 Proc. 96, 3. Doye, J. P. K. et al. Coarse-graining DNA for simulations of DNA nanotechnology. Phys. Chem. Chem. Phys. 15, 20395–20414

4. Snodin, B. E. K. et al. Introducing improved structural properties and salt dependence into a coarse-grained model of DNA. 5. Šulc, P., Romano, F., Ouldridge, T. E., Doye, J. P. K. & Louis, A. A. A nucleotide-level coarse-grained model of RNA. J. Chem. Phys.

6. Schickinger, M., Zacharias, M. & Dietz, H. Tethered multifluorophore motion reveals equilibrium transition kinetics of single DNA 7. Jun, H. et al. Autonomously designed free-form 2D DNA origami. Sci. Adv. 5, 1–9 (2019). 8. Gerling, T., Wagenbauer, K. F., Neuner, A. M. & Dietz, H. Dynamic DNA devices and assemblies formed by shape-complementary, non-base pairing 3D components. Science (80-. ). 347, 1446-1452 (2015).