

# Structural Dynamics and Topological Properties of Supercoiled DNA Ropes/Braids

L Russell<sup>1</sup>, J W Shepherd<sup>2</sup>, S Guillbaud<sup>3</sup>, J A L Howard<sup>2</sup>, O Henrich<sup>1</sup>, and M C Leake<sup>2,4</sup>

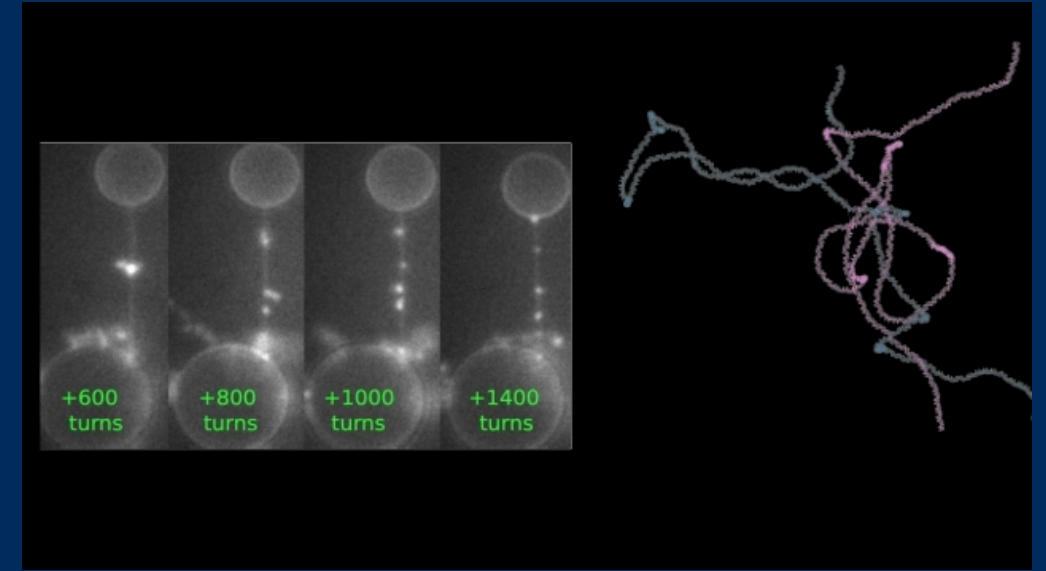
1. Department of Physics, University of Strathclyde, 2. School of Physics, Engineering, and Technology, University of York, UK; 3. Irida Ltd, UK; 4. Department of Biology, University of York, UK

DNA achieves an incredible million-fold compaction within the cell nucleus by wrapping, folding and looping in a multi-hierarchical manner creating domains with varying degrees of organisation. As a result, DNA often exists in a supercoiled state, and studying it is crucial for understanding gene expression and regulation in both prokaryotes and eukaryotes.

Supercoiled DNA undergoes large structural rearrangements, leading to the formation of plectonemes (loop-like, intertwined structures). Topological properties are critical here in determining interactions within cell environments, exemplified by DNA where its response to mechanical perturbation is as important as biochemical properties to its cellular roles.

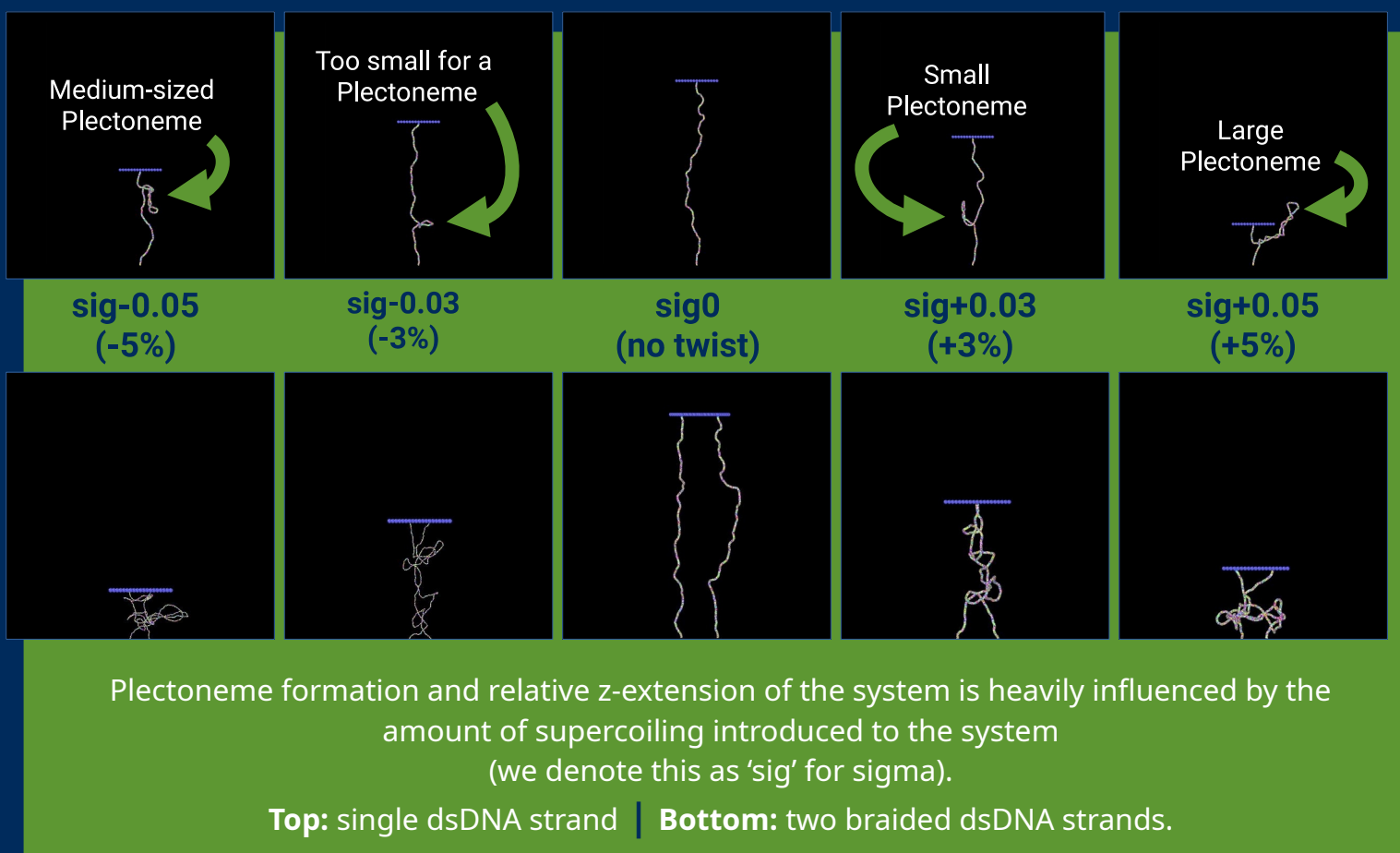
On top of supercoiling, and particularly during DNA replication, transcription and repair, DNA often presents itself in multi-stranded assemblies such as ropes and braids. While these structures are common in the cellular context, our understanding of their mechanical properties is far from complete.

Here, we present results of a combined study of DNA braids and ropes using the oxDNA coarse-grained DNA model [1,2] and the unique COMBI-Tweez experiment [3], which allows simultaneous control of DNA torque and stretch permitting directly imaging of structural changes in plectonemes. We quantify the effective spring elastic constant of DNA braids and the plectoneme size distribution, diffusivity and dynamics depending on topology and supercoiling state.



Left | Experimental; white spots highlight plectonemic and close proximity locations.

Right | Computational; an example of plectoneme formation within the upper left blue strand.



Write the points  $\curvearrowright$  (points of self-overlap) are typically unevenly distributed with varying degrees of spatial separation in braided dsDNA plectonemes.

Plectoneme formation in **Braids** is far more complex than **Single**

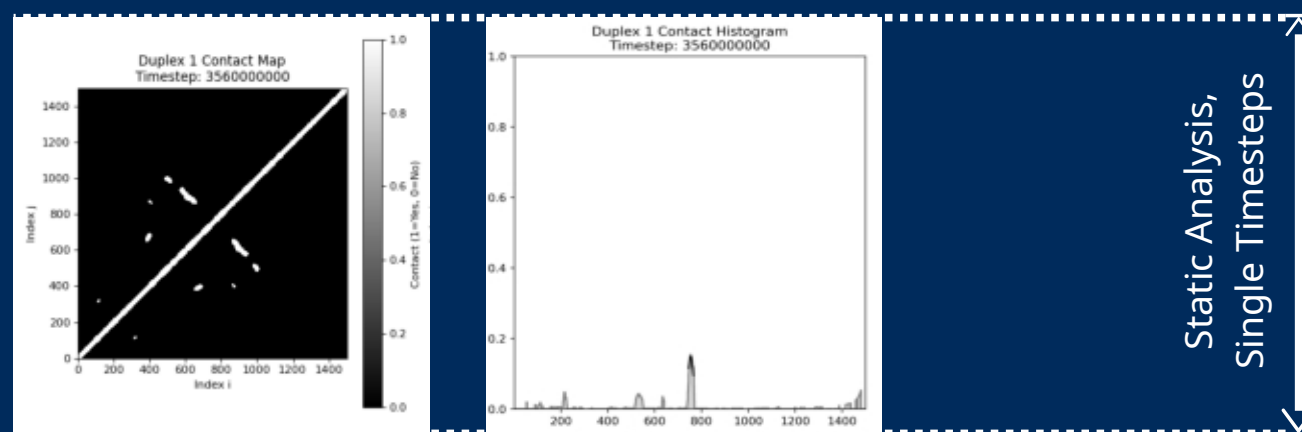
Write the points  $\odot$  (points of self-overlap) are easily detectable and relatively equally spaced in single dsDNA plectonemes.

## Plectoneme Detection

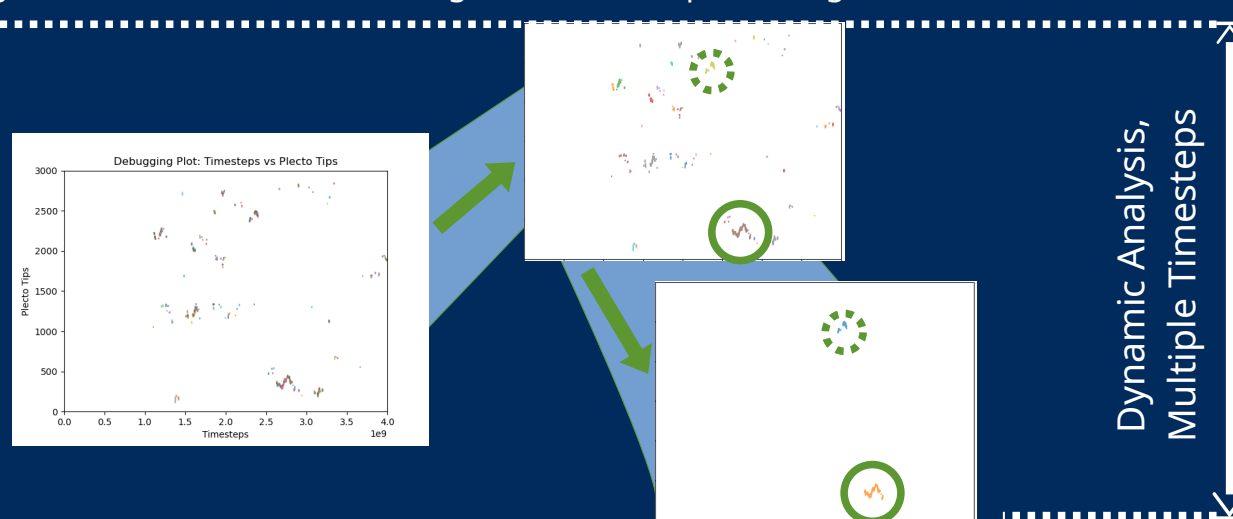
Plectoneme formation in single dsDNA strands is generally well defined, typically with relatively straight non-plectonemic regions at either ends and geometrically tight formation of the plectoneme itself; writhe locations are in close proximity, and there is little gap or offset between opposing regions of the plectoneme. As such, simple linear distance criterion often to a good job in reliably detecting plectonemes [4,5].

In contrast, the introduction of a second intertwined dsDNA strand results in a far more diverse conformational landscape, where 1D detection methods fail to distinguish between true plectonemes and just regions where two points of the same strand are nearby.

Instead, we build a pairwise squared-distance matrix with a binary contact threshold, collapsing this into a per-base contact profile by summing along perpendicular diagonals. Gaussians are then mapped to this data.



Tips are mapped into individual plectoneme tracks by tip proximity and timestep continuity. Temporally close tracks are merged, and short/invalid events are filtered out. The 'debug' plots below illustrate how we can monitor our algorithm at each stage, with the final result allowing for direct comparison against visualisation tools.



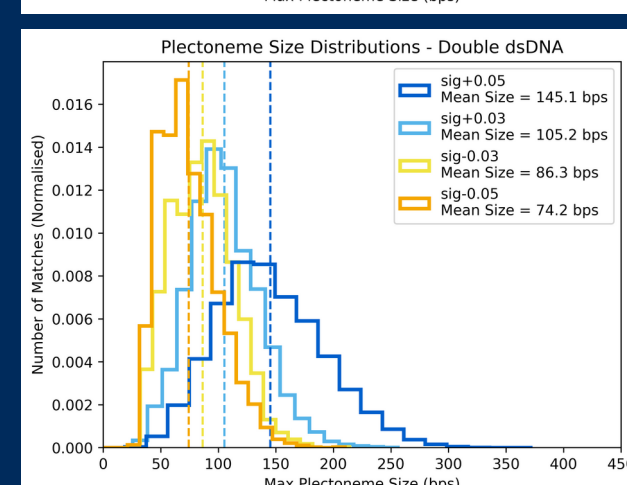
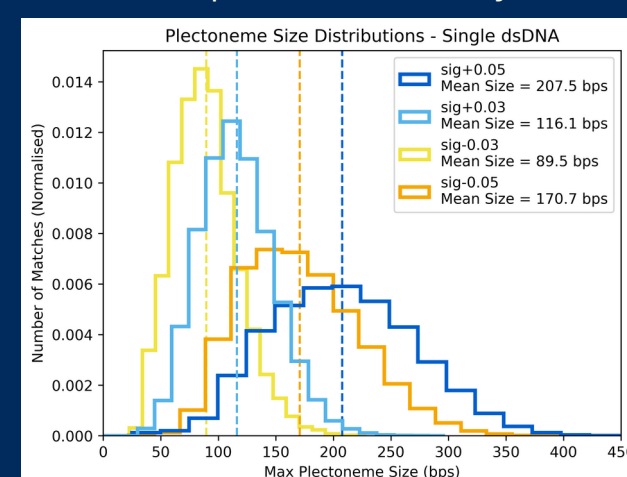
## Example Results

Our plectoneme detection algorithm records plectoneme sizes (based on Gaussian widths), as well as tip location (based on the mean of Gaussian start-end locations). In the columns below, we show results for single (**top**) and braids (**bottom**).

### Size Distributions

In single, sizes are generally symmetric across supercoiling densities, with supercoiling magnitude having a stronger influence on typical plectoneme size than supercoiling sign (under-vs-over-twist).

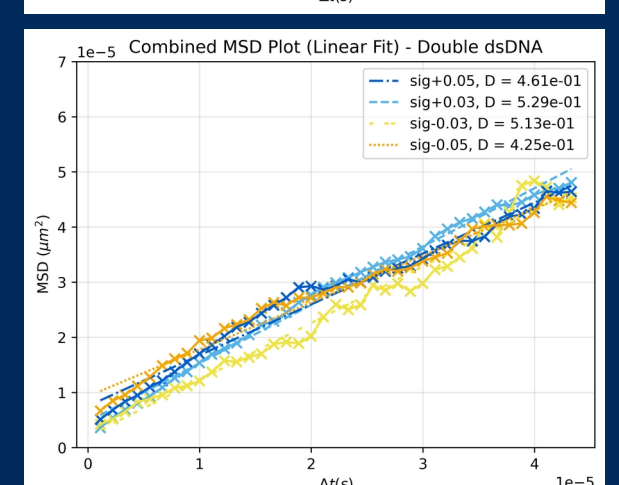
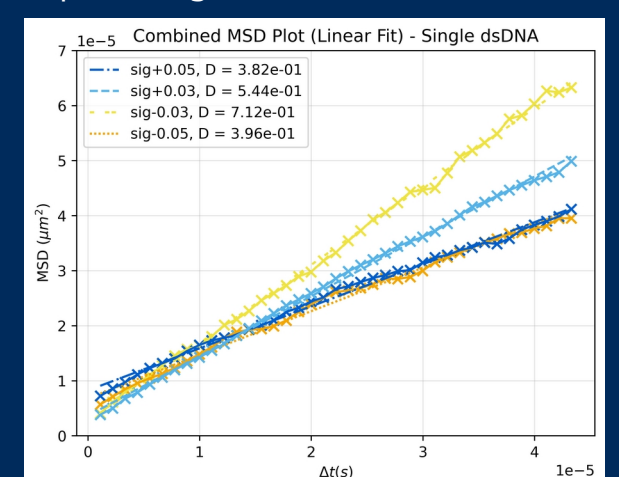
In braids, sizes shift towards smaller values. This reduction is most pronounced at higher supercoiling magnitudes, where the presence of a second duplex substantially limits



plectoneme growth, while the effect is less noticeable for  $\sigma = \pm 0.03$  where sizes are already relatively small.

### Mean-Squared-Displacement

Our results for single dsDNA appear within a reasonable range of known values [4,6]. Interestingly, the introduction of the second dsDNA in braids appears to flatten out the MSDs and show signs of convergence across supercoiling densities.



## References

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