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Abstract: 175P

Benchmarking biophysical readouts of nanoscale chromatin compaction in live cells.

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Inside the cell nucleus DNA is packaged into a multilayered structure called chromatin, which controls DNA template access and the sequences of DNA transcribed. In the field of developmental cell biology, there is a lot of interest in methods that can measure chromatin accessibility in a living cell, since the DNA sequences that chromatin makes accessible to transcription are cell type dependent and can change in response to biochemical cues. One promising way to measure live cell chromatin accessibility on a spatiotemporal scale relevant to transcription, is to quantitatively map the localisation and real-time diffusive route of different-sized fluorescent tracers throughout this porous structural framework by fluorescence fluctuation spectroscopy (FFS). The only problem is that the biological parameters output by FFS are complex to interpret and have not been benchmarked against gold standard ensembled based methods, such as micrococcal nuclease (MNase) digestion coupled with next generation sequencing (MNase-seq). Thus, in recent work we directly compared FFS based assessment of chromatin with MNase digestion with the aim of deriving a pipeline for biologists to explore chromatin accessibility at the single cell level.