Single molecule data set for the paper titled (Data for Figure4 in the paper):

A rhythmically pulsing leaf-spring DNA-origami nanoengine that drives a passive follower

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The user will find all the necessary data and analysis codes conveniently provided and properly labeled. For instance, the folder labeled "5mMNTP" contains data related to the 5mM of each NTP condition, as detailed in the paper. Each folders consist of three replicates for each condition.

1. The Movies to be analyzed have to be in “.trace” format containing 1024 pixel y and 2048 pixel X data. A mapping move of the same file format is also needed to start the analysis process.
2. Step1-Mapping: Use bright fluorophore beads to take a small movie that is used to generate mapping between the two channels. Use SM\_Mapping code for this. It should generate a text file containing the mapping parameters.
3. Step2-Trace generation: SM\_analysis code is used to find and generate traces. A mapping file describing the relation between the two channels of the movie is needed to run this code. Load the text file that is generated in step1. Proper threshold values were empirically chosen so that most of the visible peaks are chosen for analysis. “.traces”, ”.pks” and an image “.tif” file is generated.
4. The initial trace screenings are used to remove traces that do not pass certain intensity criteria. SM\_traceInitialScreeningV2 code is used for this part.
5. The screaned traces are loaded in SM\_traceViewing code to see and choose SM traces individually. When you select a trace and click on Save trace check box, an “AwesomeTrace” folder is generated in the same folder where the trace file resides. This folder will save the traces that are selected for latter review.
6. SM\_Trace\_Viewing\_timecCalculations code is used to save multiple segments of the trace and calculate the time between those sections.
7. The SM\_Histogram codes are used to plot histograms of the FRET data.