Pipeline to analyse tracking date from the AFS.

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This will provide an overview of how the analysis of the AFS data of strep-biotin was done using a python.

Preparing the traces for any analysis pipeline for the AFS.
Anchor point determination.
Drift correction.
Loop it over all bead s of interest

- Load all traces, posiiton, time and power.
- Clean outlines from the pos traces
- Determine the anchor point when non force is applied by taking the mean for X & Y and minimum for Z.
- Subtract the Anchor point.the pos traces will be centred around 0
- Compute the average of the motion of all the stuck reference beads.
- Determine and subtract anchor point for the averaged reference trajec
- Compute a rolling average of the average reference to correct drift in the bead of interest
- Recompute anchor point post drift correction for the bead of interest.

- Compute the length of the tethered
- Calibrate the force using PSD from traces.
- Identify the rupture time and define load time and loading rate and unbinding