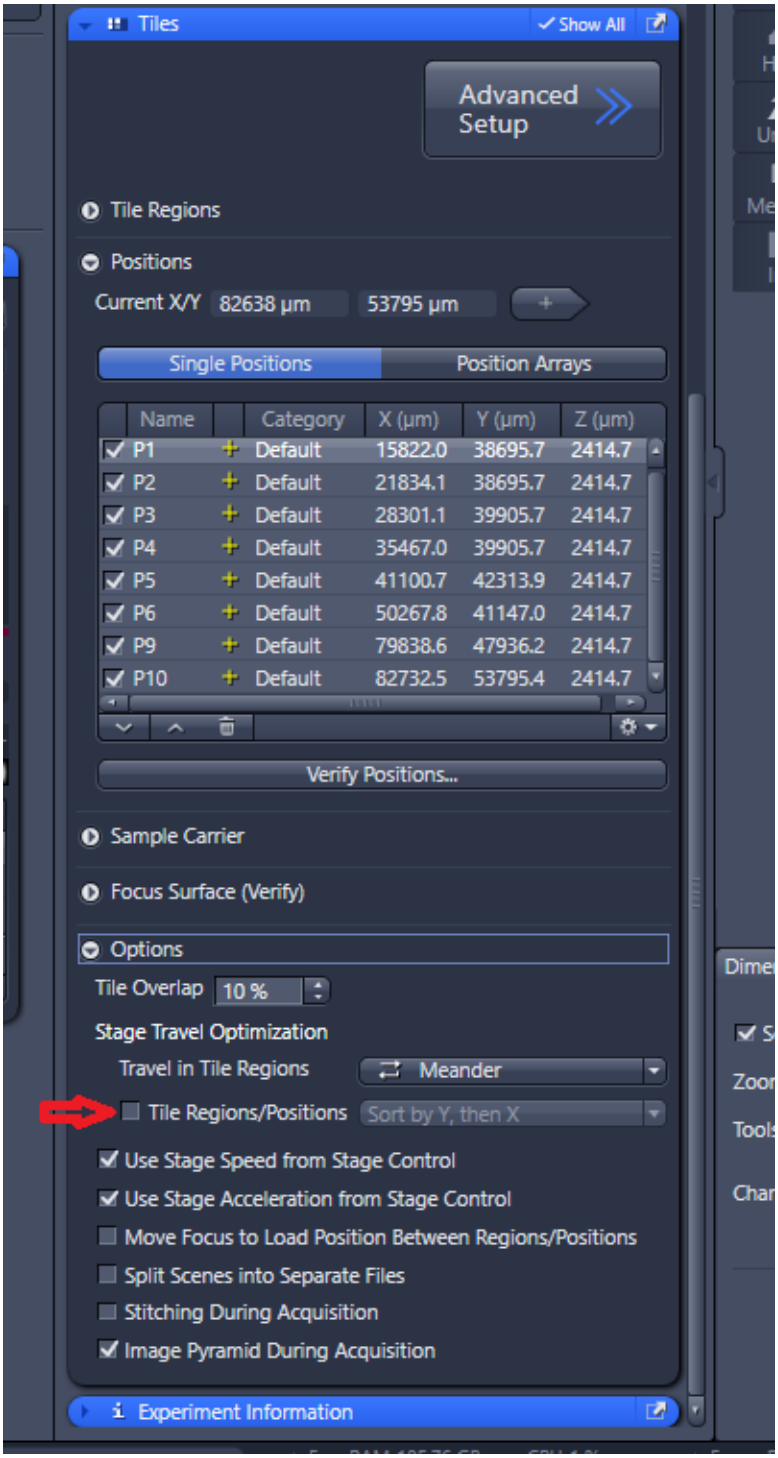
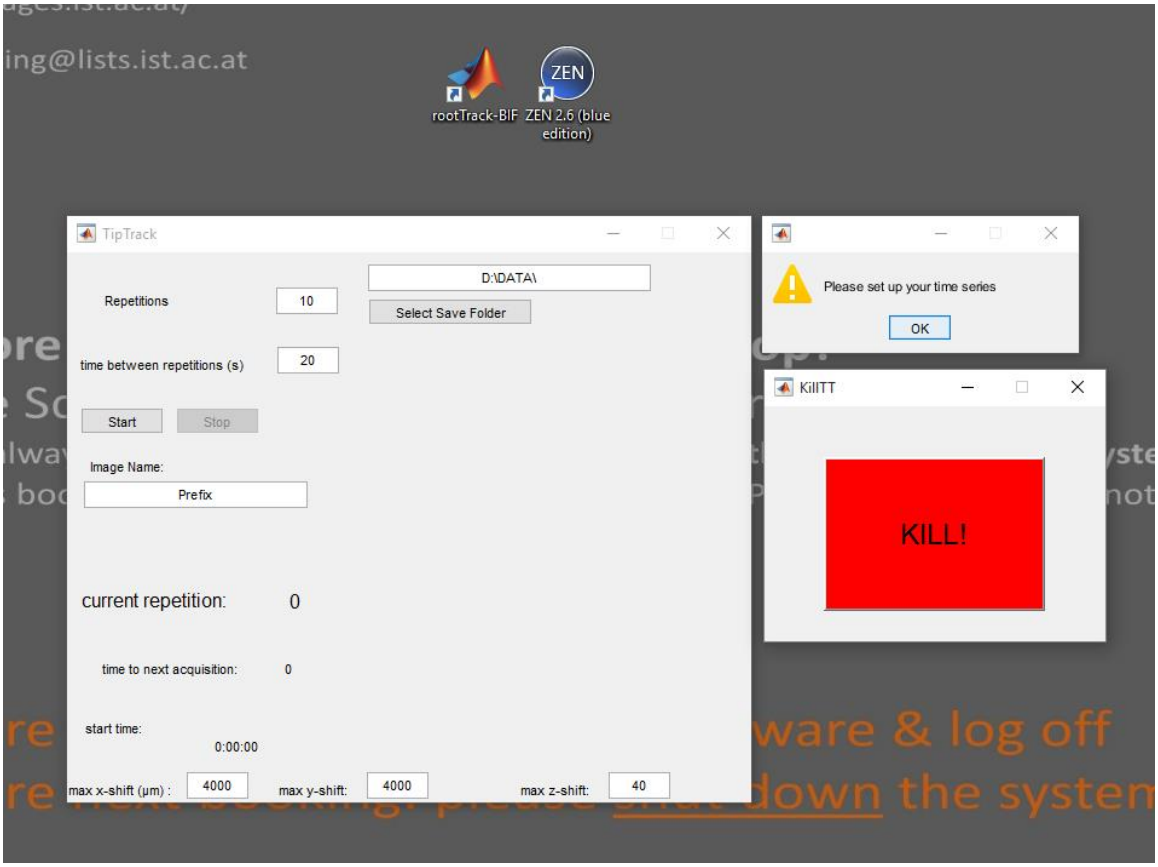
Using the root tracker

1. The first step is to define a experiment in Zen Blue. It should be a **single time frame**. Multi-color series and Z-stacks are possible, but not necessary. Time series will be generated by running the experiment multiple times automatically via the Root Tracker matlab script.

2. Define one or more positions in the 'Tiles' menu. The option **'Tile regions/positions' must be unchecked**. Otherwise the tracker will not work.



3. Open the rootTrack-BIF shortcut next to the Zen icon to start the root tracker. The program starts automatically:



4. Fill in the number of iterations (*repetitions*) and the interval between them (in seconds). Choose a folder on the data drive to save the files (*select data folder*) and press *start*.

5. To end the root tracker, press the *end root tracker* button.

Handling the files

The root tracker software creates separate files for each time frame, each one containing all the tracked elements as separate scenes. In order to sort the time series correctly the Bioimaging Facility provides two different macros.

1. To download the macro, visit **bif.pages.ist.ac.at**. Under *Image analysis* choose *Image analysis tools* and then *Image Analysis Scripts*.

2. Under *BIF FIJI macros* Choose **Root tracker concatenator** (concatenateTrackedImages.ijm), or choose ***Convert_roottracker*** under *BIF Python Scripts*.