

Automatic video tracking has had a major impact on animal behavior studies. One of the problems with using this to track the positions of animals has been keeping the animals distinct. To solve this problem for groups of fish, we will be using python code to track patterns of brightness as a visual identifier to track the fish using data from the labs of Dr. Keene, Dr. Duboue, and Dr. Kowalko, who all work with Mexican cavefish on the Jupiter campus.

1 Introduction

While visually pleasing, schooling is a rather challenging topic that has long befuddled animal scientists, due to the fact that to perform proper analysis of the animals' behavior, a vast quantity of positional data is needed. This has been alleviated recently with advances in technology, since scientists can now use computers to track the animals' positions. While this technically was possible before, this would require a person sitting in front of a video manually tracking the positions of each of the animals in question, which is what the program that we are writing aims to eliminate.

In particular, the group that this paper gets its data from is looking at Mexican Cavefish, which are both unique as an evolutionary remnant, which allows us to gain insight into the history of how schooling behavior has changed over time, and rather simplistic which is a boon for simplicities sake. In addition, one of the quirks of Mexican Cavefish is that different groups have startling evolutionary differences such as one of the groups having not evolved schooling, despite being nominally the same species as the ones that did. However, one issue that arises is that it is impractical to quantify fish behavior without automated tracking. As such, this project aims to provide a program that tracks the fish so that the labs can analyse them.

Since fish motion has become so much easier to work with, some groups that were studying the fish are using this opportunity to study the lives and motion of different types of fish in much more detail and with much more data than they were before. One of these is an association of groups out of Jupiter, which are working on Mexican cavefish. These labs, headed by Dr. Keene, Dr. Duboue, and Dr. Kowalko, collectively known as the cavefish trilab, are currently interested in the evolution of behavior of Mexican Cavefish, which necessitates a lot of video of the fish. Over the last few years the cavefish trilab has been collaborating with Dr. Fily, to apply physics techniques of collective grouping. He has developed a software to track the fish, which is currently in use by the labs, but has the issue with maintaining the identities of the fish throughout the experiment, so this project aims to fix that. Since the trilab is working with video of cavefish, this presented an opportunity to apply these techniques to clean up the video they have produced.

Before understanding the nature of the problem, we must say a few words about the process. The process starts by picking out the dark spots in the video caused by the contrast between the fish and the light background of the tank.



Figure 1: The two fishes

Once we have the positions of the fish, we can compare how the fish has moved from frame to frame by comparing the distances between their last known positions.



Figure 2: Before and after an overlap

However, we quickly run into the issue that the program doesn't respect continuity. As we can see below, when the program can't figure out which fish is which after an overlap, Figure 3, it takes a guess based off distances, Figure 4, but can get them wrong such as the situation on the right.

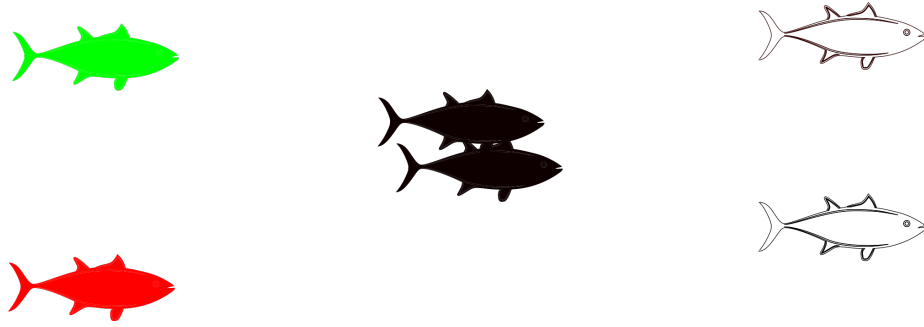


Figure 3: The program doesn't respect continuity

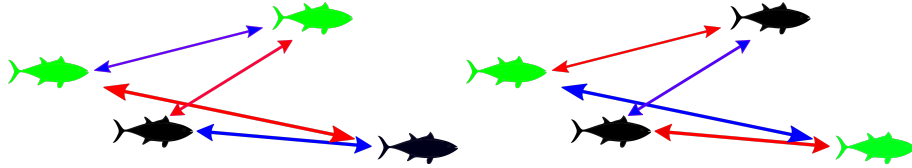


Figure 4: maintained identities (blue) and swapped identities (red) for two scenarios

If the software swaps the fish, it will look like the fish traveled longer than it should have. Below we have the fish as it tracks up to an overlap and goes past it, so you can see where the error would occur.

To do this, we are applying two approaches in tandem, both a more common naive technique that tends to fail in areas where the fish are close together but is computationally light and works well when the fish are far apart; and a second one of comparing a unique identifier for each fish from moment to moment to find the fish with the same identifier which is much more accurate, but computationally intensive, which we got from the paper on the idTracker program from when they tried to tackle the same problem. The reason we are using two processes to track the fish is that a common issue of the more common and simpler first method of automatic tracking is that whenever the position of the fish have been confused, the tracker has no way to regain the fishes' position and track which fish is which. To solve this issue, we need a way to track the fish from moment to moment in the cases where this common approach fails, which leads us to the second method.

We can extend this frame by frame comparison over the regions where the fish are visually distinct. However, in ranges where the positions of the fishes are reported as overlapping, this approach won't work due to the construction of the tracking program.

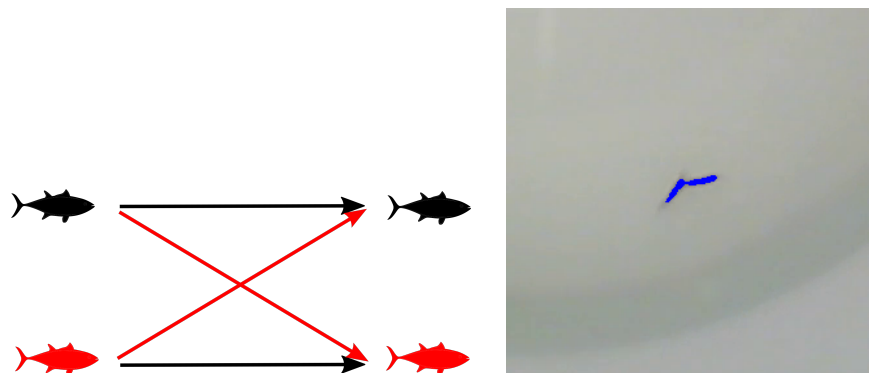


Figure 5: Left: A basic swap check, longer(wrong) distances are in red. Right: An example of an Overlap

Instead, during these ranges, we have to take the more involved approach of comparing a visually distinctive feature of the fishes from frame to frame.

2 Previous work

The main process by which we are computing the difference between the fish is a process laid out in the paper on idTracker [**idTracker**]. The authors of the paper also had a problem with the approach of tracking distances between the fishes position in that the approach both had too much error, and that the error tended to compound in on itself over the length of the tracking process. To combat this, the paper proposed a process by which each fish would be given a unique identifier, which the authors decided would be the fishes intensity map, which was created by taking readings of the brightness of the fish and noting unique spots. The process then compares the identifiers frame by frame, to determine which fish is which. We are emulating this process by using a 2d histogram to plot their intensity maps, and using this to compare the frame data.

One thing to note about this process is that it is in no way unique. Since this is a common problem across all biological diciplines that deal with animals on a small scale, multiple solutions have com forth for resolving this issue. Some of the more notable ones are: idTracker.ai, which is an upgrade to the idTracker program using machine learning; trex (cite trex.run), which is another program that using machine learning; and deeplabcut, which also uses machine learning, but is optimized for posture tracking in animals. These programs are in a position where they are adjacent to what the labs we are working with need, they each have pitfalls htat make them nonideal. Most prominently, the labs would prefer not to have to train programs to get accurate results, with the biggest offender of this being deeplabcut, in addition to not wanting to deal with the computationally insensitive nature of machine learning. This is in addition to several of the programs giving poor results when used in test cases due to optimization issues, with trex being the worst culpreate for this. Instead the deccision was made to create a program that was optimized for use by the labs.

3 Results

3.1 Introduction

The basic setup of the labs we are taking data from is a tank with two fishes in it and a camera trained on them, as seen below.

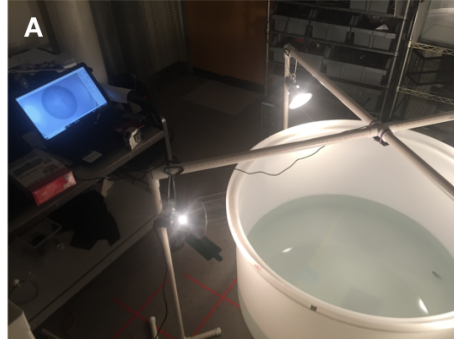


Figure 6: An example frame of the video

This setup produces a video for us to use, of which an example frame is shown below.



Figure 7: An example frame of the video

Since we need to track the fish in the setup, we need feed the video captured from this setup to the analysis program. In this case we are using trilab-tracker for this(cite <https://github.com/yffily/trilab-tracker>)(only using image recognition portions, and then taking over from there) since it has been formulated expressly for this purpose. The trilab-tracker then returns an array for each

of the fish containing the pixels and their colors. Once we have the fish saved in a format that we can analyze, the next step is to segment the data into regions based on the number of fish it detects. We do this because the distance based unswapping approach doesn't work on regions where there is only one fish detected, so we need to tell the program where it can use that approach.

3.2 Distance Based Unswapping

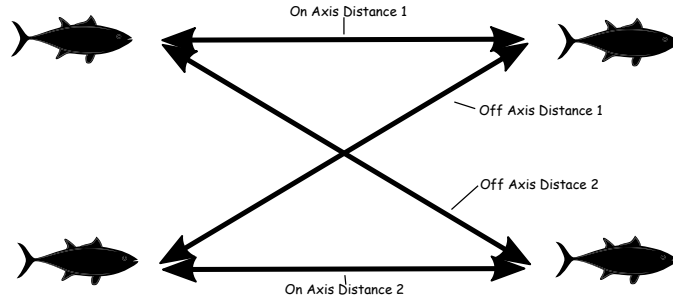


Figure 8: Basic overview of unswapping logic

The first approach we tried is taking the positions of the fish and comparing how close they were to their previous positions to check for swaps. This approach works on the regions where there are two fish detected (“nonoverlapping range”), and so we need to confine it to those regions.

3.3 Histogram Based Unswapping

In the overlapping (or regions where one fish is detected), we need an identifier for the fish, so we will use bright spots on fish as this identifier. Once we have those identifiers, the easiest way to compare these identifiers is to create histogram of the brightness of the fish. We can then have the program compare the slight differences, because even though look same, they are different enough that the code can pick up the differences. However, one issue that we ran into is that the fish we are using are subpar because they are too uniform in brightness.

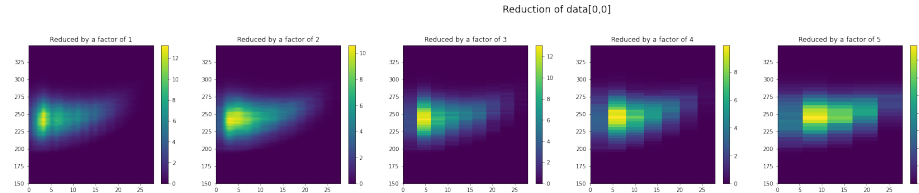


Figure 9: The histograms

3.4 Accuracy

One of the first things that I noticed when I compared the results of the unswapping with the manual check was that there was a relatively low accuracy rate. This is probably due to the fish being too uniform, as once we switched to a slightly more accurate fish recognition program, we can expect a slightly more accurate result.

4 Methods

One of the things that quickly becomes apparent is that the fish are present as a series of dark pixels against a white background, which means that we can feed the image of a frame to a different software (in this case trilab-tracker) to generate a list of pixels that compose the fishes for tracking. This software returns the fish as either a pair of arrays for the regions where it detects two fish, and a single array where it detects one fish of the form [frame][fish][xpixels, ypixels][color]. Once we have the fish in an array form for ease of operation, we need to partition the data into sections of overlapping and non overlapping regions so that we can apply different approaches to each.

```
1 i2=0
2 nonOverlappingRange=[]
3 while i2<len(fish):
4     i1=i2
5     while i1<len(fish) and len(fish[i1])!=2:
6         i1+=1
7     i2=i1
8     while i2 < len(fish) and len(fish[i2])==2:
9         #find the first overlapping index
10        i2+=1
11    nonOverlappingRange.append([i1,i2])
12 print(nonOverlappingRange)
```

Once we have the data sorted into regions, we can begin working on the nonoverlapping ones. The attack for this section is to track the distance between the fish to determine if there was a swap, by comparing the on and off axis distances of the two possible positions of the fish. The downside of this approach is that it only works in areas in which the tracker returns that there is two fish, so we will first need to determine what regions are overlapping and nonoverlapping. Once we have these nonoverlapping regions, we can begin performing the swap check.

```

1 def swapStatus(pos,i):
2     '''
3     Detect swaps between consecutive frames based on
    proximity.
4
5     Input:
6         pos:Postionts. Array with shape (Nframes,Nfish
7         ,Ndimensions),
8         i: Frame index. Int.
9
10    Output:
11        Int. 0 if no swaps, 1 if swapped, 2 if
12    overlapping.
13    '''
14    nFish=pos.shape[1] #Number of fish
15    distanceMatrix=[np.linalg.norm(pos[i+1][0]-pos[i
16    ] [0]),
17                    np.linalg.norm(pos[i+1][1]-pos[i
18    ] [1]),
19                    np.linalg.norm(pos[i+1][0]-pos[i
20    ] [1]),
21                    np.linalg.norm(pos[i+1][1]-pos[i
22    ] [0])]
23    swapCriteron=(distanceMatrix[0]+distanceMatrix[1])
24    -(distanceMatrix[2]+distanceMatrix[3])
25    if abs(swapCriteron)<1e-10:
26        return 2 #Overlapping
27    elif swapCriteron>0:
28        return 1 #Swapped
29    elif swapCriteron<0:
30        return 0 #Normal
31    else:
32        return -1

```

Once we have this data for the nonoverlapping ranges, we have to switch approaches for the overlapping regions. Since we can't compare the distances with the software only reporting a single fish, we are forced to use a different technique., we are using the technique of comparing the histograms of the brightness of the fishes before and after an overlapping range, as proposed by the paper on `idTracker[idTracker]`. The process for this is for us to feed the arrays directly into numpy's `histogram2d`, which allows us to compute the histograms with a minimal amount of effort other than determining the correct bins. After that we need to manipulate the data slightly so that the histograms are taken as the average over the nonoverlapping regions for more accuracy, and are then saved out for comparison.

```

1 for i in trange(60, desc='nonOverlappingRange'):
2     for k in range(2):
3         countSum=0
4         countDif=0
5         pairData=[]
6         for j in range(*nonOverlappingRange[i]):
7             fishPixels = fishU[j][k]
8             m,l=np.triu_indices(fishPixels.shape[0],k
=1)
9             d=np.sqrt((fishPixels[l,0]-fishPixels[m
,0])**2+(fishPixels[l,1]-fishPixels[m,1])**2)
10            bSum=fishPixels[l,2]+fishPixels[m,2]
11            bDif=fishPixels[l,2]-fishPixels[m,2]
12
13            heightValuesSum,_,_=np.histogram2d(d,bSum,
bins=(binsDist,binsSum))
14            histSum+=heightValuesSum
15            countSum+=1
16            heightValuesDif,_,_=np.histogram2d(d,bDif,
bins=(binsDist,binsDif))
17            histDif+=heightValuesDif
18            countDif+=1
19            histSum/=countSum
20            histSumList[i,k]=histSum.copy()
21            histDif/=countDif
22            histDifList[i,k]=histDif.copy()

```

This produces a histogram, similar to the one seen below.

We can then feed this representation into a simple value comparison to check for swaps. When rendered to a more human readable form, we can either get a list of frames, or a graphs as shown below.



Figure 10: The graphs from the histograms

A An appendix