Collective Animal Behaviour: Fish Schools

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Contents

Abstract

This report will look into modelling fish in a number of different ways. A basic model will initially be used and then built upon to make the interactions between fish more realistic. Initially the fish have one interaction zone surrounding them, then it gets increased to three, one smaller than the original one and one much larger. After the three zones are implemented a field of view is incorporated so that the fish cannot see all the way around themselves. When the model has been built up a predator is then introduced so that the interactions can be investigated. Once the predator has been introduced, the model is then modified in order to make the movement of both the predator and the fish more realistic. This produces unexpected behaviour for the predator when it swims towards the mean location of the fish.

1 Introduction

In nature a large group of animals are seen to act together as a unit, for example, large flocks of starlings, schools of fish, swarms of locusts and even herds of wildebeest. Some group together for protection or foraging for food, but others for heat. The increase in protection is due to that as a group they can have a larger knowledge of what is going on around them. Being in a group means that when one individual spots something, for example a predator, then the whole group can learn more quickly than if they were on their own.

One of the most fascinating things about observing large groups of animals is looking at the patterns which they create. In the UK large flocks of starlings are known as murmurations and produce spectacular aerial displays, which can be witnessed all across the country, in cities as well as in rural areas. Schools of fish have similar collective behaviour to starlings and produce some unique patterns: in some situations fish are known to swim in a torus, (Figure 1.1). In nature fish are known to swim in a torus when the school wants to stay stationary, for example when they are spawning, or when they are being attacked and wish to confuse the predator [1].

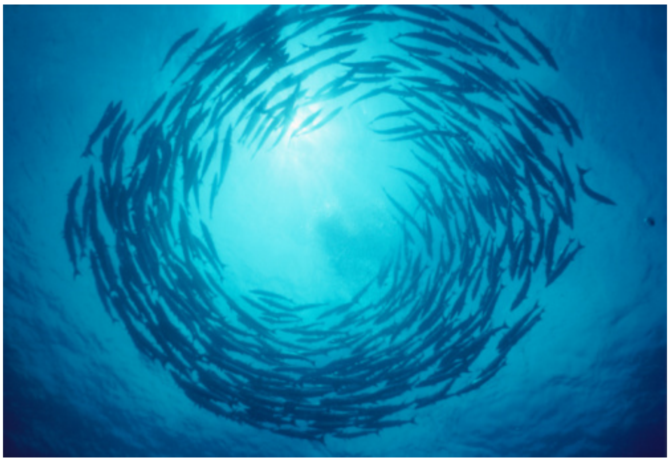


Figure 1.1: Fish sometimes swim in a torus when they are being attacked by a predator or the school wants to stay stationary before spawning. Picture copyright: Jeff Rotman [2].

Over recent years there have been many different approaches for modelling groups of animals with no leader. Vicsek *et al.* [3] used an agent based model to examine self-driven particles. These self driven particles can be thought of as fish, birds or even bacteria. The model they used looked at fixed distances from a particle to its neighbours in order to update positions and directions. Whereas in a similar model Huth *et at.* [4] used a fixed number of neighbours to update the direction and position of each fish. There have also been papers comparing the two to see which is most realistic. In 2007, a paper was written by Ballerini *et al.* [5] that states it is more likely that the fish interact on average with a fixed number of neighbours rather than those within a fixed distance. A completely different method of modelling the movement of fish was used by Faugeras *et al.* [6], in their paper they used advection-diffusion PDEs. The difficulties when using this model are apparent when expressing the time and spacial advection-diffusion coefficients. In the paper by Faugeras *et al.* they simplified the advection and diffusion by using a suitable parameter.

There have also been experiments tracking fish and recording the distances between each fish. The results of one of these experiments was compared to simulated results in the paper by Huth *et al.* [4]. They used the the closest n neighbours model, and their simulated results agreed with the experimental data.

This report looks at models of fish schools, examining how the parameters of a model control simulated fish behaviours. A basic model will be built upon and at each stage the model will be looked at in order to see where the behaviours differ. The model starts with one interaction zone sounding each fish. After some analysis it is possible to distinguish different behaviours when the radius of the interaction zone is changed

Then making the model more complex, the interaction zone is split into three distinct zones. Each zone causes different effects to how each fish will interact with its neighbours. After some analysis of the model with three zones, removing zones individually allows the roles of the different zones to be interpreted. The size of each zone is then changed to see the effects on the alignment of the fish schools.

A field of view is introduced to make the model more lifelike. This causes a blind spot behind each fish. Repeating the same analysis of the model with three zones on the field of view model any effects the blind spot has on each version of the model can be observed. The report will also look at how altering the size of the field of view changes behaviour seen.

In the penultimate section, the report finally investigates how the introduction of a predator will affect the school with the parameters fixed. There are two ways in which the fish react to the predator: swim directly away from the location of the predator; and swim away with an angle determined by a normal distribution. For each of the two versions this report will analyse the simulated fish.

2 Basic Model

The simplest model this report looks at is a self propelled particle scheme that was devised by Vicsek *et al.* [3]. In this model a fish changes its direction by aligning itself with the average direction of its neighbours within a certain distance [3]. Random noise is added to the new direction to allow for the imprecise accuracy by which a fish can asses its neighbours' directions. The initial state of the model gives each fish a random position and velocity;

$$\underline{x} = (x, y),$$
$$\underline{v} = (v\cos\theta, v\sin\theta).$$

Where θ is the direction of the fish such that $-\pi \leq \theta \leq \pi$. We have split the velocity into its components in the x and y direction. The magnitude of the velocity, $|\underline{v}| = v$, is constant. Hence for every fish, i,

$$f_i = (x_i, y_i, v_{x,i}, v_{y,i}),$$

where $i = 0, \ldots, N$, and N is the number of fish. In order to analyse the fish and their behaviour their positions are updated for many time steps.

2.1 Updating the Location and Direction of the Fish

The update step starts by calculating the distances between all the fish using Pythagoras' theorem. The distance between fish i and j is given by

$$d_{i,j} = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2}, \tag{1}$$

where fish i and fish j have positions (x_i, y_i) and (x_j, y_j) respectively. When updating the f_i vector the new velocity components become

$$v_{x,i} = \frac{1}{N}\sum_{d_{i,j}<D} v_{x,j}, \tag{2}$$
$$v_{y,i} = \frac{1}{N}\sum_{d_{i,j}<D} v_{y,j},$$

where D is a fixed radius, set as a parameter around each fish, and the index j refers to the fish within this region. This updates the direction the fish is swimming. The Euler time stepping method, $x = \delta t \cdot x + x_0$, calculates its new position. The new vector for fish i therefore is,

$$f_i = (x_i + v_{x,i} \cdot dt,\ y_i + v_{y,i} \cdot dt,\ v_{x,i},\ v_{y,i}),$$

where dt is a short time interval. When updating the f_i vectors, the current position and direction of each fish are used. Therefore, in the final step when updating the fish over one time step there are two vectors for each fish, $f_{i,current}$ and $f_{i,new}$. The fish move forward one time step by setting

$$f_{i,current} = f_{i,new}.$$

It is not known that fish average their neighbours direction, maybe they follow a leader or a fish to their left or the closest few fish. Even if they do average their neighbour's direction there will be some error due to the opacity of the water or the refraction of light in water. To mirror this in our model some noise is added in calculating which direction to travel in next. To include this uncertainty in the model the angle at which the updated fish i is going to swim is perturbed by a noise term, ω, where

$$-\sigma\frac{\pi}{2} < \omega < \sigma\frac{\pi}{2}.$$

This ensures that when $\sigma = 1$ there is a possibility that the fish can be perturbed by an angle up to $\frac{\pi}{2}$ radians. So the fish direction of travel

$$\theta = \arctan\left(\frac{v_{y,i}}{v_{x,i}}\right),$$

where $v_{y,i}$ and $v_{x,i}$ are calculated using the equations (2), becomes,

$$\theta^* = \arctan\left(\frac{v_{y,i}}{v_{x,i}}\right) + \omega. \tag{3}$$

This gives the new velocity components

$$v_{x,i} = \cos\theta^*,$$
$$v_{y,i} = \sin\theta^*.$$

Figure 2.1 shows how using equations (2) and (3) in order to update the position and direction of five fish looks pictorially. In Figure 2.1a a radius of size 6 is drawn around the first fish to be updated. The distances between all fish are calculated using equation (1). Then the fish within this radius are coloured orange. The dark purple fish shown in Figure 2.1b is where the fish being updated would go if there was no noise, i.e. traveling in the average direction of the orange fish. Since we want to have noise, here $\sigma = 0.5$, the pale purple arrows represent where the fish will move to. Repeating this for all five fish Figure 2.1c is produced. From this we can easily see where each fish will move to. Finally in Figure 2.1d, all the fish have moved simultaneously to their new positions.

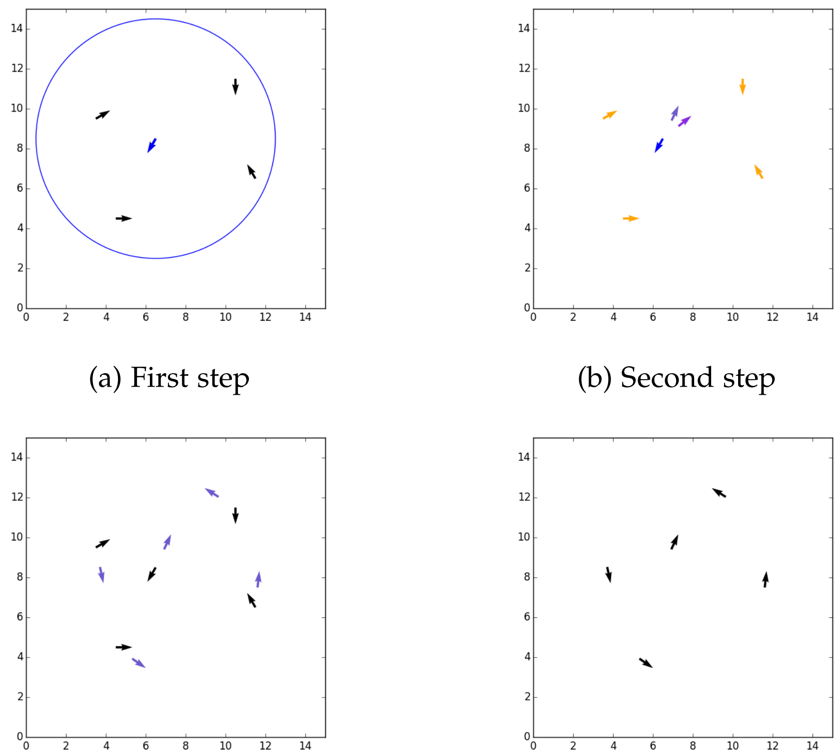
2.2 Analysis of the Basic Model

Table 2.1 shows the parameters used throughout the analysis of this model.

Parameter	Symbol	Value Range	Unit
Number of fish	N	40-200	Dimensionless
Velocity	v	0.25-1	Length per second
Time step	dt	1.0	Seconds
Noise	σ	0.0 - 1	Radians
Radius of Alignment	D	2.0 - 15.0	Length

Table 2.1: Parameters of the basic model.

When running simulations of the basic model boundary conditions are required. The boundaries can either be very large so that the fish never reach



(a) First step (b) Second step

(c) Penultimate step (d) Last step

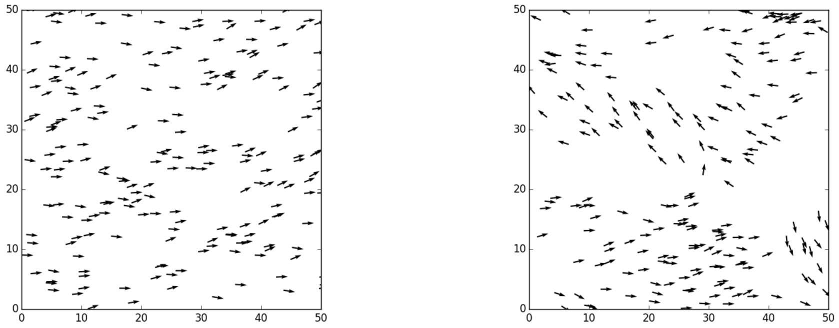
Figure 2.1: Updating the location and position of five fish using equations (2) & (3).

them or the boundaries can be smaller and periodic. For the work on the basic model the boundaries are set to be periodic. The size of the boundaries are set to be 50×50 so it takes about

$$\frac{nx}{v} = \frac{50}{1} = 50$$

time steps to cross the grid.

The value of D heavily dictates the patterns observed, as shown in Figure 2.2. In Figure 2.2a the value for D, $D = 15$, is approximately a third of the width of the domain, here the fish are all aligned. However, in Figure 2.2b where the value for D is a third smaller, $D = 5$, the fish group together and are aligned within these groups, but different groups might not be aligned with each other.



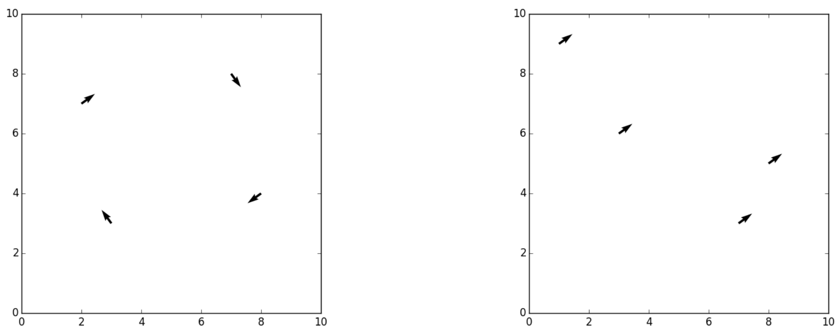
(a) $D = 15$. (b) $D = 5$.

Figure 2.2: Two simulations with $N = 200$ fish where the area is 50×50 units, $\sigma = 0.2$. The alignment in (a) is $a = 0.98$ and in (b) is $a = 0.10$.

How well a school of fish are aligned can be quantified. This is done using

$$a = \frac{1}{Nv} \left| \sum_{i=1}^{N} v_i \right|, \tag{4}$$

where $v_i = (v_{x,i}, v_{y,i})$. This gives us $0 \leq a \leq 1$. Where $a = 0$ is perfect non-alignment (Figure 2.3a) and perfect alignment is when $a = 1$ (Figure 2.3b).



(a) $a = 0$. (b) $a = 1$.

Figure 2.3: Pictorial representation of alignment values calculated using equation (4)

In Figure 2.2 the alignment changes as the radius of alignment is changed. However, the radius only has a small impact on the alignment values. This is implied by Figure 2.4 and the mean values of alignment in Table 2.2. What can be deduced is that for the first 15 time steps of the simulation, the simulation with $D = 1.0$ has the lowest alignment, whereas the when $D = 15.0$ has the highest alignment.

Due to the random nature of where the fish start and their random orientation it is not always the case that the simulations with a smaller radius of alignment have a lower alignment measurement. However, when averaging over many simulations a smaller radius gives lower alignment. Using an example of a school of fish with a small D value the group may split into two distinct groups swimming in opposite directions, they would not interact with each other because of the small interaction zone. In their own school they would be very well aligned, however, alignment of all the fish will be approximately $a = 0$. A similar simulation with a large D value will have a large alignment since the only disturbance is coming from the noise parameter.

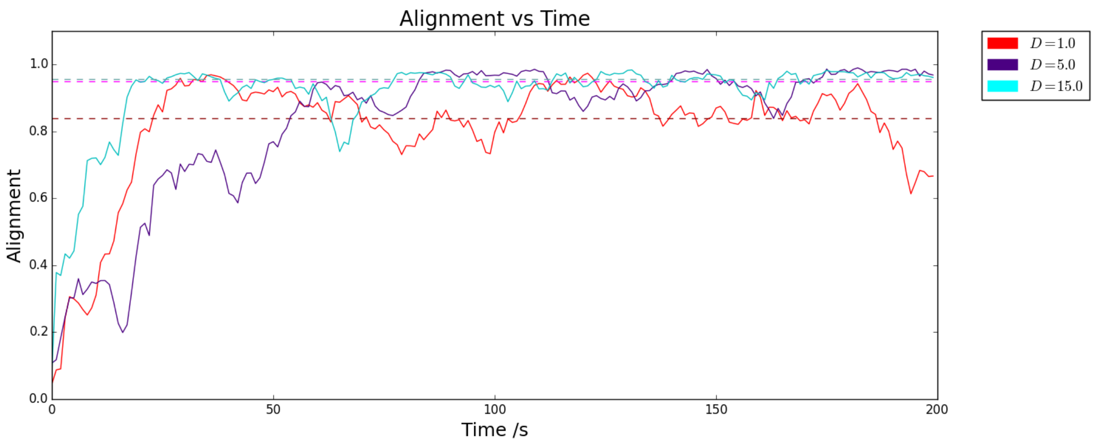


Figure 2.4: Running 3 simulations with the parameters $N = 40$, $v = 0.25$ and $\sigma = 0.2$.

D	Mean a Value	Standard Deviation
1.0	0.84	0.07
5.0	0.95	0.04
15.0	0.96	0.02

Table 2.2: Mean and standard deviation values for three simulations run with different D values. The mean and standard deviation are calculated over the last 70 time steps.

The relatively small size of the domain leads to high a values for all D values. Repeating the simulations above in a larger domain, of size 500×500, where the fish start in a 50×50 square in the centre removes this phenomenon. In Figure 2.5 alignment is plotted against time. The alignment values in the plot are considerably smaller than values when the domain was 50×50. This is because the fish now have a much larger space to swim in, they never reach the boundaries. Calculating the mean alignment values, Table 2.3, over the last 70 time steps gives an indication of the statistically steady mean. The standard deviations over the three simulations are very similar.

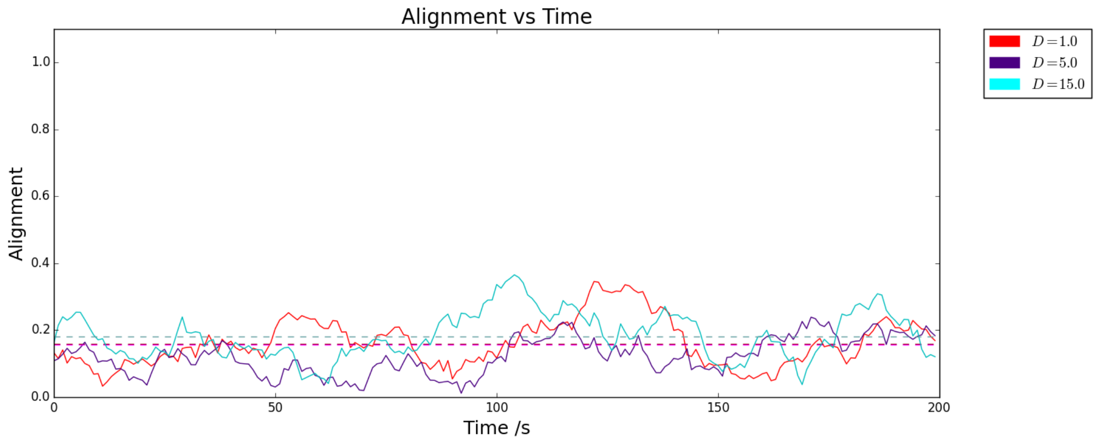


Figure 2.5: Running 3 simulations with the parameters $N = 40$, $v = 0.25$ and $\sigma = 0.2$ in a larger domain, 500×500.

D	Mean a Value	Standard Deviation
1.0	0.16	0.07
5.0	0.16	0.05
15.0	0.19	0.07

Table 2.3: Mean and standard deviation values for three simulations run with different D values in a domain of size 500×500

Altering the noise parameter and keeping D constant produces Figure 2.6. For noise, $\sigma = 0.0$ (the red line), after some initial time the fish all become perfectly aligned and stay aligned for the rest of the run. This occurs since there is no noise to make them deviate from being aligned once they have achieved it. When increased to $\sigma = 0.2$, the noise has been increased by just a small amount and the fish never reach perfect alignment. In fact they reach an average value of $a = 0.73$, shown in Table 2.4. This is due to the noise term moving them them out of alignment. When increasing the noise methodically the alignment doesn't decrease linearly. It decreased slowly at the beginning then faster near the middle then slowly again when at the highest σ values used. There appears to be three different behaviours shown here. The first is when $\sigma = 0.0$, here the fish are perfectly aligned and stay aligned. The second comes from $0.0 < \sigma \lessapprox 0.6$ where the fish are relatively well aligned with small oscillations. then the final behaviour comes from $0.6 \gtrapprox 1.0$ where the fish have a very low alignment value with large, very frequent oscillations. The simulation ran with $\sigma = 0.6$ appears to be a boundary as it spend some of the time acting like the simulation where $\sigma < 0.6$ and the rest of the time like $\sigma > 0.6$.

This suggests that as the noise increases the average alignment decreases while the oscillations, or standard deviation, about this average stay similar.

σ	Mean a Value	Standard Deviation
0.0	1.00	0.00
0.2	0.73	0.17
0.4	0.62	0.17
0.6	0.52	0.21
0.8	0.32	0.14
1.0	0.24	0.11

Table 2.4: Mean and standard deviation of the alignment values for the six simulations run with different noise. The mean and standard deviation are calculated over the last 200 time steps.

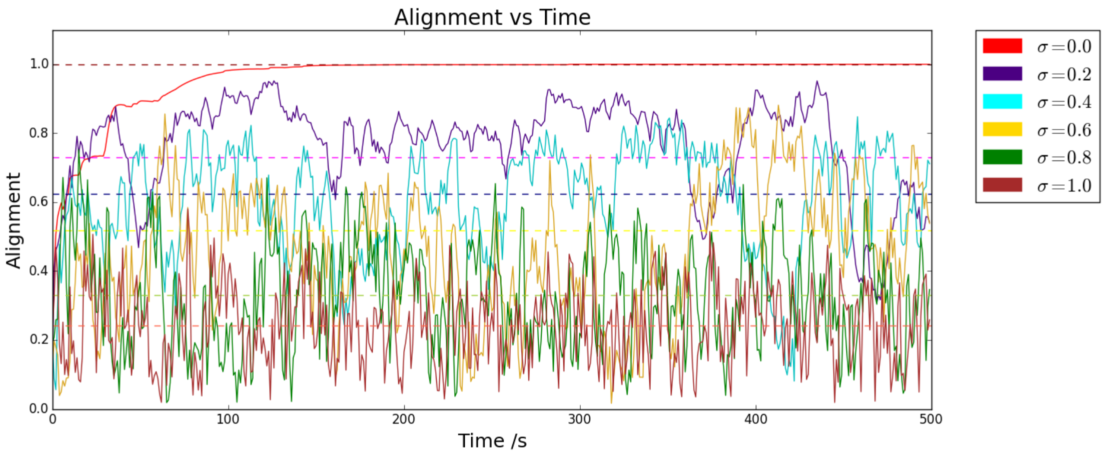
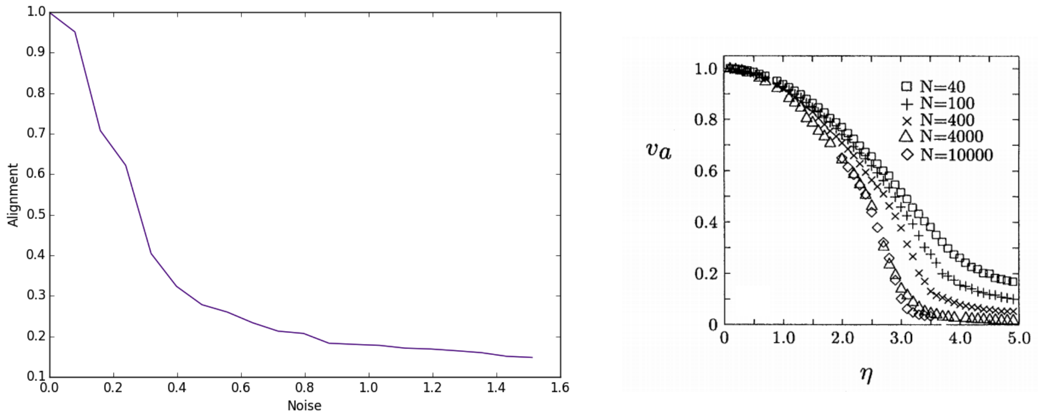


Figure 2.6: Alignment over time plot for six simulations keeping $N = 40, v = 0.31$ and $D = 7.0$ while varying σ.

Figure 2.6 shows that alignment decreases as the noise increases. To investigate Figure 2.7a, alignment against noise (σ) was produced by running 20 simulations each with a different noise value, ranging from $\sigma = 0$ to $\sigma = \frac{5}{\pi}$.



(a) When $N = 40$ this is a rapid but relatively smooth decline in alignment.

(b) Figure taken from the paper by Vicsek *et al* (1995) [3].

Figure 2.7: Alignment vs noise plots from simulations ran using (a) our model and (b) using the model by Vicsek *et al.* [3] where $v_a = a$ and $\sigma = \eta \frac{2}{\pi}$.

The value $\sigma = \frac{5}{\pi}$ was chosen in order to compare with the figure in the paper by Vicsek *et al* (1995) [3] since they calculate their noise parameter differently, $\sigma = \eta \frac{2}{\pi}$. The alignment value for each noise was calculated by averaging over 15 simulations with the same noise value. Figure 2.7b has five different lines. The line given by squares is equivalent to the purple line in Figure 2.7a. The purple line is not as smooth as the Vicsek *et al.* plot. In their paper they did not give information about how each point was calculated. If the two figures were produced using the same method then Figure 2.7b was made using a larger number of σ values and each was most likely averaged over a larger number of simulations.

2.3 Different Behaviours in the Basic Model

Running multiple simulations of the basic model we produce the results in Table 2.5. From the observations in Table 2.5, we can see that there are two different behaviours in this model. The first behaviour observed is when $0 < D < 9$. In this range of alignment radii the fish clump together and swim within these groups. The second, when $D \geq 9$, the fish all become aligned almost instantly. In the region $8 < D < 10$ the fish move slightly closer together before becoming aligned, this implies that the distinction between the two behaviours is not a sharp transition.

D Value	Observations	Alignment
15.0	aligned	0.98
14.0	aligned	0.98
13.0	aligned	0.98
12.0	aligned	0.98
11.0	aligned	0.98
10.0	aligned	0.98
9.0	aligned	0.98
8.0	clumping	0.97
7.0	clumping	0.97
6.0	clumping	0.95
5.0	clumping	0.90

Table 2.5: Observations varying D values, keeping $N = 200$ and $\sigma = 0.2$ in a 50×50 domain.

3 A Model with Three Zones of Interaction

3.1 Update Equations and Initial Analysis

So far there has only been one interaction zone around each fish. This section introduces two other zones of interaction; a repulsion zone and an attraction zone. A fish will have different update steps depending on where its closest neighbours are.

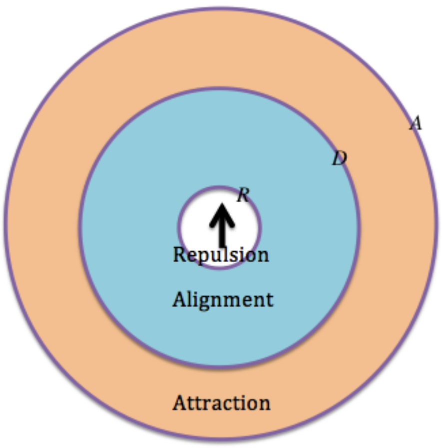


Figure 3.1: Three zones of interaction: attraction, alignment, repulsion

The new zone of interaction are defined as follows.

1. The inner zone with radius R surrounding the fish acts as a repulsion zone, i.e. stops collisions from occurring. The fish being updated will be repelled from the fish within this zone. Hence the angle at which it will

next swim, before the noise term is added, is

$$\theta = \arctan\left(\frac{\frac{1}{N}\sum_{(d_{i,j}<R)} y_j - y_i}{\frac{1}{N}\sum_{(d_{i,j}<R)} x_j - x_i}\right) + \pi. \tag{5}$$

That is, calculate the average position of the fish within this region, relative to fish i, then find the angle between fish i and this point. By adding π the new updated angle will point directly away from the average position of its nearest neighbours.

2. In the middle, alignment zone, where the radius is D, such that $R < D$, the update steps are very similar as in Section 2 with the distances taken into account changed. That is

$$\begin{aligned} v_{x,i} &= \frac{1}{N}\sum_{(R<d_{i,j}<D)} v_{x,j}, \\ v_{y,i} &= \frac{1}{N}\sum_{(R<d_{i,j}<D)} v_{y,j}. \end{aligned} \tag{6}$$

Note that here the update equation looks at the velocity components of its neighbours where in Equation (5) the positions of the fish are used.

3. The final outer attraction zone has a very similar update step to that of the repulsion zone. In the repulsion zone the fish are updated to swim directly away the current average position of its nearest neighbours, however, in this zone the fish swims towards the average position of its neighbours between D and A. Hence the update equation is

$$\theta = \arctan\left(\frac{\frac{1}{N}\sum_{(D<d_{i,j}<A)} y_j}{\frac{1}{N}\sum_{(d_{i,j}<A)} x_j}\right) \tag{7}$$

where A is the radius of attraction around the fish.

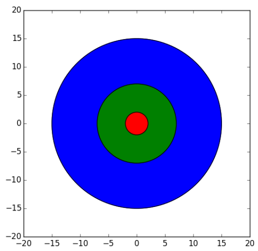
If there are no fish in the first zone then it looks at the second, and if there is none in the second then it looks in the third. If there are no fish in any interaction zone then the fish keeps its current direction.

For simulations in this Section all fish will be given a direction, $\theta = \frac{3}{4}\pi$ in order to see the effect of the repulsion zone

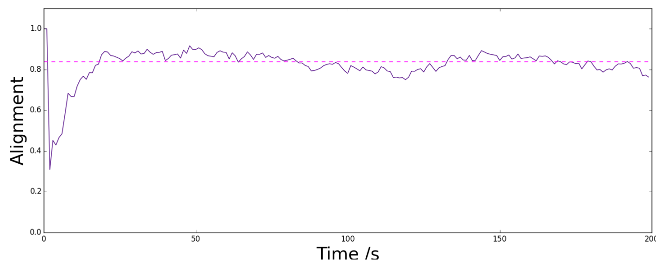
Table 3.1 shows the parameters used analysing the three zones model.

Parameter	Symbol	Value Range	Unit
Number of fish	N	$40 - 200$	Dimensionless
Velocity	v	$0.25 - 1$	Length per second
Time step	dt	1.0	Seconds
Noise	σ	$0.0 - 1$	Radians
Radius of Repulsion	R	$0.0 - 6.0$	Length
Radius of Alignment	D	$2.0 - 14.0$	Length
Radius of Attraction	A	$7.0 - 15.0$	Length

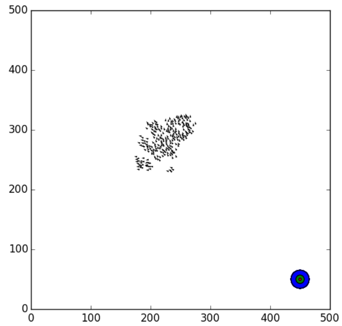
Table 3.1: Parameters of the three zone model.



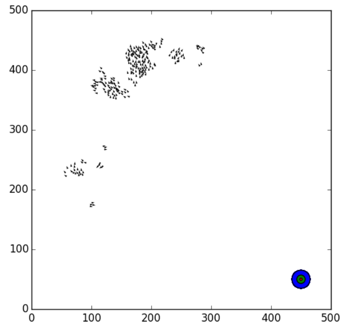
(a) Zone of interaction



(b) Alignment vs Time



(c) School at $t = 50$



(d) School at $t = 190$

Figure 3.2: Parameters set to $R = 2.0, D = 7.0, A = 15.0, \sigma = 0.2$. The circles from (a) are then placed in the bottom corner of (b) and (c) to give an idea of the scale of the interaction zones relative to the whole area within the new larger periodic boundaries.

Running a simulation of the three zone model we can produce a number of plots, shown in Figure 3.2. Figure 3.2a pictorially shows the relative sizes of the zones of interaction about the centre point, the fish. Here red represents the repulsion, green the alignment, and blue the attraction zone. It is set up so that the repulsion radius is small, to stop fish from colliding. Here we will use a radius of 2 units, i.e distance travelled in two time steps. The alignment zone is of a similar size to that in Section 2, since the repulsion zone is radius 2 units the alignment radius is set to be 7 units. Finally the attraction zone is large, 15 units, since for protection fish want to swim together. The boundaries have been increased in order to witness the behaviour of the fish without the fish instantaneously moving from one side of the domain to the other.

From the two snapshots of the fish simulation it can be seen that fish start off as one school and eventually splinter off into a number of smaller schools. This can be quantified by the alignment values, as a large school will have a high alignment value where as a group of smaller schools may have a much lower alignment value, but the difference here is small.

In a similar fashion to Section 2, it is possible to plot how the alignment changes over time: Figure 3.2b shows how the alignment in the 3 zone model changes with $\sigma = 0.2$. The mean value is $a = 0.84$ with a standard deviation of 0.03, which is similar to that of the basic model as the mean has slightly increased, whereas the standard deviation has decreased. Hence the inclusion of the other two new interaction zones has caused the standard deviation value to reduce. The sharp dip at the beginning of the simulation's alignment values is as a result of the repulsion zone. The repulsion zone update equations force the fish to swim directly away from the fish that are too close, so since the density of the initial fish is quite high it is very likely that most fish will have neighbours within their repulsion zone. This causes them to flip direction which will have a massive disturbance on the total alignment.

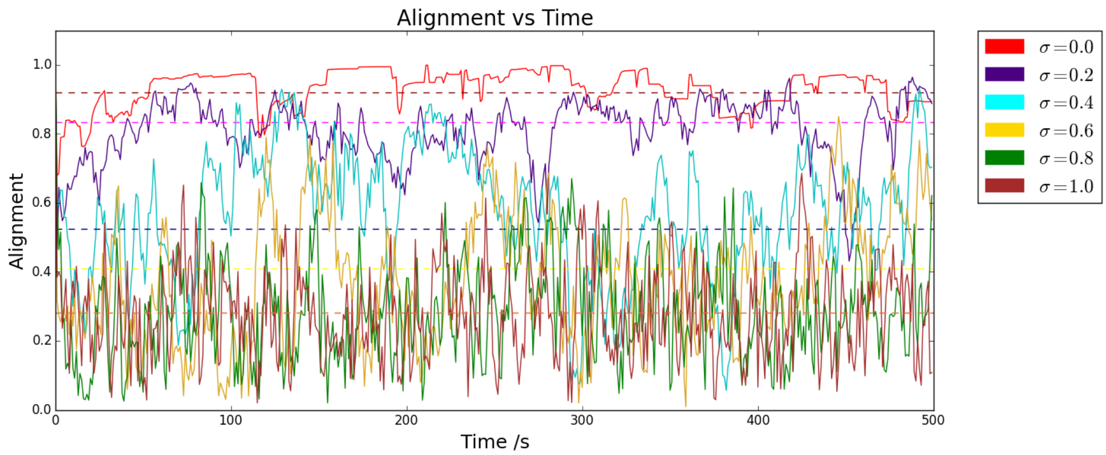


Figure 3.3: The alignment vs time plot for the 3 zones model, with $N = 40, v = 0.31, R = 2, D = 7$ and $A = 15$ constant in a domain of 50×50.

As in Section 2, running six simulations with different σ values allows investigation into how the noise parameter effects the alignment in the new model. Figure 3.3 shows how alignment changes over time when the value of σ is systematically decreased for the three zone model. Comparing this with Figure 2.6, as all parameters are the same, it can be observed that the oscillations about the averages are larger in the three zones model. Also observe that the time taken for simulations to become steady takes longer due to the repulsion zone keeping fish apart. This is also causes the simulation with a $\sigma = 0.0$ to never reach perfect alignment.

Comparing the mean values in Table 3.2 and Table 2.4 notice that for four of the σ values the mean alignment is smaller. For the value of alignment at $\sigma = 0.2$ in the three zone model the value is higher than that of the basic model. However, comparing the standard deviations the deviation is larger in the basic model making the alignment value similar. The alignment values for $\sigma = 1.0$ are similar, explained using the same argument.

σ	Mean a Value	Standard Deviation
0.0	0.92	0.04
0.2	0.83	0.09
0.4	0.52	0.17
0.6	0.41	0.16
0.8	0.28	0.12
1.0	0.28	0.13

Table 3.2: Mean and standard deviation values for the six simulations ran with different σ values. The mean and standard deviation are calculated over the last 200 time steps.

The following section discusses the different behaviours found when altering the three radius parameters, R, D, A. In Section 3.2 the parameters which are fixed are $N = 250$, $\sigma = 0.2$ and $v = 1$.

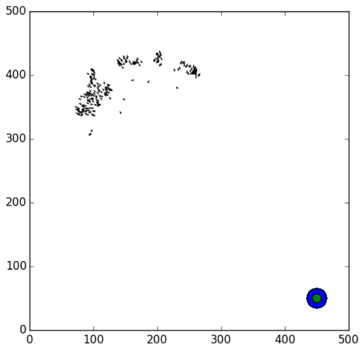
3.2 Removing Zones: The Roles of Different Zones

By removing individual interaction zones one by one it is possible to see what effect that zone had on the behaviour of the fish. A different way of thinking of removing the repulsion zone is setting $R = 0$, doing this there can be no fish within zero distance of the fish, so the repulsion update equations get passed over unused. By removing the repulsion zone observe that groups still form as the attraction and alignment zone bring groups together and keep them together respectively. Removing the alignment zone and attraction zone is done similarly by setting $D = 2$ and $A = 7$ respectively.

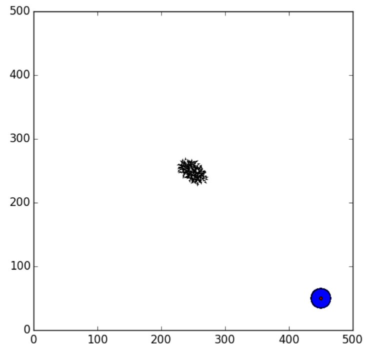
The snapshots shown in Figure 3.4 show the location and direction of the fish at the final time step. There are clear differences between each two zone model and the full three zone model.

Comparing the snapshots of the model with no repulsion to the full model, i.e. comparing Figure 3.4d and Figure 3.4a, the most significant difference is how tightly packed the fish are together. This is what we would expect since there is no code to stop the fish getting too close and colliding.

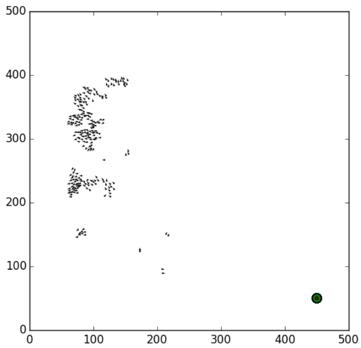
However, the main difference between these two models can be seen in their alignment vs time plots, Figure 3.2b and Figure 3.5a. As was mentioned in Section 3.1 the full model alignment vs time plot has a large drop before becoming statistically steady. The removal of the repulsion zone also removes



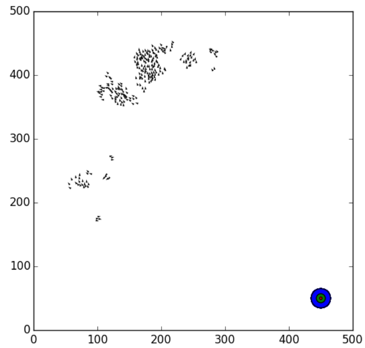
(a) No repulsion zone



(b) No alignment zone



(c) No attraction zone



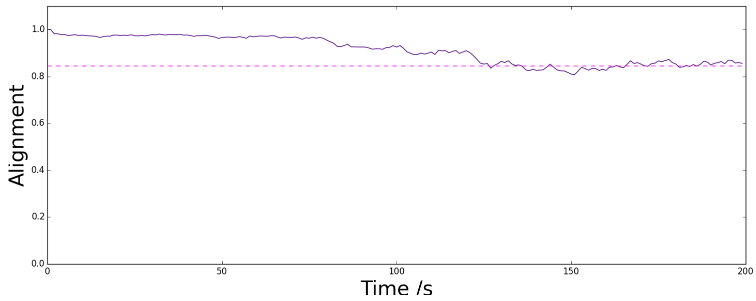
(d) Full-Model

Figure 3.4: Snapshots from Four Different models.

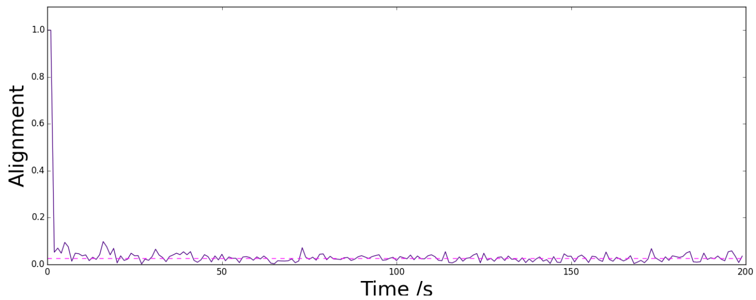
this drop, so the conclusion that the drop was made by the repulsion zone is reinforced here. Interestingly the mean alignment value, Table 3.3, for the full model is very similar with a smaller standard deviation. This is as a result of the random nature of the model.

Analysing the full model compared to the model without the alignment zone, the differences are more apparent. In the model with no alignment, the school of fish barely move from their initial position. By considering how an individual fish would update its position this behaviour is easily deciphered. An individual fish with neighbours in its repulsion zone would update to swim directly away from them. As soon at it has reached the point where there are no longer fish in the repulsion zone, it then looks at its neighbours in the attraction zone, since there is no alignment zone. It then updates to swim towards those neighbours. This eternal switching of directions would keep the fish within the initial 50×50 positions, but taking into account the noise parameter, which we set to be 0.2, explains why the shape changes over the 200 time steps.

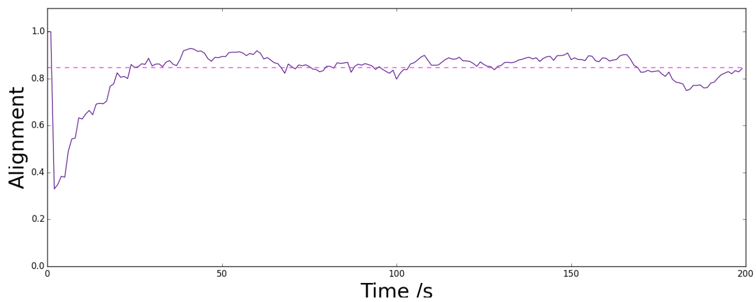
Just how little the fish move is even more apparent when looking at the trajec-



(a) No repulsion zone



(b) No alignment zone



(c) No attraction zone

Figure 3.5: Alignment vs time plots for different models.

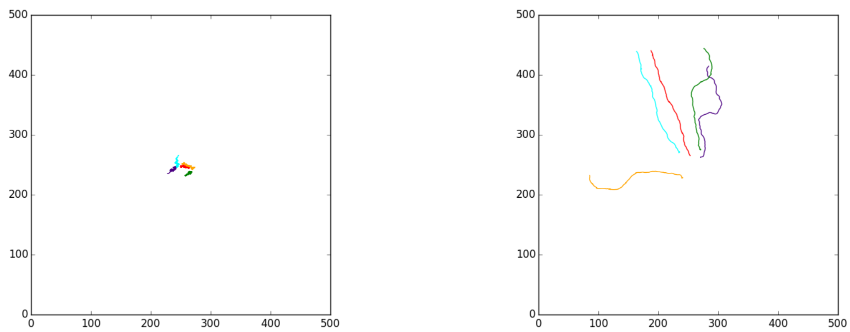
tories of five fish, Figure 3.6a, compared to those of the full model, Figure 3.6b. The fish in the full model travel much further than those in smaller two zone model. The two zone model stays in the centre whereas in the three zone model they move away.

The differences become even more evident in the large contrast between the alignment vs time plots, Figure 3.2b and Figure 3.5b. The alignment after the first few time steps stays below 0.05 and then comparing the two mean values from Table 3.3, the full model has a mean value almost 50 times larger.

Finally, comparing the full model with the model with no attraction zone it can be seen that there are fewer schools of fish in the full model. This is a result of the attraction zone keeping the current schools together, without this it is difficult to rejoin a school since the fish uses the update equation where it keeps going in its current trajectory.

R	D	A	Mean	Standard Deviation
2.0	7.0	15.0	0.93	0.02
0.0	7.0	15.0	0.83	0.03
2.0	2.0	15.0	0.02	0.01
2.0	7.0	7.0	0.79	0.03

Table 3.3: Mean and standard deviations when removing individual zones from the three zone model.



(a) A model with no alignment zone. (b) The full three zone model.

Figure 3.6: Trajectories of five fish over 200 time steps.

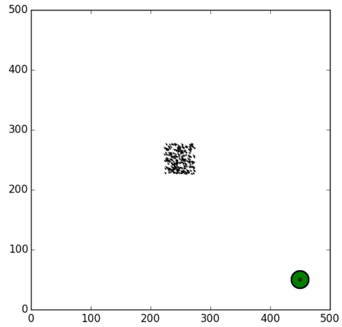
3.3 How the Zone Size Changes Alignment

Adding zones to the basic model to form two and three zone models shows some new distinct behaviour patterns. This Section explores the differences when the radii of the zones are at the extremes, that is to say radii that have a difference of $v \times dt = 1$ unit. As with all the simulations ran in a 500×500 domain the fish are in fact initialised in a 50×50 square in the centre.

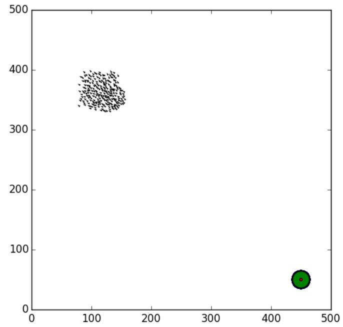
3.3.1 Maximal Alignment

Starting with a simulation with maximal alignment zone, where the distance parameters are set to $R = 2, D = 14, A = 15$, here the behaviours are very different to those seen so far in the three zone model. The fish swim together as one school and are still approximately square at the end of the simulation. Since the alignment zone is the largest, the alignment equations, Equation (6), are used more frequently than the ones for repulsion and alignment. This causes the fish to assume the direction average of its neighbours, this is observed as the fish being very well aligned.

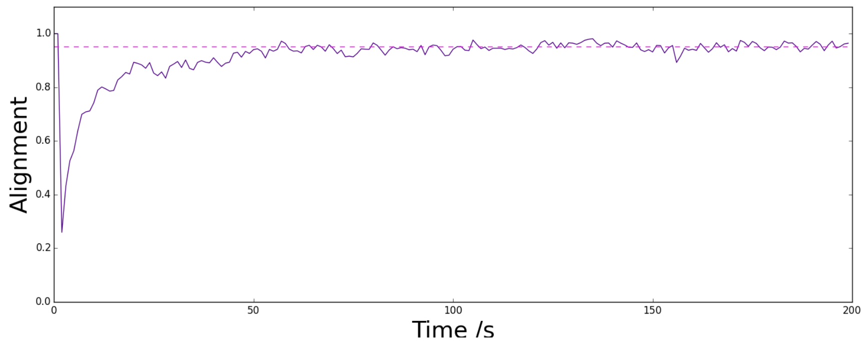
Figure 3.7a shows the school in its initial position. The fish are located in a 50×50 square in the middle of the x and y domains. At the end of the simulation, Figure 3.7b, the square shape is still clearly recognisable. This reinforces the idea that the fish become aligned very quickly and stay very aligned. Then looking at the alignment vs time plot, Figure 3.7c, it has the initial dip, which is a characteristic of the three zone model. It then becomes almost level very close to the maximal alignment value. This is what would be expected by examining the snapshots of the fish' movement.



(a) School at $t = 0$.



(b) School at $t = 190$.



(c) Alignment vs Time

Figure 3.7: A simulation with distance parameters, $R = 2, D = 14, A = 15$. The first two showing snapshots of the movement of the fish over the 200 time steps. The lower figure shows how alignment changes over time.

3.3.2 Minimal Attraction

When changing the radii parameters to reflect a minimal attraction zone, $R = 2, D = 7, A = 8$, the observations are similar to having no attraction zone. The only observable difference in the snapshots is the number of groups the initial school breaks into. With the parameters set at $R = 2, D = 7, A = 15$ there are 9 observable groups, whereas now with the attraction zone much smaller there are now 15 groups. When comparing the alignment vs time plots for the model with parameters $R = 2, D = 7, A = 8$ with the model with no attraction zone no differences are discovered. Here Equation (7) is rarely used since the difference between the D and A values is only the distance travelled in one time step.

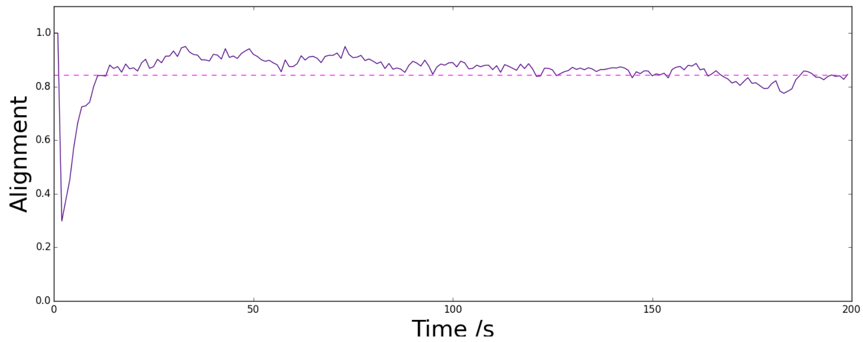


Figure 3.8: Alignment values over time from a simulation with distance parameters, $R = 2, D = 7, A = 8$. Showing the alignment values again time.

3.3.3 Maximal Repulsion

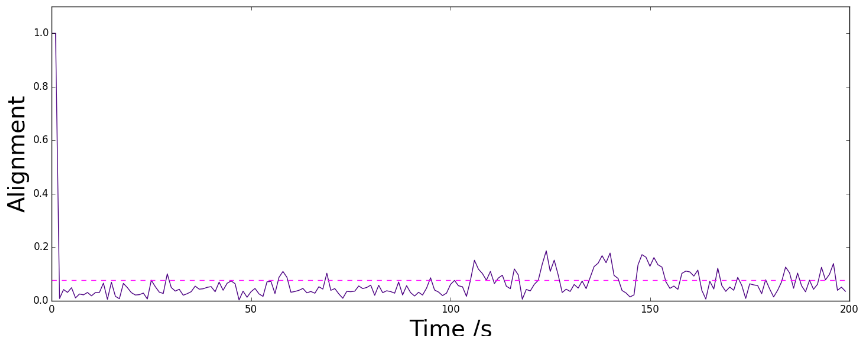
The parameters needed to simulate a maximal repulsion zone are $R = 6, D = 7, A = 8$. This gives a behaviour with certain similarities to that of the model with no alignment, however, there are some noticeable differences. The main similarity between these two models is shown by the alignment vs time plot, Figure 3.9a. The two alignment vs time plots have alignment values that stay below 0.2 and oscillates about the mean with a lower frequency to that of the two zone model.

However, looking at the snapshot of the simulation at $t = 160$, Figure 3.9b, both similarities and differences are observed between this and the full three zone model at the beginning of this section. In both models the fish stay close to the initial positions, but when comparing the trajectories of five fish for both models, Figure 3.9c and Figure 3.6a, it is clear to see that some fish in the maximal repulsion model move much further than in the no alignment model. This can be explained by thinking of what having a large repulsion radius means for the update steps. In the no alignment model, the fish are simulated to be repelled if they are closer than 2 to their neighbours. In the current model however, the fish are repelled if they are within 6 from their neighbours. So they are repelled to a distance further away from each other than in other models.

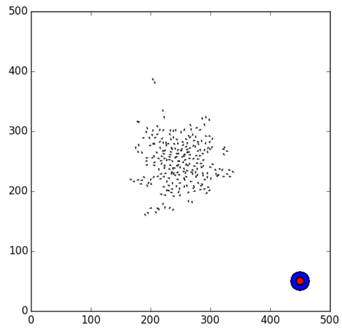
3.3.4 Minimal Alignment

The final parameter set to be analysed is the parameters for minimal alignment. This is to be expected to be similar to the previous Section and to the two zone model from Section 3.2 with no alignment. The parameters used are $R = 2, D = 3, A = 15$. These are then used to simulate fish producing the figures in Figure 3.10. As expected the alignment vs time plot, Figure 3.10a, is remarkably similar to that of of previous models mentioned above. The alignment stays very low and oscillates about the mean with a high frequency.

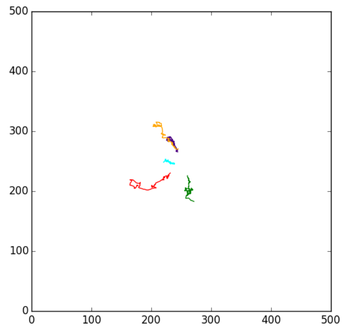
From the trajectory plot, Figure 3.10c, the behaviour of the fish looks remark-



(a) Alignment vs Time



(b) Simulation of school at $t = 160$



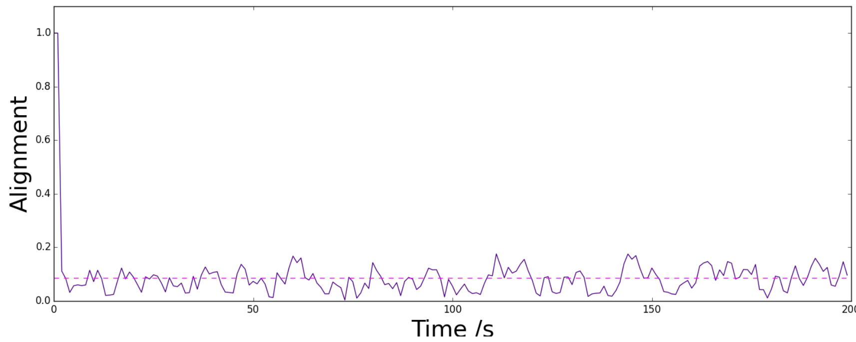
(c) Trajectories of five fish

Figure 3.9: Alignment, snapshot and trajectories from a model with parameters set to maximal repulsion, $R = 6, D = 7, A = 15$.

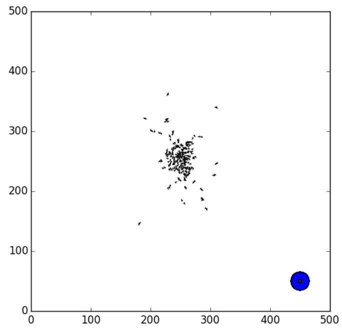
ably similar to that of the two zone model in Section 3.2 when alignment was removed. However, when considering the snapshot taken at $t = 190$ the fish actually move much further from the initial positions than the two zone model. This is explained by how the fish update their positions and directions. When a fish no longer has neighbours in the repulsion zone, there is a small distance window where it can now align with its closest neighbours. When it has no neighbours repelling, but ones aligned, they then have the chance to break away from the main school. Nonetheless the window of alignment is so small that most of the fish behave as though the zone was not there.

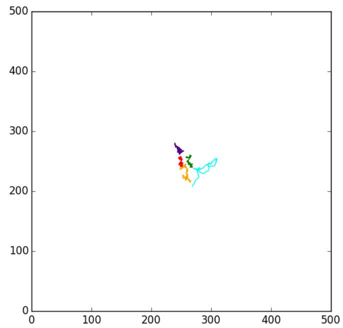
4 A Model with Limited Field of View

In previous sections, all the fish have been able to see all the way around themselves. This is not entirely realistic, since a fish is unlikely to be able to see its own tail. To put this in simulations a field of view is introduced, where each fish can see α radians in each direction. A similar field of view method is used in a paper by Couzin *et al.* [7].



(a) Alignment vs Time





(b) Simulation of school at $t = 190$ (c) Tracking five individual.

Figure 3.10: Alignment, snapshot and trajectories from a simulation with minimal alignment parameters. $R = 2.0, D = 3.0, A = 15.0$

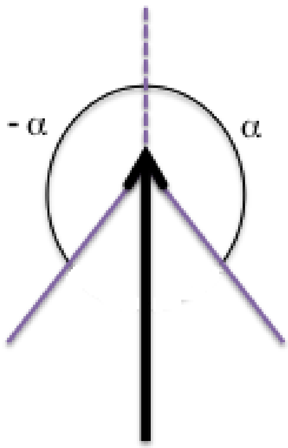


Figure 4.1: Field of view for a fish

4.1 Update Equations and Initial Analysis

In order to include a restricted view into the model, the angle between the direction of fish i and the position of fish j must be calculated, Figure 4.2. This is done by finding the location of fish j with respect to the location of fish i then calculating the angle towards this point. This angle is called $\gamma_{i,j}$. Then $\gamma_{i,j}$ is made relative to the direction of fish i by

$$\beta_{i,j} = \theta_i - \gamma_{i,j} - \pi,$$

where θ_i is the direction of fish i. There are now two stages to the update step, the first is whether the neighbouring fish can be seen. The second follows from Section 3, the zone of interaction the neighbour is in. For the first update stage, to determine which neighbours to take into account, a simple rule is used:

- If $|\beta_{i,j}| > \alpha$, then don't include this fish in the update process,
- If $|\beta_{i,j}| < \alpha$, then include this fish in the update process.

The second stage follows Section 3 where only the appropriate neighbours are used.

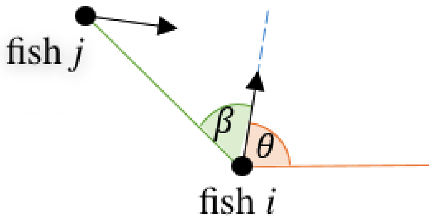
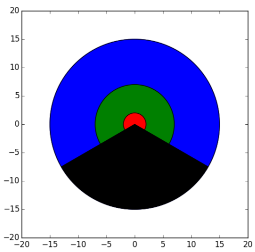
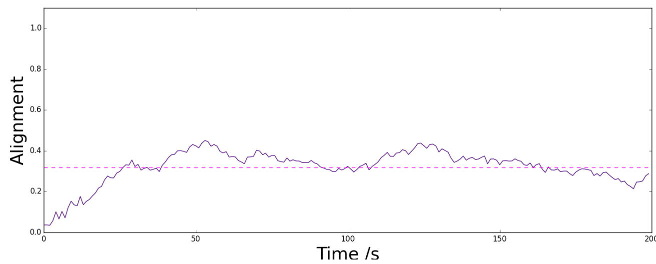


Figure 4.2: For each fish pairing the angle β must be found

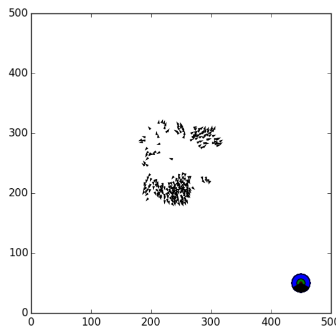
The full three zone model with a restricted view produces Figure 4.3. As in Section 3 Figure 4.3a pictorially shows the three interactions zones with the blind spot blacked out.



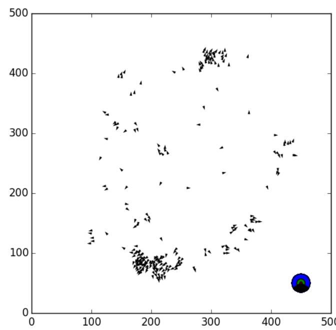
(a) Zone of interaction



(b) Alignment vs Time



(c) Simulation of school at $t = 50$



(d) Simulation of school at $t = 190$

Figure 4.3: From a simulation where $R = 2.0, D = 7.0, A = 15.0, \alpha = \frac{2\pi}{3}$

There are large differences between the three zone model and the field of view model. The simulation that produced Figure 3.2 uses the same parameters as Figure 4.3, the only difference is which fish are used in the update process, as some fish will be in the blind zone. When each fish has a restricted view the alignment becomes much lower, 0.32 down from 0.84. A large decrease is expected because each fish can not see all surrounding neighbours. From the snapshots, Figure 4.3c shows that initially the two simulations start similarly but then after the remaining time steps become much more spread out and can become isolated (Figure 4.3d).

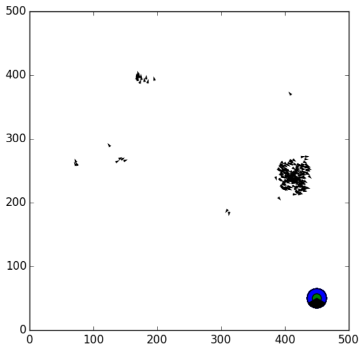
Now that a field of view has been introduced some of the behaviour seen in Section 3 may have changed. The following sections will repeat the analysis of the three zones model in order to see what implications the restricted view has. The parameters used to analyse this model are shown in Table 4.1. Now the fish are given a random direction at the start of the simulations since the role of the repulsions zone is no longer under investigation.

Parameter	Symbol	Value Range	Unit
Number of fish	N	200	Dimensionless
Velocity	v	1.0	Length per second
Time step	dt	1.0	Seconds
Noise	σ	0.2	Radians
Radius of Repulsion	R	$0.0 - 6.0$	Length
Radius of Alignment	D	$2.0 - 14.0$	Length
Radius of Attraction	A	$7.0 - 15.0$	Length
Angle of View	α	$\frac{\pi}{16} - \frac{7\pi}{16}$	Radians

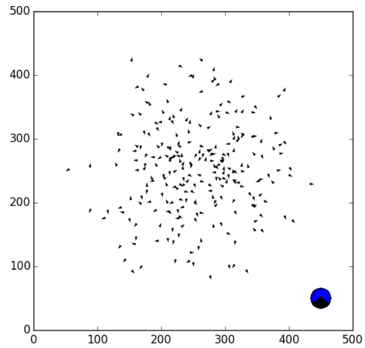
Table 4.1: Parameters of the three zone model with a field of view.

4.2 Removing Zones When View is Restricted

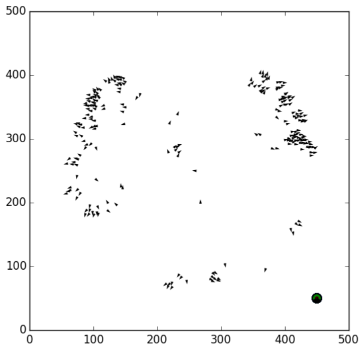
Similarly to Section 3.2, zones are removed individually. Figure 4.4 shows snapshots of the simulations at the end of their runs. There are massive differences between each of these three simulations and there are some differences with their counterparts from Section 3.2.



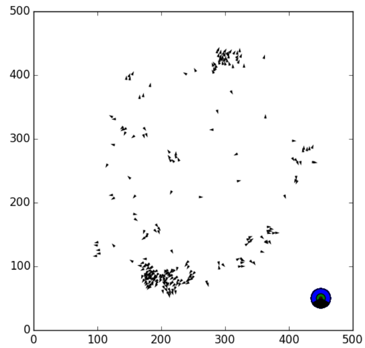
(a) No repulsion zone



(b) No alignment zone



(c) No attraction zone



(d) Full field of view model

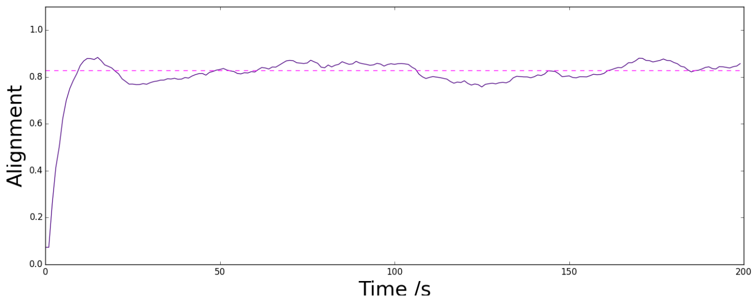
Figure 4.4: Snapshots from four different models.

Starting with the model with no repulsion zone, we see that by restricting the field of view most of the fish stay together in one school, Figure 4.4a. This is the only version of the three zone model, with or without the restricted view, with the distance parameters set to $R = 2.0, D = 7.0, A = 15.0$ that does so. This is because the fish can be really close together, since there is no repulsion zone, and then align. Some of the fish become leaders of the school since they cannot see that there are other fish following them. Moving on to compare the alignment over time plots for the models with and without a field of view, there is only one observable difference when comparing the statistically steady behaviour of the field of view model with the previous three zones model.

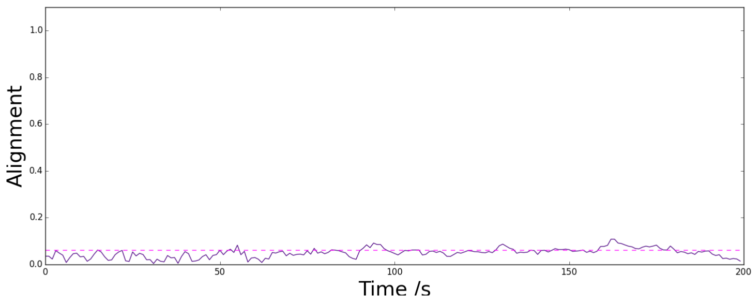
In Figure 4.5a the alignment levels off at a =0.83, whereas in Figure 3.5a the alignment settles at a =0.85. Since the two alignment vs time graphs are similar and the mean alignment values are almost the same these two model variations give the same behaviour.

Comparing the two models with no alignment zones there is a startling difference. Before in Section 3.2 the fish stayed in the 50$\times$50 square they started in. However, due to the fish now having a blind spot and therefore not always seeing any fish, the fish spread out much more. Having said this the alignment over times graphs, Figure 3.5b and Figure 4.5b, are remarkably similar when the aligament values are statistically steady. The alignment stays very low in the restricted view model because fish are swimming in every direction, so their alignment value will be approximately 0.

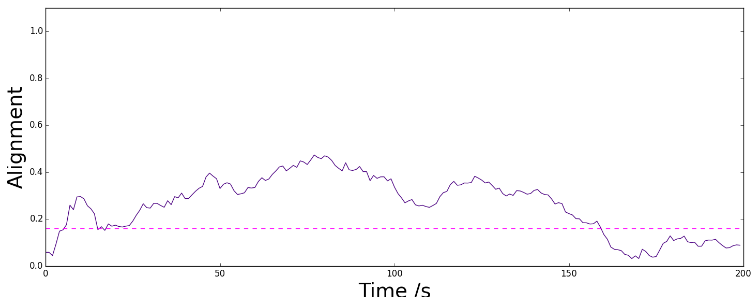
There is significant differences between the two models with no attraction. When the field of view is implemented the fish swim out almost radially, Figure 4.4c. As with the model with an unrestricted view the school of fish splinter into many groups since there is no update process keeping the group together. When comparing the two alignment over time graphs the differences become even more evident. Figure 3.5c shows the alignment dropping down and then rising back up to level out at a =0.85. Whereas in Figure 4.5c the alignment is always below 0.5. It starts much lower then rises for a short period of time before settling to give a final mean value of a =0.16.



(a) No repulsion zone



(b) No alignment zone



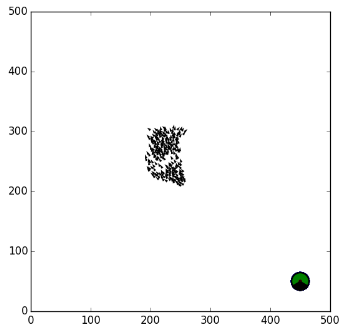
(c) No attraction zone

Figure 4.5: Alignment vs time plots for different models with a restictive view.

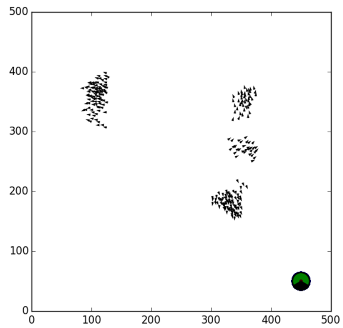
4.3 Changing the Size of Zones When View is Restricted

Exploring what happens in the three zone model when the radii of the zones are at the extremes, was discussed in Section 3.3. Now this section will investigate if any of these behaviours change when a field of view is introduced.

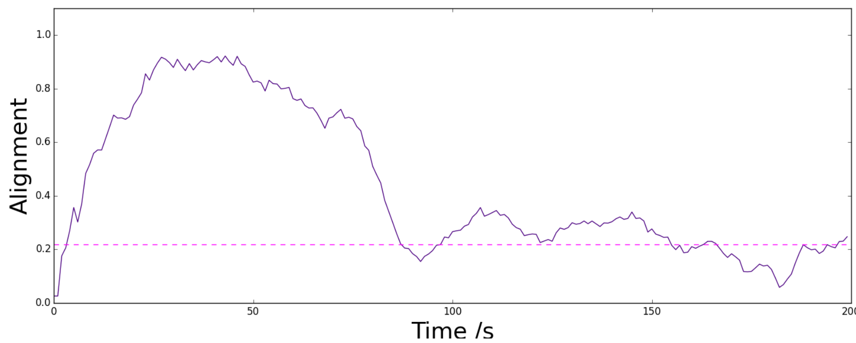
4.3.1 Maximal Alignment



(a) Simulation of school at $t = 40$



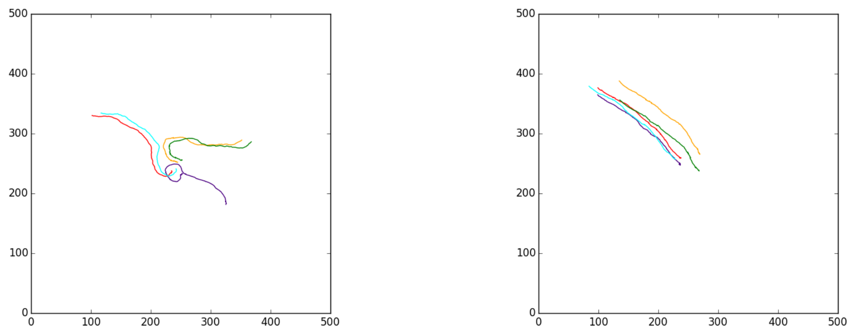
(b) Simulation of school at $t = 190$



(c) Alignment vs Time

Figure 4.6: A simulation with $R = 2.0, D = 14.0, A = 15.0, \alpha = \frac{2\pi}{3}$ to mimic maximal alignment.

Comparing the snapshots of a simulation with maximal alignment significant differences are observed. In Section 3.3.1 the fish stay together in a square shaped school. In this restricted view model, the fish stay together for approximately a quarter of the time, Figure 4.6a. However, after this time the group splinters off into a few individual schools, Figure 4.6b. Since approximately half the fish swim in one direction and the other half in the opposing direction the alignment significantly drops when the school splits. This can be seen in the alignment over time graph, Figure 4.6c, at $t \approx 90$ the alignment decreases to around a =0.2 whereas before this drop the alignment as reaching a =0.8. The differences are made even more clear when comparing the two trajectory plots for five randomly selected fish, Figure 4.7.



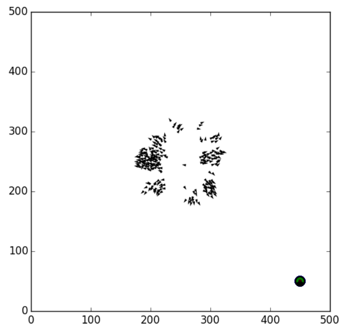
(a) Field of view model.

(b) Three zone model.

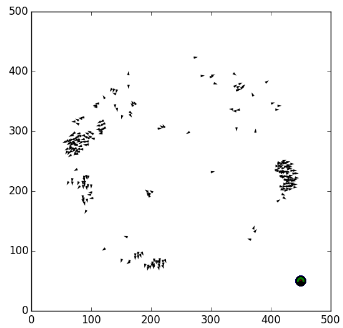
Figure 4.7: Trajectories from five random fish for both the three zone model and the field of view model. Each model has distance parameters set to $R = 2, D = 14, A = 15$.

4.3.2 Minimal Attraction

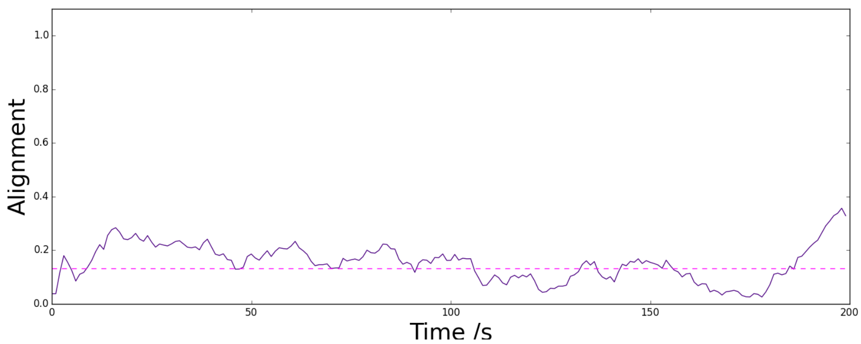
When previously looking at minimal attraction, Section 3.3.2, it was found that it was very similar to that of the two zone model, with only repulsion and alignment zones. However, when looking again at the minimal alignment with a restricted view this is no longer the case. The fish break away from the initial school approximately radially to form a number of smaller school after only 50 time steps, Figure 4.8a. These then break up over and over again until at $t = 190$ there are a larger number of groups, some only consisting of one fish (Figure 4.8b).



(a) Simulation of school at $t = 50$



(b) Simulation of school at $t = 190$



(c) Alignment vs Time

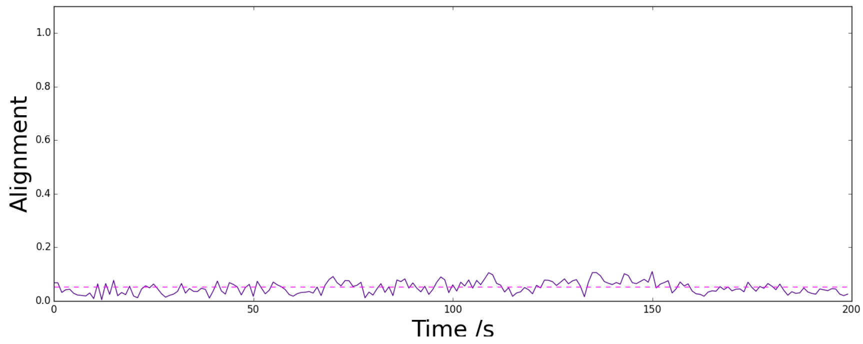
Figure 4.8: $R = 2.0, D = 7.0, A = 8.0$

The alignment over time graphs reinforce the differences between the two minimal attraction models. Figure 3.8 showed the alignment value being very high, over a =0.8, after less than 25 time steps. However, when the field of view is restricted the alignment value becomes a =0.4. This is caused by the fish swimming approximately radially from the initial positions. The alignment is calculated using the velocity, where the velocity includes the direction of travel. This causes the alignment to be very low.

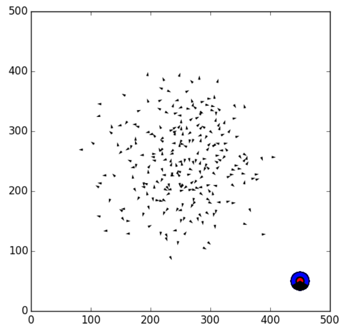
4.3.3 Maximal Repulsion

The maximal repulsion models where $R = 6, D = 7, A = 15$ can be said to be the same. Firstly comparing the alignment over time graphs, Figure 3.9a and Figure 4.9a, the alignment after an initial time period oscillates over the mean value with a high frequency. The mean value for both models is less than a =0.1 and the oscillations, or standard deviation, are very small.

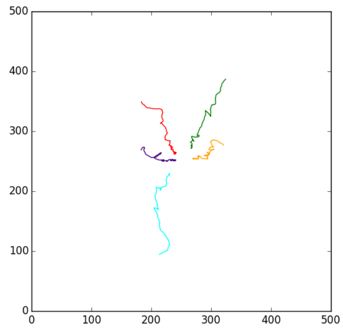
Moving on to compare the snapshots at $t = 160$, the visual behaviour of these two models is also very similar. The main noticeable difference is between the distance travelled by some of the fish. In Figure 3.9b the fish spread to an area between 150 and 350 in the x domain and 150 and 400 in the y. However, when the view is restricted the fish now spread to a region between 80 and 420 in x and 80 and 400 in y. This can also be seen in the trajectory plots. The length of the blue trajectory in Figure 4.9c, is much more stretched out than any of the



(a) Alignment vs Time



(b) Simulation of school at $t = 160$



(c) Trajectories of five fish

Figure 4.9: Alignment, snapshot and trajectories for a simulation with $R = 6.0, D = 7.0, A = 15.0$

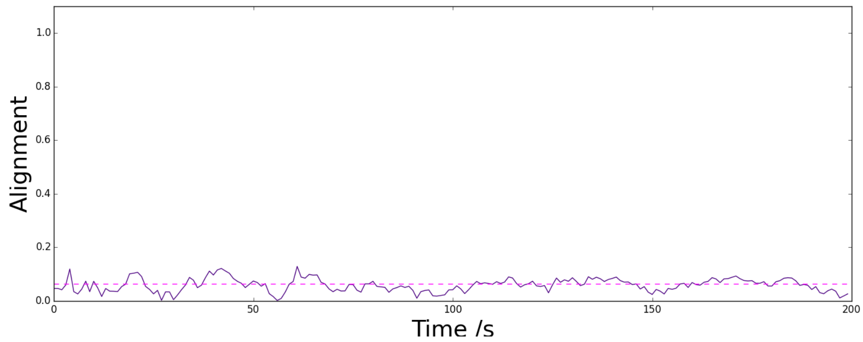
trajectories in Figure 3.9c.

From this it is possible to conclude that the size of the repulsion zone affects the behaviour more than the implementation of the field of view. When the repulsion zone is smaller the restricted view effects are more apparent, however with a large repulsion zone the effects are not so easily noticed.

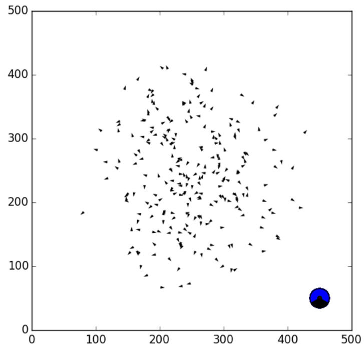
4.3.4 Minimal Alignment

Just like in Section 3.3.2 the behaviour is very similar to that of the model with no alignment, Section 4.2. When comparing the snapshots for the final time step, shown in Figure 4.4b and Figure 4.10b, there are no apparent differences even when comparing the distances the fish have spread out to.

The only difference between these models can be seen by comparing the alignment over time graphs, Figure 4.5b and Figure 4.10a. Considering the graphs as a whole they look very similar, however, when considering only up to $t = 100$ there are small differences. For the minimal alignment case the alignment oscillates over the mean value but the mean value is only calculated over the final 70 time steps to allow for models to become statistically steady. When the alignment zone was removed the oscillations were approximately



(a) Alignment vs Time



(b) Simulation of school at final time step

Figure 4.10: Alignment and snapshot for a simulation with $R = 2.0, D = 3.0, A = 15.0, \alpha = \frac{2\pi}{3}$ mimicking minimal alignment.

half the size and were all below the final mean value. After this time however, the two models appear identical.

4.4 Altering the Size of the Field of View

So far the angle of view has been set to $\alpha = \frac{2\pi}{3}$. In this section the radii will be fixed to $R = 2, D = 7, A = 15$ and the angle will be altered. Table 4.2 shows the range of angles used to investigate the effect the size of the field of view has on the behaviour of the fish. Note a full field of view has been included.

When looking at the final snapshots, Figure 4.11, there is a change in behaviour when the fish are able to see behind themselves for the first time. Looking at the first three snapshots within Figure 4.11, the fish all move out radially and rarely form schools. This is due to the small number of fish been seen due to the large blind spot and hence few fish are included in the update equations. Moving on to look at the Figures 4.11c to 4.11f it is possible to see small schools forming. When $\alpha = \frac{\pi}{2}$ very few schools form, from this it easily follows that $\alpha = \frac{\pi}{2}$ must be the boundary, or very close to the boundary, between two different behaviours.

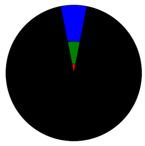
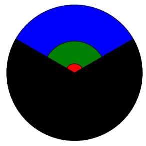
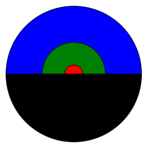
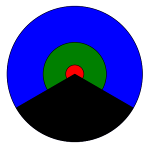
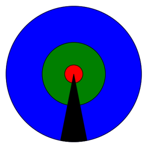
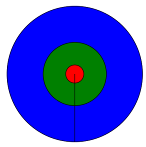
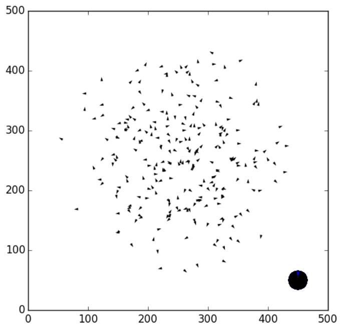
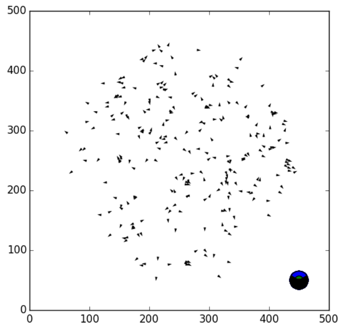
α / radians	Schematic	α / radians	Schematic
$\frac{1}{16}\pi$		$\frac{1}{3}\pi$	
$\frac{1}{2}\pi$		$\frac{2}{3}\pi$	
$\frac{15}{16}\pi$		π	

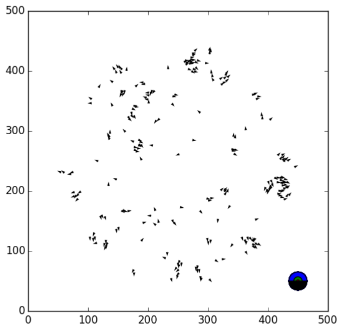
Table 4.2: Angles used to observe change in behaviour when restricted view is altered, schematics also included.



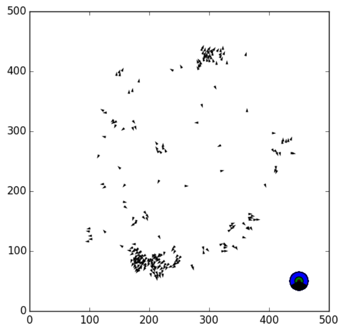
(a) $\alpha = \dfrac{1}{16}\pi$



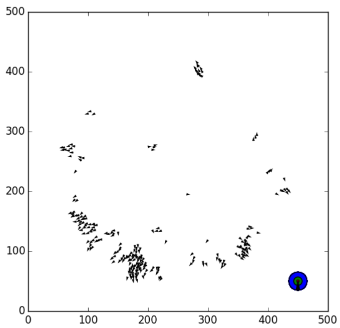
(b) $\alpha = \dfrac{1}{3}\pi$



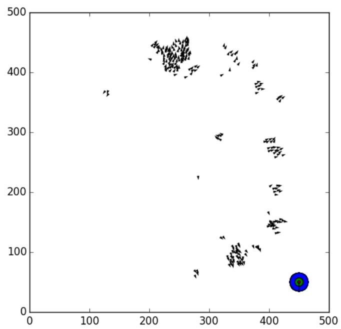
(c) $\alpha = \dfrac{1}{2}\pi$



(d) $\alpha = \dfrac{2}{3}\pi$

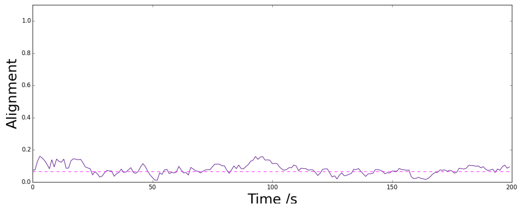


(e) $\alpha = \dfrac{15}{16}\pi$

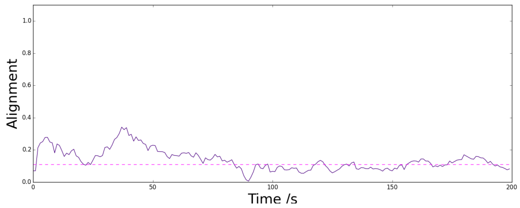


(f) $\alpha = \pi$

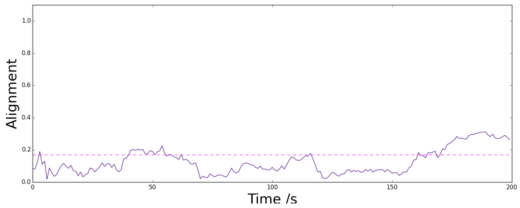
Figure 4.11: Final snapshot where $R = 1, D = 7, A = 15$ for each α value



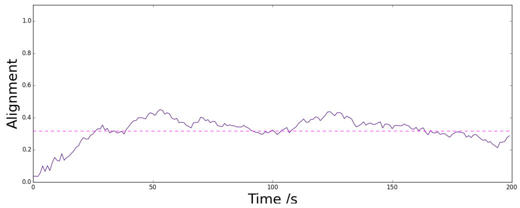
(a) $\alpha = \dfrac{1}{16}\pi$



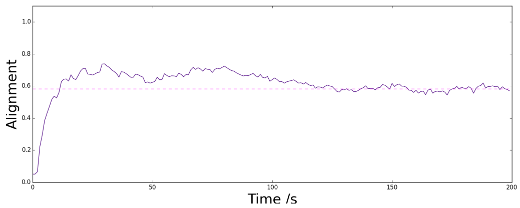
(b) $\alpha = \dfrac{1}{3}\pi$



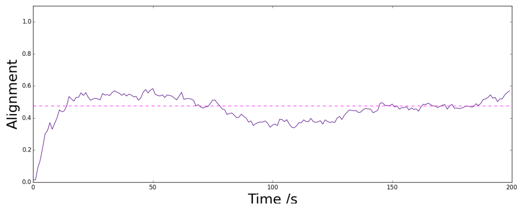
(c) $\alpha = \dfrac{1}{2}\pi$



(d) $\alpha = \dfrac{2}{3}\pi$



(e) $\alpha = \dfrac{15}{16}\pi$



(f) $\alpha = \pi$

Figure 4.12: Alignment over time graphs for each of the α values, with radii set to $R = 1, D = 7, A = 15$. The time tick marks are the same as previous alignment over time plots.

This is then reinforced when considering the alignment over time graphs; Figure 4.12. Figure 4.12a and Figure 4.12b have very similar changes in alignment after an initial time. From the snapshots of these two simulations, Figure 4.11a and Figure 4.11b, this is what was expected. Figure 4.12c shows the alignment changing over time when $\alpha = \frac{1}{2}\pi$. The alignment is much more erratic, for short periods of time it is close to zero, then it increases up to a =0.2 for another short period of time. This continues throughout the simulation until approximately $t = 170$. At this point the alignment increases above a =0.2, this is due to the fish beginning to school, causing the total alignment to increase.

Figures 4.12d to 4.12f clearly show that after a certain point the fish do become more aligned. Each of the three figures show the fish becoming aligned up to a certain value and then staying very close to this value for the rest of the simulation. Figure 4.12e shows the fish become most aligned with an α value of $\frac{15}{16}\pi$. Looking at the snapshots for the end of these simulations, it is clear that when $\alpha = \frac{2}{3}\pi$ the alignment is lower since there are a number of fish swimming in each direction.

Comparing the last two figures, Figure 4.11e and Figure 4.11f, it is clear which of the two have a higher alignment. The model with $\alpha = \frac{15\pi}{16}$ has an alignment value of approximately a =0.1, higher than that of the full vision model. Considering how similar the shapes of these two graphs look this is probably down to the random nature of the starting locations and orientations. This is easier to see in the combined plot shown in Figure 4.13.

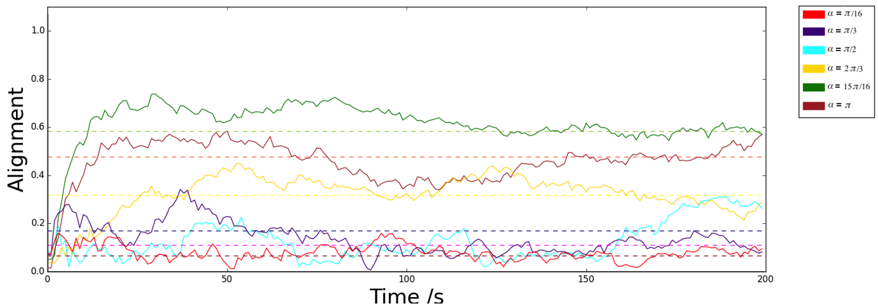


Figure 4.13: Combined alignment over time plot for the six simulations in Figure 4.12

5 Including a Predator

In this final section a predator will be introduced to observe how the simulated fish react to danger. There are three subsections where in each there is a different update procedure for either the fish or predator or both. In the first subsection when the fish enter the predator interaction zone the fish swim directly away from the predator and the predator follows a fixed trajectory. In the second, the predator will swim towards the mean position of the fish while the fish will swim directly away from the predator once they enter the interaction zone. In the final subsection, the amount a fish reacts to a predator is determined by a normal distribution.

5.1 Fish Repelled Directly Away from a Predator Following a Fixed Trajectory

To implement a simulated predator, the distance between each fish and the predator is calculated,

$$d_{p,i} = \sqrt{(x_i - x_p)^2 + (y_i - y_p)^2}.$$

If $d_{p,i} < P$, where P is the radius of repulsion around the predator, then the fish are repelled from the predator. The fish are repelled in so that they swim directly away from the predator, Figure 5.1.

The update equation for all fish i such that $d_{p,i} < P$ is

$$\theta = \arctan\left(\frac{y_i - y_p}{x_i - x_p}\right) + \pi \tag{8}$$

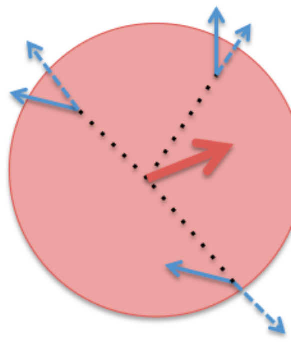
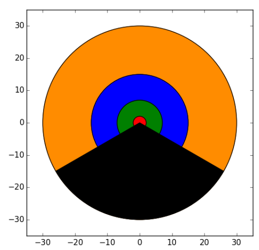


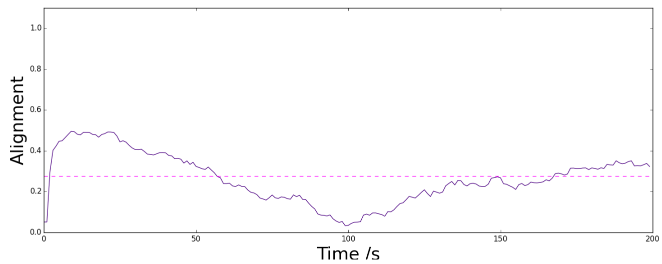
Figure 5.1: Each fish, blue, updates to swim directly away from the predator, red, taking the direction of the dashed arrows.

and since the predator is following a fixed trajectory its direction is constant.

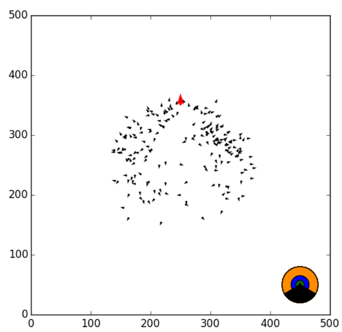
Figure 5.2 is made by running a simulation with parameters $R = 2.0, D = 7.0, A = 15.0, \sigma = 0.2$ and $P = 30.0$. To make a clear contrast to the fish the predator has a higher velocity, $v_p = 1.5$ units per second. The predator is set to start below the fish swimming at an angle of $\frac{\pi}{2}$.



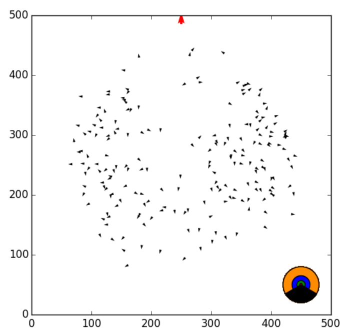
(a) Zone of interaction



(b) Alignment vs Time



(c) Simulation of school at $t = 100$



(d) Simulation of school at $t = 190$

Figure 5.2: From a simulation where $R = 2.0, D = 7.0, A = 15.0, \alpha = \frac{2\pi}{3}$ and $P = 30.0$.

As with running the initial simulations in Sections 2, 3 and 4 a schematic of the interaction zones around each fish is included, Figure 5.2a. The new orange sector is the predator interaction zone, if a predator is within this zone then the fish reacts to it. However, if there is no predator then the update equations for this zone are passed over.

From the alignment over time graph observe that the total alignment decreases to almost zero at approximately $t = 100$. Looking at the snapshot for this time, Figure 5.2c, each of the fish are facing away from a centre point. This causes the alignment to be very low. From both the alignment over time plot and the final snapshot, the fish attempt to realign in schools once the danger has passed.

5.2 Predator Attracted Towards Mean Location of Fish

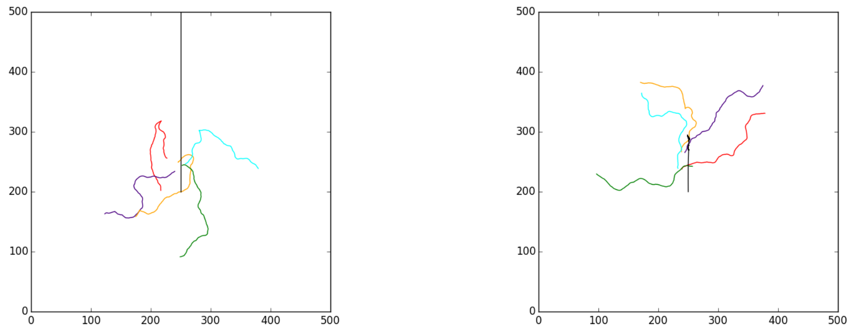
Now the update process for the predator is changed so that it swims directly towards the mean position of the fish. Now there is a non trivial update equation for the predator. In the previous section the predator followed its initial direction with no deviations. Now we set the predator direction to

$$\phi = \arctan\left(\frac{\frac{1}{N}\sum_j y_j}{\frac{1}{N}\sum_j x_j}\right),$$

whilst the direction of the fish continue to be updated by using equation (8).

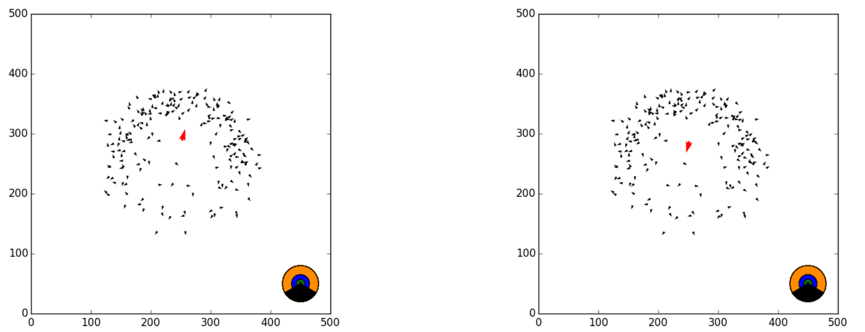
Running a simulation with the same parameters as in Section 5.1 there are noticeable differences. By firstly looking at the trajectories of five randomly located fish and the predator, shown in Figure 5.3, the major difference is the length of the black line. The distance traveled by the predator is much shorter when it is attracted to the mean location of the fish. This enables the fish to swim past the predator, whereas before when the predator was following a straight line, the fish were repelled from the predator and could not pass it.

To explain what happens the the predator and why it does not travel much further than the centre of the domain consider Figure 5.4. When updating its current direction and hence its location the predator calculates the mean location of the fish. At $t = 120$ the mean location was just in front of the predator, however, after just one tilmestep the location becomes behind it. Hence the predator switches its direction. This is as a result of the fish surrounding the predator and therefore confusing it. In an article published by Havforskningsinstituttet [1], a marine institute in Norway, Nilon and Vibó state that fish swim in circles in order to confused predators. This is confirmed by this simulation, despite the fish not circling the predator.



(a) Fixed Trajectory (b) Towards Mean Location

Figure 5.3: Trajectories of five fish and the predator, shown by the black line, using two method of updating the predator.



(a) $t = 120$ (b) $t = 121$

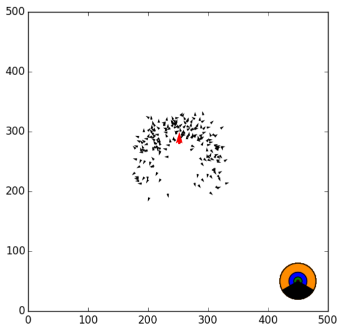
Figure 5.4: Snapshot of the simulation at two consecutive time steps.

When the fish circle the predator the alignment becomes very low. The alignment settles to a value of 0.12 and stays very close to this value once it achieves statistical stability.

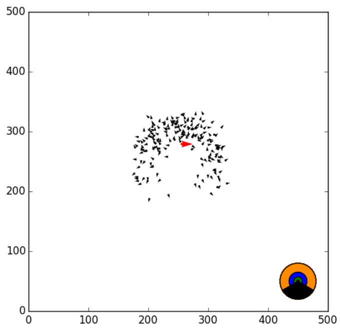
5.3 Amount the Predator and Fish Can Turn is Restricted

The amount a fish or predator can change its angle each time step so far has been solely down to the fish it is interacting with. In the case of the predator this is the position of all the fish. Now the change of angle is restricted to a maximum change of $\pm\tau_f$ and $\pm\tau_p$ for the fish and predator respectively.

When running a simulation, with $\tau_f = \frac{2\pi}{3}$ and $\tau_p = \frac{\pi}{2}$, the visual appearance looks very similar. However, when comparing two snapshots of consecutive time steps, Figure 5.5, it is possible to observe where the restriction has been implemented.
When comparing the alignment over time graphs, Figure 5.6 for the models with and without the turning being restricted there is only a slight difference.



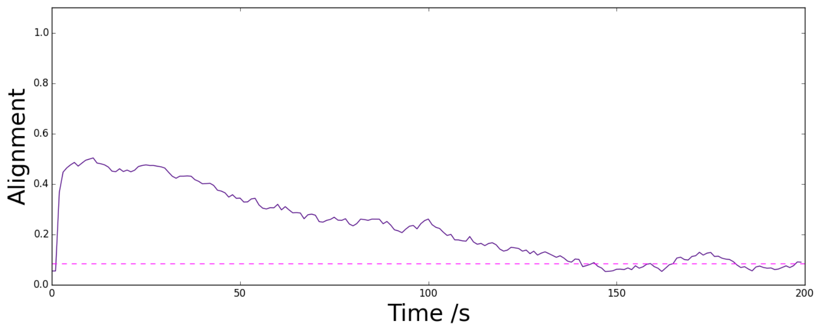
(a) $t = 61$



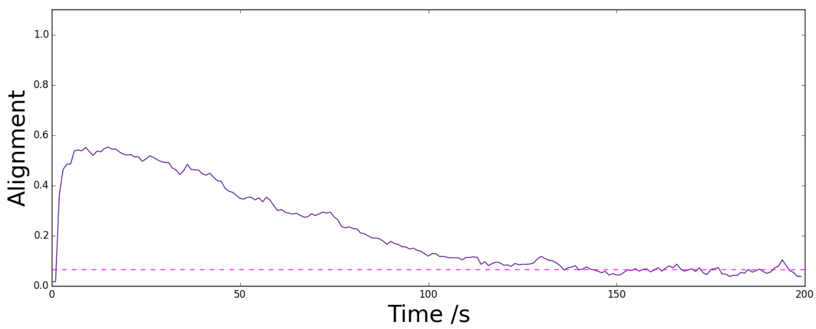
(b) $t = 62$

Figure 5.5: Snapshot of the simulation at two consecutive time steps.

When the turning becomes restricted the alignment becomes lower significantly earlier.



(a) Not restricted



(b) Resticted

Figure 5.6: Alignment over time graphs when (a) the turning is unrestricted and (b) when turning of the fish is restricted to $\frac{2\pi}{3}$ and the predator to $\frac{\pi}{2}$.

5.4 The Amount Fish React Determined by a Gaussian Distribution

In this final section the amount the fish reacts to the predator is determined by a gaussian distribution. To find the appropriate distribution the height, centre position and spread has to be found. Since the x-axis will represent the distance away from the predator, the value of the function is required to be larger the closer it get to 0 in order to implement the sense of danger in the fish. The closer the fish are the more they react. The distribution is shifted so that it is centered on 0.0. Since the fish currently react to the predator when it is within 30 units a distribution with a similar spread is needed. The spread, or standard deviation, is therefore set to 12. This is chosen so that the values at ± 30 are small. The scale of the distribution is set so that the maximum value of the distribution is 1.0 so that the values given by the distribution can be used as the fraction of a full turning away from the predator. Combining this information gives the following function,

$$f(d_p, \mu, \sigma) = e^{-\frac{(d_p)^2}{288}}.$$

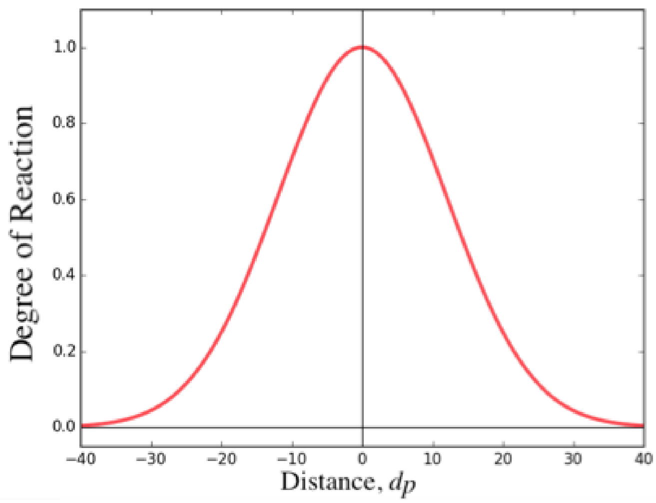


Figure 5.7: The gaussian distribution. The x values represent the distance away from the predator and the y values are then calculated to represent the percentage of reaction to the predator. Hence fish closer to the predator will react more to those further away.

In order to use the values from the gaussian distribution the change in angle, δ, must be calculated

$$\delta = \theta - \beta.$$

Where θ is the fish' current direction and β is the direction the update equations have calculated. The amount of this change used is now determined by the modified distribution. A fish at distance d_p from the predator gives a value n from the gaussian distribution. The new angle at which it will travel is

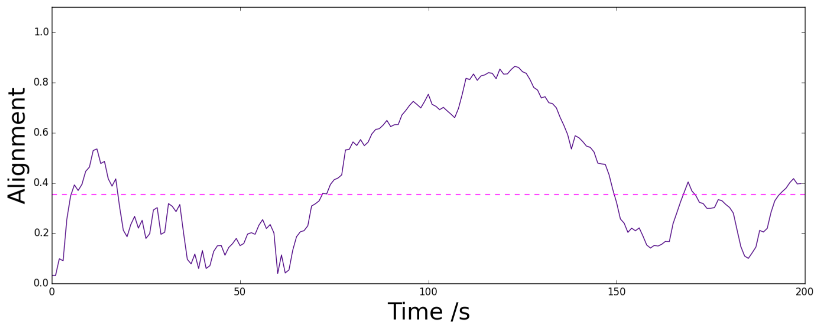
$$\eta = n(\theta - \beta).$$

It is now possible to run a simulation with parameters as in Table 5.1. This produces the results shown in Figure 5.8. Comparing these figures with the figures from previous predator models the differences are large. Starting with the alignment over time graph, Figure 5.8a, in previous predator models the alignment decreased initially. In Figure 5.2b the alignment starts to increase after $t = 100$, the approximate time the predator has passed through the school. Whereas in the other two models where the predator follows the mean, at $t \approx 100$ the alignment is very low and stays low until the end of the simulation. In this model, where turning is restricted as to a normal distribution, the fish alignment increases in the first few time steps. This is due to the fish further away aligning with the fish which have a large restriction to their change in angle. This causes the school to break up into smaller schools and hence the overall alignment drops much earlier, at around $t = 60$. Figure 5.8b shows there are a number of smaller schools where approximately half are traveling up and right whereas the other half are travelling down and left. But as seen from $t > 60$ they have the potential of re-aligning again once the danger has passed.

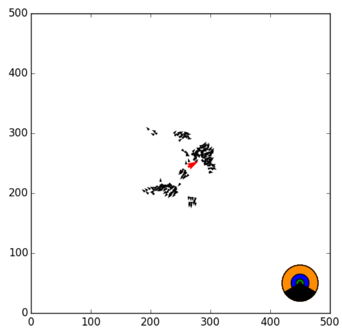
Quantity	Symbol	Value
Number of fish	N	200
Velocity	v	1.0
Noise	σ	0.2
Radius of repulsion	R	2.0
Radius of alignment	D	7.0
Radius of attraction	A	15.0
Predator repulsion radius	P	30.0
Predator velocity	v_p	1.5

Table 5.1: Parameters used in the modified normal distribution model.

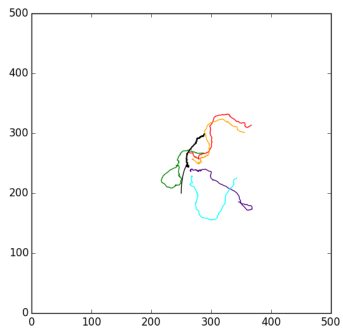
Moving on, the trajectory plot of the predator, shown as a black line, now has a much longer length. This is due to the mean position of the fish no longer approximately being the position of the predator. Now the predator appears to chase the school containing the fish, represented by the red and yellow lines.



(a) Alignment over time.



(b) Snapshot of fish at $t = 60$.



(c) Trajectories of 5 fish and predator.

Figure 5.8: Alignment, snapshot and trajectories from a simulation using the modified normal model, with parameters set to those in Table 5.1.

6 Conclusion

A basic model is initially used to to see how the noise effects the alignment values of schools of fish. Then the model is modified to incorporate three regions of interaction, a repulsion, alignment and attraction zone. The radii parameters are then increased or decreased to see how the ratios of the radii affect the alignment. Then a restricted field of view is introduced, where α is the angle to which the fish can see to the left and to the right. By changing the size of α the effects of the blind spot can be observed in the alignment values. Finally a predator is added in order to see how fish simulated with a restricted view react to danger.

Good alignment values come from models where the noise parameter is small, $\sigma \leq 0.2$. Good alignment is also seen when the size of the alignment parameter is almost as large at the size of the attraction parameter. This produces a school of fish with almost perfect alignment. When a field of view is introduced the best alignment comes from when the fish have a small blind spot. This gives better alignment values than when the fish have a unrestricted view.

When the noise value is large, $\sigma \geq 0.8$, the alignment values are very small. The alignment is also poor when the repulsion zone is large and when the alignment zone is small, $a \approx 0$. When introducing a field of view the fish have poor alignment when the blind spot covers over 50% of the region surrounding each fish.

The alignment values are also very low when a predator is introduced. However, when the predator is following the mean location of its prey, the fish successfully manage to confuse the predator by encircling it. This ensures the mean location of the fish to be approximately the current location of the predator. When the turning of the fish is restricted and determined by a gaussian distribution, the predator then appears to chase after small groups of fish.

To follow on from this report, a simulation looking into 3D would be interesting to see if any of the models examined would produce results such as a torus shaped school. This was previously managed by Couzin *et al.* in their paper published in 2002 [7]. It would also be interesting to see if the same results could be found if the update steps look at a fixed number of fish to interact with instead of the fish within a fixed distance.

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