A FIRST STEP TOWARD THE CALCULATION OF A CONNECTIVITY MATRIX FOR THE GREAT BARRIER REEF

CHRIS BOWDEN

University of Reading
Department of Mathematics

Supervisor: Dr Emmanuel Hanert

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Abstract

Coral reef systems such as the Great Barrier Reef are fundamental to the food industry, tourism revenue and coastal protection of tropical regions. Due to recent human activity, the health of these coral reefs is under threat. It is therefore necessary to design marine reserves in order to protect and help sustain coral populations. An understanding of the connectivity between reefs or systems of reefs can help decide on the size and spacing of marine reserves.

To follow the paths of coral eggs released from reefs in simple domains, a particle tracking algorithm is developed in conjunction with a current hydrodynamic model of the Great Barrier Reef. The hydrodynamic model makes use of the $P_1^{NC} - P_1$ finite element formulation which is presented. Particle positions are updated by means of the Lagrangian algorithm.

This study suggests that the construction of connectivity matrices for reef systems should take into account both short and long range dispersal strategies by considering different species of coral and how their mechanisms of reproduction affect the dispersal time of their larvae.

Acknowledgements

Firstly I would like to thank NERC for their generous grant, making it possible for me to study this course. I would also like to thank Emmanuel Hanert for all of his advice and ideas given while supervising this project.

I would like to thank all of my fellow MSc students for making the computer room an enjoyable and relaxing place to study. Many thanks also go to my girlfriend for all of the patience and reassurance she has given me throughout the course.

Lastly I would like to thank my Dad for all of the time, effort and money he spent on getting my program to run on all six computers in the house. Without his help I would not have managed to get all of the results needed before the time for the project ended.

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Figure 1: Map of locations of threatened corals reefs and sites that show signs of promise. Image taken from Bryant et al. (1998).

Fishing, tourism and economic resources of tropical areas are all built upon healthy coral ecosystems. Worldwide, the food, tourism revenue, coastal protection (barrier coral reefs protect shorelines from erosion and storm damage) and new medications that the reefs pro-

Figure 2: Map of locations of protected reef areas. Image taken from Bryant et al. (1998).

Carr 2003). The currents therefore control the transport of coral eggs between reefs, and hence determine the connectivity of reef populations. So what can be gained from investigating the connectivity between reef populations? Due to the damage inflicted to coral reefs by the various di□erent processes described above, marine reserves must be designed to protect coral reef populations. Bryant et al., 1998, found that at least 40 countries did not have any marine protected areas for conserving their coral reef systems. A map of marine protected areas is given in Figure 2. The size and spacing of these reserves is not only critical to the sustainability of the protected populations but can also greatly influence unprotected populations outside of the reserves (Shanks et al., 2003). It is therefore important to have an understanding of how populations of corals in reefs or islands are being sustained. Is a reef or island self-replenishing or does it rely on the transport of coral eggs from other reefs and islands? To what extent does a reef or island replenish other populations? The answers to these questions can help determine how large marine reserves are made and how far apart they should be. Understanding the connectivity between coral reefs can help to identify which reefs or systems of reefs should be protected in order to enhance other unprotected populations.

The purpose of this study is to develop a tool for use in conjunction with a current hy-

included in the model. The results of this study are in the form of connectivity matrices produced for each domain.

Chapter 1

An unstructured-mesh hydrodynamic model of the GBR

The model provided by Emmanuel Hanert is presented in [1] as a model that solves the discretized shallow water equations (SWEs) on a fully unstructured mesh of approximately 850,000 triangular elements. The model domain covered most of the GBR from the Great Keppel Island to the Forbes Island in the North[1]. In this study, the model will run on the much smaller, simpler domains mentioned earlier that only contain a few islands. This chapter will outline the main features of the model and give examples of the output generated.

1.1 The shallow water equations and boundary conditions

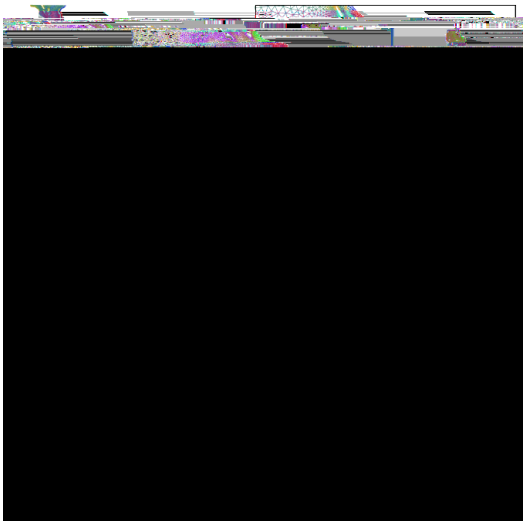
1.1.1 The shallow water equations

The SWEs are comprised of the continuity equation and the horizontal momentum equations, they are presented below using the same notation as in [1]:

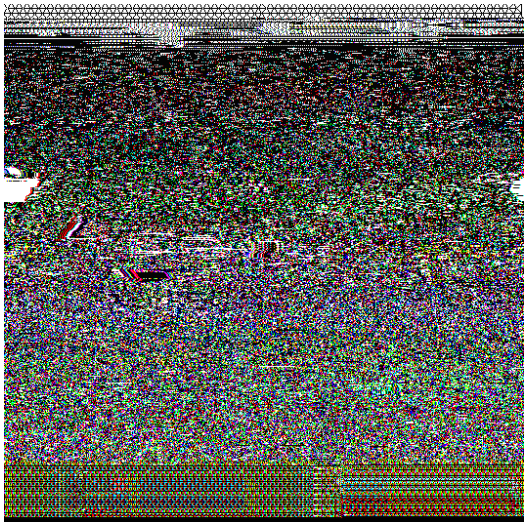
$$\begin{aligned}
\frac{\partial \eta}{\partial t} + \frac{\partial (Hu)}{\partial x} + \frac{\partial (Hv)}{\partial y} &= 0, \qquad (1.1)\\
\frac{\partial u}{\partial t} + u\frac{\partial u}{\partial x} + v\frac{\partial u}{\partial y} - fv + g\frac{\partial \eta}{\partial x} &= \frac{1}{H}\left[\frac{\partial}{\partial x}(\nu H\frac{\partial u}{\partial x}) + \frac{\partial}{\partial y}(\nu H\frac{\partial u}{\partial y})\right] + \frac{\tau_x}{\rho H} - \frac{g\,\mathrm{u}}{C^2 H}u,\\
\frac{\partial v}{\partial t} + u\frac{\partial v}{\partial x} + v\frac{\partial v}{\partial y} + fu + g\frac{\partial \eta}{\partial y} &= \frac{1}{H}\left[\frac{\partial}{\partial x}(\nu H\frac{\partial v}{\partial x}) + \frac{\partial}{\partial y}(\nu H\frac{\partial v}{\partial y})\right] + \frac{\tau_y}{\rho H} - \frac{g\,\mathrm{u}}{C^2 H}v,
\end{aligned}$$

1.2 Criteria for the mesh

The model is based on an unstructured mesh, and so the size and shape of the triangular



(c) Fine mesh resolution around islands and course mesh resolution in open waters, image taken from [1]



(d) Fine mesh resolution around islands and open boundaries. Images courtesey of Emmanuel Hanert

Figure 1.1: Model resolution

the solution is calculated using a 3^{rd} order Adams-Bashforth time marching scheme. The main features of these methods are described below.

1.3.1 The $P_1^{NC} - P_1$ finite element formulation

Let's remind ourselves of the equations we wish to solve:

$$\frac{\partial \eta}{\partial t} + \quad \cdot (H\mathbf{u}) = 0, \tag{1.2}$$

$$\frac{\partial \mathbf{u}}{\partial t} + \mathbf{u} \cdot \quad \mathbf{u} + f\mathbf{k} \times \mathbf{u} + g \quad \eta = \quad 1$$

where $\bar{\Omega}$ is the closure of Ω. Now let $\partial\Omega_e$ be the boundary of each element Ω_e, and let the outward unit normal to $\partial\Omega_e$ be $\mathbf{n}_e$. Let Γ be the collection of all the interelement boundaries $\Gamma_I = \partial\Omega_e \cap \partial\Omega_f$ with $e > f$ so that:

$$\bar{\Gamma} = \bigcup_{I=1}^{N_\Gamma} \bar{\Gamma}_I \quad \text{and} \quad \Gamma_I \cap \Gamma_m = \emptyset \quad \text{for} \quad I = m,$$

where N_Γ is the number of elements in Γ. Each $\Gamma_I \subset \Gamma$ is associated with a unique normal vector $\mathbf{n}$ which point from Ω_e to Ω_f. The finite element method uses the weak formulation of equations (1.2) and (1.3). This form is built in such a way that the solution for the elevation is continuous everywhere whereas the solution for the velocity can be discontinuous between elements. It therefore needs constraints to impose the continuity of the velocity between the elements. The weak form of the SWEs, obtained by taking the dot product of equations (1.2) and (1.3) with test functions $\hat{\eta}$ and $\hat{\mathbf{u}}$ respectively, is as follows:

Find $\eta(x, t) \in E$ and $\mathbf{u}(x, t) \in U$ such that

$$\sum_{e=1}^{N_E} \int_{\Omega_e} \frac{\partial \eta}{\partial t}\hat{\eta} - H\mathbf{u} \cdot \nabla \hat{\eta} \, d\Omega + \sum_{e=1}^{N_E} \int_{\partial\Omega_e} H\hat{\eta}\mathbf{u} \cdot \mathbf{n}_e \, d\Gamma = 0 \quad \forall \hat{\eta} \in E, \tag{1.4}$$

$$\sum_{e=1}^{N_E} \int_{\Omega_e} \frac{\partial \mathbf{u}}{\partial t} \cdot \hat{\mathbf{u}} - (\nabla \cdot (\mathbf{u}\hat{\mathbf{u}})) \cdot \mathbf{u} + f(\mathbf{k} \times \mathbf{u}) \cdot \hat{\mathbf{u}} + g\nabla\eta \cdot \hat{\mathbf{u}} - \frac{1}{H}(\nabla \cdot (\nu H \nabla \mathbf{u})) \cdot \hat{\mathbf{u}}$$
$$- \frac{\tau}{\rho H} \cdot \hat{\mathbf{u}} + \frac{g}{C^2 H}\mathbf{u} \cdot \hat{\mathbf{u}} \, d\Omega + \sum_{e=1}^{N_E} \int_{\partial\Omega_e} (\mathbf{u}\mathbf{u} \cdot \mathbf{n}_e) \cdot \hat{\mathbf{u}} d\Gamma + \sum_{I=1}^{N_\Gamma} \int_{\Gamma_I} [\mathbf{u}] \cdot [\mathbf{a}(\hat{\mathbf{u}})] d\Gamma$$
$$= 0 \quad \forall \hat{\mathbf{u}} \in U, \tag{1.5}$$

where $[\mathbf{s}] = \mathbf{s}_{|\Omega_e} - \mathbf{s}_{|\Omega_f}$ is the jump of $\mathbf{s}$ on an interior edge of Γ_I, $\mathbf{s}_{|\Omega_e}$ denotes the restriction of $\mathbf{s}$ on Ω_e, and E and U are suitable function spaces[3] to which $\hat{\eta}$ and $\hat{\mathbf{u}}$ belong. The function $\mathbf{a}$ satisfies the previously mentioned continuity constraint while maintaining the weak formulation of the differential equations. The function $\mathbf{a}$ satisfies:

$$\mathbf{a}(\hat{\mathbf{u}}) = \begin{cases} \mathbf{u} \cdot \mathbf{n}(\lambda - 1/2)\hat{\mathbf{u}} & \text{on } \Omega_e, \\ \mathbf{u} \cdot \mathbf{n}(\lambda + 1/2)\hat{\mathbf{u}} & \text{on } \Omega_f, \end{cases}$$

where $\lambda \in [-1/2, 1/2]$. The choice of λ

by choosing $\lambda = \frac{1}{2}\text{sign}(\mathbf{u}(\mathbf{x}) \cdot \mathbf{n}(\mathbf{x}))$. Choosing the upwind parametrization that is usually selected (Houston et al., 2000; Hanert et al., 2004), with some standard algebra (Houston et al., 2000; Hanert et al., 2004) the weak formulations (1.4) and (1.5) can be rewritten as:

Find $\eta(x, t)$ E and $\mathbf{u}(\mathbf{x}, t)$ U such that

$$\sum_{e=1}^{N_E} \int_{\Omega_e} \frac{\partial \eta}{\partial t} \hat{\eta} - H\mathbf{u} \cdot \hat{\eta} \, d\Omega + \sum_{I=1}^{N_\Gamma} \int_{\Gamma_I} (H\mathbf{u} \cdot \mathbf{n} \, [\hat{\eta}] + [H\mathbf{u} \cdot \mathbf{n}] \, \hat{\eta} \, d\Gamma = 0 \quad \hat{\eta} \quad E, \tag{1.6}$$

$$\sum_{e=1}^{N_E} \int_{\Omega_e} \frac{\partial \mathbf{u}}{\partial t} \cdot \hat{\mathbf{u}} - (\cdot(\mathbf{u}\hat{\mathbf{u}})) \cdot \mathbf{u} + f(\mathbf{k} \times \mathbf{u}) \cdot \hat{\mathbf{u}} + g \cdot 7$$

(Hanert et al., 2005).

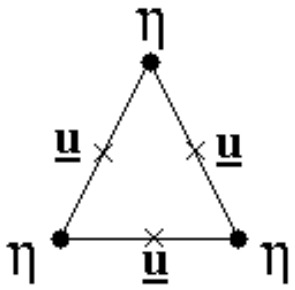


Figure 1.3: Position of elevation and velocity nodes on an element

(1.6) and (1.7) is performed:

$$\underbrace{H\mathbf{u}^h \cdot \mathbf{n}\,[\varphi_i]\,d\Gamma}_{=0} + \int_{\Gamma_I} [H\mathbf{u}^h \cdot \mathbf{n}]\;\varphi_i \;\; d\Gamma \approx 0. \qquad (1.8)$$

(Note that where previously $H = h + \eta$, in (1.8) η has been replaced with the finite element approximation η^h giving $H = h + \eta^h$).

The first term in (1.8) vanishes because of the continuity across the P_1 shape functions - there is no jump in the elevation shape function, i.e. $[\varphi_i$

where

$$F_\eta^n = - \quad \cdot (H\mathbf{u}^n),$$

and

$$F_{\mathbf{u}}^n = -\mathbf{u}^n \cdot \quad \mathbf{u}^n - f\mathbf{k} \times \mathbf{u}^n - g \quad \eta^n + \frac{1}{H}\left(\quad \cdot (\nu H \quad \mathbf{u}^n)\right) + \frac{\tau}{\rho H} - \frac{g \ \mathbf{u}^n}{C^2 H}\mathbf{u}^n.$$

Rearranging again to leave η^{n+1} and $\mathbf{u}^{n+1}$ on the left hand sides of our equations gives:

$$\begin{aligned} \eta^{n+1} &= \eta^n + \frac{\Delta t}{12}(23F_\eta^n - 16F_\eta^{n-1} + 5F_\eta^{n-2}), \\ \mathbf{u}^{n+1} &= \mathbf{u}^n + \frac{\Delta t}{12}(23F_{\mathbf{u}}^n - 16F_{\mathbf{u}}^{n-1} + 5F_{\mathbf{u}}^{n-2}). \end{aligned}$$

As η^n and $\mathbf{u}^n$ are vectors taking values over the whole domain, we obtain the following matrix system of linear equations:

$$\begin{bmatrix} A & 0 \\ 0 & B \end{bmatrix} \begin{bmatrix} U^{n+1} \\ H^{n+1} \end{bmatrix} = \begin{bmatrix} R_U \\ R_H \end{bmatrix} \tag{1.14}$$

where U^{n+1} and H^{n+1} are the values of η and $\mathbf{u}$ on the mesh nodes, defined as

$$U^{n+1} = \begin{bmatrix} u_i \\ v_i \end{bmatrix} \quad \text{and} \quad H^{n+1} = (\eta_j),$$

where $1 \le i \le N_S$ and $1 \le j \le N_V$. The matrix A on the left hand side of equation (1.14) is diagonal. In terms of computation e□ciency this is a major advantage as it means that we do not have to invert any large matrices or 'lump' any terms. The matrix B is not diagonal, and so here the 'lumping' technique is required to put the o□ diagonal terms onto the diagonal. With both the spatial and time discretization the elements of the matrices A and B are:

$$A_{ij} = \sum_e \int_{\Omega_e} \psi_i \psi_j \, \mathrm{d}\Omega \tag{1.15}$$

$$B_{ij} = \sum_e \int_{\Omega_e} \varphi_i \varphi_k \, \mathrm{d}\Omega \quad \delta_{ij}. \tag{1.16}$$

Equation (1.16) can be interpreted as adding all of the terms $\int_{\Omega_e} \varphi_i \varphi_k \, \mathrm{d}\Omega$ to entry B_{ij} when $i = j$.

2.1 Choosing an advection-diffusion algorithm

2.1.1 Eulerian or Lagrangian?

The tracking of a group or cluster of particles in a flow could be done by either:

- considering a group of particles as a passive tracer and monitor its concentration c (Eulerian formulation), or
- following each particle individually and, given its velocity, update its position at each time step (Lagrangian formulation).

In a 2-D approach, the concentration c of a passive tracer is governed by the Eulerian equation

$$\frac{\partial(hc)}{\partial t} = - \quad \cdot (\mathbf{u}hc - hk \quad c) \tag{2.1}$$

where t, $h(> 0)$ and $k(> 0)$ denote time, water depth and the horizontal diffusivity respectively ([6]), and $\mathbf{u}$ is the depth averaged velocity. According to [6], accurate numerical simulations of (2.1) are not easy to obtain due to difficulty in finding accurate Eulerian discretizations of the advective operator $- \quad \cdot (\mathbf{u}hc)$. Thus the Lagrangian algorithm is often used to predict the fate of water-borne propagules near coral reefs, for example sewage, coral eggs and larvae, plankton, fish and crown-of-thorn starfish (Sammarco & Andrews 1988, 1989, Wolanski et al., 1989, 1997, Black et al. 1990, 1991, Dight et al. 1990, Oliver et al. 1992, Black 1993), [6]. For this reason, this study will use the Lagrangian approach. The Lagrangian algorithm, as given in [6], reads:
At time $t_n = n\Delta t$ $(n = 1, 2, 3, \ldots)$, where Δt is a suitable time increment, the position $\mathbf{x}_n = (x_n, y_n)$ of a water-borne propagule is updated by:

$$\mathbf{x}_{n+1} = \mathbf{x}_n + \mathbf{v}\Delta t + \frac{\mathbf{R}_n}{\sqrt{r}}\sqrt{2k\Delta t} \tag{2.2}$$

where the velocity $\mathbf{v}$ is set to $\mathbf{u}$, $\mathbf{R}_n$ is a vector of zero mean random numbers with variance r and k is the horizontal diffusivity. It is believed that the concentration of particles, which

2.2 Integration of the advection-di□usion algorithm with the model

Before the advection-di□usion model can be written, some work needs to be done in order

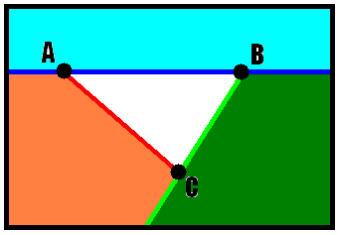


Figure 2.1: Each edge of a triangle splits 2-D space in half, image from [11]

product of the vectors $(B - A)$ and $(P - A)$ gives a vector pointing in to the page. Conversely, taking the cross product of $(B - A)$ and $(Q - A)$ gives a vector pointing out of the page.

- Moreover, taking the cross product of $(B - A)$ with the vector from A to any point above the line AB results in a vector pointing out of the page, while using any point below AB produces a vector pointing into the page. So all that is needed to distinguish which side of a line a point lies on is the appropriate cross product.
- Now all that is needed to be done is to work out which direction the cross product should point in. To caclulate this, a reference point that is always on one side of the line is needed. The third vertex of the triangle will do nicely.

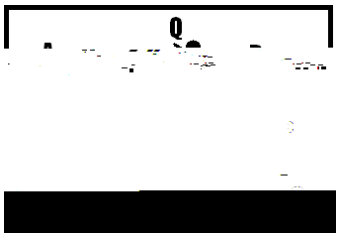


Figure 2.2: How do we mathematically determine which point is in the triangle? Image from [11]

Any point P where $(B-A)\times(P-A)$ does not point in the same direction as $(B-A)\times(C-A)$ isn't inside the triangle. If the cross products do point in the same direction, then P needs to be tested with the other lines as well. If the point is on the same side of AB as C and is also on the same side of BC as A and on the same side of CA as B, then it is in the triangle.

The Barycentric technique

The Barycentric technique is another conceptually simple technique for determining whether

a point is in a triangle or not, it requires slightly more algebra than the 'same side technique' but computes faster. This is the technique that will be employed in the model.

The three points of a triangle define a plane in space. Let A be the origin of this plane. Through combinations of the vectors $(B - A)$ and $(C - A)$ any point in the plane can be reached. In particular, the point P can be described as

$$P = A + u(B - A) + v(C - A)$$

If u or v is greater than one or less than zero then the point is outside of the triangle as it is too far from A in one of the directions $\pm(B - A)$ or $\pm(C - A)$. Furthermore if $u + v > 1$ then the point is outside of the triangle as the combination $A + u(B - A) + v(C - A)$ has taken the point past edge BC. If any of these tests fail then the point cannot be in this triangle. P is easily found given u and v, but what is needed is to find u and v given P. The position of P is given above as one equation in two unknowns. Two equations in two unknowns are produced as follows.

For ease of notation let $(P - A) = V_0$, $(B - A) = V_1$ and $(C - A) = V_2$ so that

$$P - A = u(B - A) + v(C - A)$$

becomes

$$V_0 = uV_1 + vV_2.$$

To get two equations in two unknowns, take the dot product of both sides with V_1 and then with V_2 to give

$$\begin{aligned} V_0 \cdot V_1 &= u(V_1 \cdot V_1) + v(V_2 \cdot V_1) \\ V_0 \cdot V_2 &= u(V_1 \cdot V_2) + v(V_2 \cdot V_2). \end{aligned}$$

Solving this pair of simultaneous equations gives us u and v:

$$\begin{aligned} u &= \frac{(V_2 \cdot V_2)(V_0 \cdot V_1) - (V_2 \cdot V_1)(V_0 \cdot V_2)}{(V_2 \cdot V_2)(V_1 \cdot V_1 - (V_2 \cdot V_1)(V_1 \cdot V_2)} \\ v &= \frac{(V_1 \cdot V_1)(V_0 \cdot V_2) - (V_1 \cdot V_2)(V_0 \cdot V_1)}{(V_2 \cdot V_2)(V_1 \cdot V_1) - (V_2 \cdot V_1)(V_1 \cdot V_2)}. \end{aligned}$$

So given the vertices of an element and the position of a point P, whether or not P lies in the element is worked out by simply calculating u and v as above and checking whether or not $u, v \in [0, 1]$ and $u + v < 1$.

2.2.2 Using the P_1 and P_1^{NC} weight functions to determine velocity at a point

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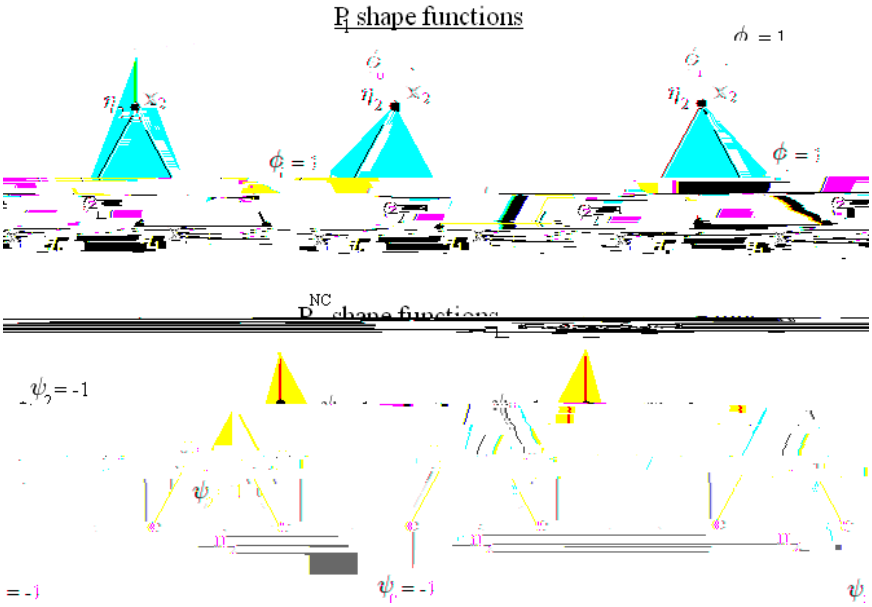


Figure 2.3: Shape functions

and so for each i there are three equations in three unknowns. For example for $i = 0$:

$$\begin{aligned} \varphi_0(x_0) &= 1 = \alpha_0 x_0 + \beta_0 y_0 + \gamma_0 \\ \varphi_0(x_1) &= 0 = \alpha_0 x_1 + \beta_0 y_1 + \gamma_0 \\ \varphi_0(x_2) &= 0 = \alpha_0 x_2 + \beta_0 y_2 + \gamma_0. \end{aligned}$$

Solving these simultaneous equations, for $i = 0$ for example, gives:

$$\begin{aligned} \alpha_0 &= \frac{y_1 - y_2}{(x_0 - x_2)(y_1 - y_2) + (x_2 - x_1)(y_0 - y_2)}, \\ \beta_0 &= \frac{x_2 - x_1}{(x_0 - x_2)(y_1 - y_2) + (x_2 - x_1)(y_0 - y_2)}, \\ \gamma_0 &= \frac{x_1 y_2 - x_2 y_1}{(x_0 - x_2)(y_1 - y_2) + (x_2 - x_1)(y_0 - y_2)}, \end{aligned}$$

α_1, α_2, β_1, β_2, γ_1 and γ_2 are found in the same way. A general form for α_i, β_i and γ_i can be written using the modulo operation:

$$\alpha_i = \frac{y_{(i+1)|3} - y_{(i+2)|3}}{(x_{i|3} - x_{(i+2)|3})(y_{(i+1)|3} - y_{(i+2)|3}) + (x_{(i+2)|3} - x_{(i+1)|3})(y_{i|3} - y_{(i+2)|3})},$$

$$\beta_i = \frac{x_{(i+2)|3} - x_{(i+1)|3}}{(x_{i|3} - x_{(i+2)|3})(y_{(i+1)|3} - y_{(i+2)|3}) + (x_{(i+2)|3} - x_{(i+1)|3})(y_{i|3} - y_{(i+2)|3})},$$

$$\gamma_i = \frac{x_{(i+1)|3}\ \ y_{(i+2)|3} - x_{(i+2)|3}\ \ y_{(i+1)|3}}{(x_{i|3} - x_{(i+2)|3})(y_{(i+1)|3} - y_{(i+2)|3}) + (x_{(i+2)|3} - x_{(i+1)|3})(y_{i|3} - y_{(i+2)|3})},$$

where $(i + k)|3$ stands for $(i + k)$mod3. In this general form the φ_is can be calculated using a single function that takes the position of a point (or particle) as an argument. From this the ψ_is can be calculated and hence the velocity at any point in the domain.

2.2.3 Construction of the diffusion term

The Lagrangian algorithm consists of an advective and a diffusive term. So far the steps to implmenting advective term $\mathbf{v}\Delta t$ (where $\mathbf{v}$ is set to $\mathbf{u}$ as in equation (2.1)) have been considered. The construction of the diffusive term $\frac{\mathbf{R}_n}{\sqrt{r}}\sqrt{2k\Delta t}$ requires

- a vector $\mathbf{R}_n = (R_x, R_y)$ of zero mean random numbers taking values in $[-1, 1]$,
- calculation of the variance of these random numbers
- a choice for the diffusivity parameter k.

The components of $\mathbf{R}_n$ are obtained using the `srand` and `rand` functions defined in the standard C++ library. Two random numbers R_1 and R_2 between 0 and 200 are produced and translated to the interval $[-1, 1]$ using the formulae

$$R_x = R_1/100 - 1,$$
$$R_y = R_2/100 - 1,$$

giving 201 possible values for each of R_x and R_y.

The variance r of these 201 random variables, call them x_k, is calculated using the standard formula:

$$r = \sum_{k=0}^{k=200} (x_k - \bar{x})^2 = 0.33667.$$

As for the choice of di□usivity parameter k, a range of values will be tested. The model only allows particles to be released from a finite number of points around the islands, however many particles can be released from each point. In order to find the best value to represent the dispersion of coral eggs in the flows through the two and four island domains, values of 0.5, 1.0 and 2.0 (as used in [

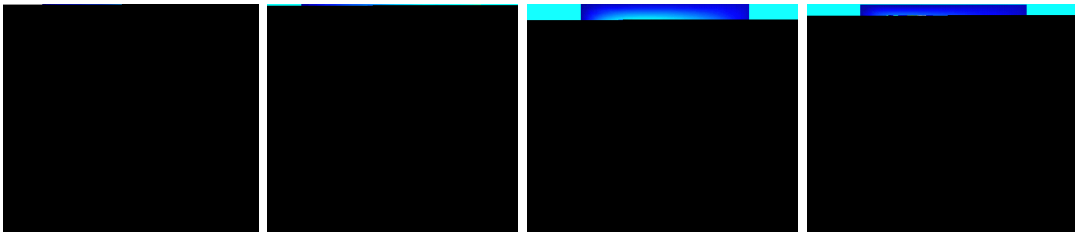


Figure 2.4: Stommel elevation fields at various time steps

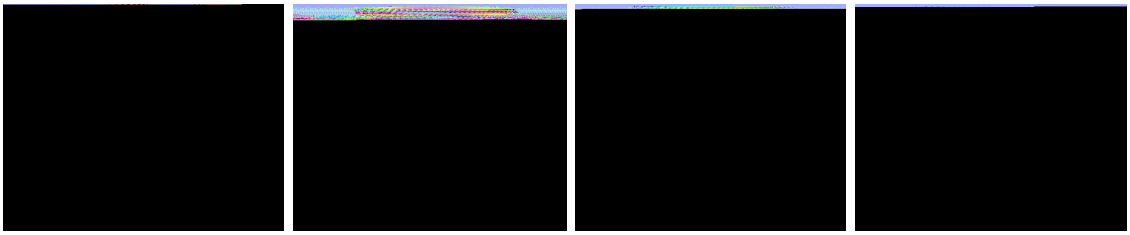


Figure 2.5: Stommel velocity fields at various time steps

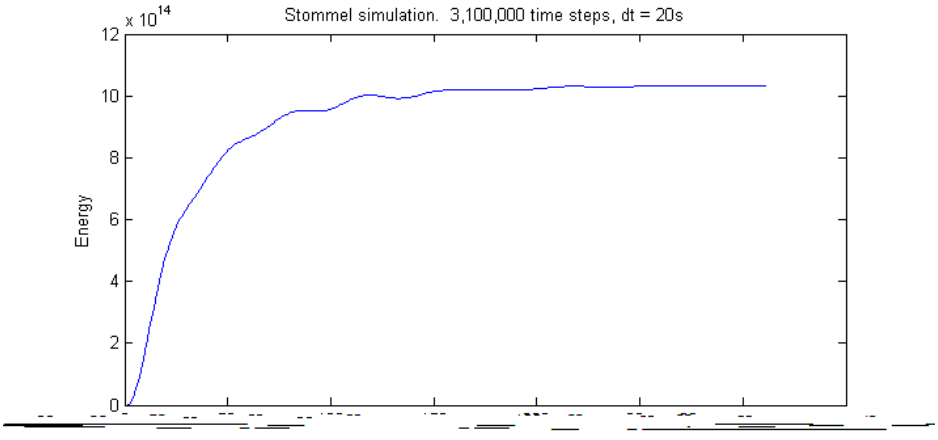
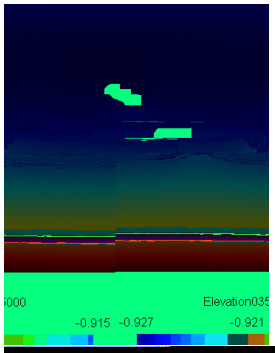
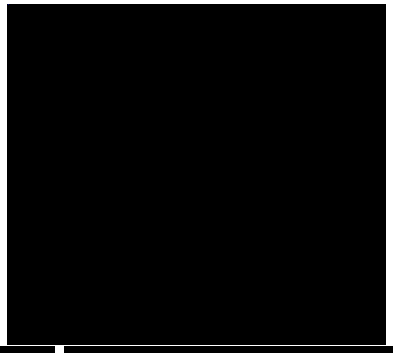
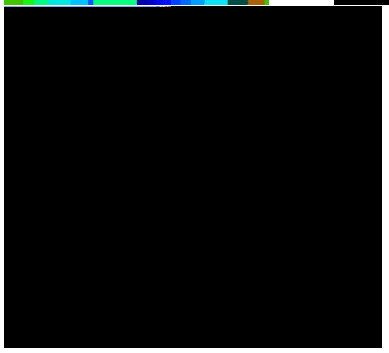
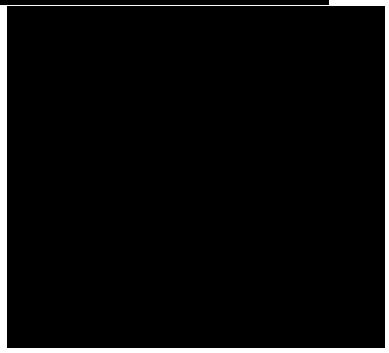
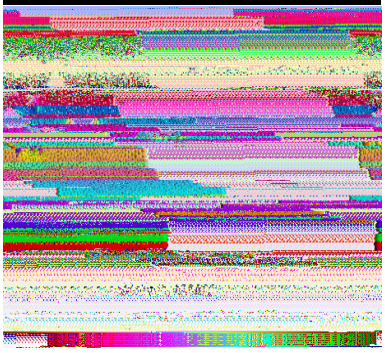
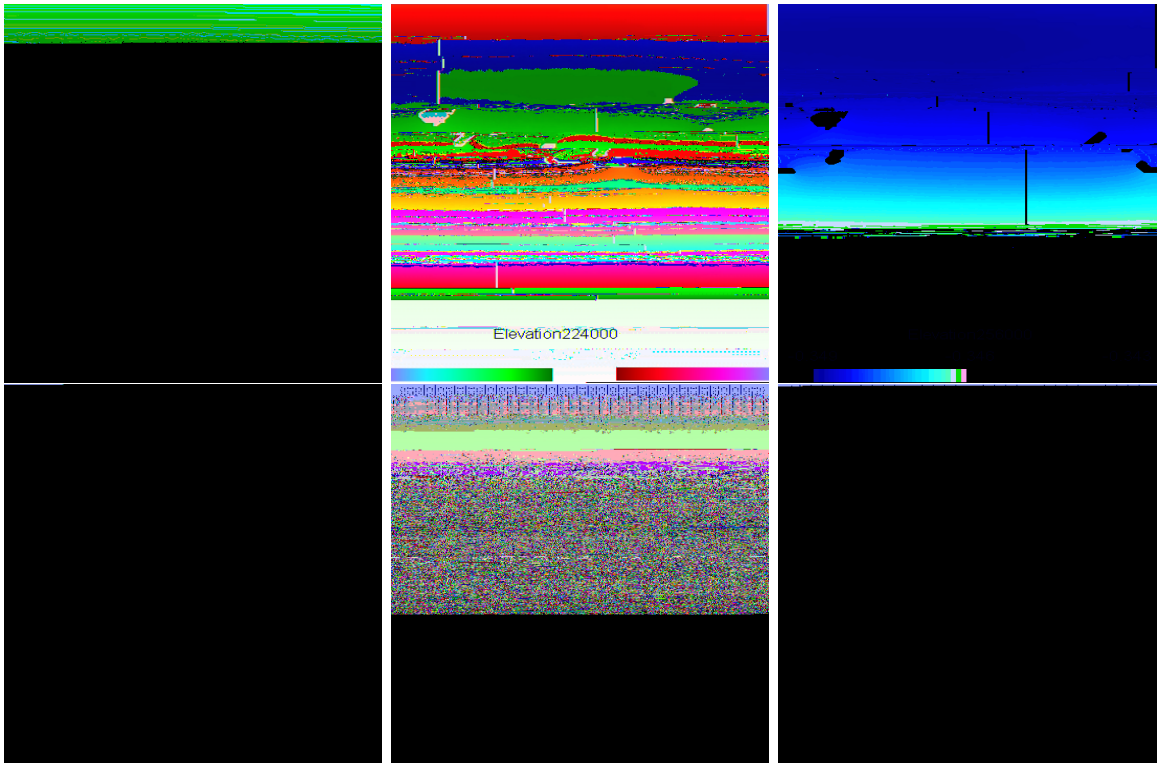


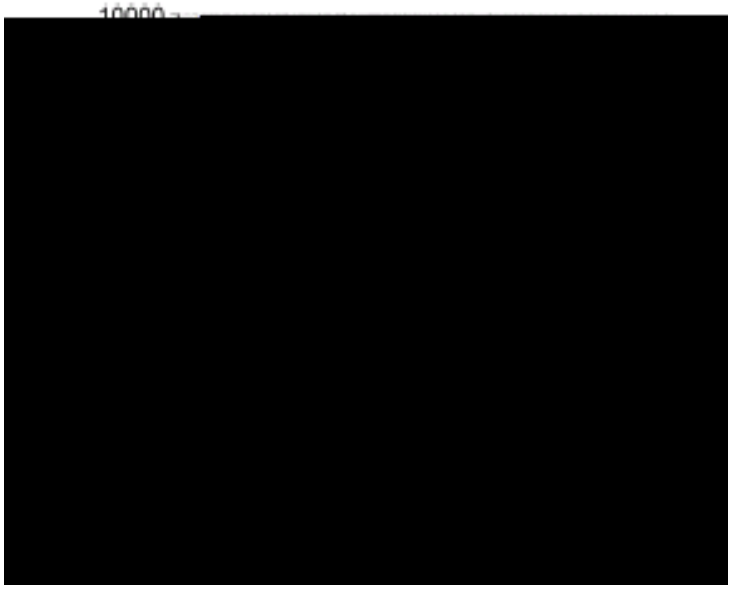
Figure 2.6: Energy in the Stommel simulation

Figure 2.7: A particle released into the Stommel simulation

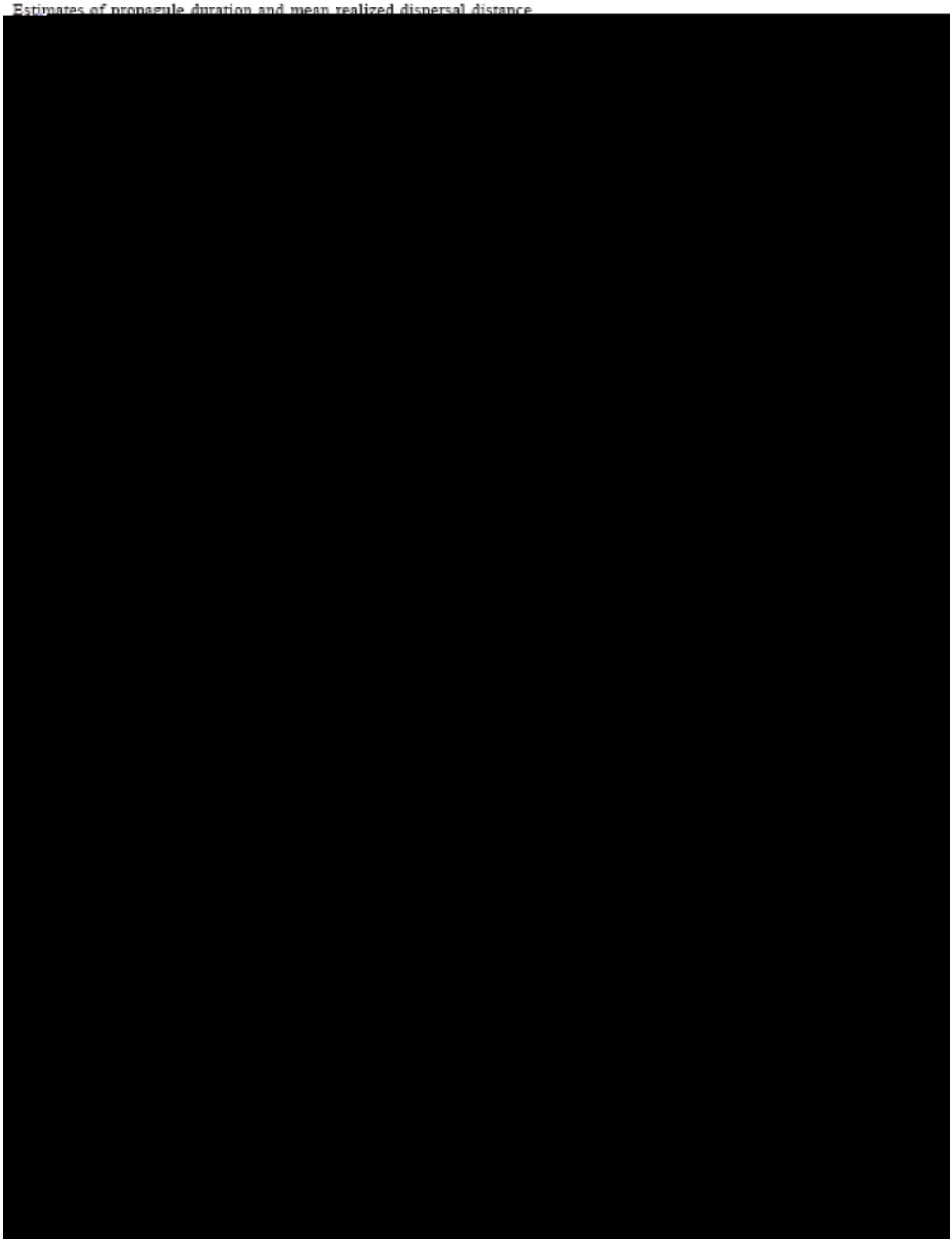

Elevation035
-0.915 -0.927 -0.921



Elevation224000



Estimates of propagule duration and mean realized dispersal distance



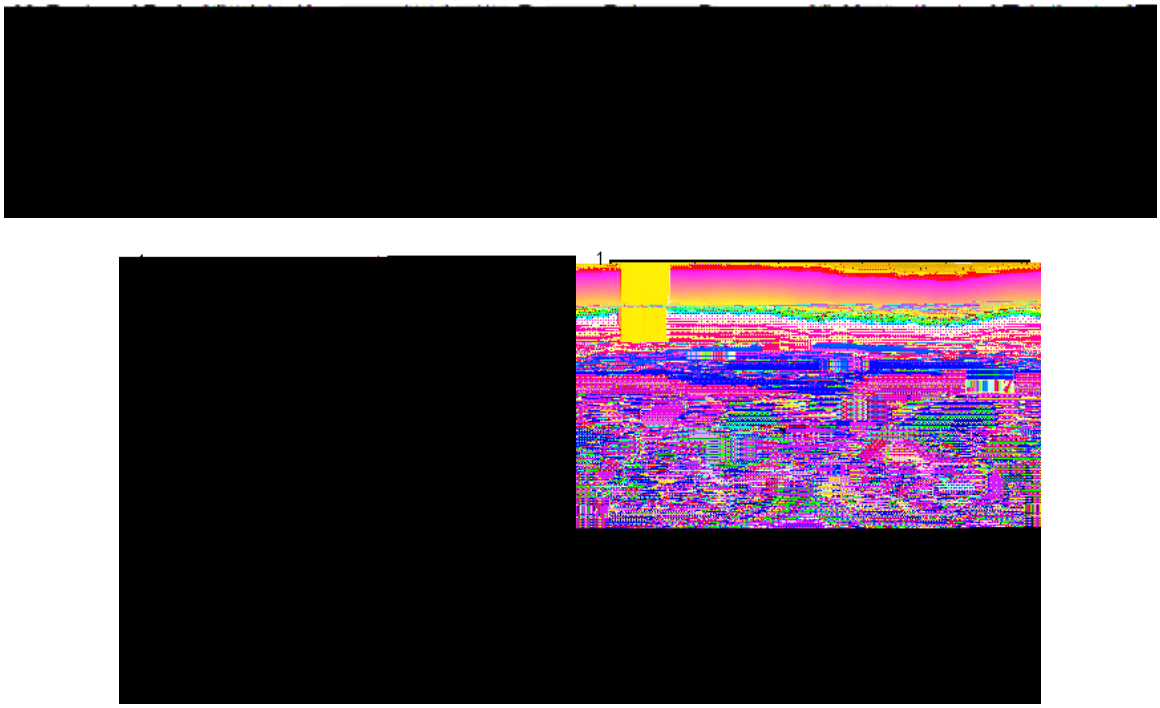


Figure 2.12: Radii around islands inside which propagules are assug1(ropa0010-1mto0-1ms00ttIrope)]TΩ

Chapter 3

Results

3.1 Two island domain

In the Stommel test case, the system became steady after about 3,000,000 time steps when energy became constant. In the case of the two and four island domains, the energy does not become constant as the elevation is being forced on the two open boundaries. A plot of the energy against the number of time steps reveals that the energy in the system oscillates:

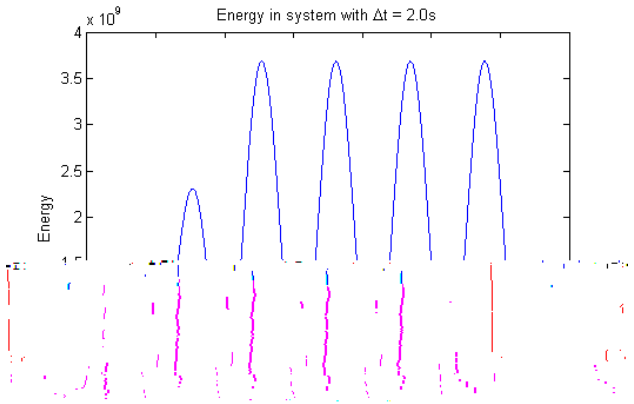


Figure 3.1: Plot of the energy in the two island system against the time step

The particles are therefore released once the energy in the simulation starts to oscillate over constant range (at 25000 time steps when Δt is set to 2.0 seconds). The results are

displayed to show the simulated dispersal times for the three types of coral larvae given in Figure (2.11) - *Pocilloporids* (4 hours), *Acroporids* (24-72 hours) and *Balanophyllia elegans* (3 days). Results are given in sets corresponding to diffusivity values 2.0, 10.0, 25.0 and 50.0 m^2s^{-1}. Plotted for each are the positions of particles and either the elevation or velocity fields for corresponding time frame. The two sets of results that best represent the behaviour for each time frame are given in this chapter, the rest can be found in Appendix A. In order to consider the islands in this domain individually, the lower island will be referred to as island one and the upper island will be referred to as island two.

3.1.1 Dispersal time = 4h (*Pocilloporids*)

Summary of results:

- for all values of the diffusivity the the particles stayed within the radii of the islands,
- as a result the connectivity matrices indicate that all propagules stayed within the vicinity of the parent reef.

Figure 3.2 displays a table of the minimum, maximum and mean distances travelled from the point of release by particles at increasing time steps.

Figure 3.2: Minimum, maximum and mean distances dispersed from initial release points for the two island domain initial four hour period

Dispersal time (mins)	Di□usivity k (m^2s^{-1})	Min. dispersal distance (m)	Max. dispersal distance (m)	Mean dispersal distance (m)
33	2.0	0.0025	0.6409	0.1336
66	2.0	0.0132	5.3517	1.0824
99	2.0	0.0239	13.7286	3.2116
132	2.0	0.0239	13.7286	3.2116
165	2.0	0.0364	24.238	6.5938
198	2.0	0.0284	22.7876	6.0714
33	10.0	0.0023	0.6076	0.1304
66	10.0	0.0095	5.3047	1.0872
99	10.0	0.0161	13.64	3.1884
132	10.0	0.0242	20.2072	5.3745
165	10.0	0.0359	23.9935	6.5632
198	10.0	0.0299	22.5723	6.053
33	25.0			

3.1.2 Dispersal time = 24h - 72h (*Acroporids, Balanophyllia elegans*)

Summary of results:

- At low values of di□usivity the particles still stay within the radii of the islands,
- but now at higher values of di□usivity some particles start to oscillate in and out of one of the islands.
- The two extremes are displayed, k = 2.0m

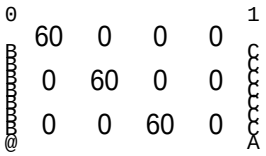
3.2 Four island domain

At this point it is necessary to consider the computational and time restraints on this study. For the CFL condition to be satisfied for the four island domain, it is necessary to change the time step from Δt = 2.0s to Δt = 0.25s, i.e. one iteration corresponds to just a quarter of a second. As a result, the time taken for the energy to oscillate between a steady range increases to 200,000 time steps (see Figure 3.5). The execution time for the program to reach this point is about 44 hours. For the program to then simulate the dispersal of particles for

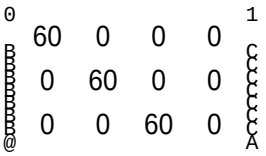
3.2.2 Longer dispersal times

The four island simulation was run until the end of the time allocated for this study, the evolution of the connectivity matrix is given below. Particles are released once the system has reached a steady state at 200,000 time steps. The final time step is 425,000 which corresponds to a simulation of propagules in the water column for 29.5 hours.

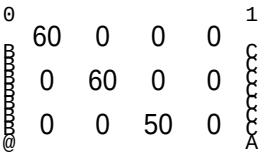
Initially, particles start to leave the fourth island and then after some time leave the third island:



Time step = 200000

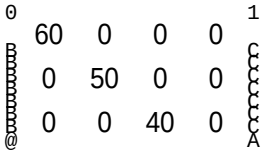


Time step = 227000

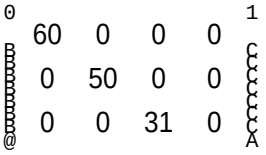


Time step = 250000

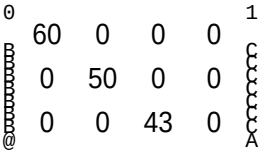
Particles then begin to leave the second island and others move in and out of the third and fourth islands:



Time step = 270000

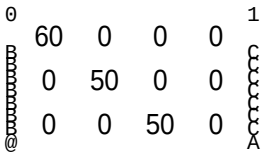


Time step = 280000

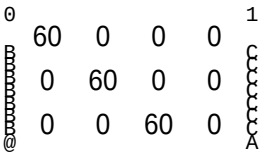


Time step = 300000

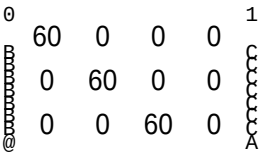
After 300,000 time steps particles start to return to their parent islands:



Time step = 310000



Time step = 330000

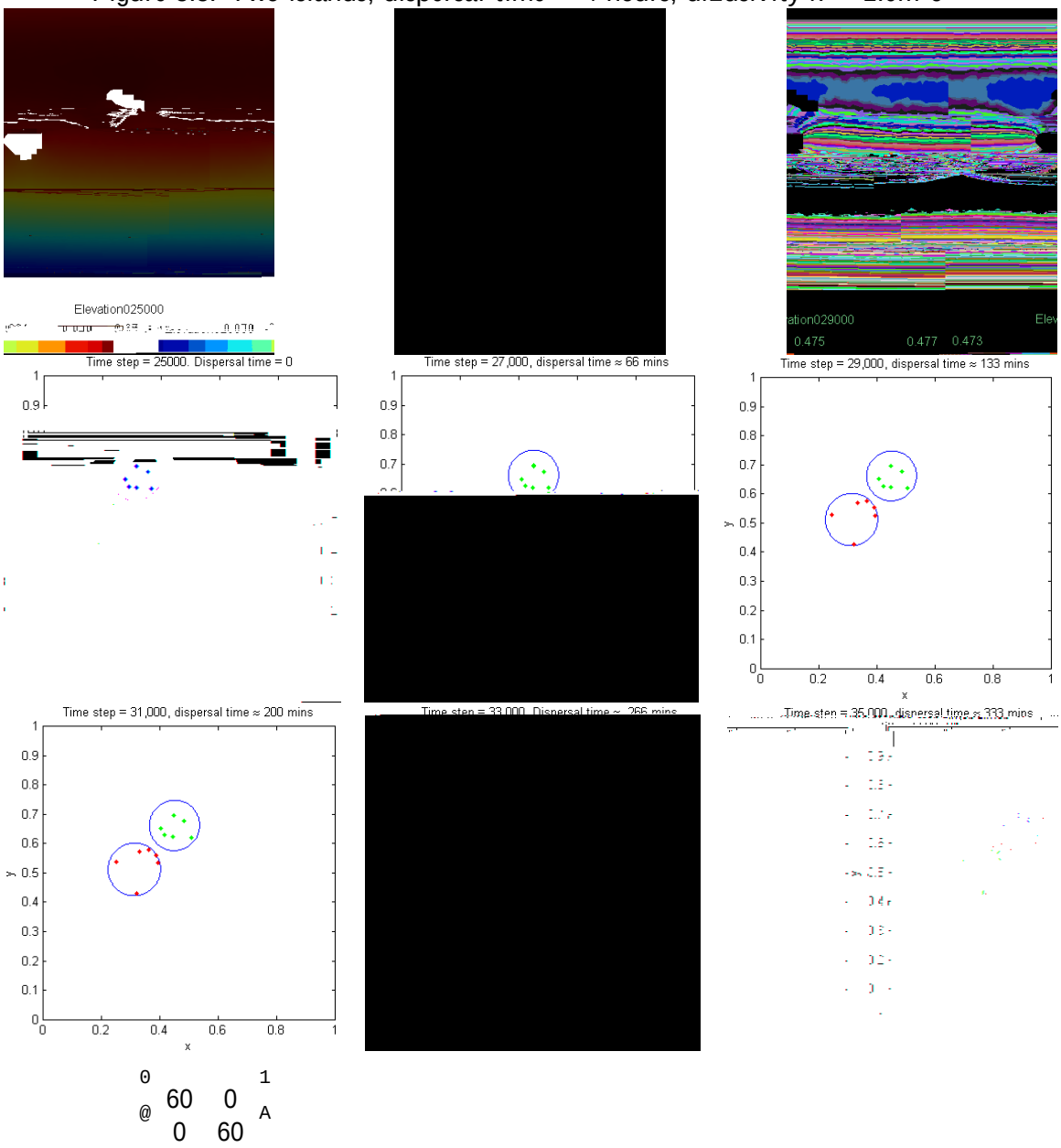


Time step = 340000

Particles remain at their initial islands until 370,000 time steps when a few start to move from the first island:

$$\begin{bmatrix} 60 & 0 & 0 & 0 \\ 0 & 60 & 0 & 0 \\ 0 & 0 & 60 & 0 \\ 0 & 0 & 0 & 60 \end{bmatrix}$$

Figure 3.3: Two islands, dispersal time ≈ 4 hours, di□usivity $k = 2.0\text{m}^2\text{s}^{-1}$

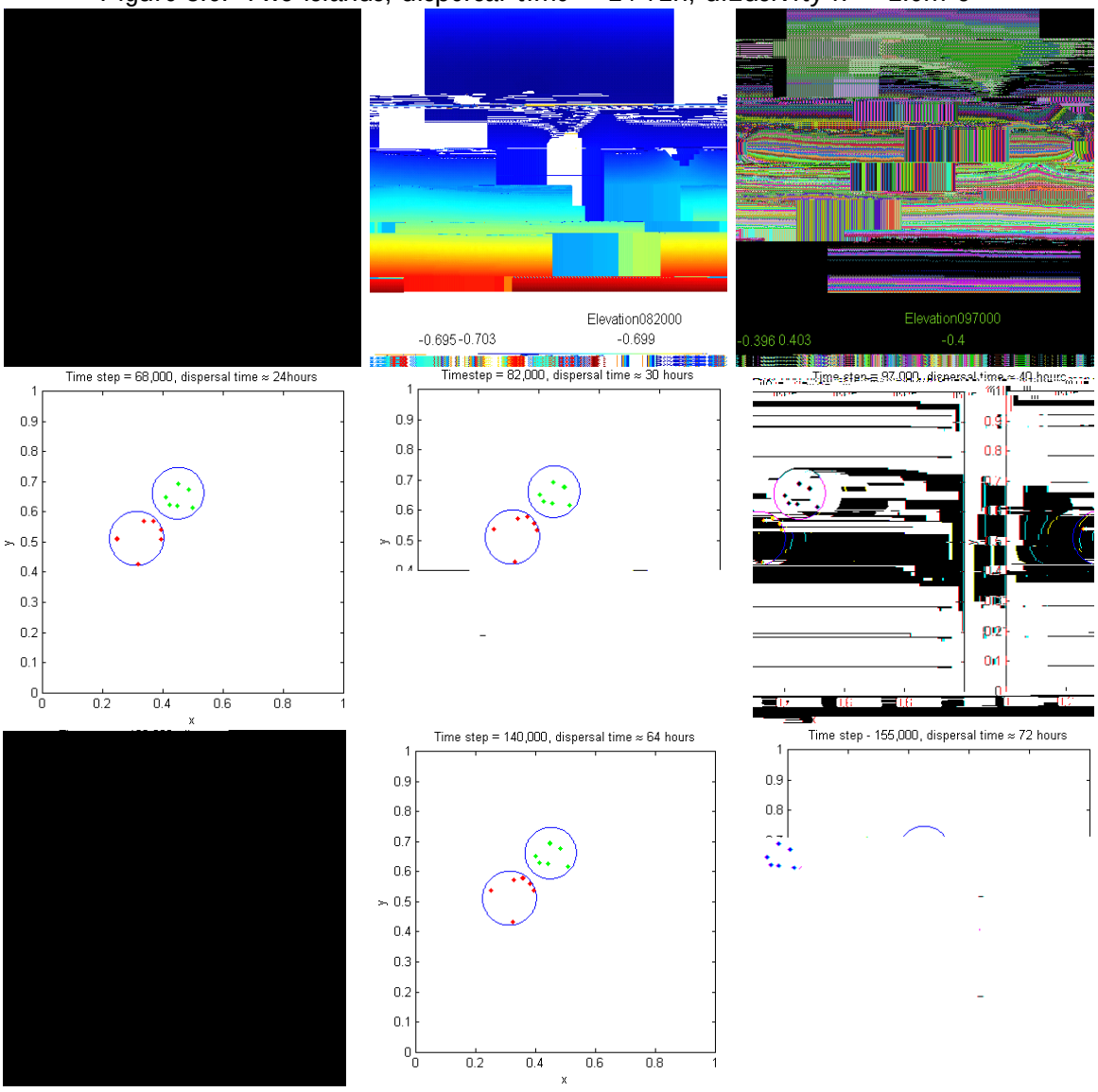



```
0       1
@ 60  0 A
  0  60
```

Figure 3.5: Minimum, maximum and mean distances dispersed from initial release points for the two island 24-72 hour period

Dispersal time (hours)	Di□usivity k (m^2s^{-1})	Min. dispersal distance (m)	Max. dispersal distance (m)	Mean dispersal distance (m)
24	2.0	0.0058	2.195	0.2774
32	2.0	0.0332	15.6949	3.9506
40	2.0	0.0462	14.2177	3.7792
48	2.0	0.0039	4.8538	0.547

Figure 3.6: Two islands, dispersal time ≈ 24-72h, di□usivity k = 2.0m^{2}s^{-1}



$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 68000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 82000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 97000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 126000

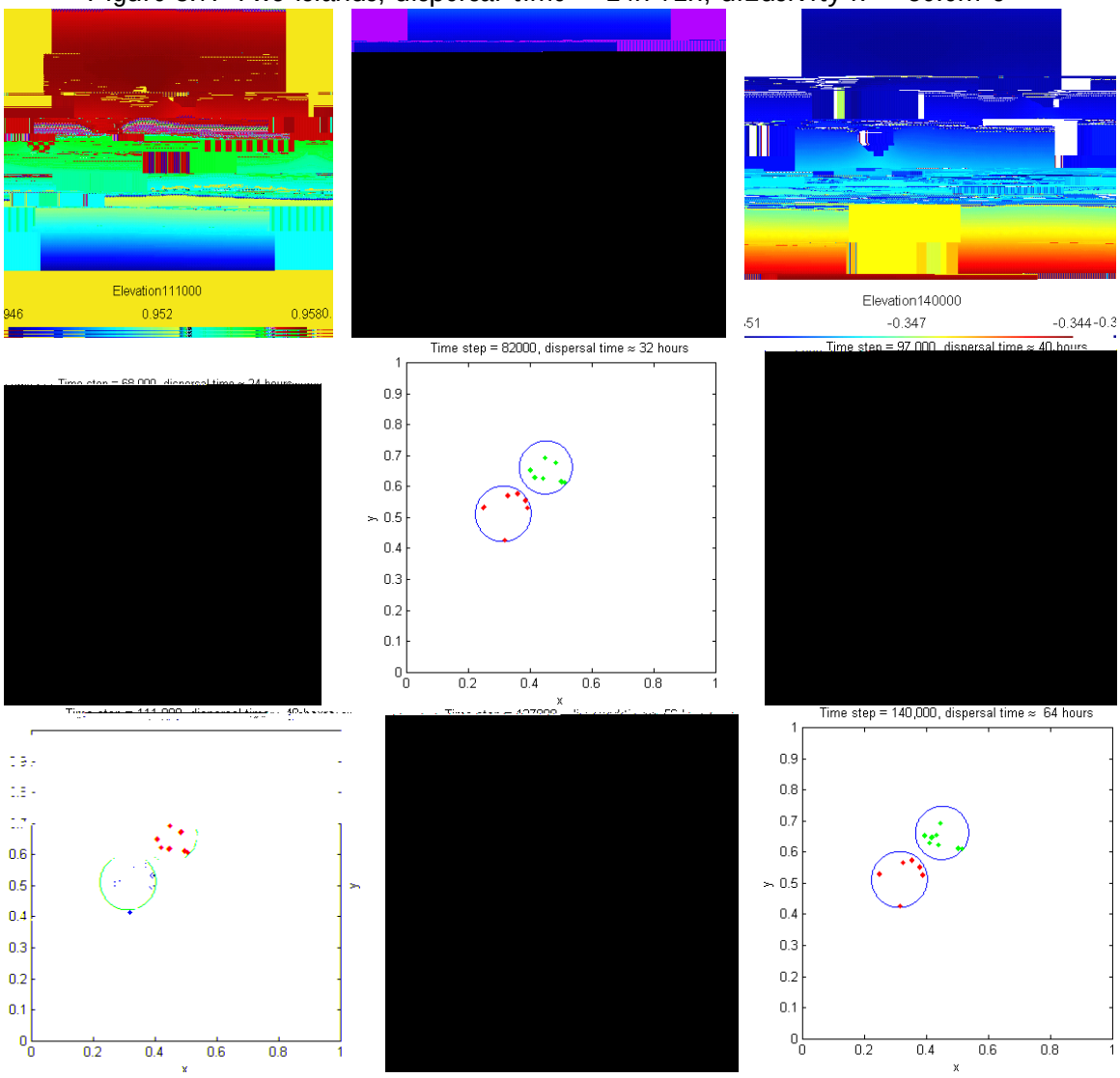
$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 140000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 155000

Figure 3.7: Two islands, dispersal time ≈ 24h-72h, di□usivity k = 50.0m^{2}s^{-1}



0 1
@ 50 0 A
0 60

Time step = 68000

0 1
@ 60 0 A
0 60

Time step = 82000

0 1
@ 60 0 A
0 60

Time step = 97000

0 1
@ 50 0 A
0 60

Time step = 111000

0 1
@ 54 0 A
0 60

Time step = 127000

0 1
@ 60 0 A
0 60

Time step = 140000

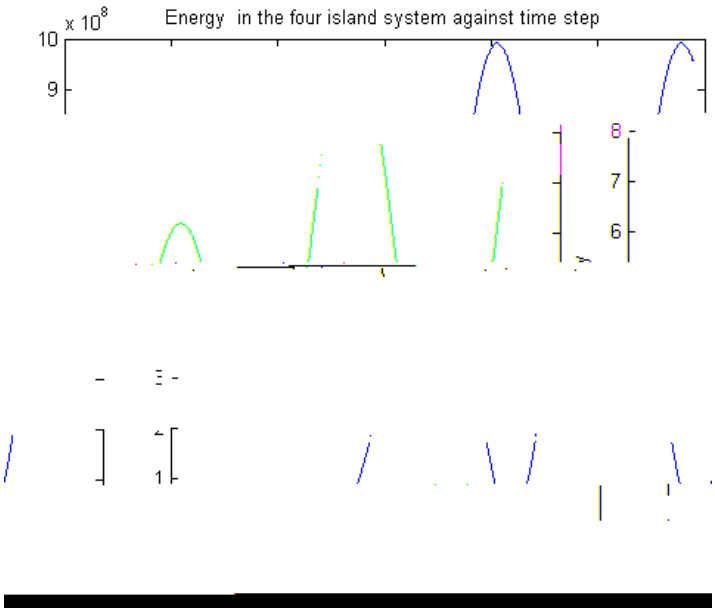
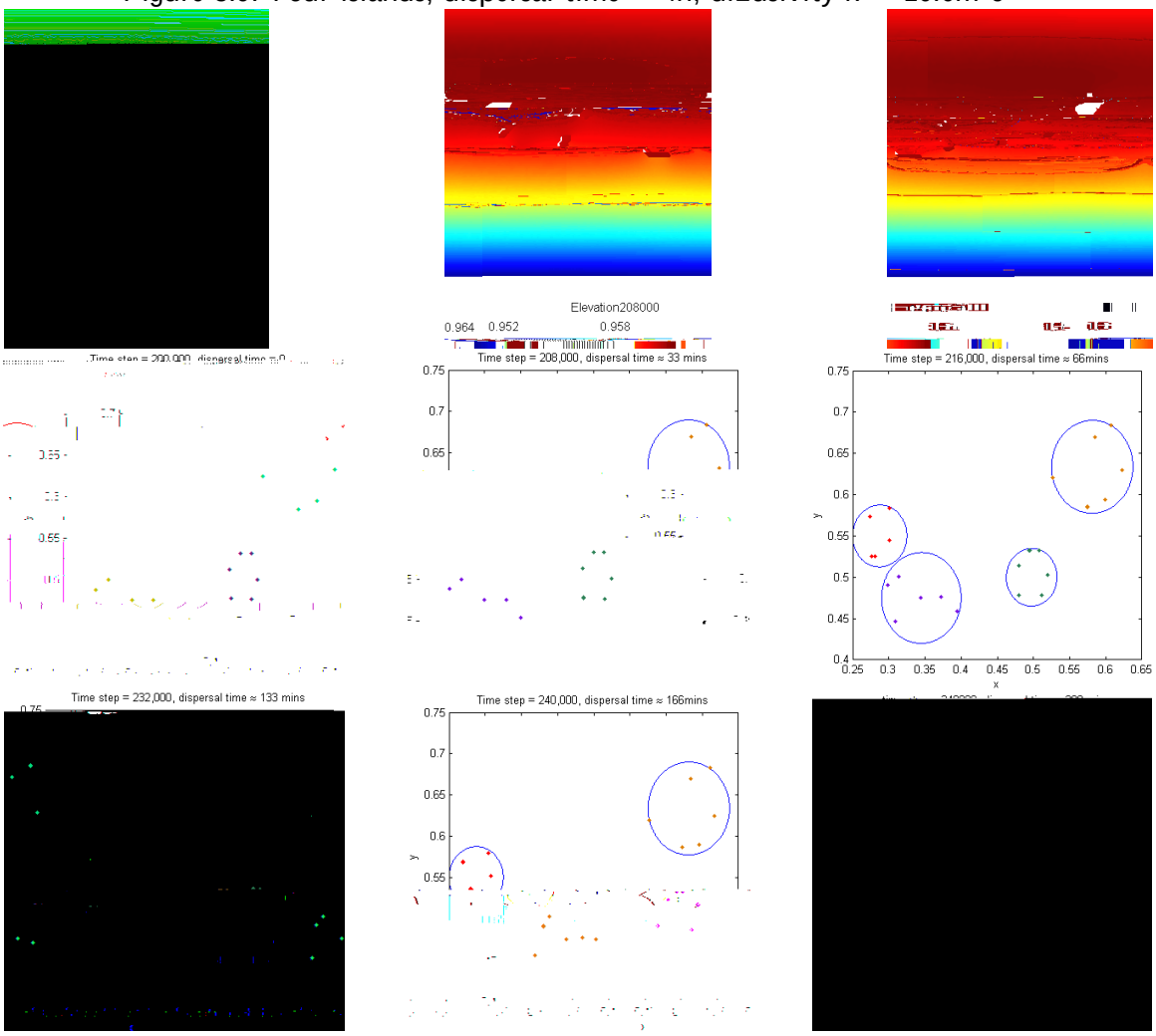


Figure 3.8: Energy in the four island system

Figure 3.9: Four islands, dispersal time ≈ 4h, di□usivity $k = 10.0\text{m}^2\text{s}^{-1}$



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B

Chapter 4

Discussion of results and conclusions

4.1 The two island domain

4.1.1 The four hour simulation

the model is simulating this, it must be noted that the method of using radii inside which particles are assumed to settle is purely hypothetical, and so this is of course speculation.

4.1.2 The 24-72 hour simulation

In the 24-72 hour simulation, corresponding to the dispersal times for *Acroporids* (24-72 hours) and *Balanophyllia elegans* (72 hours), whether or not particles left the vicinity of the islands depended on value of the diffusivity k. At a value of $k = 50\text{m}^2\text{s}^{-1}$ particles started to leave the lower island. However, having left the vicinity of the island they then proceeded to return, leave again and then slowly return by the end of the 72 hour time frame. This oscillating behaviour can also be seen for all of the other values of k in the table given in Figure 3.6. For dispersal times up to 40 hours, the maximum and average dispersal distances increase but then drop at 48 hours. For the remaining 24 hours the maximum and average disperal distances rise and fall as the particles move back and forth.

So do the model simulations represent the behaviour of either *Balanophyllia elegans* larvae or *Acroporids* larvae? The distances travelled by the particles indicate that the simulations are closer to that of the *Acroporids* larvae. Of course the dispersal distances for this larvae are only really relevant to the regions where the data was sourced from (Rib Reef, Pandora Reef and Myrmidon Reef in the Great Barrier Reef, Australia, Sammarco and Andrews (1989)), not necessarily the simple two island domain in this study! A further study could

4.2 The four island domain

4.2.1 The four hour simulation

4.3 Summary of conclusions

Factors that could be taken into account when building a connectivity matrix for the Great Barrier Reef could be:

- The type of coral larvae being dispersed. The species of corals with the highest population in each island or reef could be simulated.
- The di□erent dispersal strategies - both the long range and short range strategies could be taken into account, this would require a model that simulates a the dispersal of coral larvae over a long period of time (> 300h or even as far as a yearly dispersal distance) while keeping track of species of larvae that only disperse short distances.

Chapter 5

Further work

In addition to the suggestions made in Chapter 4, further work that could be done directly on this project is summarised in the sections that follow.

5.1 The modified Lagrangian algorithm

In this study the Lagrangian algorithm was used to update the position of particles:

$$x_{n+1} = x_n + v\Delta t + \frac{R_n}{\sqrt{r}}\sqrt{2k\Delta t} \tag{5.1}$$

This algorithm assumes a constant diffusivity k and depth h. This is not ideal for the domains studied as the depth changes with the elevation and the bathymetry of the islands, and the diffusivity will vary according to how far the particles are from the islands (i.e. how far they are from the turbulent features such as eddies in the wake of islands). An algorithm could be implemented to include varying h and k. It is noted in [6] that when h or k is not constant the Lagrangian algorithm (5.1

as

$$\frac{\partial(hc)}{\partial t} = - \quad \cdot [(\mathrm{u} + kh^{-1} \quad h)hc - k \quad (hc)]. \tag{5.3}$$

Equation (5.3

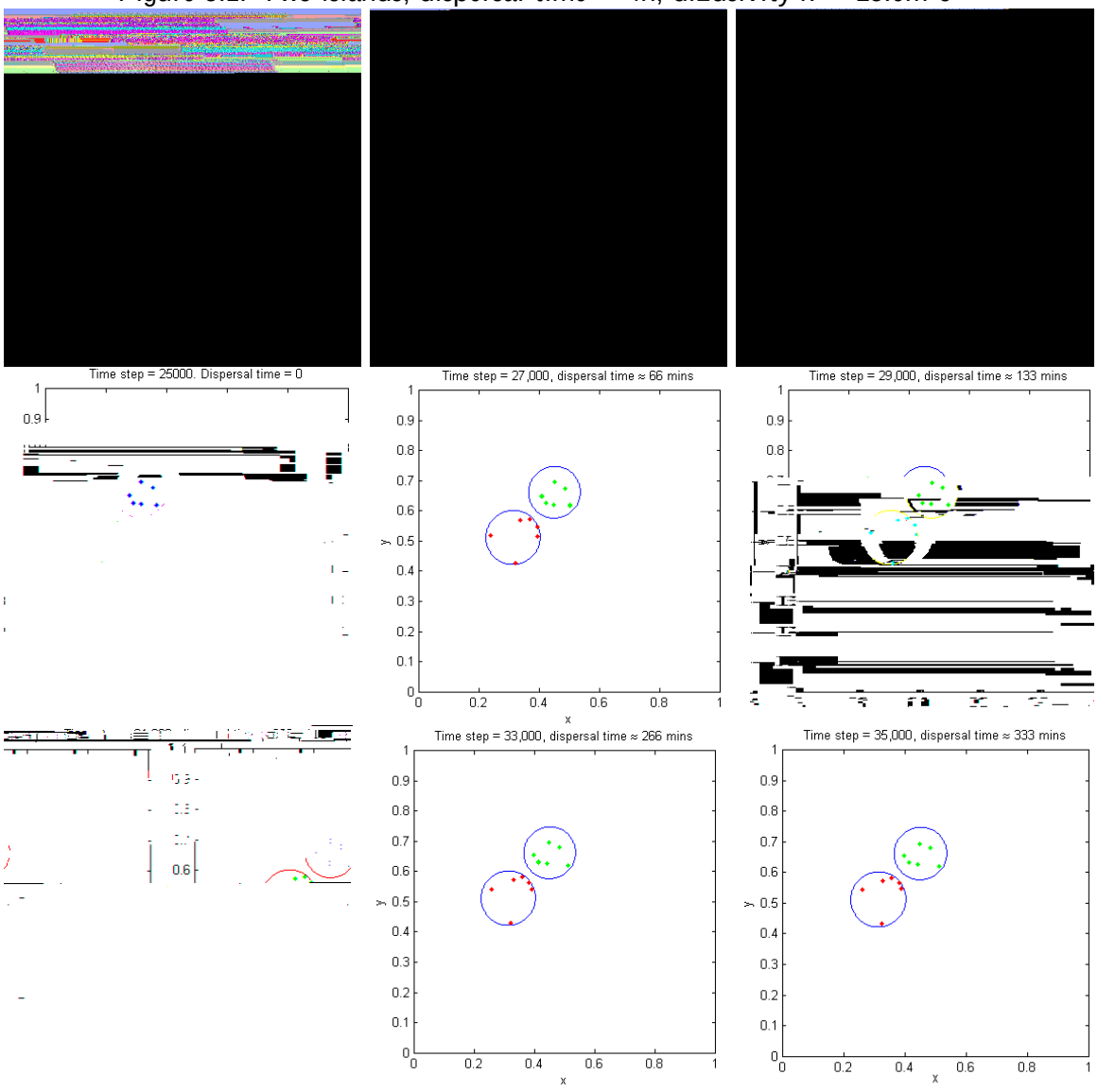
5.4 Di□erent species of Coral

The coral species mentioned in this study all have small dispersal distances and times relative to the distances and times that would be considered when thinking about designing marine reserves. Shanks et al. (2003) mentions two evolutionary stable dispersal strategies: dipsersal < 1km with propagules spending less than 100 hours in the water column, or > 20km with propagules spending over 300 hours in the water column. Much longer simulations could be run in order to investigate corals whose larvae travel distances over 20km.

Appendix A

Included in this appendix are the remaining plots of particle positions for the two island four hour and 72 hour simulations.

Figure 5.1: Two islands, dispersal time ≈ 4h, di□usivity $k = 25.0\text{m}^2\text{s}^{-1}$



$$\begin{pmatrix} 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 25000

$$\begin{pmatrix} 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 27000

$$\begin{pmatrix} 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 29000

$$\begin{pmatrix} 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 31000

$$\begin{pmatrix} 60 & 0 \\ 0 & 60 \end{pmatrix}$$

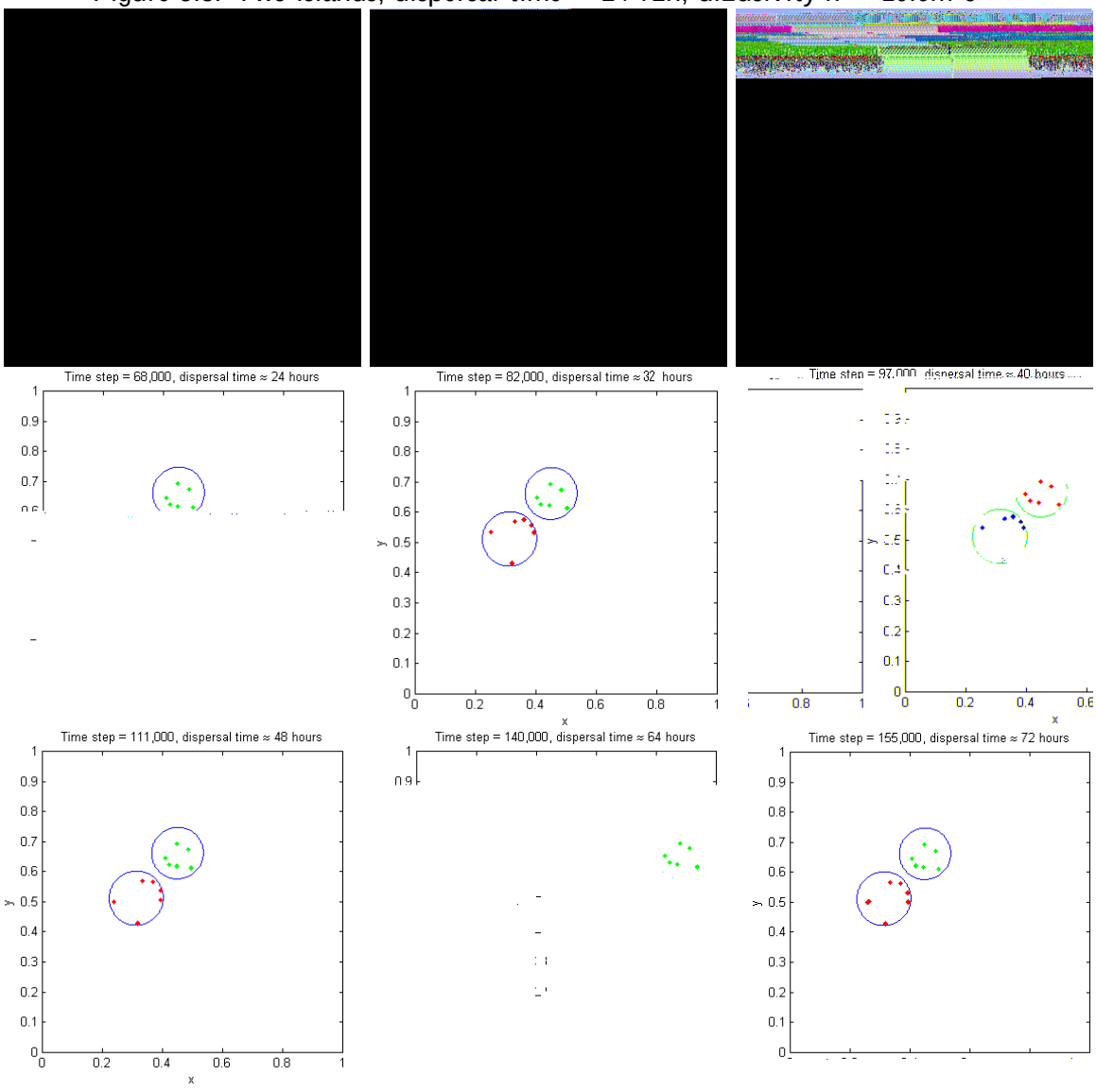
Time step = 33000

$$\begin{pmatrix} 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 35000

Figure 5.2: Two islands, dispersal time ≈

Figure 5.3: Two islands, dispersal time ≈ 24-72h, di□usivity $k = 10.0\text{m}^2\text{s}^{-1}$



$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 68000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 82000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 97000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 111000

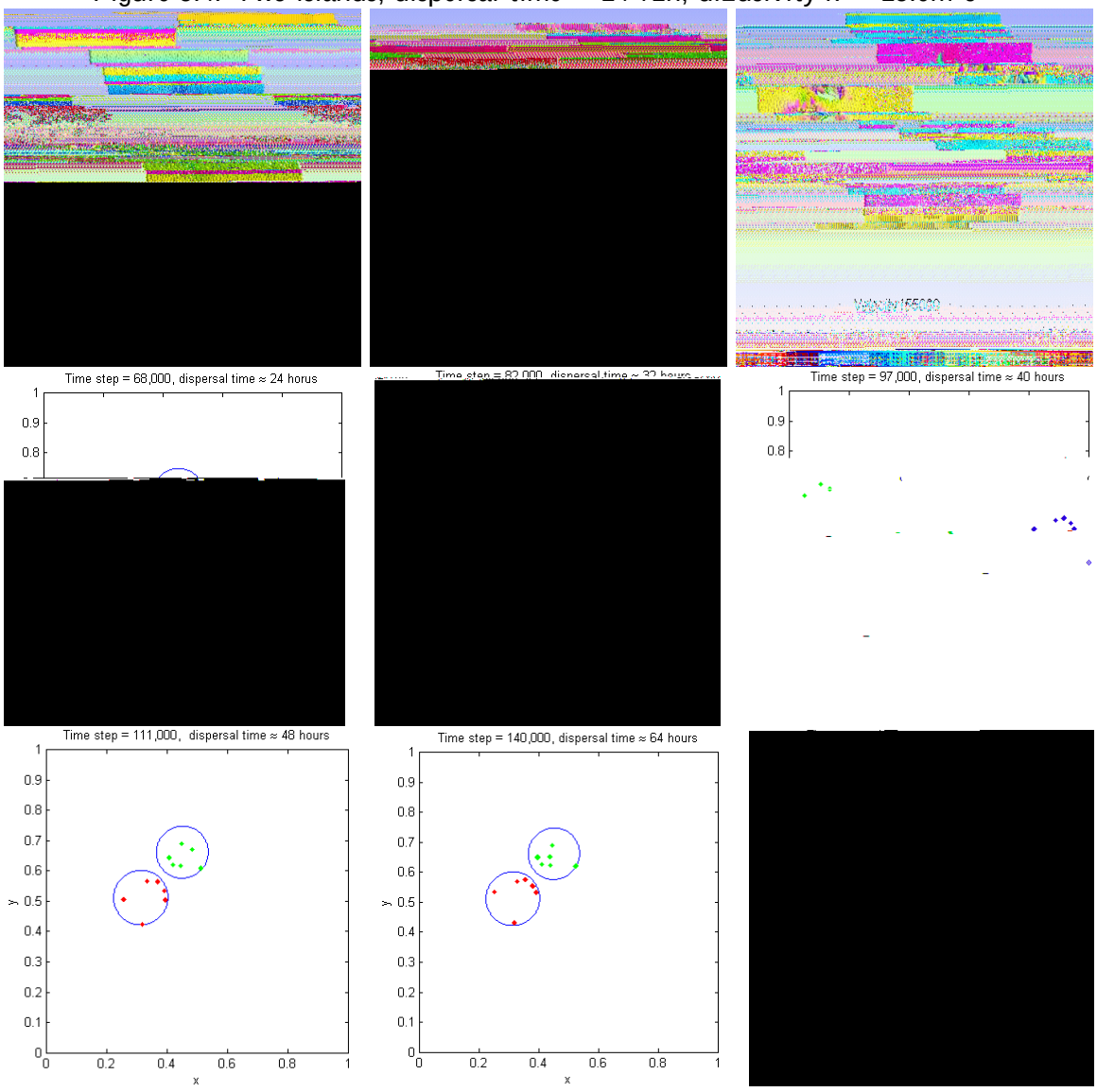
$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 140000

$$\begin{matrix} 0 & & 1 \\ @ & 60 & 0 \\ & 0 & 60 \end{matrix} \; A$$

Time step = 155000

Figure 5.4: Two islands, dispersal time ≈ 24-72h, di□usivity k = 25.0m^{2}s^{-1}



$$\begin{pmatrix} 0 & 1 \\ 58 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 68000

$$\begin{pmatrix} 0 & 1 \\ 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 82000

$$\begin{pmatrix} 0 & 1 \\ 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 97000

$$\begin{pmatrix} 0 & 1 \\ 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 111000

$$\begin{pmatrix} 0 & 1 \\ 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 140000

$$\begin{pmatrix} 0 & 1 \\ 60 & 0 \\ 0 & 60 \end{pmatrix}$$

Time step = 155000

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