

# Complex Network Analysis for Marine Models

Subtitle (optional)

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# Chapter 1

## Numerical Considerations

### 1.1 Test case to assess the implementation of the overturner model

This note is an adaptation of Eric Deleersnijder's working paper [Del11].

#### 1.1.1 Governing equations

Let us consider a water domain, whose width is denoted  $B(t, \mathbf{x})$ , where  $t$  is the time and  $\mathbf{x} = (y, z)$  is the position vector. The continuity equation is

$$\frac{\partial B}{\partial t} + \nabla \cdot (B\mathbf{u}) = 0, \quad (1.1)$$

where  $\mathbf{u}(t, \mathbf{x})$  is the latitudinally-averaged meridional velocity. Assuming that mixing along the parallels is sufficiently efficient, we may study the concentration of a passive tracer by means of a two-dimensional model. The latitudinally-averaged concentration of the tracer  $C(t, \mathbf{x})$  obeys the following partial differential equation :

$$\frac{\partial (BC)}{\partial t} + \nabla \cdot (B\mathbf{u}C) = Q\delta(\mathbf{x} - \mathbf{x}_1) + \nabla \cdot (B\mathbf{K} \cdot \nabla C), \quad (1.2)$$

where  $\mathbf{K}$  is the diffusivity tensor (symmetric and positive definite);  $\delta$  is the Dirac delta function with  $\delta(\mathbf{x} - \mathbf{x}_n) = \delta(x - x_n)\delta(y - y_n)$ ;  $Q(t)$  is the rate of release of a lineic source of length  $B$  along the latitude direction located at  $\mathbf{x} = \mathbf{x}_1$ . If  $C(t, \mathbf{x})$  represents the density of the tracer in water, then  $Q(t)$  is the mass of tracer released per second by the source.

Equation (1.2) is the so-called conservative form of the model. The convective form is obtained by combining equations (1.1) and (1.2):

$$\frac{\partial C}{\partial t} + \mathbf{u} \cdot \nabla C = \frac{Q}{B}\delta(\mathbf{x} - \mathbf{x}_1) + \frac{1}{B}\nabla \cdot (B\mathbf{K} \cdot \nabla C). \quad (1.3)$$

#### 1.1.2 An idealised model

For our test case to be interesting, we must be able to compute its analytical solution. Accordingly, we make some simplifying assumptions which will allow us to compute the solution analytically. First, we assume a constant width  $B$  and a constant velocity field

$$\mathbf{u}(t, \mathbf{x}) = v\mathbf{e}_y + w\mathbf{e}_z, \quad (1.4)$$

where  $\mathbf{e}_y$  and  $\mathbf{e}_z$  are the unit vectors associated respectively with the  $y$ - and  $z$ -coordinate axis. Furthermore, the diffusivity tensor is supposed constant and diagonal :

$$\mathbf{K} = \begin{pmatrix} K_{yy} & 0 \\ 0 & K_{zz} \end{pmatrix}, \quad (1.5)$$

where  $K_{yy}, K_{zz} > 0$ . Finally, we consider a sudden pointwise release of tracer at  $t = 0$ . Hence,  $Q(t)$  is of the form :

$$Q(t) = M\delta(t), \quad (1.6)$$

where  $M$  is the mass of tracer released at  $t = 0$ .

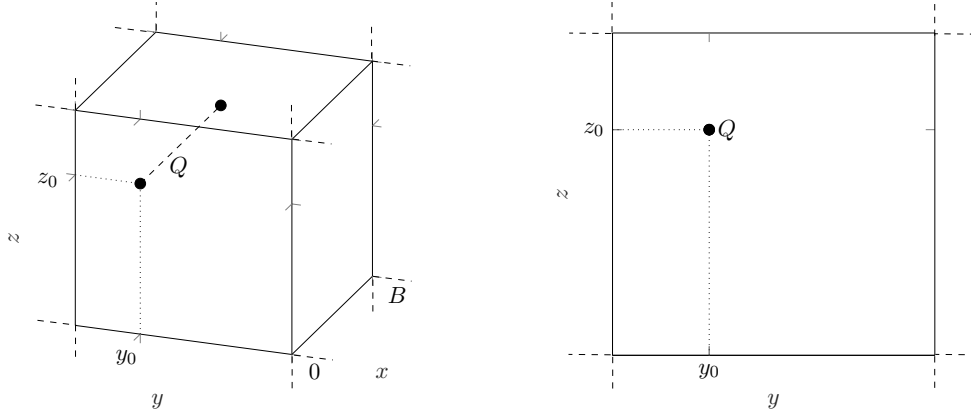
Under these assumptions, equation (1.3) simplifies to :

$$\frac{\partial C}{\partial t} + v \frac{\partial C}{\partial y} + w \frac{\partial C}{\partial z} = J\delta(t)\delta(y - y_1)\delta(z - z_1) + K_{yy} \frac{\partial^2 C}{\partial y^2} + K_{zz} \frac{\partial^2 C}{\partial z^2}, \quad (1.7)$$

where  $J := M/B$ . For the sake of simplicity, we can forget about the fact that our model is width-integrated and consider that it is a purely two-dimensional model with a point-source

$$Q := J\delta(t). \quad (1.8)$$

A part of the physical meaning of the model is lost but this makes representations of the problem easier.  $C$  now represents the two-dimensional density (i.e., in  $[kg/m^2]$ ) of the tracer in water.  $J$  can then be regarded as the mass of tracer released by the sudden point source at  $\mathbf{x} = \mathbf{x}_1$ . The three- and two-dimensional interpretations of the problem are represented on figure 1.1.



**Figure 1.1** – Illustration of the 3D and 2D interpretations of the model.

### Test case 1 : infinite domain

The first (an most simple) test case is to consider an infinite domain, i.e.

$$-\infty < y, z < \infty, \quad (1.9)$$

with nonzero velocities  $v$  and  $w$ . This test case provides a check that our numerical implementation handles the diffusion and advection processes properly both in the  $y$ - and  $z$ -directions. The parameters are chosen from the values of the overturner model :

$$v = \frac{\Psi}{H} = 4 \times 10^{-4} [m/s], \quad w = \frac{\Psi}{L} = 1.33 \times 10^{-7} [m/s], \quad (1.10)$$

and

$$K_{yy} = K_h = 10^3 [m^2/s], \quad K_{zz} = K_{v_2} = 10^{-4} [m^2/s]. \quad (1.11)$$

For the length scales of the overturner model, those diffusivities corresponds to Péclet numbers

$$Pe_y = \frac{v}{K_{yy}/L} = 6, \quad Pe_z = \frac{w}{K_{zz}/H} = 6.67. \quad (1.12)$$

Hence, in both the  $y$ - and  $z$ -directions, the transport is neither dominated by advection nor by diffusion. This is interesting as a test case since it allows to assess how the numerical solver handles both physical processes in both directions. Finally,  $J = 50\,000$  particles are released at  $t = 0$  at the location  $(y_1, z_1) = (0, 0)$ .

## Test case 2 : semi-infinite domain

Another interesting case is to consider a semi-infinite domain with a wall at  $z = 0$  :

$$-\infty < y < \infty, \quad 0 < z < \infty. \quad (1.13)$$

This is useful to assess how our numerical model handles no-through boundary conditions. Again, the parameters values are related to the ones from the overturner model :

$$v = \frac{\Psi}{H} = 4 \times 10^{-4} [m/s], \quad w = 0 [m/s], \quad (1.14)$$

and

$$K_{yy} = K_h = 10^3 [m^2/s], \quad K_{zz} = K_{v_1} = 10^{-1} [m^2/s]. \quad (1.15)$$

Notice the choice of  $K_{zz}$  : it is chosen equal to  $K_{v_1}$ , which is  $10^3$  times larger than  $K_{v_2}$ , the value chosen for test case 1. The goal here is to assess that the boundary condition is well handled by the solver. Since  $w = 0$ , only the vertical diffusivity could possibly drive the particles towards the wall. By increasing  $K_{zz}$ , we ensure that more particles will bounce against the wall, which is relevant in this context.  $J = 50\,000$  particles are released at  $t = 0$  at the location  $(y_1, z_1) = (0, H)$ .

### 1.1.3 Analytical solution and properties

#### Green's function

In order to build the analytical solution of the problem, we need to compute the Green's function associated to this particular problem. We derive the Green's function  $G$  associated to test case 1. We will show later how this function can be used to compute the concentration for both test case 1 and test case 2.  $G(t, t', \mathbf{x})$  is zero for  $t < t'$  and is the solution of

$$\begin{cases} \frac{\partial G}{\partial t} + v \frac{\partial G}{\partial y} + w \frac{\partial G}{\partial z} = K_{yy} \frac{\partial^2 G}{\partial y^2} + K_{zz} \frac{\partial^2 G}{\partial z^2} \\ G(t, t', y, z)|_{t=t'} = \delta(y)\delta(z) \end{cases} \quad (1.16)$$

for  $t \geq 0$ , and on an infinite domain  $-\infty < y, z < \infty$ . It can be shown that [source ? ou le papier de deleersnijder suffit ?](#)

$$G(t, t', y, z) = \frac{\exp \left[ -\frac{(y-s_v)^2}{4K_{yy}\tau} - \frac{(z-s_w)^2}{4K_{zz}\tau} \right]}{4\pi\sqrt{K_{yy}K_{zz}\tau}}, \quad (1.17)$$

where  $\tau = t - t'$  and

$$\mathbf{s}(t, t') = (s_v(t, t'), s_w(t, t')) = \left( \int_{t'}^t v d\xi, \int_{t'}^t w d\xi \right) = (v\tau, w\tau). \quad (1.18)$$

$G$  has some interesting properties. The "mass" of the solution is

$$m(t, t') \equiv \int_{\mathbb{R}^2} G(t, t', \mathbf{x}) d\mathbf{x} = 1. \quad (1.19)$$

The "center of mass" is located at

$$\mathbf{r}(t, t') \equiv \frac{1}{m(t, t')} \int_{\mathbb{R}^2} \mathbf{x} G(t, t', \mathbf{x}) d\mathbf{x} = \mathbf{s}(t, t'). \quad (1.20)$$

The variance of the solution is

$$\sigma^2(t, t') \equiv \frac{1}{m(t, t')} \int_{\mathbb{R}^2} |\mathbf{x} - \mathbf{r}(t, t')|^2 G(t, t', \mathbf{x}) d\mathbf{x} = 2(K_{yy} + K_{zz})\tau. \quad (1.21)$$

### Test case 1

The analytical solution of test case 1 is now obtained with the help of the Green's function derived above by computing the convolution between  $G$  and the source terms :

$$\begin{aligned} C(t, \mathbf{x}) &= \int_0^t \int_{\mathbb{R}^2} G(t, t', \mathbf{x} - \mathbf{x}') J \delta(t) \delta(\mathbf{x} - \mathbf{x}_1) d\mathbf{x}' dt' \\ &= JG(t, 0, \mathbf{x} - \mathbf{x}_1). \end{aligned} \quad (1.22)$$

The concentration profile for test case 1 is thus

$$\frac{J}{4\pi\sqrt{K_{yy}K_{zz}t}} \exp \left[ -\frac{(y - s_v)^2}{4K_{yy}t} - \frac{(z - s_w)^2}{4K_{zz}t} \right]. \quad (1.23)$$

The total mass of tracer present in the domain is

$$m(t) \equiv \int_{\mathbb{R}^2} C(t, \mathbf{x}) d\mathbf{x} = J. \quad (1.24)$$

Note that this number is independant of the transport processes.

The mass center is located at

$$\begin{aligned} \mathbf{r}(t) &\equiv \frac{1}{m(t)} \int_{\mathbb{R}^2} \mathbf{x} C(t, \mathbf{x}) d\mathbf{x} \\ &= \int_{\mathbb{R}^2} \mathbf{x} G(t, 0, \mathbf{x} - \mathbf{x}_1) d\mathbf{x} \\ &= \int_{\mathbb{R}^2} (\mathbf{x} - \mathbf{x}_1) G(t, 0, \mathbf{x} - \mathbf{x}_1) + \mathbf{x}_1 G(t, 0, \mathbf{x} - \mathbf{x}_1) d\mathbf{x} \\ &= \mathbf{x}_1 + \mathbf{s}(t, 0), \end{aligned} \quad (1.25)$$

where properties (1.19) and (1.20) are used to perform the last step.

Finally, the variance of the solution is

$$\begin{aligned} \sigma^2(t) &= \frac{1}{m(t)} \int_{\mathbb{R}^2} |\mathbf{x} - \mathbf{r}(t)|^2 C(t, \mathbf{x}) d\mathbf{x} \\ &= \int_{\mathbb{R}^2} |(\mathbf{x} - \mathbf{x}_1) - \mathbf{s}(t, 0)|^2 G(t, 0, \mathbf{x} - \mathbf{x}_1) d\mathbf{x} \\ &= 2(K_{yy} + K_{zz})t, \end{aligned} \quad (1.26)$$

where property (1.21) is used.

## Test case 2

To compute the solution to test case 2, a little trick must be applied. Consider the problem on an infinite domain with two sudden point sources of equal intensity located at  $z = H$  and  $z = -H$ . By symmetry, one can see that the concentration of that problem in the region  $[-\infty, \infty] \times [0, \infty]$  is precisely the concentration of test case 2. Hence, we can use the Green's function  $G$  derived for test case 1 to compute the concentration. In this case, the convolution has to be performed with two point sources :

$$\begin{aligned} C(t, \mathbf{x}) &= \int_0^t \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} J \delta(t') \delta(y' - y_1) [\delta(z' - z_1) + \delta(z' + z_1)] G(t, t', y - y', z - z') dy' dz' dt' \\ &= J \int_0^t \delta(t') [G(t, t', y - y_1, z - z_1) + G(t, t', y - y_1, z + z_1)] \\ &= J [G(t, 0, y - y_1, z - z_1) + G(t, 0, y - y_1, z + z_1)]. \end{aligned} \quad (1.27)$$

The concentration of the tracer for test case 2 is thus

$$C(t, y, z) = \frac{J}{4\pi\sqrt{K_{yy}K_{zz}t}} \exp\left[-\frac{(y - s_v)^2}{4K_{yy}t}\right] \left\{ \exp\left[-\frac{(z - z_1)^2}{4K_{zz}t}\right] + \exp\left[-\frac{(z + z_1)^2}{4K_{zz}t}\right] \right\} \quad (1.28)$$

The mass is obtained as

$$m(t) \equiv \int_0^{\infty} \int_{-\infty}^{\infty} C(t, y, z) dy dz = J, \quad (1.29)$$

i.e. the number of particles released at  $t = 0$ . This result is obvious since there is no other source or sink, and we impose a no-through condition at the boundary.

NOTE : Le calcul du centre de masse me pose problème dans la direction  $z$ . On trouve assez facilement que  $r_y = y_1 + s_v = y_1 + vt$ . Par contre dans la direction  $z$ , il faut calculer

$$\int_0^{\infty} z \left\{ \exp\left[-\frac{(z - z_1)^2}{4K_{zz}t}\right] + \exp\left[-\frac{(z + z_1)^2}{4K_{zz}t}\right] \right\} dz.$$

Pas sûr qu'une solution simple existe... Je m'attends à une expression du type " $H + (\dots)$ ", où  $(\dots)$  est un terme qui permet de tenir compte du décalage du centre de masse selon  $z$  à cause du rebond sur le mur, et qui serait donc une fonction de  $K_{zz}$ ,  $t$  et  $z_1$ .

Cependant, le calcul du centre de masse ne me paraît pas indispensable et même si cela m'intrigue, j'ai dû m'efforcer de lâcher l'affaire pour ne pas passer la journée dessus. (D'autant plus que je peux les approximer numériquement à partir de l'expression analytique de la concentration.)

## 1.2 Validation of the numerical solver

This section aims to show that the numerical results obtained with the solver are in good agreement with the analytical ones. As the combination of the two test cases cover the main features of the overturning model, this constitutes a validation of the solver.

Both test cases are simulated for 1 year with a time step of 1 hour, and  $J = 50\,000$  particles are released at  $t = 0$ . The concentration is computed at the final time  $T = 1$  year on the domain  $[y_{min}, y_{max}] \times [z_{min}, z_{max}]$ , where the subscripts *min* and *max* stands for the minimal and maximal position at time  $T$  amongst all the particles. The notation  $C(y, z)$  will be used to denote  $C(T, y, z)$  in the next. That domain is divided into  $20 \times 20$  boxes, and the (normalized) concentration in a box is computed as the number of particles in that box divided by the total number of particles  $J$ .

### 1.2.1 Test case 1

Figure 1.2 shows a comparison between the numerical result and the analytical solution for the (normalized) concentrations. Dark (resp. light) shaded areas correspond to zones where the numerically computed concentration is "above" (resp. "below") the exact concentration. Figures 1.3a and 1.3b represent respectively a cut of the concentrations at fixed  $y = r_{y,exact}$  and at fixed  $z = r_{z,exact}$ . The numerically computed concentration  $C_{num}$  seems to be an appreciable approximation of the exact concentration  $C_{exact}$ . To be more specific, the maximal local error is

$$\|C_{exact} - C_{num}\|_{\infty} = 1.037 \times 10^{-3}. \quad (1.30)$$

The centers of mass are located at

$$\mathbf{r}_{exact} = (12\,614.4, 4.2) [m], \quad \mathbf{r}_{num} = (10\,985.3, 4.4) [m]. \quad (1.31)$$

The relative error is

$$\mathbf{e}_r = \left| \frac{\mathbf{r}_{exact} - \mathbf{r}_{num}}{\mathbf{r}_{exact}} \right| = (1.29 \times 10^{-1}, 4.75 \times 10^{-2}), \quad (1.32)$$

where the division is taken element-wise on the vectors. The 2-norm of the relative error is

$$\|\mathbf{e}_r\|_2 = 1.38 \times 10^{-1}. \quad (1.33)$$

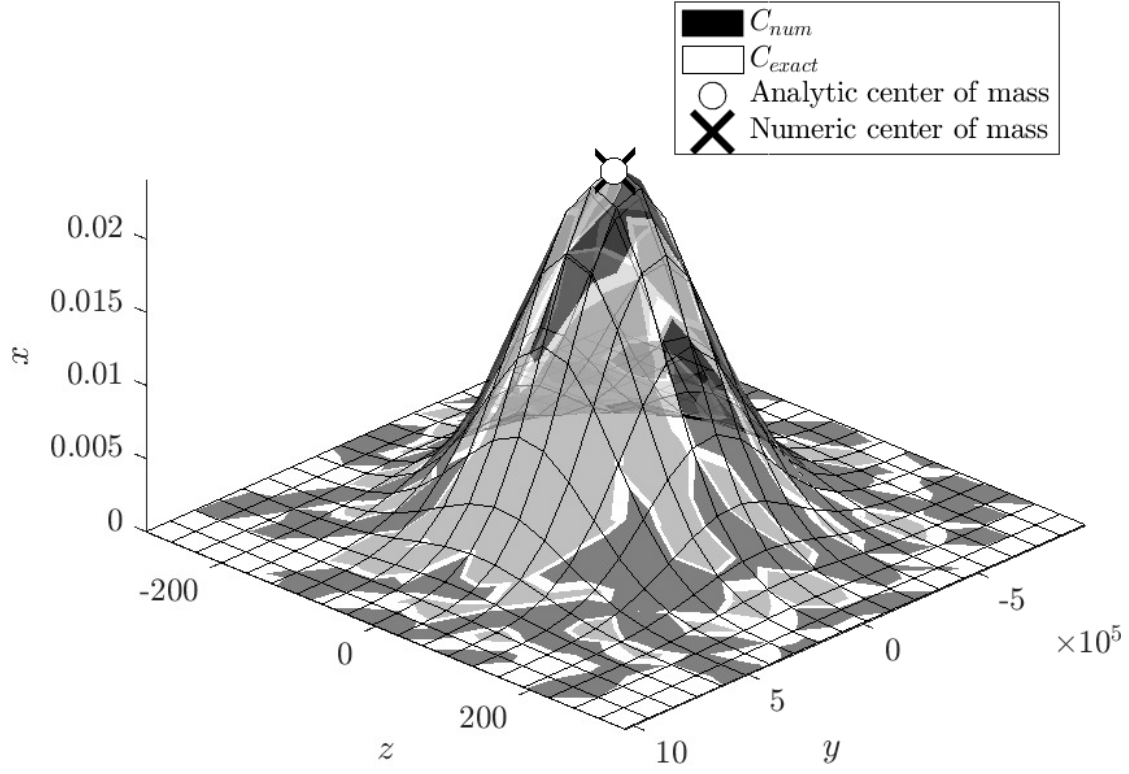
This can be seen as a quantification of the error on advection. To quantify the error on diffusion, we compute the variance of the concentration :

$$\sigma_{exact}^2 = 6.31 \times 10^{10} [m^2], \quad \sigma_{num}^2 = 6.35 \times 10^{10} [m^2]. \quad (1.34)$$

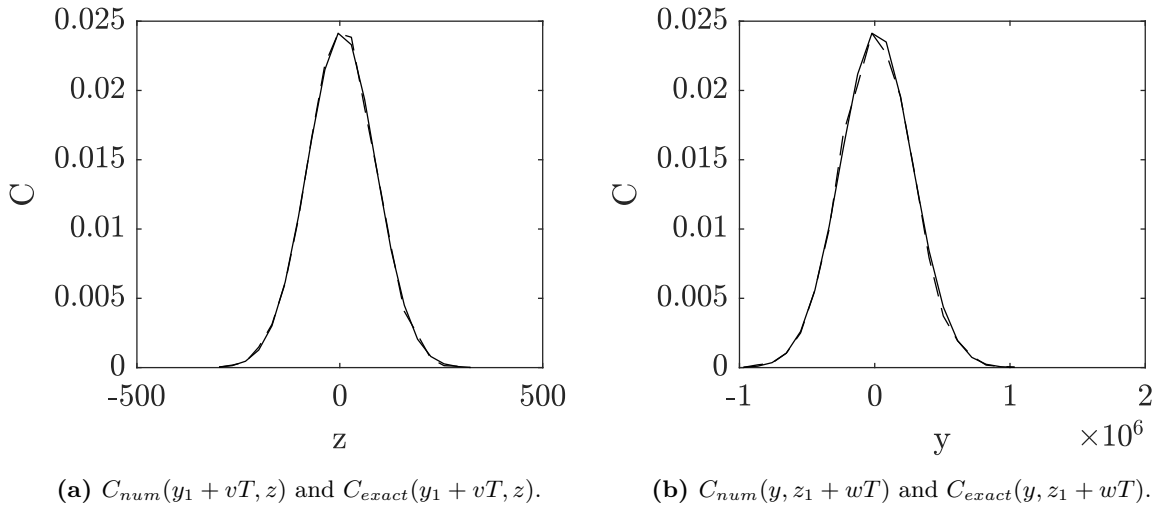
The relative error is

$$e_{\sigma^2} = \left| \frac{\sigma_{exact}^2 - \sigma_{num}^2}{\sigma_{exact}^2} \right| = 7.26 \times 10^{-3}. \quad (1.35)$$





**Figure 1.2** – Comparison of the concentrations obtained analytically and numerically. The "centers of mass" of the concentration obtained numerically (black cross) and numerically (white bullet) are also shown on the figure.



**Figure 1.3** – Cut of the concentrations at fixed  $y = r_{y,exact}$  and at fixed  $z = r_{z,exact}$ . The dashed line represent  $C_{num}$  and the continuous line is for  $C_{exact}$ .

### 1.2.2 Test case 2

Figure 1.4 shows a comparison between the numerical result and the analytical solution for the (normalized) concentrations for test case 2. Since we do not have analytical expressions of the center of mass and of the variance for this test case, the "exact" values are approximated numerically thanks to the analytical expression of the concentration. Figures 1.5a and 1.5b represent respectively a cut of the concentrations at fixed  $y = r_{y,exact}$  and along the boundary  $z = 0$ . The big picture about test case 2 is the presence of a boundary with no-through condition. A first verification is to check if all the particles are still in the domain, which is indeed the case. Although this might seem trivial here, it is sometimes a real challenge to ensure that no particle crosses the boundary, especially for geometrically complex domains. Besides, one can see on figure 1.5b that the concentration profile is well approximated along the boundary. Indeed, the maximal local error at the boundary is

$$\|C_{exact}(y, 0) - C_{num}(y, 0)\|_{\infty} = 3.53 \times 10^{-4}, \quad (1.36)$$

The maximal local error on the whole domain is

$$\|C_{exact} - C_{num}\|_{\infty} = 1.097 \times 10^{-3}. \quad (1.37)$$

The centers of mass are located at

$$\mathbf{r}_{exact} = (1.26 \times 10^4, 5.06 \times 10^3) [m], \quad \mathbf{r}_{num} = (1.10 \times 10^4, 5.05 \times 10^3) [m]. \quad (1.38)$$

The relative error is

$$\mathbf{e}_r = \left| \frac{\mathbf{r}_{exact} - \mathbf{r}_{num}}{\mathbf{r}_{exact}} \right| = (1.29 \times 10^{-1}, 1.825 \times 10^{-3}). \quad (1.39)$$

The 2-norm of the relative error is

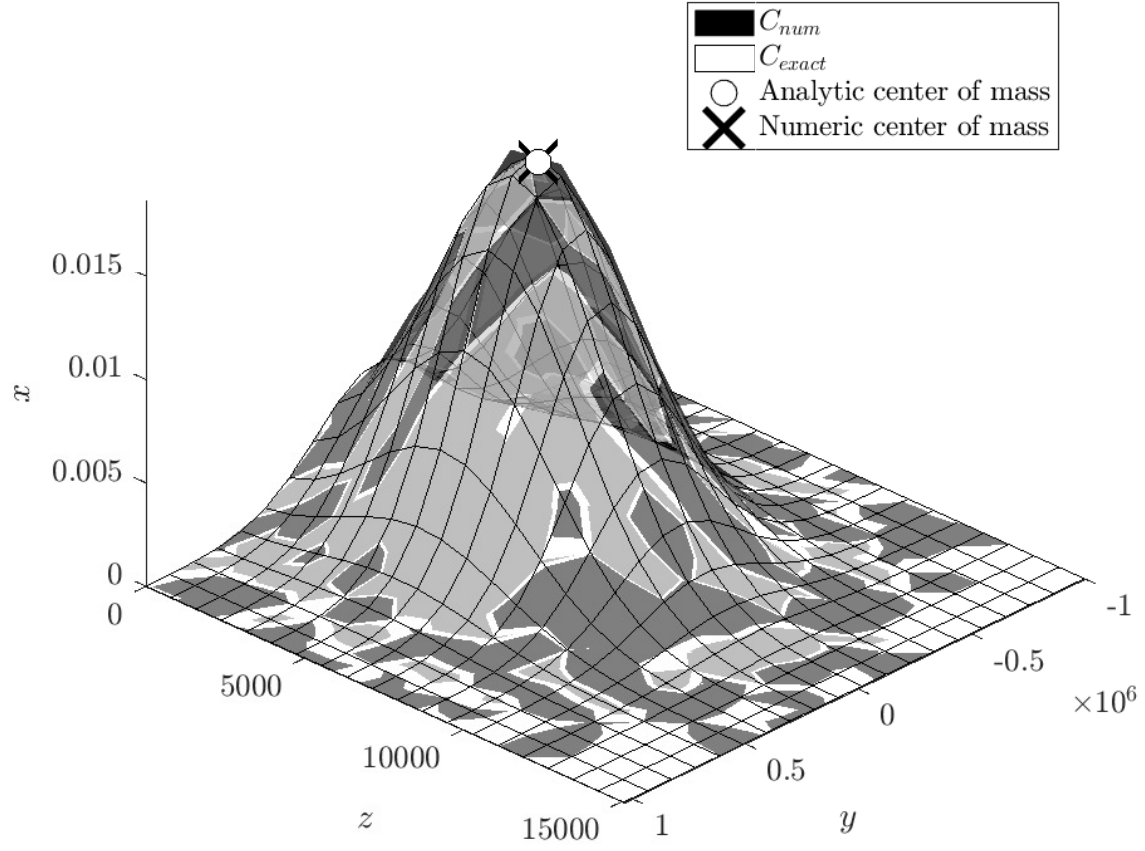
$$\|\mathbf{e}_r\|_2 = 1.29 \times 10^{-1}. \quad (1.40)$$

This can be seen as a quantification of the error on advection. To quantify the error on diffusion, we compute the variance of the concentration :

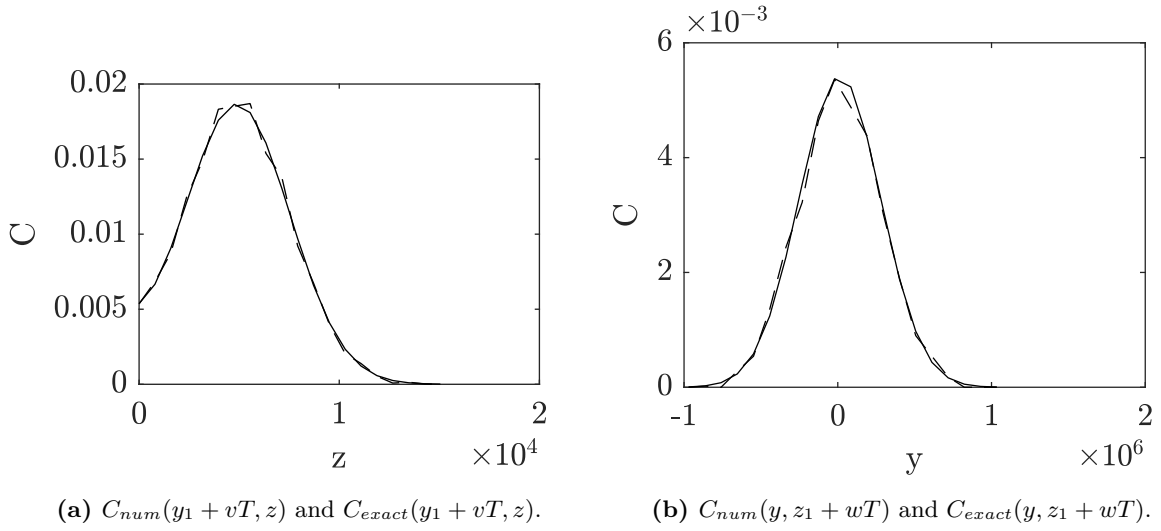
$$\sigma_{exact}^2 = 6.39 \times 10^{10} [m^2], \quad \sigma_{num}^2 = 6.35 \times 10^{10} [m^2]. \quad (1.41)$$

The relative error is

$$e_{\sigma^2} = \left| \frac{\sigma_{exact}^2 - \sigma_{num}^2}{\sigma_{exact}^2} \right| = 4.85 \times 10^{-3}. \quad (1.42)$$



**Figure 1.4** – Comparison of the concentrations obtained analytically and numerically. The "centers of mass" of the concentration obtained numerically (black cross) and numerically (white bullet) are also shown on the figure.



**Figure 1.5** – Cut of the concentrations at fixed  $y = r_{y,exact}$  and at fixed  $z = r_{z,exact}$ . The dashed line represent  $C_{num}$  and the continuous line is for  $C_{exact}$ .

## Chapter 2

# Clustering

### 2.1 The stability criterion for graph communities

This section is devoted to the explanation of The partition of a graph into communities (or clusters) as been widely studies those last two decades. Clustering is indeed a great tool to gain insight into the underlying structure of a system represented by a network. In some cases, one can even build a simplified functional description base on the clusters. Many partitioning methods have been proposed, each relying on a particular measure to quantify the quality of a community structure. Such methods include normalized cut,  $(\alpha, \epsilon)$  clustering or modularity and its variants and extensions. See for instance [For10] for a 2010 survey. In this work, we choose the stability approach, initially presented in [DYB10] and further expended in [LDB09] and [DSYB13]. The stability method presents a number of advantages. First, it does not require the number of communities to be specified beforehand, ensuring a natural partitioning of the graph. Second, it is flexible in the sense that it does not seek a *unique* optimal partition. Instead, it reveals several community structures, each appearing to be the most relevant at particular values of the Markov time. The latter acts as an intrinsic resolution parameter, as will be explained shortly. Finally, it is probably the most unifying approach since many of the standard partitioning measures find an interpretation through the stability framework.

#### 2.1.1 Discrete-time stability as an autocovariance

The stability criterion is based on the two-way relationship between graphs and Markov chains: On one hand, any graph has an associated Markov chain where the states are the nodes of the graph and the transitions probabilities between states are given by the weights of the edges. On the other hand, any Markov chain can be represented by a graph whose edges are weighted according to the transition probabilities. Concretely, consider a graph of  $N$  nodes whose  $N \times N$  weighted adjacency matrix is denoted  $\mathbf{A}$ . Let  $\mathbf{k} = \mathbf{A}\mathbf{1}$ ;  $k_i$  is the total weight of the outgoing edges from node  $i$ . Let  $\mathbf{K} = \text{diag}(\mathbf{k})$ . Then, by normalizing the rows of  $\mathbf{A}$  we get the matrix  $\mathbf{M} = \mathbf{K}^{-1}\mathbf{A}$ , the transition probability matrix.  $\mathbf{M}$  is row-stochastic and  $[\mathbf{M}]_{ij}$  is the probability to go from node  $i$  to node  $j$ . If  $\mathbf{p}_t$  is the  $N \times 1$  probability vector at Markov time  $t$ , then the dynamics of the discrete-time Markov process are given by :

$$\mathbf{p}_{t+1} = \mathbf{p}_t \mathbf{K}^{-1} \mathbf{A} = \mathbf{p}_t \mathbf{M}. \quad (2.1)$$

This Markov perspective provides a dynamical interpretation of the partitioning problem : at a given time scale, natural clusters corresponds to sets of states from which escape is unlikely

within that time scale. Hence, the stability measure of the quality of a clustering is based on the statistical properties of a dynamical process taking place on the network.

Consider a finite-state Markov process  $\mathcal{M}$  and a partition  $\mathcal{P}$ . Suppose that  $\mathcal{M}$  is ergodic, i.e. that it is possible to go from every state to every state and that the Markov process is aperiodic. Note that this implies that any initial state will asymptotically reach the same stationary solution. Let  $P(\mathcal{C}, t)$  be the probability that a random walker is in community  $\mathcal{C}$  at that  $t$  if it was initially in  $\mathcal{C}$ , when the system is at stationarity. Discounting the probability of such an event to take place by chance at stationarity and summing over all communities of  $\mathcal{P}$  leads to the definition of the stability of the partition  $\mathcal{P}$  :

$$r(t; \mathcal{P}) = \min_{0 \leq s \leq t} \sum_{\mathcal{C} \in \mathcal{P}} P(\mathcal{C}, s) - P(\mathcal{C}, \infty). \quad (2.2)$$

By ergodicity, the memory of the initial condition is lost at infinity and  $P(\mathcal{C}, \infty)$  is thus equal to the probability that two independant walkers are in  $\mathcal{C}$  at stationarity. Equation (2.2) tells us that only the communities in which a random walker is likely to stay brings a positive contribution to stability, where *likely to stay* means that the probability for a walker to be in its initial community at time  $t$  is larger than the probability of that event occuring by chance at stationarity. Note that taking the minimum for all times up to  $t$  implies that the stability of the clustering at time  $t$  is large only if it is large for all times preceding  $t$ . This allows to assign a low stability to partitions where there is a high probability of leaving the community and coming back to it later.

Let us developp definition (2.2) to express it in matrix form. We consider a discrete-time Markov process, or Markov chain. Let  $\mathbf{M}$  be the transition probability matrix of a finite state Markov chain, namely that  $[\mathbf{M}]_{ij}$  is the probability of going to state  $j$  at time  $t + 1$  if we are in state  $i$  at time  $t$ . Let  $\boldsymbol{\pi}$  be the stationnary distribution of the ergodic Markov chain, given by  $\boldsymbol{\pi} = \boldsymbol{\pi}\mathbf{M}$ , and  $\boldsymbol{\Pi} = \text{diag}(\boldsymbol{\pi})$ . Finally, let  $\mathbf{H}_{\mathcal{P}}$  be the indicator matrix of the partition  $\mathcal{P}$ . If  $N$  is the number of states and  $c$  the number of communities in  $\mathcal{P}$ ,  $\mathbf{H}_{\mathcal{P}}$  is a binary  $N \times c$  matrix such that

$$[\mathbf{H}_{\mathcal{P}}]_{ik} = \begin{cases} 1 & \text{if node } i \text{ is in community } k, \\ 0 & \text{otherwise.} \end{cases} \quad (2.3)$$

Using those notations, the *clustered autocovariance matrix* at time  $t$  is defined as

$$\mathbf{R}_t = \mathbf{H}_{\mathcal{P}}^{\top} (\boldsymbol{\Pi} \mathbf{M}^t - \boldsymbol{\pi}^{\top} \boldsymbol{\pi}) \mathbf{H}_{\mathcal{P}}, \quad (2.4)$$

where  $\top$  is the transposed sign and  $\mathbf{M}^t$  is  $\mathbf{M}$  at the power  $t$ . Finally, the stability of the *clustering*  $\mathcal{P}$  is expressed as

$$r(t; \mathcal{P}) = \min_{0 \leq s \leq t} \sum_{i=1}^c [\mathbf{R}_s]_{ii} = \min_{0 \leq s \leq t} \text{trace}(\mathbf{R}_s). \quad (2.5)$$

The definitions above stands all for a given partition  $\mathcal{P}$ . As we are interested in the optimal clustering in the sense of stability, we search the partition that maximize the stability. Clearly, the optimal partition might be different for each different Markov time  $t$ . Computing the optimal partition for each Markov time  $t$  gives the *stability curve of the graph* :

$$r(t) = \max_{\mathcal{P}} r(t; \mathcal{P}). \quad (2.6)$$

We understand thus how Markov time acts as an intrinsic resolution parameter : as Markov time grows, the number of communities decreases. This is quite intuitive since there are more possibilities for a random walker to escape a community, when the time scale increases. Hence, communities get bigger or coarser with Markov time increasing. Interestingly, one can prove that in the case of *undirected networks*, stability at time 1 is equivalent to the well-known configuration

modularity measure. But this equivalence does not hold for directed networks and therefore does not concern the present work.

At this stage, an important remark has to be made about the assumption of ergodicity. The verification of this assumption is often far from being obvious, especially in the case of big undirected networks. The trick in that case is to introduce "à la Google" random teleportations.<sup>1</sup> Let  $\tau$  be the *teleportation probability*. Then, if a random walker is located on a node with at least one outlink (which is always the case for the network that we consider), it follows one of the outlinks with probability  $1 - \tau$ . Otherwise, the node is called a *dangling node* and the random walker is teleported with a uniform probability to another random node. The corresponding perturbation of the transition probability matrix is, in the most general case :

$$\widetilde{\mathbf{M}} = (1 - \tau)\mathbf{M} + \frac{1}{N}[(1 - \tau)\mathbf{d} + \tau\mathbf{1}]\mathbf{1}^\top, \quad (2.7)$$

where  $N$  is the number of nodes,  $\mathbf{d}$  is a binary  $N \times 1$  vector whose entries are equal to 1 if the corresponding node is a dangling node and 0 otherwise, and  $\mathbf{1}$  is the  $N \times 1$  unity vector. In the case that we will consider in the next section,  $\mathbf{d}$  is the zero vector. This perturbation is known to make the dynamics ergodic, ensuring the existence and uniqueness of the stationary solution  $\boldsymbol{\pi}$ .

### 2.1.2 Extension to continuous time

From a general viewpoint, the discrete process can be interpreted as an approximation of its continuous counterpart : whereas the state of the discrete-time random walker can only change at unit-time intervals, the continuous-time random walkers undergoes a waiting time between each change of state which is itself a random variable. More precisely, it is a continuous memoryless random variable distributed exponentially with unit expectation. Obviously, the transition probabilities from one node to the other are the same for both processes, only the time at which the jump occurs may vary. The continuous-time process corresponding to (2.1) is governed by the so-called *Kolmogorov equation* :

$$\dot{\mathbf{p}} = \mathbf{p} \text{diag}\{\boldsymbol{\lambda}(\mathbf{k})\} \mathbf{K}^{-1} \mathbf{A} - \text{diag}\{\boldsymbol{\lambda}(\mathbf{k})\} \mathbf{p}, \quad (2.8)$$

where  $\lambda_i(\mathbf{k})$  is the rate at which random walkers leave node  $i$ . Two particular cases of this process are implemented by the stability software : the *normalised Laplacian dynamics* and the *standard (combinatorial) Laplacian dynamics*. The former correspond to the choice  $\boldsymbol{\lambda}(\mathbf{k}) = \mathbf{1}$ . Hence, the expected waiting time is 1 at every node. The latter corresponds to  $\boldsymbol{\lambda}(\mathbf{k}) = \mathbf{k}/\langle \mathbf{k} \rangle$ . In that case, the average waiting time at node  $i$  is  $\langle \mathbf{k} \rangle / k_i$ . Hence, the expected waiting time at a given node is smaller (resp. larger) than 1 if the total weight of the outgoing edges from that node  $i$  is larger (resp. smaller) than the average total weight of the outgoing edges on the network. However, the expected waiting time over the whole network is  $\langle \langle \mathbf{k} \rangle / \mathbf{k} \rangle = 1$ . The corresponding governing equations are respectively

$$\dot{\mathbf{p}} = \mathbf{p} \mathbf{K}^{-1} \mathbf{A} - \mathbf{p} = \mathbf{p} \mathbf{M} - \mathbf{p} \quad (2.9)$$

for the normalized Laplacian and

$$\dot{\mathbf{p}} = \mathbf{p} \frac{\mathbf{A}}{\langle \mathbf{k} \rangle} - \frac{\mathbf{K}}{\langle \mathbf{k} \rangle} \mathbf{p} \quad (2.10)$$

for the combinatorial Laplacian.

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<sup>1</sup>In the original PageRank proposed by S. Brin and L. Page in 1998 (ref. [GP98]), this consist essentially in applying a perturbation to the transition probability matrix between web pages in order to ensure that at least one row of the matrix is positive, which implies the convergence of the Power Method. If we note the teleportation probability  $\tau$ , the perturbation can be interpreted as follows : a web surfer follows a link in his current page with probability  $1 - \tau$  and jumps to an arbitrary web page with probability  $\tau$ .

### 2.1.3 Assessing the robustness of a partition

We present here two mechanisms commonly used to assess the relevance of a particular partition. One simple way is to consider that a robust partition should not be altered by a small modification of the quality function. Such a modification could be for example a perturbation of the Markov time  $t$  at which the partition has been found. From this point of view, robust partitions correspond to *plateaux* in the stability curve of the graph. In other words, robust partitions should be persistent over a wide interval of Markov time.

The second indicator of the robustness of a partition that we will take into account in this work follows from considering that a robust partition is one that is persistent to small modifications of the optimization algorithm. The central tool to quantify this approach of the robustness of a partition is the *normalized variation of information* [Mei07]. This is a popular way to compare two partitions. Let  $p(\mathcal{C})$  be the probability for a node to be in community  $\mathcal{C}$ , i.e.  $p(\mathcal{C}) = n_{\mathcal{C}}/N$  where  $n_{\mathcal{C}}$  is the number of nodes in community  $\mathcal{C}$ . The variation of information between partitions  $\mathcal{P}_1$  and  $\mathcal{P}_2$  is defined by :

$$\text{VI}(\mathcal{P}_1, \mathcal{P}_2) := \frac{H(\mathcal{P}_1, \mathcal{P}_2) - H(\mathcal{P}_1) - H(\mathcal{P}_2)}{\log(N)} = \frac{H(\mathcal{P}_1|\mathcal{P}_2) + H(\mathcal{P}_2|\mathcal{P}_1)}{\log(N)}, \quad (2.11)$$

where  $\log(N)$  is a normalization factor;  $H(\mathcal{P}) = -\sum_{\mathcal{C}} p(\mathcal{C}) \log[p(\mathcal{C})]$  is the Shannon entropy;  $H(\mathcal{P}_1, \mathcal{P}_2)$  is the Shannon entropy of the joint probability  $p(\mathcal{C}_1, \mathcal{C}_2)$  that a node belongs to both a community  $\mathcal{C}_1$  of  $\mathcal{P}_1$  and a community  $\mathcal{C}_2$  of  $\mathcal{P}_2$ . This yields  $p(\mathcal{C}_1, \mathcal{C}_2) = n_{\mathcal{C}_1 \cap \mathcal{C}_2}/N$ , and  $H(\mathcal{P}_1, \mathcal{P}_2) = -\sum_{\mathcal{C}_1 \in \mathcal{P}_1} \sum_{\mathcal{C}_2 \in \mathcal{P}_2} p(\mathcal{C}_1, \mathcal{C}_2) \log[p(\mathcal{C}_1, \mathcal{C}_2)]$ ; and  $H(\mathcal{P}_1|\mathcal{P}_2)$  is the conditional Shannon entropy of partition  $\mathcal{P}_1$  given  $\mathcal{P}_2$ , which is defined in a standard way from the joint distribution:  $p(\mathcal{C}_1|\mathcal{C}_2) = p(\mathcal{C}_1, \mathcal{C}_2)/p(\mathcal{C}_2) = n_{\mathcal{C}_1 \cap \mathcal{C}_2}/n_{\mathcal{C}_2}$ , and the expression of  $H(\mathcal{P}_1|\mathcal{P}_2)$  follows straightforwardly. The latter can be interpreted as the additional information needed to describe  $\mathcal{P}_1$  once  $\mathcal{P}_2$  is known. This measure of the difference between two partitions is then used as follows: for each Markov time, an ensemble of Louvain optimisations of stability are performed, starting from different random initial node ordering. Remember that the problem being  $\mathcal{NP}$ -hard, we rely on a heuristic algorithm — the Louvain method — that finds a good partition for a given Markov time, but not necessarily the optimal partition. Hence the partition found may differ if a different initial condition is provided. The normalized variation of information allows then to quantify how different the optimised partitions are. Therefore, a low variation of information indicates optimised partitions that are very similar to each others, hence that a small modification of the algorithm barely alters the partition. From the point of view of the field of dynamical system, robust partitions have thus an attractor with a large basin of attraction for the optimisation method.

### 2.1.4 Software

In order to compute stability partitions in the next of this work, we make use of Michael Schaub's free software *PartitionStability*. This C++ implementation of the stability method with a MATLAB<sup>®</sup> interface is available at <https://github.com/michaelschaub/PartitionStability>. It relies on the Louvain algorithm [BGLL08] to optimize the stability quality function. This heuristic algorithm has been initially developed for modularity optimisation. However one can show that stability can be written as the *modularity* of a time-dependent network evolving under the Markov process [LDB09]. Hence, the Louvain method can almost straightforwardly be applied to stability optimisation.

## 2.2 Clustering of the overturner problem

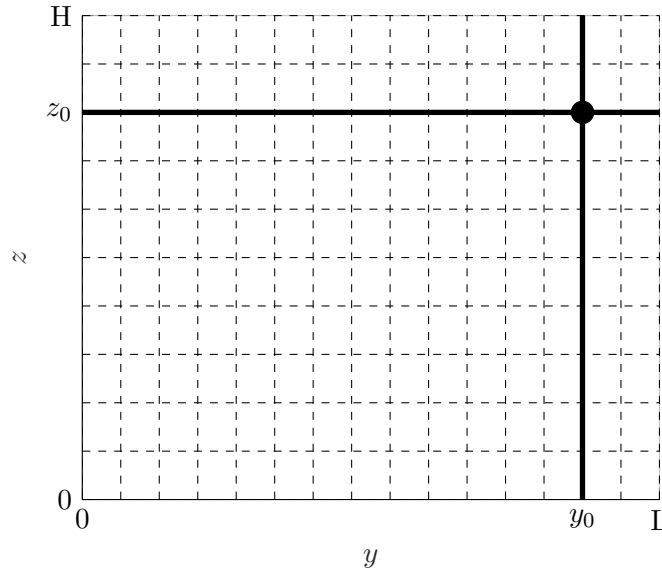
This section presents the results of applying a community-detection algorithm on the overturner problem. First, we explain how the method is applied and then we present the results for a given set of data's.

### 2.2.1 Description of the method

In order to apply a clustering algorithm on the overturner problem, we have to define how the model can be considered as a graph. To this end, the domain is decomposed into  $n_{box,y} \times n_{box,z}$  boxes. Figure 2.1 represents an example of such a domain decomposition with  $n_{box,y} = 15$  and  $n_{box,z} = 10$ . For any time  $T$ , the corresponding directed graph is build as follows : each node represents a box, and there is an edges between nodes  $i$  and  $j$  if the probability  $m_{ij}^T$  that a particle ends up in box  $j$  after a time  $T$  if it started in box  $i$  is nonzero. The weight of that edge is then  $m_{ij}^T$ . Since the problem is stationnary,  $m_{ij}^T$  depends only on the time range  $T$ , not on the initial time. Hence, the initial time can indifferently be considered as being zero. The adjacency matrix  $\mathbf{M}(T)$  of the graph is build from the weights  $m_{ij}^T$  :  $[\mathbf{M}(T)]_{ij} = m_{ij}^T$ . For any time  $T$ ,  $\mathbf{M}(T)$  is row-stochastic :

$$\mathbf{M}(T) \cdot \mathbf{1} = \mathbf{1}, \quad (2.12)$$

where  $\mathbf{1}$  is the unit column vector of size  $n_{box,y}n_{box,z}$ .



**Figure 2.1** – Illustration of the decomposition of the domain into boxes with  $n_{box,y} = 15$  and  $n_{box,z} = 10$ .

To estimate the probabilities  $m_{ij}^T$ , the program is runned for a time  $T$  with each box containing initially  $J$  uniformly distributed particles.  $m_{ij}^T$  is then numerically estimated as the number of particles  $p_{ij}$  having started in box  $i$  and ending up in box  $j$ , divided by  $J$ . This *box counting* method has been extensively used to estimate the concentration in studies using random walk modelling, see e.g. [Rid98]. As pointed in [SHD07], this method suffers some drawbacks. The estimated transition probability depends on the choice of the boxes, in particular of their size and their center. Moreover, the number of boxes cannot be chosen to be too large; otherwise the estimated concentration tends to become very irregular or noisy. Finally, the resolution of the estimated concentration is limited to the size of the boxes, as it cannot be described in a box more precisely than a constant. But it is the perfect method for our problem since the volume



average over such boxes (the nodes) is precisely what we want. Note however that other methods exist for estimating the concentration that might be better suited for other studies. For example, the *kernel estimation* method allows to reduce drastically the number of particles, and does not suffer from the resolution limit inherent to the box counting method. This method is briefly presented in [SHD07]. Classical references are [Sil86] and [WJ95].

### **2.2.2 Results**

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