

The thing with the Golgi apparatus

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Abstract

Title: Quantifying the Golgi

Abstract: The Golgi apparatus is a key component in intracellular trafficking, maturing and directing proteins essential to the cell. Despite years of research, a model coupling Golgi size and function to the cells' transport properties is lacking. In this thesis we develop such a model, describing the Golgi as an active droplet. New experimental data sheds more insight in the spatial organization of the trafficking and I have also devised two new methods relying on image gradients and neural networks to analyze this data and confront it with our model.

Contents

ABSTRACT

i

1 INTRODUCTION

- 1.1 The secretory pathway: a biological perspective
- 1.2 This thesis

2 MODEL FITTING

- 2.1 The concept
- 2.2 Step 1 - Smoothing and denoising
- 2.3 Step 2 - Derivatives
- 2.4 Step 3 - Segmentation
- 2.5 Step 4 - Fitting

3 DATA ANALYSIS

- 3.1 Rush
- 3.2 Analysis of fluorescence
- 3.3 Analysis of time derivative
- 3.4 Analysis of LS-fit
- 3.5 Analysis of constrained LS-fit
- 3.6 Conclusion

4 PHYSICS INFORMED NEURAL NETWORKS

- 4.1 Neural Networks
- 4.2 Physics Informed Neural Networks
- 4.3 Conclusion

5	INTRODUCTION TO GOLGI AS A PHASE SEPARATED DROPLET	
5.1	Phase separation	
5.2	Effective droplet	
5.3	Golgi as an active droplet	
6	GOLGI MODEL	
6.1	Two-component model	
6.2	Conclusion	
7	CONCLUSION	

APPENDIX I: SOME EXTRA STUFF

REFERENCES

1

Introduction

The cell is a highly dynamic object and requires dozens of proteins for proper functioning. Most of these proteins are produced in the Endoplasmic Reticulum (ER), an organelle found in eukariotic cells around the nucleus. Secretions from the ER don't travel directly to their destination. Rather, they move through the cell to the Golgi apparatus, after which they move to their destination. The Golgi doesn't only act as some sort of sorting centre, but it also matures the proteins coming in. The Golgi apparatus is thus a key component in intracellular trafficking, more specifically the secretory pathway. Years of research have quantified key proteins for maturation and secretion, but a model coupling Golgi function and shape to transport parameters is lacking. In order to understand more about the Golgi, we believe such a model is required. In this thesis we do so. We furthermore wish to confront our model with real-life data.

NEEDS LONGER, something about biophysics? Quantitative biology? Vesicles?

This chapter serves as an introduction to the thesis. We start by painting a biological picture of the Golgi and shortly summarizing the quantitative work done on the golgi so far. Armed to the teeth with new biological knowledge, we present the framework for our thesis and give a (qualitative) background on phase separation and biological data analysis to justify our hypothesis. We end this chapter with an overview of the rest of the thesis.

1.1 THE SECRETORY PATHWAY: A BIOLOGICAL PERSPECTIVE

The long journey of a protein starts in the endoplasmatic reticulum. The ER is

Once a vesicle is released from the ER from an ERES, it is transported by

Many different types of cells have golgi apparatuses, with different appearances of the Golgi. It consists of several independent completely functional subunits known as stacks. In plants for example, these stacks are distributed throughout the cell, whereas (normally) they form a single ribbon next to the nucleus in mammals. The exact reason for this is not yet known, and we leave this question for what it is. We focus only on mammalian cells.

As stated, in mammals the golgi forms a single big organelle known as a ribbon and that each ribbon consists of fully functional stacks. Each stack consists of a number of compartments known as cisternae. We show a ribbon in figure ref and a stack in figure ref. Cisternae are flattened membranes and look like a disk, so a stack is literally a stack of these cisternae disks. The membrane is made of vesicular material from the ER. The golgi is not isotropic: absorption of vesicles happens on one side, known as the cis-face (cis-compartments) while secretion happens on another - the trans-face. Compartments inbetween are known as medial compartments. Vesicles fusing with the cis-face releasing their contents. Depending on the final location of the proteins, the proteins will be modified ('matured') and sent on. The Golgi thus acts like a post office, receiving mail and sending it on to the right receiver.

Exactly how this sorting and maturing inside the Golgi happens is not sure. Two main models are currently contenders. The first one is known as maturation (?) and assumes that the cargo proteins move through each cisterna as a multi stage step, each cisterna has a specific task and the cargo moves from one cisterna to the next. The other model is called cisternal maturation and states that each cisterna matures as a whole, moving through each step. Each model offers explanations for some observations, but not all.

Cargo exiting the Golgi is packed into a vesicle and moves to the target

1.1.1 QUANTITATIVE WORK ON GOLGI SO FAR

One such model is offered by Hirschberg ref in their 1997 paper. They follow a virus fused to a fluorescent protein from the ER through the Golgi to the plasma membrane. They determine the fluorescence in each area in time. The model they've developed is simple although seems to fit quite nicely. It's a kinetic model, meaning they have a rate for each step (see figure ref). Although this model fits their data, their model does not take into account several crucial features such as size of the Golgi, transport properties etc. All transport from the ER to the Golgi is reduced to a single kinetic parameter. EXPLAIN MODEL MORE CLEARLY.

1.2 THIS THESIS

1.2.1 BIOLOGICAL IMAGE ANALYSIS

Over the years many different techniques for analyzing biological movies and images have been developed. We can group them roughly by type of technique or type of microscopy. Save several types of super resolution techniques, we can define fluorescent images, where some fluorescent particle is attached to the cargo and bright and dark field, where we use normal light to view at the images. The RUSH experiments only allow us access to fluorescence images.

In analysis techniques we can roughly make two categories: single particle tracking and everything else. In single particle tracking, small fluorescent beads or particles are used which are a very small spot in a video and which we can localize. From frame to frame we can follow the particles to obtain a trajectory for each particle. From these trajectories we can then obtain transport properties. These techniques are very popular and powerful, but we require us to be able to track the particles. Unfortunately, for the data we have we cant.

Other methods which don't require single particle tracking often look at correlations. The correlation function G is actually connected to the local transport properties. Unfortunately we need quite a bit of data to get some decent results out of this. Furthermore, this assumes that the particles are passive, which is not a given. Other techniques requires shifting the concentration profile to find the velocity, but we don't get any diffusion from this. Authors ref give another methods for calcuting the derivative and minimizing this, its called PIV. All these methods are cool but still very specific.

Last years a lot of different methods for data analysis have come up. We can place the image analysis in a broader perspective to make use of these techniques. consider a movie: its taken as a number of frames, with each frame consisting of a bunch of points. We can regards each

All these questions give rise to a more gener

1.2.2 GOLGI AS A PHASE-SEPARATED DROPLET

Why do we think we can describe the Golgi as a phase separated droplet? First and foremost, phase separation turns out be quite important in biology and shows quite some promising feature such as able to predict the growth of the centrosome or even cell division. A second stronger argument is the biogenesis of the Golgi. Roughly speaking, there are two ways for an organelle to form. One could follow some sort of template, while a

second way is self organization. Ronchi et al use laser nano-surgery to completely remove the Golgi apparatus and next observe the *de novo* formation of the Golgi. They identify a few stages: in the beginning, vesicles are released from the ER but nothing happens. Without Golgi, the microtubular transport is not working so the vesicles stay around the ERES. After some concentration, stack-like structures are formed, including the cisterna like topology. After microtubules have recovered/been built, these move the golgi to its location next to the nucleus and the mtoc. This sounds peculiarly like a phase transition: once a certain critical concentration is reached, the solvent phase separates. In this case, the golgi would be modeled as a dense droplet in a sea of dilute phase; the cytoplasm.

The cytoplasm isn't a simple dilute phase though; its where the transport from the ER to the Golgi/droplet takes place. The transport of the vesicles from the ER to golgi takes place mainly across microtubules. We hypothesize we can model this as some kind of flow, next to diffusion and to model the golgi as a marriage between a flow model and phase separation.

ures form around ERES (Ronchi) and then later move towards mtoc.

We think we can describe this using an active droplet. Our model basically consists of two parts: We hypothesize that we can describe the transport between the ER and the golgi as a advection-diffusion equation and use a Cahn-Hilliard equation (see next section) to describe the phase separation. We thus need a way to couple the transport model to the phase separation model.

1.2.3 STRUCTURE AND MAIN QUESTIONS

This thesis consists of two parts. Part I contains my work related to the analysis of the RUSH experiments, while part II discusses the model I have developed for the Golgi. Although our image analysis was developed with the RUSH data in mind, it answers to a more general question: *how do we fit a

2

Model fitting

In the introduction we stated the question:

How can we fit a model to spatiotemporal data if that model is a PDE?

In this chapter we present the answer in the form of a system which allows us to fit PDE-models to data. We start of with a section describing the general idea and subsequent sections elaborate on each step.

The system principally works for any type of data and model, but was developed originally to analyze data from the RUSH experiments. We illustrate our system with several examples and have chosen to use real data from the RUSH experiments (specifically, MANII) over synthetic data. In figure fig. 2.1 we show four typical frames of the MANII movie. Characteristically, MANII moves from the ER to the Golgi and remains there. The upper left frame shows the first frame with all the cargo in the ER, in the lower left and upper right the intermediate regime is shown (i.e. cargo moving) and in the lower right frame all the cargo has moved into the Golgi.

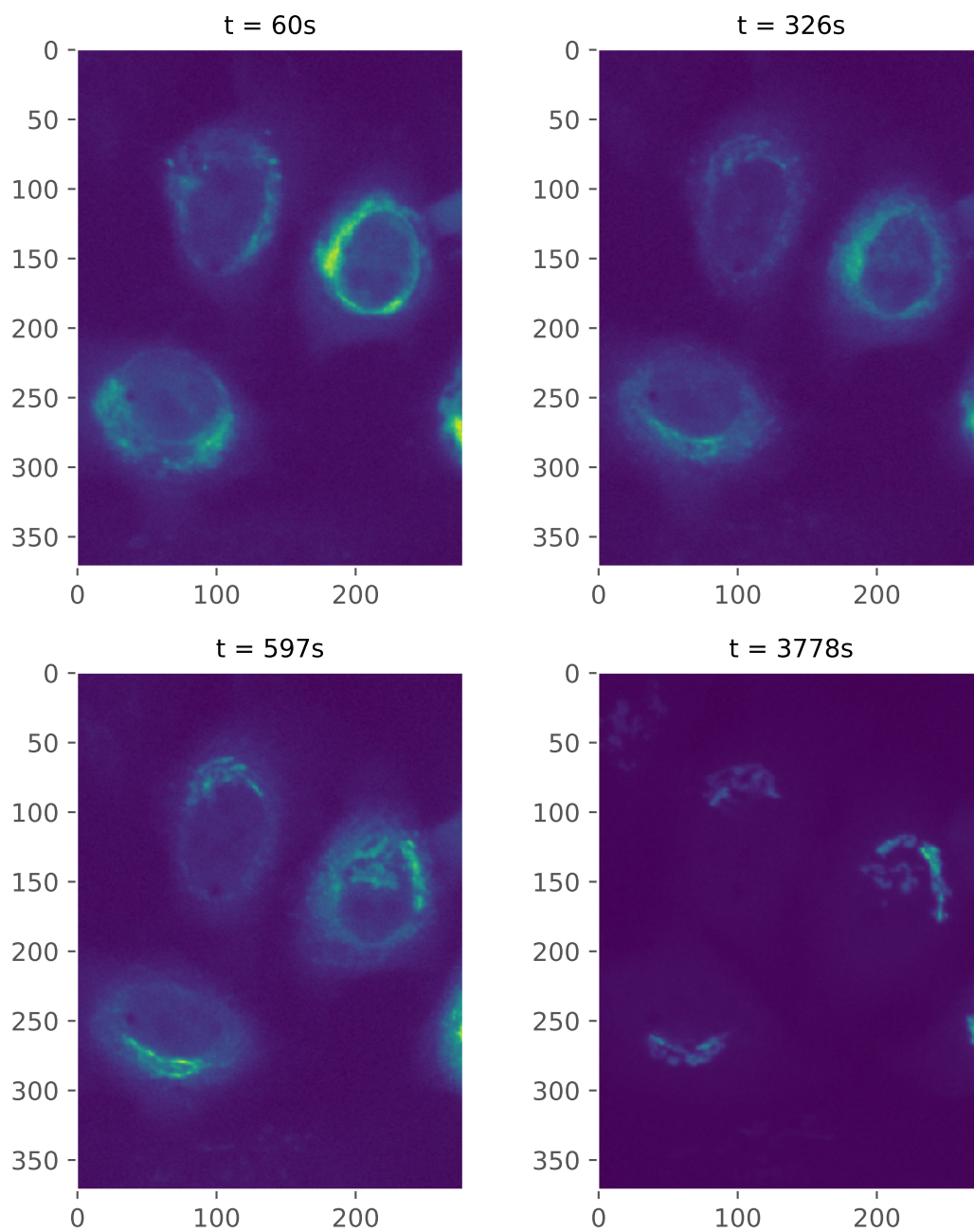


Figure 2.1: Four frames ($t = , , ,$) showing a typical MANII cycle of the RUSH experiment.

2.1 THE CONCEPT

Assume we have some experimental data describing some process $f(x, t)$. We have also developed a model for this process in the form of a PDE:

$$\partial_t f(x, t) = \lambda_1 \nabla^2 f(x, t) + \lambda_2 \nabla f(x, t) + \lambda_3 f(x, t) + \lambda_4 \quad (2.1)$$

We now wish to know if this model fits the data $f(x, t)$ and the value of coefficients λ_i . To do so, consider each spatial term of $f(x, t)$ in eq. 2.1 as some variable x_i and $\partial_t f$ as y , so that we can rewrite it as:

$$y = \lambda_1 x_1 + \lambda_2 x_2 + \lambda_3 x_3 + \lambda_4$$

If we have access to the variables x_i and y , we can perform least squares fitting to obtain the coefficients λ_i . In other words, if we can calculate the spatial and temporal derivatives, we can fit the model to the data. Once we know the coefficients, we can use our model to propagate the first frame of the data and compare our model to the experimental data.

Although the concept seems trivial, its implementation is all but. Data is rarely noiseless and obtaining accurate derivatives from noisy data is notoriously hard. We can also have different models in different areas of the data, so that we need to segment the data or the coefficients λ_i might not be constant but space- and time- dependent. The process of fitting the data thus has several steps:

1. Denoising and smoothing
2. Calculating derivatives
3. Segmenting
4. Fitting

In the next sections, we describe each step separately. Note that the method we present here has been developed empirically: there's no theoretical background as to why this particular combination should work optimally. Instead, it's been developed while analyzing the data, adapting each step on the go.

2.2 STEP 1 - SMOOTHING AND DENOISING

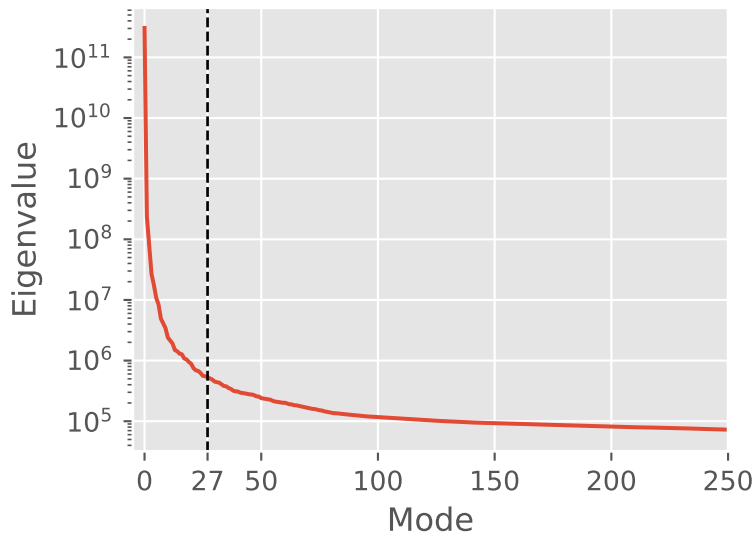
The first step in our pipeline is to denoise and smooth the data. The smoothing is necessary for accurately calculating the derivatives. Denoising still is a very active area of research

(especially in life sciences) and dozens of different methods exist¹. For example, one could Fourier transform the signal and use a high pass filter, but this would also get rid of small and sharp features. After evaluating several methods, we have settled on the so-called ‘Wav-InPOD’ method, introduced by 3 in 2016. In 4 they show that this methods outperforms several other advanced methods. WavInPOD combines Proper Orthogonal Decomposition (POD) with Wavelet filtering (Wav). Both subjects are vast (especially Wavelet transform) and we’re only interested in the result of the technique, so we only present a short introduction here, adapted from 3.

POD is a so-called dimensionality reduction technique and is very closely related to the more well-known Principal Component Analysis (PCA) in statistics. In physics it’s often used to analyze turbulent flows⁵. In POD we wish to describe a function as a sum over its variables:

$$f(x, t) = \sum_n^r \alpha_n(x) \varphi_n(t)$$

where α_n and φ_n are called respectively the spatial and temporal modes. Associated with each mode n is an energy-like quantity E_n . Modes with a higher ‘energy’ E_n contribute more to the signal f than modes with a lower energy and we can thus approximate the signal by selecting the k modes with the highest energy. A typical log10 energy spectrum has a ‘knee’ in the values, as shown in figure fig. ?? . Modes with an energy below the knee are noise, and modes above the knee are signal.



The wavelet transform is very similar to the Fourier transform, but uses wavelets as its basis. A fourier transform gives the frequency domain with infinite precision, but tells nothing about the locality of the frequencies (.i.e when each frequency is present in a signal). By using a wavelet (a wave whose amplitude is only non-zero for a finite time), we sacrifice precision in the frequency domain but gain information on the locality instead. Performing a wavelet transform transforms the signal into the sum of an approximation and its details and we can filter this analogous to a fourier filter. Due to its locality however, noise is filtered out, by sharpness is retained.

WavinPOD combines these two techniques by applying wavelet filtering to the POD modes. In detail, one first decomposes the problem with a POD transformation. The energy spectrum of this transformation is shown in figure fig. ?? and we select a cutoff of 27. All retained modes are wavelet filtered and are then retransformed to give the denoised and smoothed signal. In figure fig. 2.2 we show the results of the smoothing in the time and spatial domain. In the left panel we show the signal of a single pixel in time, while we plot a line of pixels in a single frame in the right panel. The red lines denote the original (unfiltered) signal, the blue line the effect of just applying a POD and the black one the result of the WavInPOD technique. Note that the effect of the wavelet filtering is to smooth the signal significantly and in comparing the original data to the filtered data that we've retained the sharpness of the features whilst obtaining a smooth signal.

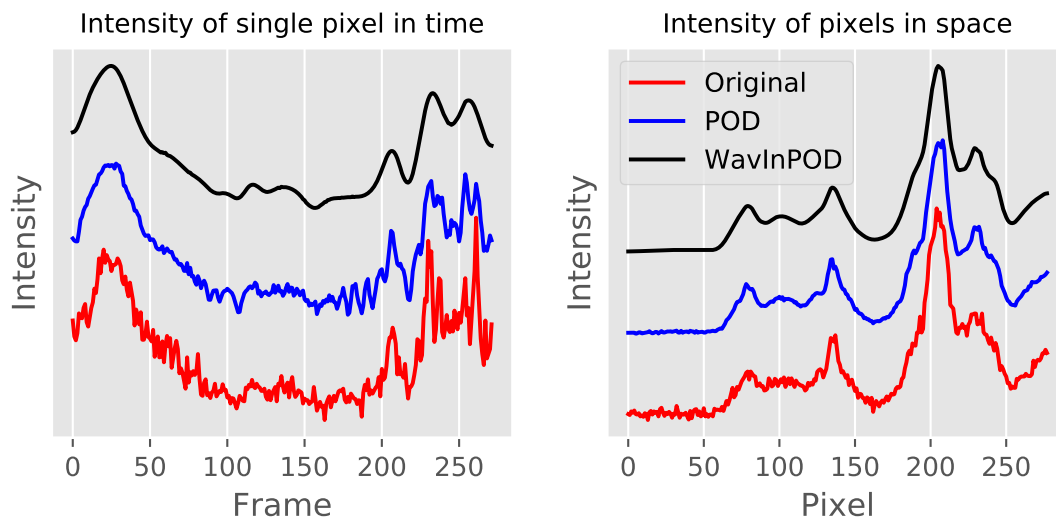


Figure 2.2: Effect of POD with a cutoff of 27 and wavelet filtering with a level 3 db4 wavelet. Left panel shows the result in the time domain, right panel in the spatial domain. Lines have been offset for clarity.

2.3 STEP 2 - DERIVATIVES

After having denoised the images, we calculate the spatial and temporal derivatives. Obtaining correct numerical derivatives is hard and becomes much more so in the presence of noise⁷. Next to a finite-difference scheme, one can for example (locally) fit a polynomial and take its derivative or use a so-called tikhonov-regularizer⁸. The computational cost of these methods is high however and don't scale well to dimensions higher than one. For our spatial derivatives these methods are thus not available. In fact, obtaining the gradient of a 2D discrete grid has another subtlety which we need to adress.

Naively, one could obtain the gradient of a 2D grid by taking the derivative using a finite difference scheme with respect to the first and second axis. If there are features on the scale of the discretization (\sim few pixels), such an operation will lead to artifacts and underestimate the gradient. These issues have long been known and several techniques have been developed to accurately calculate the gradient of an 'image'. The most-used one is the so-called Sobel operator. It belongs to a set of operations known as *kernel operators*. Kernel operators are expressed as a matrix and by convolving this matrix with the matrix on which the operation is to be performed, we obtain the result of the operator. We show this for the Sobel operator.

Consider a basic central finite difference scheme:

$$\frac{df}{dx} \approx \frac{f(x_{i+1}) - f(x_{i-1}))}{2h}$$

where h is defined as $x_{i+1} - x_i$. In terms of a kernel operator, we rewrite this as:

$$\frac{1}{2} \cdot \begin{bmatrix} 1 & 0 & -1 \end{bmatrix}$$

where we have set $h = 1$, as the distance between pixels is one by definition. By convolving this matrix with the matrix \mathcal{A} we obtain the derivative of \mathcal{A} :

$$\partial_x \mathcal{A} \approx \mathcal{A} * \frac{1}{2} \begin{bmatrix} 1 & 0 & -1 \end{bmatrix}$$

Finite difference

0	0	0
-1		1
0	0	0

3x3 Sobel

-1	0	1
-2		2
-1	0	1

Figure 2.3: Left panel: One dimensional finite difference kernel. Right panel: Three by three Sobel filter

As stated, this operation is inaccurate and introduces artifacts. To improve this, we wish to include the pixels on the diagonal of the pixel we're performing the operation on as well (see figure fig. 2.3). The distance between the diagonal pixels and the center pixel is not 1 but $\sqrt{2}$ and the diagonal gradient also needs to be decomposed into \hat{x} and \hat{y} , introducing another factor $\sqrt{2}$. The kernel thus obtained is the classic 3×3 Sobel filter:

$$G_x = \frac{1}{8} \cdot \begin{bmatrix} 1 & 0 & -1 \\ 2 & 0 & -2 \\ 1 & 0 & -1 \end{bmatrix}$$

Increasing the size of the Sobel filter increases its accuracy and we've implemented a 5×5 operator. Implementing the derivative operation as a kernel method is also beneficial from a computational standpoint, as convolutional operations are very efficient.

As the time derivative involves just one dimension, we make use of a second order accurate central difference scheme implemented in Numpy.

2.4 STEP 3 - SEGMENTATION

In the case of the RUSH data, obtained images and movies often contain multiple cells. Each of these cells can be further segmented into two more areas of interest: the cytoplasm, which is where we want to fit our model and the Golgi apparatus. We wish to make a mask

which allows us to separate the cells from the background and themselves and divide each cell into cytoplasm or Golgi.

Figure fig. 2.1 shows four typical frames in the MANII transport cycle. Note that no sharp edges can be observed, especially once the MANII localizes in the Golgi. No bright field images were available as well, together making use of techniques such as described in 9 unavailable. We have thus developed two methods which allow us to segment the image and the cells, based on Voronoi diagrams and the intensity.

2.4.1 VORONOI DIAGRAM

Consider again the frame on the left of figure fig. 2.1. Note that in early frames such as this one, the cargo (i.e. fluorescence) is spread circumnuclear. Applying a simple intensity based segmentation gives us a number of separate areas, which *very* roughly correspond to a cell. We can then pinpoint each cell's respective center. Given n points, Voronoi tessellation divides the frame into n areas, where point i is the closest point for each position in area A_i . The hidden assumption here is thus that each pixel belongs to the cell center it's closest too. Although this is a very big assumption, in practice we've found this to be reasonable. Furthermore, one can add 'empty' points to make the diagram match observations. Assuming small movements of the cell, this isn't an issue either for this technique, as we are assigning an area to each cell instead of very precisely bounding it. This also allows us to calculate the Voronoi diagram in the early frames and apply the segmentation to the entire movie. The result of this segmentation for MANII is shown in figure fig. 2.4. Each cell centre is denoted by a dot, while the lines denote the border between each voronoi cell.

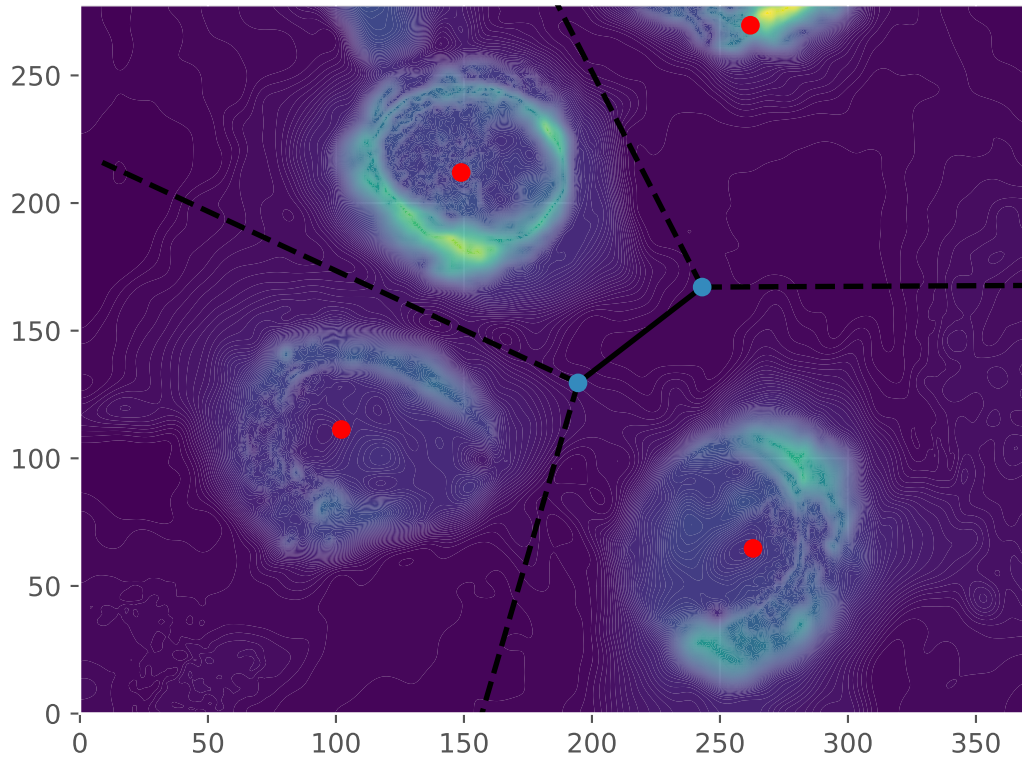


Figure 2.4: The obtained mask. Red dots are cell centers, dashed lines infinite edges and solid lines finite edges.

2.4.2 INTENSITY

The Voronoi technique works very well for an area-based approach, but for analyzing our fitting data we would like a more precise mask - although we still don't require pixel-level accuracy. From the movies, the Golgi is clearly visible and we can separate the cytoplasm from the background, with a big 'gray' area inbetween. We thus turn to an intensity based approach. We have developed the following approach for localizing the Golgi:

1. Normalize the intensity I between 0 and 1.
2. Sum all the frames in time: $\sum_n I(x, y, t_n)$. A typical result is shown in figure fig. 2.5 .
3. Threshold the image to obtain the mask. This is either done automatically through an Otsu threshold or by manually adjusting the threshold until desired result.
4. The mask is postprocessed by filling any potential holes inside the mask.

This procedure was unable to reliably separate the background from the cytoplasm. Noting that while the cytoplasm might not have the intensity as the golgi, its time derivative should be higher than the rest of the areas. We replace step two by $\log_{10} (\sum_n I(x, y, t_n) \cdot \partial_t I(x, y, t_n))$, where the time derivative has been normalized between 0 and 1. Figure fig. 2.5 shows our final results. The upper two panels show the images obtained after performing the summing operation for the Golgi and cytoplasm respectively, while the lower left panel shows the final mask obtained after thresholding these two images. For comparison, we plot frame to compare the mask to.

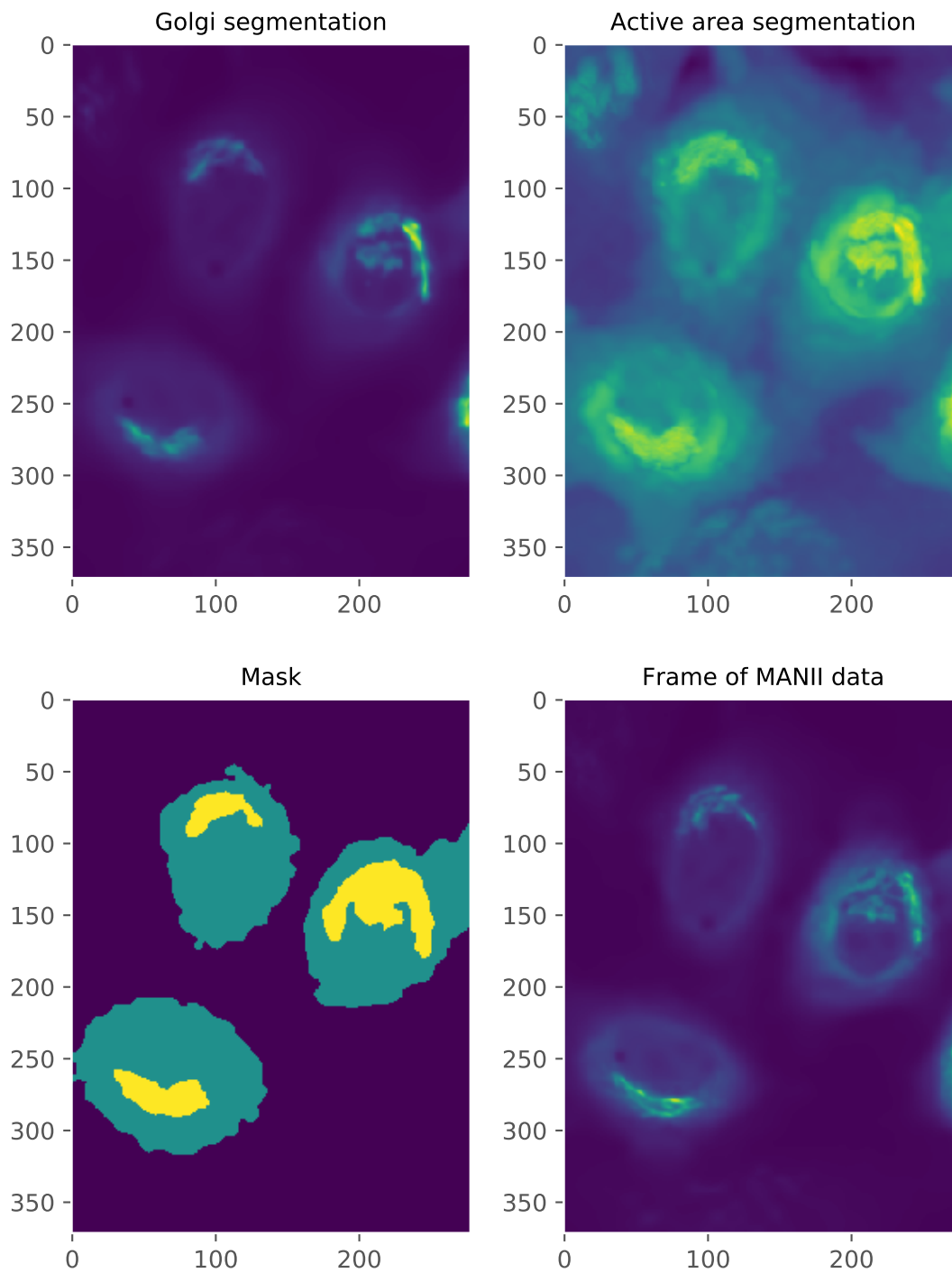


Figure 2.5: Four panels showing the different stages of making the mask. From segmenting the upper two panels we determine the golgi and active area, leading to the mask in the lower left. Compare the to the lower right.

2.5 STEP 4 - FITTING

Having gathered all the data, the final step is to fit the model. Equation eq. 2.1 assumes a model with constant coefficients. In reality, coefficients will be spatially and even temporally varying. To circumvent this issue, we assume the coefficients can be assumed to be locally constant. We thus assume that for a small area we can fit the model using constant coefficients. We perform this operation for every datapoint in a sliding-window manner, as shown in figure fig. 2.6, thus ending up with a coefficient field.

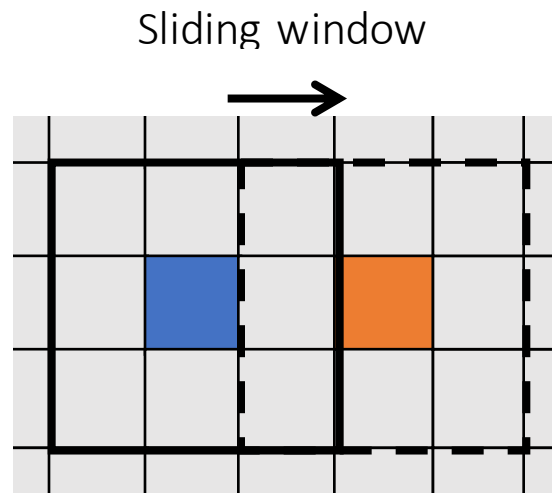


Figure 2.6: Schematic overview of the sliding window technique. The solid black line encompasses an area around its blue coloured central pixel and the fit output is assigned to that pixel. We then move the window (dashed black line) and perform the fit for the orange coloured pixel.

3

Data analysis

In the previous chapter we developed a general system to fit our advection-diffusion model to the data obtained from the RUSH experiments. In this chapter we apply said system to the MANII movies. MANII has been chosen as after arriving at the Golgi, it remains there. Dealing with only one transport direction makes everything a lot easier for us. This chapter consists of five sections:

- Section 1 presents a general analysis of the fluorescence data of the movies
- In section 2 we discuss the time derivative of the fluorescence, $\partial_t I$, as this also has some interesting points.
- Section 3 contains our analysis of the least squares fit.
- Section 4 is similar to section 3, only now we analyse a constrained fit with $D > 0$.
- Section 5 summarizes our findings and presents possible improvements for the system.

3.1 RUSH

A technique known as RUSH (Retention Using Selective Hooks) has recently (2012) been developed in the team of Frank Perez at Institut Curie to study secretory traffic. It allows for the precise timing of the release of proteins from the endoplasmatic reticulum and can

be used to follow the secretory pathway from the ER to the Golgi and even post-golgi using fluorescent live-cell imaging.

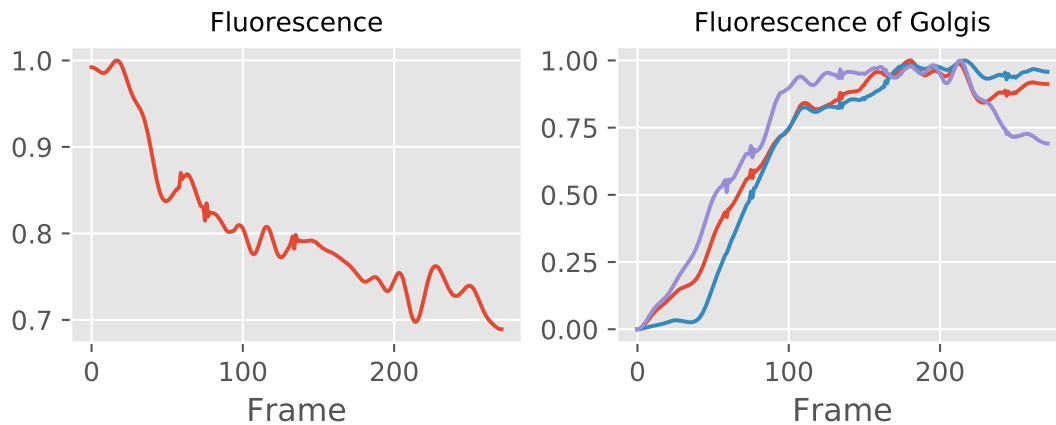
RUSH system

Figure ref shows the principle of the RUSH system. Inside a donor compartment, a hook protein is fused to a core streptavidin. A streptavidin-binding-protein (SBP) binds reversibly to the streptavidin and has both the protein to be followed attached to it (the reporter) and a fluorescent protein. Upon the addition of biotin, it binds to the streptavidin and releases the reporter complex. In this case, the reporter complex starts its secretory pathway and is released from the ER. The advantage of the RUSH system is its precise timing, non-toxicity and that it is adaptable to a wide array of cargo proteins. In this thesis we mainly focus on the α -mannosidase-II (ManII). This cargo protein has some function inside the golgi apparatus and, contrary to most proteins, is retained in the Golgi. As it is retained in the Golgi, the movies we will analyze will only contain the transport towards the golgi, so that we don't have to separate post and pre-golgi traffic. Figure ref shows several frames of the ManII transport cycle. Initially, the reporter is still in the ER and no cargo is observed in the Golgi. Then we observe a rise in the Golgi, where it remains.

Couple of frames of the ManII transport.

3.2 ANALYSIS OF FLUORESCENCE

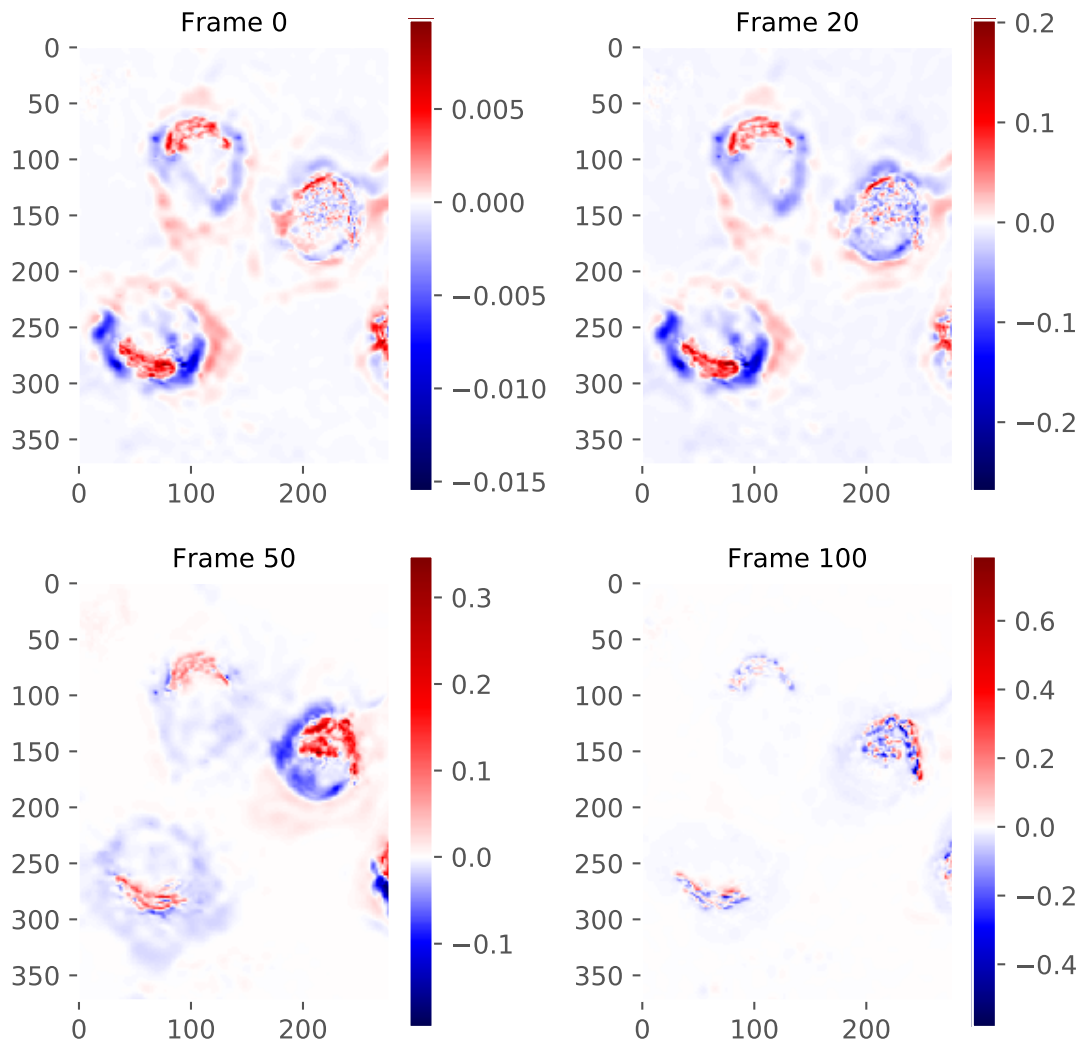
We first perform a general analysis of the fluorescence intensity. We plot the average normalized fluorescence (that is, we normalize the fluorescence between 0 and 1 to get rid of the background in our statistics, average each frame and then normalize that between 0 and 1). The average fluorescence decays with almost 30%, which is a lot. We can also observe two 'regimes': between frame 0 and 100 we roughly see a very strong decay and after frame 100 we see a slower decay. The first regime is where all the cargo moves towards the Golgi, showing that the assumption that $I \propto t$ might not necessarily be true, while the second regime is probably caused by fluorescence extinction.



In the right panel we show the fluorescence in each of the golgi bodies. This has been calculated by averaging the fluorescence in each of the golgi for each frame, taking into account the decay of the fluorescence due as shown in the left panel and finally normalizing between 0 and 1. We observe that the fluorescence increase in each of the three cells is nearly similar; although one cells transport starts later than the rest, it seems to catch up to them. All three rise mostly before frame 100 and then plateau off. This suggests a common pattern, but what exactly??

3.3 ANALYSIS OF TIME DERIVATIVE

For the fit we have also determined the time derivative of the fluorescence. This can also give us some qualitative data. We show 4 frames in figure .



We see that the initial cargo comes from an area close to the golgi and then slowly moves outwards. In the end all we see changing in time is the golgi. This shows that initially stuff gets released from an inner ring and maybe diffuses outward, before it condenses into the golgi.

3.4 ANALYSIS OF LS-FIT

We now turn towards an analysis of our LS fits. We used a window with of 7x7 in the spatial domain and 1 in the temporal domain, i.e. the fit of each frame is independent. We first

show several

3.5 ANALYSIS OF CONSTRAINED LS-FIT

3.6 CONCLUSION

Bayesian heeeeee

4

Physics Informed Neural Networks

In the previous chapters we showed the difficulties in fitting a model in the form of a partial differential equation to spatio-temporal data. The method we developed was a classical numerical approach, separating the problem into several substeps such as denoising, smoothing and numerical differentiating. In the last few years machine learning has been slowly making its way into physics. Very recently, a technique generally referred to as Physics Informed Neural Networks (PINNs) have shown great promise as both tools for simulation and model fitting (10, 11, 12, 13, 14). In this chapter, I will evaluate the use of this technique to fit the model to the RUSH data. I've divided the chapter into three parts:

- Neural Networks - This part will cover the basics of neural networks: their inner workings, how to train them and other general features.
- Physics Informed Neural networks - In this second part we introduce the concept behind PINNs, use it to solve a toy problem and apply it to our RUSH data.
- Conclusion - Finally we summarize the results and observations from the previous sections.

4.1 NEURAL NETWORKS

Artificial Neural Networks (ANNs) are networks inspired by biological neural networks. Contrary to other ways of computing, ANNs are not specifically programmed for a task -

instead, ANNs are *trained* using a set of data. Research on artificial neural networks started in the '40s but never gained any critical mass, as no efficient training algorithm was known. Once an efficient training algorithm was found in 1975 by Werbos, interest resurged but it wasn't until the late '00s that deep learning started gaining widespread traction. The use of GPU's allowed ANNs to be efficiently trained and widely deployed at reasonable cost.

The advancements in machine learning in general and especially neural networks in the last ten years have yielded a wealth of techniques and approaches. In supervised learning, the network is given pre-labeled data so that it is trained by learning the mapping from the given inputs to the given outputs. Other types such as supervised learning, where the network needs to learn to discriminate between unlabeled data, and reinforcement learning don't have any obvious use for PINNs yet and I've thus chosen to omit them. In the next sections, I'll present the mathematics of an ANN and show how they are trained using the so-called *backpropagation* algorithm.

4.1.1 ARCHITECTURE

An excellent introduction is given by Michael Nielsen in his freely available book "Neural networks and deep learning." The following section has been strongly inspired by his presentation.

At the basis of each neural network lies the neuron. It transforms several inputs non-linearly into an output and we can use several neurons in parallel to create a *layer*. In turn, several layers in series make up a network. The layers in the middle of the network are known as *hidden layers*, as shown in figure fig. 4.1

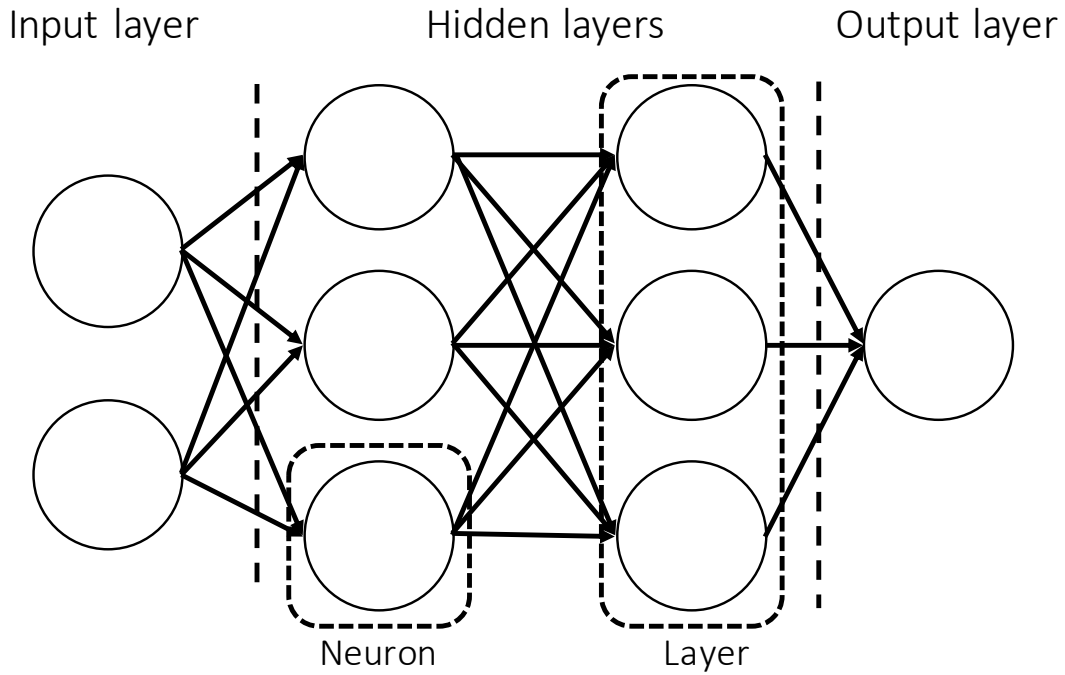


Figure 4.1: Schematic view of a neural network.

In the schematic shown in fig. 4.1, each neuron is connected to every neuron of the previous and next layer. This is known as a *fully connected* layer. Using only this type of layers, we've created a feed-forward network and it has been proven that a single hidden layer with enough neurons is a *universal function approximator*, i.e. a neural network can represent any continuous function using enough neurons.

As stated, a neuron takes several inputs and transforms them into an output. This is a two step process, where in the first step the neuron multiplies the input vector x with a weight vector w and adds a bias b :

$$z = wx + b \quad (4.1)$$

z is called the weighted input and is transformed in the second step by the neuron *activation function* σ . This in turn gives the output of the neuron a , also known as the activation:

$$a = \sigma(z) = \sigma(wx + b) \quad (4.2)$$

The role of the activation function is to introduce non-linearity into the system. The classical and often used activation function is the *tanh*, as it is bounded between +1 and -1. Since we're working with multiple layers, it is useful to rewrite function eq. 4.2 in terms of the activation a^l of layer l :

$$a^l = \sigma(z^l) = \sigma(w^l a^{l-1} + b^l)$$

where w^l and b^l are respectively the weight matrix and bias of layer l .

4.1.2 TRAINING

In supervised learning the task of training a machine means adjusting the weights and biases until the neural network predictions match the desired outputs. We thus need some sort of metric to define this 'distance' between prediction and desired output. Training the network then means minimizing the metric with respect to the weights and biases of the network. This metric is known as the cost function \mathcal{L} and the most used form is a mean squared error:

$$\mathcal{L} = \frac{1}{2n} \sum_i |y_i - a_i^L|^2 \quad (4.3)$$

where n is the number of samples, y_i the desired output of sample i and a_i^L the activation of the last function - the prediction of the network. Minimizing this is not trivial, as the problem can have many local minima. A solution can be found however using gradient descent techniques.

Gradient descent techniques are based on the fact that given an initial position, the fastest way to reach the minimum from that position is by following the steepest gradient. Thus, given a function $f(x)$ to minimize w.r.t to x , we guess an initial position x_n and iteratively change until it converges:

$$x_{n+1} = x_n - \gamma \nabla f(x_n)$$

where γ is known as the learning rate. If a global minimum exists, this technique will converge on it. More advanced versions of this technique exist which are able to deal with local minima as well, since convexity of the cost function is not at all guaranteed.

Making use of gradient descent requires knowledge of the derivatives of the cost function w.r.t to the variables to be optimized. In the case of neural networks, we thus need to know

the derivative w.r.t to each weight and bias. A naive finite difference scheme would quickly grow computationally untractable for even shallow networks. A solution to this problem was found by Werbos in the form of the backpropagation algorithm. Despite many years of ongoing research, it is still the go-to algorithm for each neural network implementation.

BACK PROPAGATION AND AUTOMATIC DIFFERENTIATION

As we wish to minimize the cost function w.r.t. to each weight w and bias b using gradient descent, we need to find the derivative of the cost function w.r.t to each. Our argument simplifies if we move away from vector notation and introduce w_{jk}^l , the weight of the j -th neuron in layer $l - 1$ to neuron k in layer l and b_j^l , the bias of the neuron j in the l -th layer. We introduce the error of neuron j in layer l as:

$$\delta_j^l = \frac{\partial C}{\partial z_j^l}$$

We can rewrite this using the chain rule as:

$$\delta_j^l = \sum_k \frac{\partial C}{\partial a_{jk}^l} \frac{\partial a_{jk}^l}{\partial z_j^l}$$

However, the second term is always zero except when $j = k$, so the summation can be dropped. Remembering eq. 4.2, we note that $\partial a_{jk}^l / \partial z_j^l = \sigma'(z_j^l)$. For the last layer $l = L$, the first term turns into the derivative of the cost function, finally giving us:

$$\delta_j^L = |a_j^L - y_j| \sigma'(z_j^L) \quad (4.4)$$

Equation eq. 4.4 relates the error in the output layer to its inputs. This in turn is a function of all the previous inputs and errors and we thus need to find an expression relating the error in layer l with the error in an layer $l+1$. Since we have an expression for the error in the last layer, we propagate the error going down the layers, hence the name *backpropagation*. Again using the chain rule gives:

$$\delta_j^l = \sum_k \frac{\partial C}{\partial z_{jk}^{l+1}} \frac{\partial z_{jk}^{l+1}}{\partial z_j^l} = \sum_k \delta_k^{l+1} \frac{\partial z_{jk}^{l+1}}{\partial z_j^l}$$

Using equation eq. 4.1, we obtain after substitution:

$$\delta_j^l = \sum_k \delta_k^{l+1} w_{kj}^{l+1} \sigma'(z_j^l) \quad (4.5)$$

Using equations eq. 4.4 and eq. 4.5, we can calculate the error in C due to each neuron. Finally, we need to relate the error in each error to $\partial C / \partial w_{jk}^l$ and $\partial C / \partial b_j^l$. Making use yet again gives us the last two backpropagation relations:

$$\frac{\partial C}{\partial b_j^l} \frac{\partial b_j^l}{\partial z_j^l} = \frac{\partial C}{\partial b_j^l} = \delta_j^l \quad (4.6)$$

$$\sum_k \frac{\partial C}{\partial w_{jk}^l} \frac{\partial w_{jk}^l}{\partial z_j^l} = \delta_j^l \rightarrow \frac{\partial C}{\partial w_{jk}^l} = a_j^{l-1} \delta_j^l \quad (4.7)$$

Now that we now that all back propagation equations, we state the algorithm. It consists of four steps:

1. Complete a forward pass, i.e., calculate the expected outcomes with the current weights and biases.
2. Calculate the error using eq. 4.4 and do a backward pass to obtain the error in each neuron using eq. 4.5. This can be used to calculate the gradients using eq. 4.6 and eq. 4.7
3. Adjust the weights and biases using the choosen optimizer (e.g. gradient descent)
4. Return to step 1 until the optimization problem converges.

Mathematically, back propagation is a special case of a technique known as automatic differentiation. Automatic differentiation is a third type of differentiation, next to numeric and symbolic. It allows for machine precision calculation of derivatives by writing it as a chain of simple operations combined with the chain rule, similar to backpropagation. Note that:

$$\delta_j^o = \frac{\partial C}{\partial x_j} \frac{\partial x_j}{\partial z_j^o}$$

so that:

$$\frac{\partial C}{\partial x_j} = a_j^\circ \partial_j^\circ$$

Thus neural networks also give us access to high precision derivatives with regard to each coordinate.

4.2 PHYSICS INFORMED NEURAL NETWORKS

On the face of things, the goal of physics and neural networks are oppsite: whereas physics tries to build an understanding of things using models to make predictions, neural networks learn a *modelless* mapping to make predictions. Recent advancements however have merged the two approaches together in a concept known as Physics Informed Neural Networks (14, 13). In this approach, we encode physical laws into the network, so that the network respects the physics. This can be used to both numerically solve equations or fit a model to spatiotemporal data. Even more so, it should allow us to infer coefficient fields.

4.2.1 THE CONCEPT

Consider a set of 1D+1 spatiotemporal data, consisting of some property $u(x, t)$ at coordinates (x, t) . The neural network can be learned the underlying physics by minimizing the cost function:

$$\mathcal{L} = \frac{1}{2n} \sum_i |u_i - a_i^L|^2$$

The process of learning requires a lot of data and is prone to overfitting. Now assume that we know that $u(x, t)$ is governed by some process which is written as a partial differential equation:

$$\partial_t u = f(\mathbf{1}, u, u_x, u_{xx}, u^2, \dots)$$

where f is a function of u or its spatial derivatives. Rewriting it as:

$$g = 0 = -\partial_t u + f(\mathbf{1}, u, u_x, u_{xx}, u^2, \dots) \quad (4.8)$$

we see that in order to satisfy the PDE, $g \rightarrow 0$. The idea of PINNs is to add this function g to the costfunction of the neural network:

$$\mathcal{L} = \frac{1}{2n} \sum_i |u_i - a_i^L|^2 + \lambda \sum_i |g_i|^2 = MSE + \lambda PI$$

where λ sets the effective strength of the two terms. Observe that the cost function is higher if the PDE is not satisfied. Minimizing the costfunction will thus mean minimizing g and hence satisfying the PDE. We effectively penalize solutions not satisfying the physics we put in equation eq. 4.8; the added term acts a ‘physics-regularizer’. Concretely, the adding of physics constrains the solution space, preventing overfitting and making the neural network much more data efficient. The most useful feature however is that we don’t need a vast set of training data to train the network, as we solve the problem *by* training the network.

We can also remove the mean squared error term from the cost function and add initial and boundary conditions, similar to the PI term. If we now train the network, it will learn the solution to the given PDE whilst respecting the given boundary and initial conditions. This alternative means of numerically solving a model doesn’t need advanced meshing of the problem domain or carefully constructed (unstable) discretization schemes, as it requires the physics to be fulfilled at every point in the spatiotemporal domain. A useful analogy here is calculating the trajectory of a launched object. A classical numerical solver would take small steps in time, updating the position and speed of the object each step. A PINN however uses a completely different approach. Given the initial (random) state of the neural network, it calculates a first trajectory and keeps adjusting the weights of the network until the cost is minimized, i.e. until we obtain a solution satisfying the included physics and initial and boundary conditions. A classical numerical approach tries once using a correct and methodical approach, whereas a PINN tries many times until the result satisfies its constraints.

We can also use this framework to fit models to spatiotemporal data by letting the coefficient of each term be a variable to be minimized as well. More concretely, where before the cost was a function of the weights and biases, $\mathcal{L} = f(w^l, b^l)$, we now let it be a function of the coefficients λ of the PDE as well: $\mathcal{L} = f(w^l, b^l, \lambda_1, \lambda_2, \dots)$. This is shown for several PDEs such as the Burgers, Schrodinger or Navier-Stokes equation in the papers of M. Raissi(14, 13). In the case of the Navier-Stokes equation, it’s shown that it’s also possible to infer the pressure field, which appears as a separate term. This is achieved by adding another output neuron to the PINN (shown in figure fig. 4.2), so that it predicts both the pressure and the flow. In theory it should also be possible to infer spatially and temporally varying *coefficient* fields. We investigate this claim in the next section.

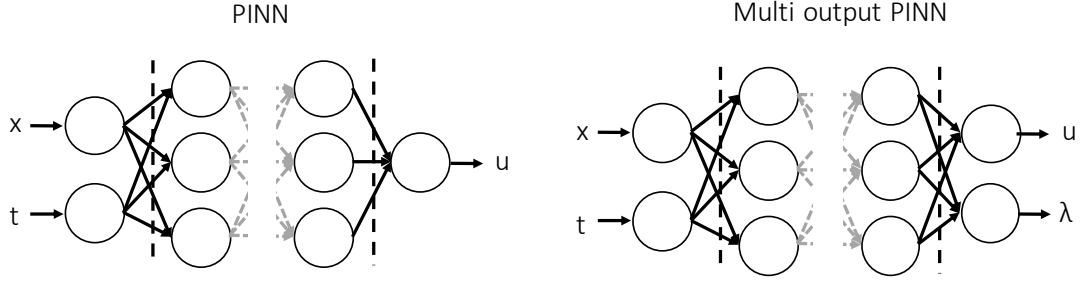


Figure 4.2: Left panel: a normal single output PINN. Right panel: a multi-output PINN. The network now also predicts the coefficients values at each data point.

4.2.2 PINNs IN PRACTICE

We now wish to evaluate the use of PINNs to analyze the RUSH data. Using a diffusive process as a toy problem, we first show how PINNs are able to accurately determine the diffusion constant, even in the presence of noise. Next, we prove that PINNs are indeed capable of inferring coefficient fields and finish by analyzing some parts of the RUSH data.

In our toy problem we have an initial concentration profile:

$$c(x, 0) = e^{-\frac{(x-0.5)^2}{0.02}}$$

diffusing in a 1D box according to:

$$\frac{\partial c(x, t)}{\partial t} = \nabla \cdot [D(x) \nabla c(x, t)]$$

on the spatial domain $[0, 1]$ with perfectly absorbing boundaries at the edges of the domain:

$$c(0, t) = c(1, t) = 0$$

If $D(x) = D$, this problem has an analytical solution through a Greens function. If the diffusion coefficient is spatially dependent though, the problem needs to be solved numerically. The code used to generate our data can be found in the appendix. Although this toy problem is simple and in 1D, our results easily generalize to higher dimensions and complexity at the cost of higher computational cost.

4.2.2.1 CONSTANT DIFFUSION COEFFICIENT

We now consider the mentioned problem with a diffusion coefficient of $D(x) = D_0 = 0.1$ and simulate it between $t = 0$ and $t = 0.5$. Using a spatial and temporal resolution of 0.01 , we have a datagrid of 101 by 51 , so that our total dataset consists of 5151 samples. The neural network consists of 6 hidden layers of 20 neurons each and $\lambda = 1$. Figure fig. 4.3 shows the ground truth for the problem and the absolute error of the neural network.

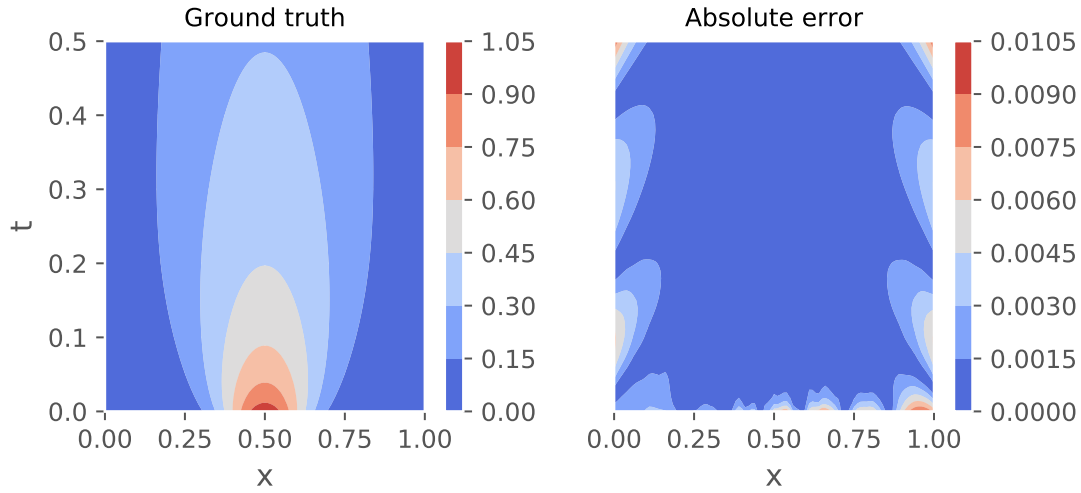


Figure 4.3: Left panel: Simulated ground truth of the problem. Right panel: The absolute error of neural network. Note that most of the error is located at areas with low concentration, i.e. signal.

The predicted diffusion coefficient is $D_{pred} = 0.100026$, giving an error of 0.026% . In 14, the authors obtain similar accuracies for significantly more complex problems such as the Schrodinger equation, which means that our accurate inference is not just due to the simplicity of the problem. Furthermore, Raissi et al. show that the result is robust w.r.t the architecture of the network. From the absolute error we observe that the error seems to be higher in areas with low concentration. This is a feature we've consistently observed: in areas with low 'signal', the neural network seems to struggle.

As good as these results are, the input data is noiseless and thus of limited practical interest. We now show that PINNs perform equally well with noisy data by adding 5% white noise to the data and performing the same procedure. The network is now doing two tasks in parallel: it's both denoising the data and performing a model fit. In the left panel of figure fig. 4.4 we show the concentration profile at times $t = 0, 0.1$ and 0.5 , with the prediction of the PINN superimposed in black dashed lines at each time. On the right panel we show

again the absolute error from the ground truth. Observe the similarities with the noiseless case: most of the error localizes in areas with low concentration.

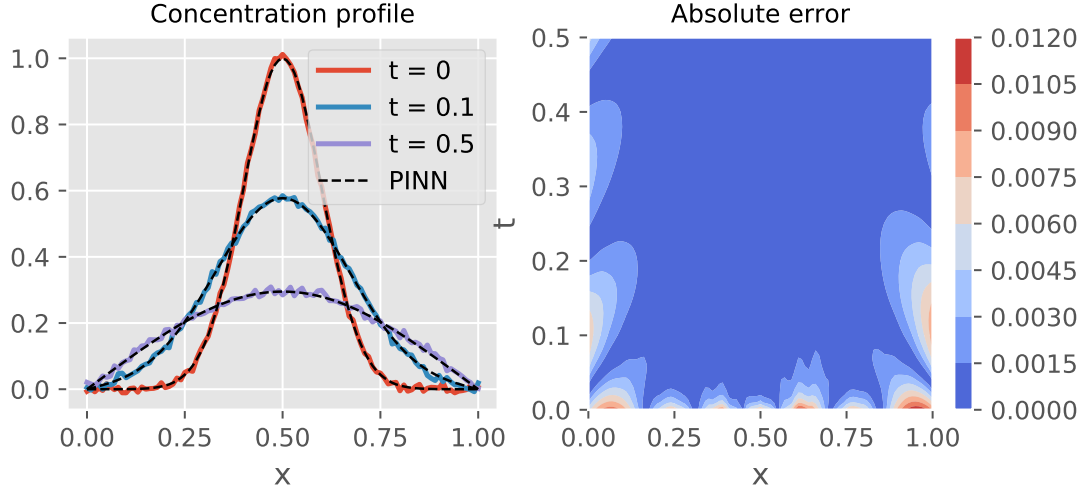


Figure 4.4: Left panel: The original noisy concentration profile with the neural network inferred denoised version super imposed. Right panel: The absolute error of neural network with respect to the ground truth. Note that most of the error is located at areas with low concentration.

The inferred diffusion constant is $D_o = 0.10052$, giving an error of 0.52% . Although the error is slightly higher than in the noiseless version, it's extremely impressive that we obtain the diffusion constant to this precision.

4.2.2.2 VARYING D

As stated, it should be possible to infer coefficient fields by using a two output neural network. One output predicts the concentration while the other predicts the diffusion coefficient. Such a network is indeed capable of generating the right coefficient field as shown in figure fig. 4.5 . Here the network has been trained on the constant diffusion coefficient data we used before including 5% white noise, so that we should observe a diffusion field constant at $D(x, t) = D_o = 0.1$. In the upper left we show the data on which the network is trained, with the upper right panel the predicted concentration profile, which shows a very good match. In the lower right panel we show the inferred diffusion field. We observe a good match in the middle of the plot, but the neural network again struggles in areas with low concentration, such as the lower left and right area. A more quantitative analysis of the predicted diffusion and concentration is presented in the lower left corner. Here we plot

the Cumulative Distribution Function (CDF) of the absolute relative error. Note that the PINN predicts the concentration very well, but struggles more with the diffusion coefficient. This is expected, as the mean squared error of the cost function is quite explicit in its use of the concentration, whereas the diffusion coefficient is determined self-consistently in the PI part. We also observed similar but distinctive results in different runs, owing to the non-convexity of the problem. Overall the result is still remarkable, given that we've inferred a diffusion field from just concentration data with 5% noise.

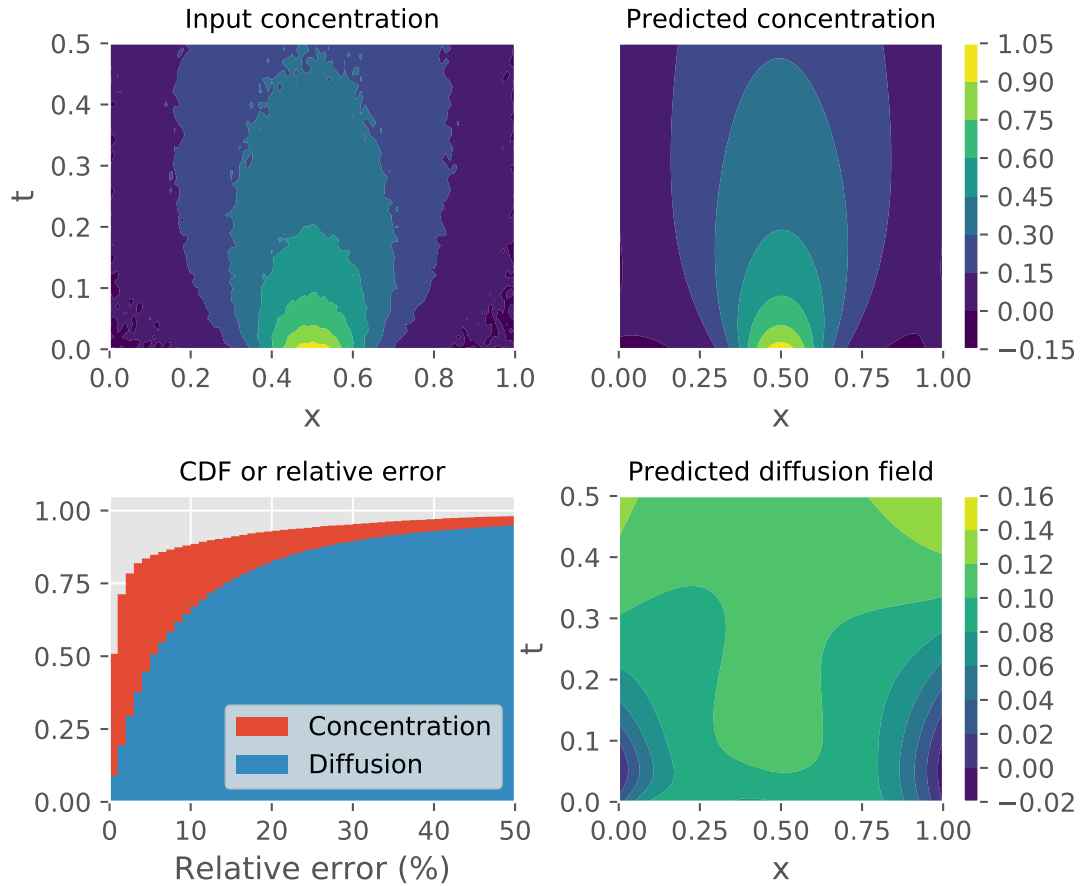
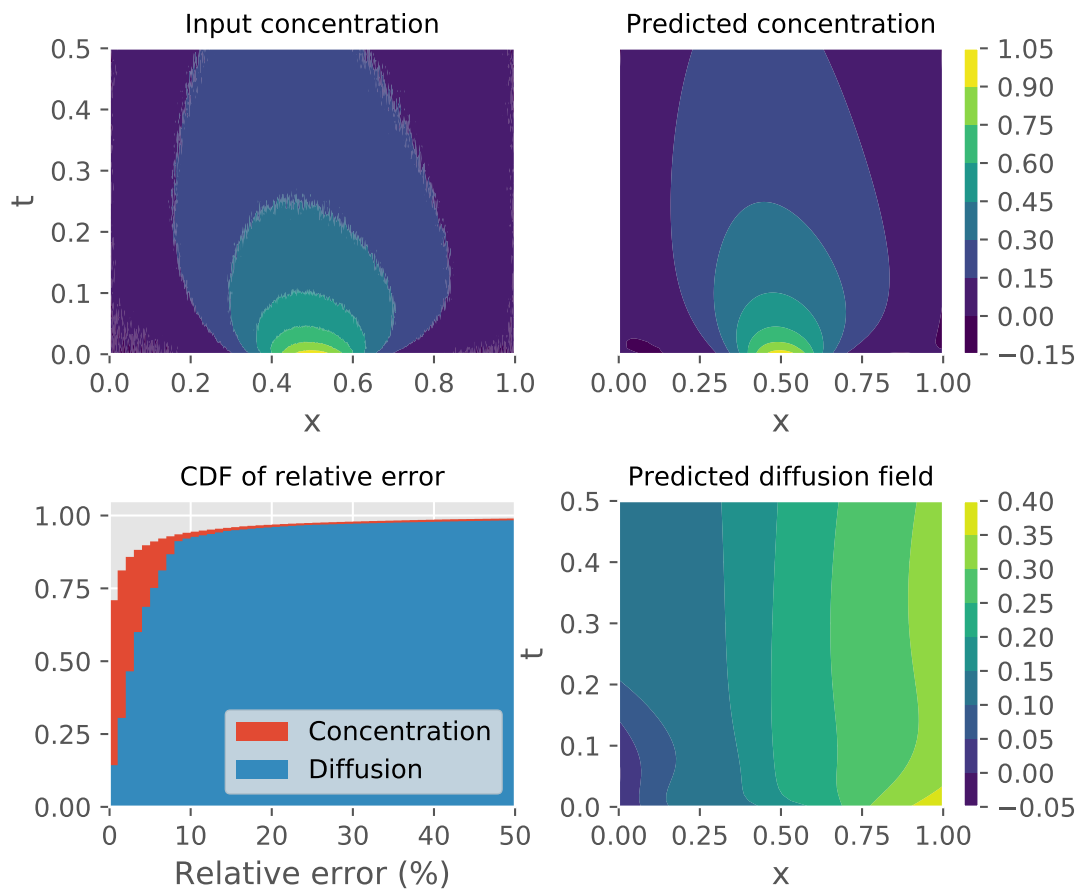
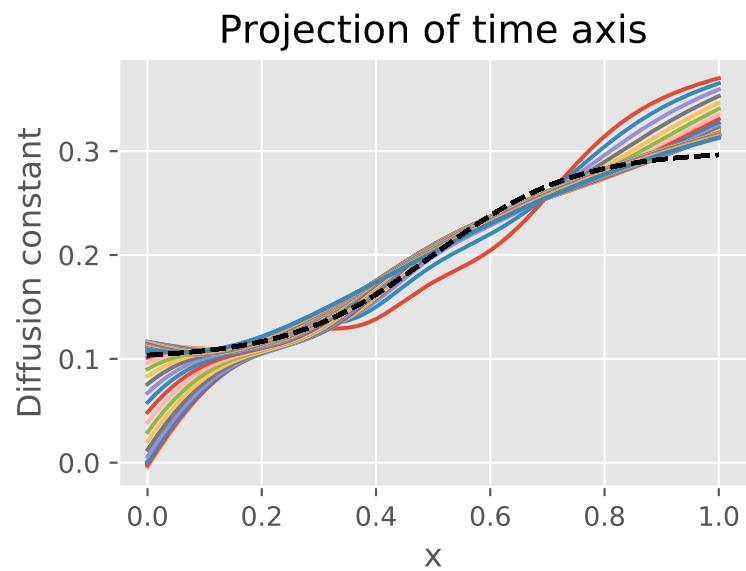


Figure 4.5: We show the training data and predicted concentration profile in the upper left and right panels. The lower right panel shows the inferred diffusion field while the lower left panel shows the CDF of the relative error of the diffusion and concentration.





4.2.2.3 REAL CELL

4.3 CONCLUSION

4.3.1 WEAK POINTS AND HOW TO IMPROVE

5

Introduction to Golgi as a phase separated droplet

In this second part of the thesis we develop a model linking the Golgi function and size to protein transport. Special attention will be devoted to adding spatial dependence, as this is what current models are lacking. IN the first section we justify our choice of a phase-separated droplet from a biological perspective. In the second section we present a short primer on phase-separation theory before presenting an approximation which makes the theory analytically tractable. We end with a section which sets up our model, which we solve and analyze in the next chapter.

5.1 PHASE SEPARATION

Consider a mixture of two molecules, type A and B. One is the solvent and one the solute. One can then try and use statistical mechanics to derive a mean-field model and get all sorts of cool results. This is quite complex and not particularly enlightening for us. Instead, we follow a method devised by Landau. We know that phase separation occurs when the free energy has two convex region, so we can construct a free energy density function f with two minima in a minimalist way as:

$$f(c) = \frac{b}{2(\Delta c)^2} (c - c_o^-)^2 (c - c_o^+)^2$$

where b characterizes interactions, $\Delta c = |c_o^- - c_o^+|$, and c_o^\pm is where the two minima of the function are located. Figure shows this free energy function. A free energy like this leads to phase separation into a dense and dilute phase. The interface has surface tension, so when we calculate the full free energy of the system we add a term for the interface:

$$F(c) = \int dV(f(c) + \frac{1}{2}\kappa \nabla^2 c)$$

We thus have constructed a Landau free energy with order parameter c . The first term accounts for the bulk energy, while the second term penalizes interfaces. Suitable choices of parameter lead either to a mixed state, where $\bar{c} = \text{constant}$ in the whole system, or to a phase separated state such as shown in figure. When we quench a system from a mixed state into a phase-separated state, this happens through a process called *coarsening dynamics*. Basically small domains form and these keep growing, showing a maze-like structure as in figure In liquid-liquid phase separation, the order parameter is conserved, as the molecules cant just change. The phases then exchange diffusion-like and can only exchange locally, so we state that:

$$\partial_t c = -\nabla \cdot \mathbf{j}$$

where \mathbf{j} is a flux. We know that \mathbf{j} is related to the chemical potential through:

$$\mathbf{j} = -\Lambda \nabla \mu$$

where Λ is an Onsager coefficient. We also know that $\mu = \delta F / \delta \phi$ so that we end up with

$$\frac{\partial \phi}{\partial t} = m \nabla^2 \frac{\delta F}{\delta \phi}$$

where $\delta / \delta \phi$ is a functional derivative. Given the landau free energy in eq , we obtain:

$$\frac{\partial \phi}{\partial t} = m \nabla^2 [f(\phi) - k \nabla^2 \phi]$$

which is known as the Cahn-Hilliard equation. The Cahn-hilliard equation is what governs the maze domain evolution shown in figure and is the basis for studies of phase separation. Due to its non-linearity its very hard to use, and many times a scaling relation is derived. However, since we want to include spatial inhomogeneity, this probably will not work. We present a different approach using effective droplets in the next section.

5.2 EFFECTIVE DROPLET

Consider phase separation in a one-dimensional box. The system will separate into a dilute and a dense phase, separated by an interface of width w :

$$c^*(x) = \frac{c_o^- + c_o^+}{2} + \frac{c_o^+ - c_o^-}{2} \tanh\left(\frac{x}{w}\right)$$

The idea of the effective droplet model is that if the width of the interface w is very small, we neglect the interfacial contribution and describe the system as two separate bulk phases. In each bulk phase we then solve a linearized version of the Cahn-Hilliard equation and match the solutions at the interface of the phases. Growth of the droplet can then be described in terms of fluxes across the interface. We show this in figure fig. ??.

We first linearize the Cahn-Hilliard equation in the bulk phases. Consider again the Cahn-Hilliard equation, where we've changed the order parameter ϕ to a concentration c :

$$\begin{aligned}\frac{\partial c}{\partial t} &= -m \nabla J \\ J &= -\nabla \mu\end{aligned}$$

$$\mu = f(c) - k \nabla^2 c \tag{5.1}$$

where $f(c) = \partial f / \partial c$. We're assuming an infinitely thin interface, so the interfacial term is negligible. Linearizing the chemical potential in c around the dense phase yields $\mu = f'(c_o^+)c$, so that eq. 5.1 becomes:

$$\frac{\partial c}{\partial t} = D \nabla^2 c \tag{5.2}$$

where we've replaced all the constant in front of the right term by D . We thus see that linearizing the Cahn-Hilliard equation in the bulk leads to a diffusion equation. The effective droplet theory is most accurate in predicting steady states and thus the time-dependence of eq. 5.2 is ignored. As we've replaced a single equation by two, we need an extra set of boundary conditions at the interface.

5.2.1 BOUNDARY CONDITIONS

To determine the droplet boundary conditions, consider a system which is phase separated and has an infinitely thin interface. The total free energy of the system is then:

$$F = V_1 f(\varphi_1) + V_2 f(\varphi_2)$$

where V_i and φ_i are respectively the volume and density of phase i and $f(\varphi_i)$ is the free energy density. In equilibrium, this free energy is minimized. Assuming incompressibility ($V_1 + V_2 = V$) and conservation of particles ($V_1 \varphi_1 + V_2 \varphi_2 = V\varphi$), we further constrain the system to two independent variables. Choosing to minimize the free energy with respect to φ_1 and V_1 gives us two conditions:

$$f'(\varphi_1) = f'(\varphi_2) = 0$$

$$0 = f(\varphi_1) + f(\varphi_2) + (\varphi_2 - \varphi_1)f'(\varphi_2)$$

Since $f'(\varphi) = \mu(\varphi)$, the first condition states that both phases must have the same chemical potential, while the second one refers to the matching of osmotic pressure. One obvious solution to these equations is a completely mixed state with $\varphi_1 = \varphi_2$. A non-trivial (phase-separated) solution exists as well, where φ_1 and φ_2 are the two minima of the free energy density function $f(\varphi)$. In our system, this corresponds to c_o^+ and c_o^- . Assuming that our droplet is locally in thermodynamic equilibrium, we can apply this solution as boundary conditions. Concretely,

$$c(R) = \begin{cases} c_o^-, & \text{Outside droplet} \\ c_o^+, & \text{Inside droplet} \end{cases}$$

Now that we have defined boundary conditions, equations such as eq. 5.2 can be solved. The solution will give us the concentration profile in each phase, but the droplet behaviour is determined by the fluxes across the interface. We show this in the next section.

5.2.2 FLUXES AND MOVEMENT OF INTERFACES

Given a concentration profile $c(x)$, the (diffusive) flux can be calculated by applying Ficks' law:

$$J(x) = -D \frac{\partial c}{\partial x}$$

Using this expression, we can calculate a flux on the inside of the interface J_{in} and on the outside of the interface J_{out} . Note that in and out respectively refer to inside and outside the droplet and not to the direction of the flux. Figure ????: eff_droplet shows a typical concentration profile of an active droplet. Observe that due to the activity of the droplet, the concentration profile inside the droplet is not flat but convex. Due to this convexity, the flux J_{in} will be pointed inwards, while the flux J_{out} will also be pointed inwards typically due to transport or production. Intuitively, J_{in} is the flux lost due to the decay or activity in the droplet, while J_{out} replaces the converted material inside with material from outside. A steady-state can be achieved once these two fluxes are equal. Note that while the system is at steady state, it is not in equilibrium, as the fluxes across the interface are not zero; the fluxes are balanced, rather than equilibrated. This is a typical characteristic of an active system.

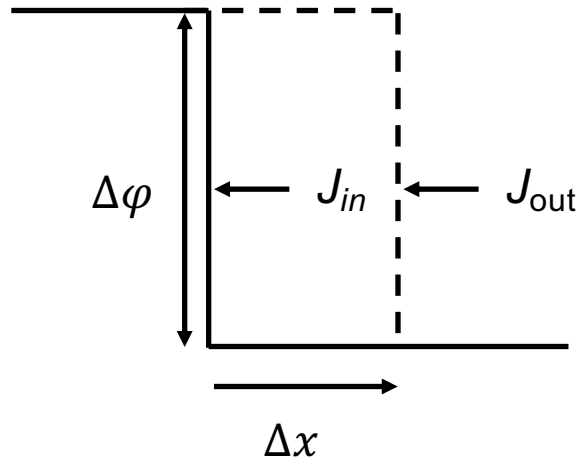


Figure 5.1: Figure illuminating the relation between a moving interface and the fluxes across it.

If the fluxes J_{in} and J_{out} are not balanced, a net flux exists, leading to either growth or decay of the droplet. We wish to derive an expression for interface speed v_n in terms of the fluxes across it. Consider figure fig. 5.1. If we wish to move the interface a distance Δx , we need a net material gain of $\Delta x \Delta c$. This net gain is supplied by a net flux in a time Δt , so that:

$$\Delta x \Delta c = (J_{in} - J_{out}) \Delta t$$

which can be rewritten as:

$$\frac{\Delta x}{\Delta t} = v_n = \frac{J_{in} - J_{out}}{\Delta c} \quad (5.3)$$

Thus if $|J_{in}| < |J_{out}|$, $v_n > 0$ and the interface will move to the right. If we consider a ‘free’ droplet (with two interfaces in 1D), the radius of the droplet is determined by both interfaces. Since the fluxes need not be similar on both sides of the droplet, not only the radius but also the position of interfaces plays a role. We thus characterize the droplet in terms of its radius R and its geometric center x_o . Consider a droplet of radius R at position x_o . The left and right interfaces move respectively with velocities v_l and v_r . In a time dt , the droplet then moves to a new position $x_o + dx$ and will have a new radius $R + dR$:

$$x_o - R + v_l dt = x_o + dx - (R + dR)$$

$$x_o + R + v_r dt = x_o + dx + (R + dR)$$

Solving this set of equations for dx and dR gives:

$$\frac{dR}{dt} = \frac{1}{2}(v_r - v_l) \quad (5.4)$$

$$\frac{dx_o}{dt} = \frac{1}{2}(v_l + v_r) \quad (5.5)$$

Equations eq. 5.4 and eq. 5.5 give the change in radius and position of the droplet. Note that these results are quasi-steady state: we’ve calculated the fluxes from stationary concentration profiles. Thus equations eq. 5.4 and eq. 5.5 are best used to calculate (quasi-) steady states and not dynamics. Nevertheless, equation eq. 5.5 shows an interesting feature: active droplets can move on their own. This movement is the result of an imbalance in fluxes between the left and right interface: the droplet center is displaced because one side of the droplet grows faster than the other. This imbalance is caused by a concentration gradient and droplets will move up the gradient, as the flux on the high concentration side will be higher than on the low side. Finally combining eq. eq. 5.3 with eqs. eq. 5.4 and eq. 5.5 yields the position and radius of the droplet in terms of the fluxes across its interface:

$$\frac{dR}{dt} = \frac{1}{2\Delta c} [(J_{in}^{x=R} - J_{in}^{x=-R}) + (J_{out}^{x=-R} - J_{out}^{x=R})]$$

$$\frac{dx_o}{dt} = \frac{1}{2\Delta c} [(J_{in}^{x=-R} + J_{in}^{x=R}) - (J_{out}^{x=-R} + J_{out}^{x=R})]$$

This completes the effective droplet model. It allows us to rewrite the non-linear Cahn-Hilliard equation into two or more separate linear problems with proper boundary conditions. Furthermore, these linear problems can be easily extended, such as by adding decay, sources or advection and we will do so in the next section. To solve a typical problem with the effective droplet theory, we thus perform the following steps:

- Identify the domains and correct equations.
- Solve equations inside each domain to obtain concentration profile.
- Calculate the fluxes across the interfaces.
- Obtain steady states at the balance of fluxes.

In the next section we present our model for the Golgi in the effective droplet model.

5.3 GOLGI AS AN ACTIVE DROPLET

- The Golgi is able to form de novo (Bevis)
- Microtubules position the golgi near the mtoc (Sengupta)
- Nocadazole depolymerizes microtubules -> golgi stacks move towards ERES (sengupta)
- Golgi size is dependent on amount of trafficking (Sengupta)
- Separate ministacks seems to be fully functional (Wei)
- Golgi disassembly is due to imbalanced trafficking: exit from ER is blocked, while outflow still continues (Ronchi)
- When golgi is completely cut out, stack like struct

In this section we introduce our model for Golgi biogenesis and maintenance. Biologically, our problem encompasses four different populations: the immature cargo, the mature cargo, the Golgi, with all dissolved in the cytoplasm. The immature cargo transforms into the Golgi material, which matures into mature cargo. Similar to ref, we model this however in a simple manner with just the immature cargo phase separating in a dilute and dense phase and the mature cargo implicitly.

As stated in the previous chapter, once the microtubules are depolymerized, the Golgi ribbon breaks into separate stacks which colocate with the ERES. If we model not the complete Golgi but a single stack, we can reduce our problem to 1D, where a droplet can move from one side of the system, representing the Golgi ribbon, to the other side, representing the ERES. This simplification permits analytical tractability. We thus end up with a 1D box where the dilute phase represents the cytoplasm, while the dense phase represents a single Golgi stack.

Proteins exiting the ERES are transported towards the ER over the microtubules. This is a stochastic process with the proteins detaching from and re-attaching to the microtubules randomly. ref shows that such a stochastic process can reduce to a Fokker-Planck equation if the attaching and detaching is much faster than the transport itself. As the Fokker-Planck equation is functionally equivalent to an advection-diffusion equation, we hypothesize that we can model protein transport using an advection-diffusion equation. Furthermore, ref reports that cargo can disappear without reaching the Golgi and we thus add a decay term to the advection-diffusion equation, resulting in the final equation for the evolution of dilute phase:

$$D\partial_x^2 c(x) - v\partial_x c(x) - ac(x) = 0 \quad (5.6)$$

We will neglect the term on the left as we're working in a quasi-static limit. The first term on the right is a diffusive, the second term advective with advection velocity v , while the last term represents the decay.

ref states that after stack-like structures are formed close to the ERES, they are transported to the ribbon by microtubules. Hence we use an advective term next to a diffusive term in the dense phase. As the dense phase represents the Golgi, we need a term to account for maturation of the proteins. Much discussion on this subject exists (see maternal vs. cis-ternal maturation), but we choose a simple decay-like term. This gives an expression very similar to the dilute phase (eq. 5.6), save for a different decay rate:

$$D\partial_x^2 c(x) - v\partial_x c(x) - kc(x) = 0 \quad (5.7)$$

Note that we assume a similar diffusion coefficient in the dense and dilute phase. Choosing different diffusion coefficients would result in slightly different length scales (see next section), but would not affect the main results. As stated, we also model the mature population implicitly, in this case having the effect that the cargo lost due to the decay term exits the system.

We now turn to the boundary values. As demanded by the effective droplet model, we set at the interface between the droplet and the dilute phase:

$$c(x_o \pm R) = \begin{cases} c_o^-, & \text{inside of interface} \\ c_o^+, & \text{outside of interface} \end{cases}$$

Our system is a 1D box of length L , with the left boundary representing the ERES, modeled as a source, and the right boundary a zero-flux boundary, so that all cargo exits the system either through decay in the dilute phase or maturation in the dense phase:

$$(-D\partial_x c + vc)|_{x=0} = J_{in}$$

$$(-D\partial_x c + vc)|_{x=L} = 0$$

We solve this set of equations in the next section.

6

Golgi model

In the previous chapter we introduced the Cahn-Hilliard equation. Its non-linearity makes it extremely hard to study and in this chapter we present an approximation known as effective droplet theory. In this chapter we introduce the effective droplet approximation, discuss our models for the Golgi apparatus and show the results for these models. We've divided the chapter into three sections:

- Effective droplet theory - In this section we introduce effective droplet theory.
- Golgi as an effective droplet- Here we introduce our model and show
- Two-component model- This third section contains a possible extension of the effective droplet model to two-components.

We end the chapter with a short summary of our conclusions.

6.0.1 SOLUTION

The general solution of equations eq. 5.6 and eq. 5.7 is given by:

$$c(x) = C_1 e^{-\frac{x}{l^\pm}} + C_2 e^{\frac{x}{l^\pm}}$$

where we have defined l^\pm as:

$$l^\pm = \frac{2D}{\sqrt{4kD + v^2} \pm v} \quad (6.1)$$

where k should be replaced by a outside the droplet. Note that l^\pm defines the lengthscale of the problem. Without advection it simplifies to $\sqrt{D/k}$ and both lengthscales becomes similar. It is here we see that the advection combined with decay leads to some sort of ‘symmetry-breaking’ in the droplet and that the effect of advection is more than just translating the droplet. We study this in the next section. Applying the boundary conditions and calculating the flux at position $x_o + R$ and $x_o - R$ gives the following fluxes outside:

$$J_{out}^{x=-R} = J_{in} \frac{(1 + \frac{l_-}{l_+}) e^{-\frac{(x_o - R)}{l_-}}}{Pe_- + Pe_+ \frac{l_-}{l_+} e^{-\frac{x_1}{l_+}}} + \frac{c_o^{out} D Pe_+ (1 - e^{-\frac{x_1}{l_+}})}{l_+ (1 + \frac{l_-}{l_+} \frac{Pe_+}{Pe_-} e^{-\frac{x_1}{l_+}})} \quad (6.2)$$

$$J_{out}^{x=R} = -c_o^{out} D \frac{Pe_- Pe_+ (1 - e^{-\frac{x_2 + L}{l_+}})}{l_+ Pe_- + e^{-\frac{x_2 + L}{l_+}} l_- Pe_+} \quad (6.3)$$

where we have introduced the coordinates x_1 and x_2 , which are defined respectively as $x_o \pm R$ and correspond to the left and right interface. We have also defined the Peclet-like numbers Pe^\pm :

$$Pe^\pm = 1 \mp \frac{vl^\pm}{D}$$

and a new combined lengthscale $l = \frac{l^+ l^-}{l^+ + l^-} = 1/l^+ + 1/l^-$. The flux on the left of the droplet consists of two terms, with the first one accounting for the influx and the second one for the interface with the droplet. The flux on the right is clearly similar, but lacks a second term since we’ve set a zero-flux boundary at $x = L$.

We now turn to the fluxes on the inside of the droplet. In this case however, the fluxes on the left and right side of the droplet are not of particular importance; considering equations eq. 5.4 and eq. 5.5, we’re interested in their sum and difference. Introducing $J_{rad} = J_{in}^{x=R} - J_{in}^{x=-R}$ and $J_{pos} = J_{in}^{x=R} + J_{in}^{x=-R}$, we obtain:

$$J_{rad} = \frac{-2c_o^+ D \sinh \frac{R}{l^-} \sinh \frac{R}{l^+}}{l} \frac{1}{\sinh \frac{R}{l}}$$

$$J_{pos} = 2c_o^{in} D \left[\frac{Pe_-}{l_-} \frac{\sinh \frac{R}{l_+} \cosh \frac{R}{l_-}}{\sinh \frac{R}{l}} - \frac{Pe_+}{l_+} \frac{\sinh \frac{R}{l_-} \cosh \frac{R}{l_+}}{\sinh \frac{R}{l}} \right]$$

The equation for the radius can also be interpreted as the maturation flux. It contains an important point with respect to the validity of effective droplet theory. Consider the limit of $R \rightarrow \infty$:

$$\lim_{R \rightarrow \infty} = -2c_o^+ \sqrt{kD} \quad (6.4)$$

where for simplicity we have set the advection speed v to zero. For an active droplet one would expect the maturation flux to scale with the radius. However, equation eq. 6.4 shows that the maturation flux saturates. The answer to this conundrum is found by studying the concentration profile in the droplet. For $R \gg l$, the concentration in the center of the drop goes to zero, which is unphysical and an artifact of the effective droplet model. Thus effective droplet theory is only valid in the region $R \ll l$. When advection is added back into the mix this point is slightly more nuanced, as advection changes the concentration profile. We show this in the next section.

The equation for the positional flux hints at the effects of the advection and maturation. In a droplet without decay, the concentration profile would be flat and the positional flux would be proportional to $c_o^+ v$. Equation tells a different story. We investigate this in depth in the next section.

6.0.2 NO DECAY IN THE DILUTE PHASE: THE EFFECT OF ADVECTION

We first study the effect of advection on the droplet by setting the decay in the dilute phase to zero. In this case the flux on the outside of the droplet becomes position-independent:

$$J_{in}^{x=-R} = J_{in}$$

$$J_{out}^{x=R} = 0$$

This is expected, as the cargo can only exit the system by decaying inside the droplet. The equations for the flux in the droplet remain unchanged because they are independent of the decay outside. Developing the internal droplet fluxes for $R \ll l^\pm$ gives:

$$J_{rad} \approx -2c_o^+ kR$$

$$J_{pos} \approx$$

Combining these equations gives us expressions for the growth rate and speed of the droplet:

$$\frac{dR}{dt} =$$

$$\frac{dx_o}{dt} =$$

Armed with these equations we can study the effect of advection. In figure .. we show the minimum concentration, dx_o/dt and dR/dt as a function of R and v .

In the left panel we show the minimum concentration as a function of R and v . The white line shows the concentration corresponding to $l = 0.5$ at $v = 0$ and we indeed see that advection increases the minimum concentration. In the middle panel we show the increase in radius dR/dt as a function of again R and v . Red colors mean positive, blue negative and white zero, so we've plotted with x's the line $dR/dt = 0$, which corresponds to a stable droplet. On the right we show dx_o/dt ; where the $dx_o/dt = 0$ line crosses with the $dR/dt = 0$ line there's a droplet with stable radius and position.

To show this more clearly, we plot the droplet radius and minimum concentration as a function of the advection velocity in figure . Observe that advection decreases the droplet radius by almost 10%, while simultaneously also increasing the minimum concentration. The advection is thus 'compacting' the droplet. By what process is this happening? To see this, consider an active droplet without advection. The concentration profile is symmetric and convex; the flux on both sides due to diffusion is inwards and thus in opposite directions. If we now turn on advection, this symmetry is broken. On the left side of the droplet, the diffusion and advection point in the same direction but on the other side they are aligned opposite. This causes an asymmetry in the concentration and a difference in the flux to the centre: more goes to it from the left than is taken away by the right, hence compacting the droplet.

Can advection stabilize a droplet? Zwicker et al show that an active droplet such as ours can divide through a shape instability. Our model is 1D however and not easily scalable to higher D's because of the advection. Simulations would be needed to state anything on this.

We can make a few conclusions about the situation. For a very specific set of parameters, the droplet can both be stable in radius and position. There's no position dependence so not that interesting. Also observe that there are only two situations: either the droplet is moving to the left infinitely, or moving to the right infinitely, as there's no stable position on either side. Which situation happens is controlled by the gradient of the concentration

versus the advection. note that we need a non-zero convection to move the droplet from one mode to the other. The explanation is simple: the convection needs to overcome the gradient to reverse droplet movement. At the inflection point, $dx_o/dt = 0$.

We now make some very speculative biological connection to the observation of Golgi properties. A strong marker is that once the microtubules are depolymerized, the stacks move away from the perinuclear area and colocate with the ERES. This is what we see when we turn off the advection, the droplet moves up the gradient to the source. A similar thing is seen with biogenesis, the stacks are made around the ERES but need microtubules to be transported to the center.

We have a model which described some features but its unstable. Can we make some position in our system inherently stable? We try in the next section by adding decay to the dilute phase.

6.0.3 DECAY IN THE DILUTE PHASE

We now wish to find a model in which the position has a stable position. So not just a set of parameters where $dx_o/dt = 0$, but a position x_o where the droplet is stable. The flux on the inside is independent of the position of the droplet, so to get a stable position we need a position dependent flux on the outside. To this end, we introduce a decay term in the dilute phase. We then end up with the full equations We first numerically solve these equations before attempting an approximation. The result is shown in figure ... and shows a ‘phase-diagram’ of our active droplet model. In the left panel we show the minimum concentration in the droplet, while the middle and right panel shows the numerical value of dx_o/dt and dR/dt , all as a function of the CoM position x_o and radius R . From the right two plots we’ve extracted the lines $dx_o/dt = 0$ and $dR/dt = 0$, which we’ve superimposed on all three panels. Where these lines cross a stable state exist. We first discuss each line independently and then discuss the stable points.

First consider the line $dR/dt = 0$, a droplet with stable radius. We observe that left of the line $dR/dt > 0$, with the opposite on the right. This means that each radius is stable: a perturbation w.r.t to the radius will not propagate. The $dx_o/dt = 0$ is more interesting. It has the appearance of a ‘finger’ and has a stable and unstable branch. The arm below the point is stable, where the arm above the point is not. This has important implications for the crossings: the lower intersection is stable w.r.t. to all perturbations, while the upper intersection is unstable. Perturbations above the dx_o/dt line will propagate, while perturbations below will move the droplet to the lower intersection.

This is all fine and dandy, but there’s one problem: the lower intersection, the stable point,

is unphysical. We characterize the droplet in terms of its center of mass x_o and radius R , meaning that the left interface is at a position $x_o - R$. The red line in the plots shows the line $x_o = R$ and everything below this line is unphysical, as it means the left interface is at a position $x_o - R < 0$, past the system edge. Why does this happen? First, in a dynamical description this wouldn't happen, as the left interface boundary condition prevents moving past. In a static description this can however since we specify the edge of the system as a flux boundary condition. Inspection of the concentration (see figure) learns that the droplet moves on top of the source: the flux inside the droplet at a point is similar to the boundary condition. In 2D this wouldn't be a problem but in our 1D description it is as the BC is specified as a flux and not as a source. That means we're left with just an unstable point. Why is this point unstable? Investigating the fluxes shows that despite the decay the left interface is an order of magnitude bigger than the right interface, thus behaviour is mainly determined by the left interface. Once the left interface starts moving due to a perturbation, the rest follows.

6.1 TWO-COMPONENT MODEL

Two components jeej

6.2 CONCLUSION

7

Conclusion

So what can we say about our project? We tried a lot but nothing worked ha-ha.

Appendix 1: Some extra stuff

Add appendix 1 here. Vivamus hendrerit rhoncus interdum. Sed ullamcorper et augue at porta. Suspendisse facilisis imperdiet urna, eu pellentesque purus suscipit in. Integer dignissim mattis ex aliquam blandit. Curabitur lobortis quam varius turpis ultrices egestas.

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