DOCUMENTATION FOR THE PYTHON LIBRARY INTCYT

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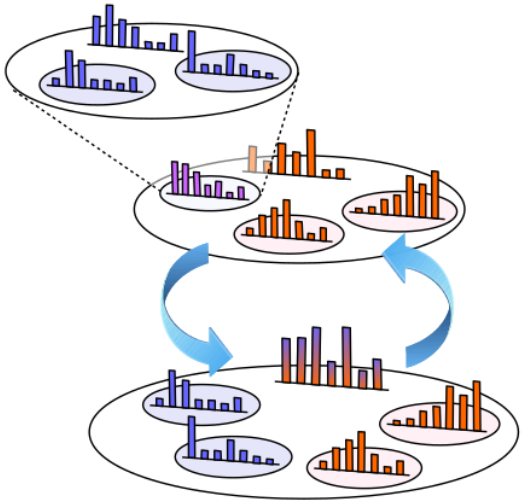


Typeset in LaTeX 2$_\varepsilon$.

Contents

Introduction

1.1. About IntCyt

IntCyt was the result of an interdisplinary collaboration [2, 3] between postdocs and students of Kellis lab (http://compbio.mit.edu/). In a few words, IntCyt is an artificial intelligence algorithm inspired from living cell dynamics, biological hierarchies and non-equilibrium principles. More technically, IntCyt is a plastic network-based unsupervised learning algorithm. The main characteristics of the IntCyt algorithm are

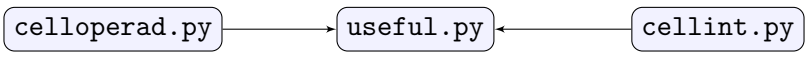
1) its ability to simultaneously learn and compartmentalize data through architectural reshaping of its network;
2) its high interpretability.

1.2. About this documentation

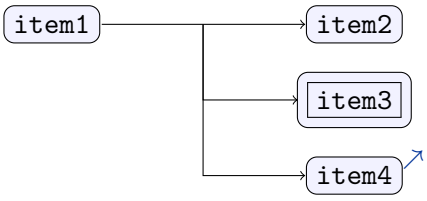
The present book contains a tutorial (see Chapter 2) explaining how to use the various methods and classes contained in `intcyt.py` as well as a description of the importable functions and importable classes of its sub-modules, which we list below:

- `useful.py` (see Chapter 3)
- `celloperad.py` (see Chapter 4)
- `cellint.py` (see Chapter 5)

The dependencies between the different chapters are shown in the following diagram.



We shall use similar diagrams to specify dependencies between functions and modules of the library too. Specifically, at the begining of a description of a class or an independent function, we give a brief description of the specifities of the item, followed by a dependency flow chart showing the different modules on which this item depend. Below, we give the example of such a flow chart.



As can be seen above, these flow charts will use three different types of boxes:

1) boxes with no specific decoration will usually frame items (such as classes and functions) that belong to the module described;
2) double boxes will frame the name of intermediate items that do not have dependencies with other items (final item);
3) boxes with clickable arrows in the top-right corner will frame items that are defined in external modules. The arrow should send the reader to that specific module;

We will also give examples and demonstrations within editor mode windows or console mode windows. The editor mode will be used to describe the code of functions and will look as follows.

file.py

```
1  class MyClass:
2    """
3    This is a comment
4    """
5    def __init__(self,arg0,arg1):  #This is the constructor of the class
6      """
7      Another comment about the code
8      """
```

The console mode will be used for examples and will look as follows.

```
>>> P.obj
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13]
```

1.3. Licensing and use of third party libraries

The library IntCyt is provided under the BSD license. Note that IntCyt is exclusively coded in python and uses third party libraries attached to the python package. Specifically, we use the libraries:

- `math` in the modules `celloperad.py` and `useful.py`;
- `random` in the module `celloperad.py`;
- `sys` in the modules `celloperad.py`, `useful.py`, and `cellint.py`;
- `time` in the module `useful.py`.

All the above are associated with the python package and are provided under the Open Source license. Similarly, the libraries used in tutorial of the present documentation (see section 2) are provided under either the Open Source license or the BSD license.

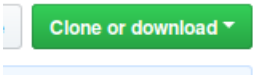
1.4. Acknowledgments

The following people have participated in one way or another to the project: Leandro Agudelo, Kevin Grove, Manolis Kellis, Anna Kondylis, Burak Kutlu, Anjanet Loon, Soumya P Ram.

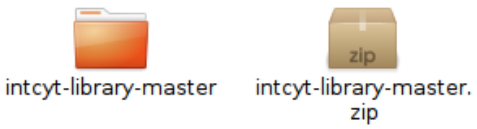
Tutorial

2.1. Installation and preparation

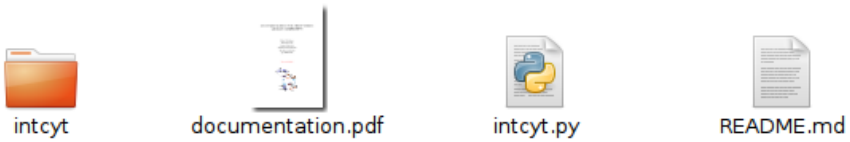
To install the library, go to https://github.com/remytuyeras/intcyt-library and download the library package by clicking on the green download button.



In your download directory, you should see a zip file named `intcyt-library-master.zip`. Copy this file in a new directory and extract its content with a zip extraction application. You should have the following display.



Now, enter the directory `intcyt-library-master`, in which you should see the following files.



The directory named `intcyt` contains the codes of the functions of the library and the python file `intcyt.py` contains the headings referring to the modules of the library. For the purpose of this tutorial, we will need three additional files:

- a python file `main.py` in which we will write an algorithm that learns a dataset of images;
- a python file `visualize.py` in which we will write a program that displays the progress of our learning algorithm;
- a python file `challenge.py` in which we will write a program that generates learning challenges for self-supervision tests;

To do this properly, create a new directory called `user` and copy the file `intcyt.py` in it.

Then, go to `user` and open the file `intcyt.py`: you should see several instances of the function `sys.path.insert` containing directory paths in their second arguments, as shown below.

intcyt.py

```
1 import sys
2 sys.path.insert(0, "intcyt/useful/")
3 from useful import *
```

Add the text `../` at the beginning of every path passed to the function `sys.path.insert`, as shown below.

intcyt.py

```
1 import sys
2 sys.path.insert(0, "../intcyt/useful/")
3 from useful import *
```

Once the paths are all updated, go back to the directory `user` and create three files named `main.py`, `visualize.py`, and `challenge.py` as well as two directory `data` and `result-load`, as shown below.

We are now ready to use the library – open the three files `main.py`, `visualize.py`and `challenge.py` and proceed to section 2.2.

2.2. Third party libraries and overall organization

In this tutorial, we will use third party libraries to open and read third party machine learning datasets. We will use

- `gzip` to read GZ files;
- `numpy` to read the MNIST dataset and the fashion-MNIST dataset;
- `scipy.io` to read the SVHN dataset;
- `matplotlib.pyplot` to display the progress of the algorithm (saved in GZ files).

In this respect, we add the following lines of code to the two files `main.py` and `challenge.py`.

main.py / challenge.py

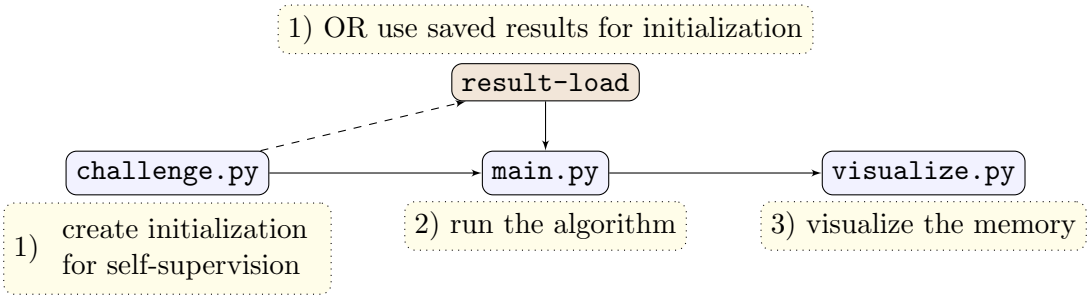
```
1 from intcyt import *
2 #------------------
3 #Libraries to open datasets
4 #------------------
5 import gzip
6 import numpy as np
7 import scipy.io as sio
```

In `visualize.py`, we will need the library `gzip` and `matplotlib` to open files and display their contents. We do so by adding the following lines of code to `visualize.py`.

visualize.py

```
1  from intcyt import *
2  import gzip
3  import matplotlib.pyplot as plt
```

The organization of this tutorial goes a sfollows: we will first focus on writing the code for `main.py` in section 2.3 and section 2.5; we will then write the code for `visualize.py` in section 2.6 and we will finish with the code of `challenge.py` in section 2.7. The following diagram shows the normal chronological use of these scripts.



The main goal of the tutorial is to use the IntCyt library to design the machine learning algorithm presented in [1]. As will be seen, this algorithm can memorize, abstract, organize and infer the data of reference machine learning datasets such as `MNIST`, `fashion-MNIST` and `SVHN`.

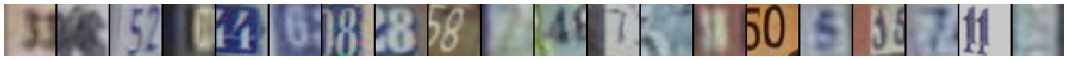
2.3. Loading datasets

In this section, we focus on the piece of code of `main.py` that allows us to load datasets into the memory. For convenience, we shall integrate the names of these datasets as options in the launch command of the script `main.py`. For example, the following launch command will instruct the script `main.py` to read and learn the data stored in the dataset `fashion-MNIST`.

```
> python main.py fashion-MNIST
```

We now present the datasets `MNIST`, `fashion-MNIST` and `SVHN` and explain how these can be downloaded and loaded in the memory.

The most challenging dataset that we will test in this tutorial is `SVHN`, which can be found at the address http://ufldl.stanford.edu/housenumbers/. This dataset contains RGB images of street numbers as shown below.



First, download the file `train_32x32.mat` linked therein. Then, copy the downloaded file `train_32x32.mat` into the directory `data` and add the following piece of code to `main.py`.

main.py

```
8  #-------------------------------------------------------------------------
9  #Loading the dataset for learning
10 #-------------------------------------------------------------------------
11 #Open the SVHN dataset
12 if len(sys.argv) > 1 and sys.argv[1] == "SVHN":
13   dic_svhn = sio.loadmat("data/train_32x32.mat")
14   #Access to the dictionary
15   dicim = dic_svhn["X"] #shape:  32, 32, 3, 73257
16   dictr = dic_svhn["y"] #shape:  73257, 1
17   image_size = [32,32,3] #height, width, depth
```

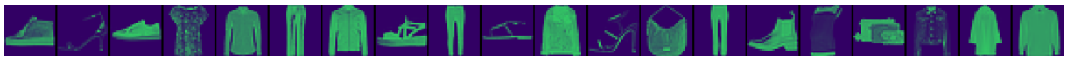
The easiest datasets that we will test in this tutorial is `MNIST`, which can be found at the address http://yann.lecun.com/exdb/mnist/. This dataset contains black and white images of hand-written numbers as shown below.

Download the files `train-images-idx3ubyte.gz` and `train-labels-idx1-ubyte.gz` linked therein, then copy these files into these directory `data` and add the following piece of code to `main.py`.

main.py

```
18  #------------------
19  #Open the MNIST dataset
20  elif len(sys.argv) > 1 and sys.argv[1] == "MNIST":
21    fim = gzip.open("data/train-images-idx3-ubyte.gz","r")
22    ftr = gzip.open("data/train-labels-idx1-ubyte.gz","r")
23    ftr.read(8)
24    fim.read(16)
25    image_size = [28,28,1] #height, width, depth
```

An intermediate-level dataset for our algorithm is the dataset `fashion-MNIST`, which can be found at the address https://github.com/zalandoresearch/fashion-mnist. This dataset contains black and white images of fashion clothes as shown below.

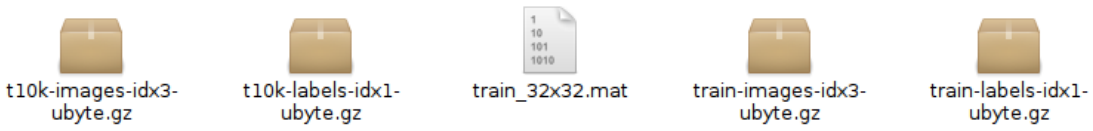


Download the files `t10k-images-idx3-ubyte.gz` and `t10k-labels-idx1-ubyte.gz` linked therein, then copy these files into the directory `data` and add the following piece of code to `main.py`.

main.py

```
26  #------------------
27  #Open the fashion-MNIST dataset
28  elif len(sys.argv) > 1 and sys.argv[1] == "fashion-MNIST":
29    fim = gzip.open("data/t10k-images-idx3-ubyte.gz","r")
30    ftr = gzip.open("data/t10k-labels-idx1-ubyte.gz","r")
31    ftr.read(8)
32    fim.read(16)
33    image_size = [28,28,1] #height, width, depth
34    categories = ["t-shirt","trousers","pullover", \
35                  "dress","jacket","sandal","shirt", \
36                  "sneaker","bag","ankle-boot"]
37  else:
38    exit(0)
```

Once all the previous operations have been completed, the directory `data` should look as follows:



Let us now move on to section 2.4, which introduces the reader to the main tools of the library IntCyt. Even though we will take care of explaining the role of the various functions that we shall use in the code of this tutorial, we will often refer to the corresponding description of this documentation for more details.

2.4. Operads, Cells and Super Cells

This section demonstrates the use of the classes `Cell` (section 4.1) and `SuperCell` (section 4.2) and `Operad` (section 4.3), which belong to the module `celloperad.py` (section 4).

Here, our goal is to construct a database on which our algorithm can operate and store information. Since we are following the construction of [1], we want this database to be a *super cell* [1, Def. 2.1]. In fact, this super cell will start as an even simpler structure called a *cell* [1, Def. 1.2]. Overtime, we will see that the cell develops into a hierarchical structure defining a proper super cell.

Mathematically, the evolution of a cell into a proper super cell happens within an operadic environment. As a result, we will start by calling an operad item. To do so, we call the constructor of the class `Operad` (section 4), which takes the dimensions of the data as an input (*i.e.* the dimensions of the images contained in the datasets). For any of our datasets, the dimensions of each data is given by a multiplication of the components of the list `image_size`. In this respect, we append the following lines of code to `main.py`.

main.py

```
39 #-----------------------------------------------------------------------
40 #Initializing the super cell
41 #-----------------------------------------------------------------------
42 #Main parameters defining the initial super cell
43 #------------------
44 dim = image_size[0] * image_size[1] * image_size[2]
45 operad = Operad(dim)
```

Viewed from a mathematical standpoint, the item `operad` is supposed to be a map sending any tuple of the form $((x_1, x_2, \dots, x_{\texttt{ary}}), y)$, where x_i and y are lists of length `dim` containing `float` values, to a set of `SuperCell` items, as illustrated below.

$$\mathcal{O}^{\texttt{dim}}_{\texttt{ary}} : \begin{pmatrix} (\texttt{float}^{\texttt{dim}})^{\texttt{ary}} & \times & \texttt{float}^{\texttt{dim}} & \to & \texttt{Set}(\texttt{SuperCell}) \\ (x_1, \dots, x_{\texttt{ary}}) & , & y & \mapsto & \mathcal{O}^{\texttt{dim}}_{\texttt{ary}}(x_1, \dots, x_{\texttt{ary}}; y) \end{pmatrix}$$

Because such an encoding is absolutely not practical – at least computationally, an `Operad` item is instead designed to only recover the algebraic properties of this mapping.

With the previous picture in mind, the super cell on which we want our algorithm to rely is, by definition, an element of a set

$$\mathcal{O}^{\texttt{dim}}_{\texttt{ary}}(x_1, \dots, x_{\texttt{ary}}; y).$$

Because the parameters `ary` and $x_1, \dots, x_{\texttt{ary}}$ are variables for the same operad $\mathcal{O}^{\texttt{dim}}$, we specify these parameters when initializing the super cell (as opposed to giving them to the operad item). In our case, we will consider a super cell whose parameter `ary`, representing its number of "organelles" [1, Def. 2.7], is equal to 20. For more clarity and flexibility, we will use a variable `ary` containing that number, as shown below.

main.py

```
46 ary = 20
```

Now, regarding the initialization of the parameters $x_1, \dots, x_{\texttt{ary}}$, we give two options: either we reload previously constructed super cells, saved in the directory `result-load`, or we create a new super cell, which will give rise to a new save file.

To control which of the previous scenarios should be considered, we add a second option to our launch command. Specifically, the system variable `sys.argv[2]` will be assumed to be either empty or contain the string `"-load"`. For example, we will use the following launch command to call our program on the dataset `fashion-MNIST` relative to the parametrization of the super cell saved in the directory `result-load`.

```
> python main.py fashion-MNIST -load
```

More specifically, the option `-load` will instruct the script `main.py` to initialize the organelles $x_1, \dots, x_{\texttt{ary}}$ with the vectors specified in a file named `load_initial.gz` located in the directory `result-load`. On the other hand, if `sys.argv[2]` is not allocated, then the parameters $x_1, \dots, x_{\texttt{ary}}$ are randomly initialized.

We take care of the option `-load` as follows. First, we open the file `load_initial.gz` in `result-load` by using the module `gzip`. Then, we use the function `usf.get_memory` (see section 3.1.10) to load the first `ary` vectors stored in the file `load_initial.gz`. These vectors play the role of our organelles $x_1, \dots, x_{\texttt{ary}}$ and are the required data to construct a `Cell` item (see section 4.1). The resulting `Cell` item is then made into a `SuperCell` item (see section 4.2), which will constitute the database of our learning algorithm.

main.py

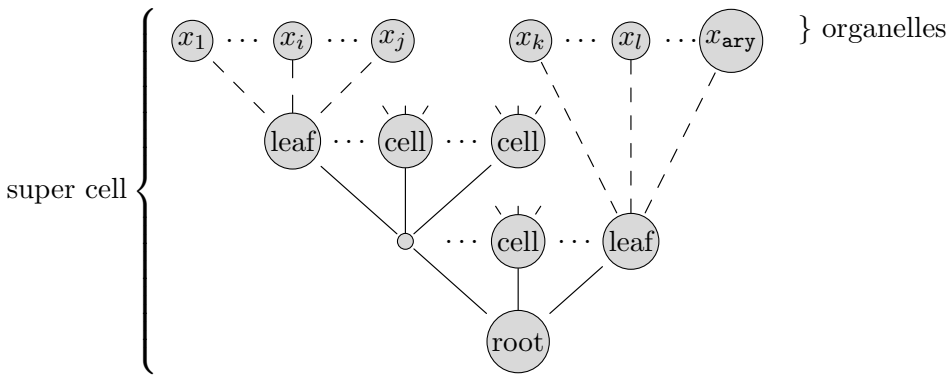
```
47 #------------------
48 #Initializing the organelles and the cytosolic content (either new ones
   or saved ones)
49 #------------------
50 if len(sys.argv) > 2 and sys.argv[2][:5] == "-load":
51   #Load a previously generated tree (height 0)
52   fload = gzip.open("result-load/load_initial.gz","r")
53   initial_organelles = usf.get_memory(fload,ary,[0])
54   fload.close()
55   c = Cell(dim,0,[0]*dim,initial_organelles[0])
56   sc = SuperCell(c)
```

On the other hand, if the system variable `sys.argv[2]` is not allocated or does not contain the string `"-load"`, then we use the function `operad.generate` (see section 4.3.5) to generate a `SuperCell` item of height 0 whose organelles are randomly initialized.

main.py

```
57 else:
58   #Generate a random tree of height 0
59   sc = operad.generate(levels = 0, arity = ary, key = lambda:
   random.randint(0,30))
```

It is now a good time to recall a few fact about the overall structure of a super cell. As explained in [1, Supp. text], a super cell is a tree structure whose leaves and junctions are each associated with a `Cell` item. As a result, we adapt the terminology of trees to super cells. In this respect, a super cell possesses: a *root cell*, a flexible number of *leaf cells*, and a flexible number of *junction cells*, which are each made of a *parent cell* and a collection of *child cells* (see [1, Conv. 2.2]). According to [1, Def. 2.7], the collection of organelles $x_1, x_2, \dots, x_{\texttt{ary}}$ of a super cell is defined as the concatenation of the collections of organelles associated with the leaf cells.



While the organelles of the leaf cells determine the collection of parameters $x_1, x_2, \ldots, x_{\texttt{ary}}$, the root cell determines the parameter y through its 'content' (see [1, Def. 1.21]). In order to record the evolution of a super cell, we will have three types of save files:

- "save_roo.gz" will contain the vectors describing the evolution of the parameter y;
- "save_org.gz" will contain the vectors describing the evolution of the organelles;
- "save_tre.gz" will contain the vectors describing the evolution of the tree structure.

Note that the file "save_tre.gz" will mostly be used for visualizations, while the other files can be considered collections of re-usable information.

In the piece of code given below, we use the three print functions `usf.print_root`, `usf.print_organelles`, and `usf.print_tree` to print the parameters defining the root, the organelles and the tree structure of the super cell in their corresponding files, respectively.

main.py

```
60 #------------------
61 #The initial sate of the super cell is saved in the memory
62 #------------------
63 fsave_roo = gzip.open("save_roo.gz","w")
64 fsave_org = gzip.open("save_org.gz","w")
65 fsave_tre = gzip.open("save_tre.gz","w")
66 usf.print_root(sc,image_size,fsave_roo,option="save")
67 usf.print_organelles(sc,image_size,fsave_org,option="save")
68 usf.print_tree(sc,image_size,fsave_tre,option="save")
69 fsave_roo.flush()
70 fsave_org.flush()
71 fsave_tre.flush()
```

2.5. Learning datasets with IntCyt

In this section, we use the IntCyt algorithm (see [1, Sec. 2]) to memorize, abstract and organize data originating from the datasets presented in section 2.3. For simplicity, our algorithm will run on a loop of 10,000 iterations. At each of these iterations, we shall read a new image in the dataset.

We read the dataset through two variables: `label` and `inputs`. At every iteration, the variable `inputs` contains a list of `float` values representing an image and the variable `label` indicates the type of image contained by `inputs`. We start with the dataset `SVHN` as follows.

main.py

```
72 #-----------------------------------------------------------------------
73 #Running the Learning algorithm
74 #-----------------------------------------------------------------------
75 for i in range(10000):
76   #------------------
77   #Get labels and inputs
78   #------------------
79   if sys.argv[1] == "SVHN":
80     label = dictr[i]
81     inputs = dicim[:,:,:,i].reshape(dim)
```

Above, the variable `label` is a `numpy.ndarray` item containing an integer and the variable `inputs` is a `numpy.ndarray` containing exactly `dim` `float` values.

In the case of `MNIST`, we read an image and its label as shown below. Again, the variables `label` and `inputs` are `numpy.ndarray` items containing numerical values.

main.py

```
82    #------------------
83    if sys.argv[1] == "MNIST":
84      buf_lab = ftr.read(1)
85      buf_inp = fim.read(dim)
86      label = np.frombuffer(buf_lab, dtype=np.uint8).astype(np.int64)
87      inputs = np.frombuffer(buf_inp, dtype=np.uint8).astype(np.float32)
```

Finally, the following panel shows how we read the dataset `fashion-MNIST`, which is very similar to the dataset `MNIST`, except that the labels here refer to the indices of the strings contained in the list `categories` defined in section 2.3.

main.py

```
88    #------------------
89    if sys.argv[1] == "fashion-MNIST":
90      buf_lab = ftr.read(1)
91      buf_inp = fim.read(dim)
92      label = map(lambda x:  categories[x], np.frombuffer(buf_lab,
    dtype=np.uint8).astype(np.int64))
93      inputs = np.frombuffer(buf_inp, dtype=np.uint8).astype(np.float32)
```

The next piece of code is introduced for optimization purposes. Specifically, because we would like to avoid overfitting the datasets, we want our algorithm to be somewhat "lazy". We do so by slowing down its learning speed, which can be done by giving it input data whose values are relatively small. In our case, we will make sure that all the input data are normalized so that their maximum values is equal to `0.0001`.

main.py

```
94    #------------------
95    #Normalization of the input vector
96    #------------------
97    inputs = 0.0001*inputs/max(inputs)
98    vector = inputs.tolist()
```

For debugging purposes, we use the function `debug_time.set` (section 3.2) to display the iteration of the loop and the type of the analyzed data in the standard output.

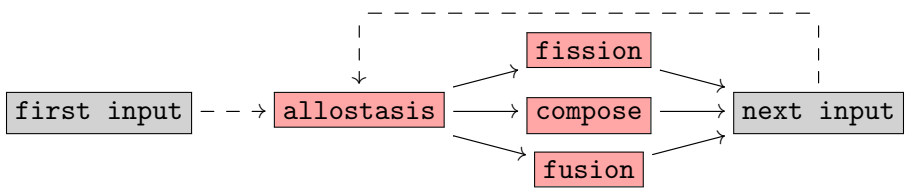
main.py

```
99    #------------------
100   #The algorithm
101   #------------------
102   debug_time.set("Learning data labeled as " + ",
    ".join(map(str,label)))
```

We can now proceed to the main part of our code, in which we use of the method `intcyt` (section 5.1). Before calling this function, we will need to fix a few parameters, which we are going to discuss in the following paragraphs.

The parameters that we are about to set up will help us control the various intermediate steps that constitute our algorithm. Let us recall from the introduction of [1, Sec. 2] that our algorithm is made of four main steps, shown in red, in the following diagram.

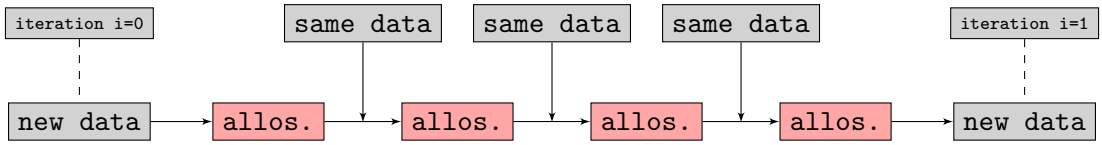
(2.1)



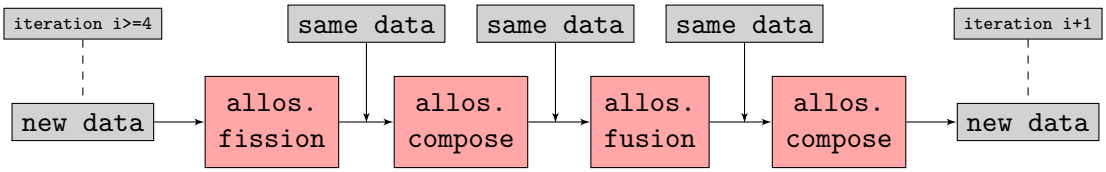
Every input given to the algorithm goes through the step `allostasis` (see diagram above), but depending on the iteration at which the algorithm is, the algorithm can proceed to either the step `fusion`, the step `fission` or the step `compose`. After one of these steps, the algorithm switches to the next input and the algorithm restarts the same process from `allostasis`. Here, it is important to note that the step `next input` does not necessarily refer to the data coming next in the dataset. Indeed, there are instances of our algorithm in which the next input is actually equal to the same data. The number of iterations done on the same data will be determined by an `epoch` number. This number determines how many times our algorithm needs to go through the cycle shown in (2.1), with the same input data, before being able to switch to the next data in the dataset. The interested reader can find more details about the reasons why the algorithm is decomposed as shown in (2.1) in [1, Sec. 2].

For this tutorial, we will focus on a version of `IntCyt` in which:

- the `epoch` number is equal to 4, which means that there are four epoch iterations before proceeding to the next loop iteration;
- during the first 4 loop iterations (*i.e.* 16 epoch iterations): we go through the step `allostatis` with no extra step `fission`, `fusion`, or `compose`, as shown below;



- after the first iteration: the step `fission` occurs at the first epoch iteration;
- after the first iteration: the step `fusion` occurs at the third epoch iteration;
- after the first iteration: the step `compose` occurs at the second and fourth epoch iteration;



In the piece of code given below, the variable `start` specifies the loop iteration at which the steps `fission`, `fusion`, and `compose` will start being used by our algorithm. The variable `epoch` contains the epoch number. The variables `fission_events`, `fussion_events` an `compose_events` contain the epoch iterations at which the events `fission`, `fusion`, and `compose` occur within an epoch period (made of 4 epoch iterations). Finally, `events` is the list of all these parameters and will be given to the function `intcyt` as an argument.

main.py

```
103  #------------------
104  start = 4
105  epoch = 4
106  fission_events = [0]
107  fusion_events = [2]
108  compose_events = [1,3]
109  events = [start,epoch,fission_events,fusion_events,compose_events]
```

We also create a `list` item `filtering` that plays the role of the various parameters ν used in [1, Def. 2.30]. This parameter allows us to control fusion events and fission events occurring in the super cell by limiting these events to particular groups of cells. Giving high values to `filtering` (*e.g* values greater than `1`) will prevent cells that are too different from

merging and will prevent cells that are similar enough from dividing. In our case, we chose the following parameterization.

main.py

```
110   #------------------
111   filtering = [1.5, #To control fission
112                1.5] #To control fusion
```

We can now start the epoch loop. We do so by adding the following lines of code to `main.py`. At the beginning of every epoch iteration, we display on the standard output the state of the super cell `sc` through the method `.stdout`. This method displays an ASCII tree that informs us about the evolution of the architecture of super cell.

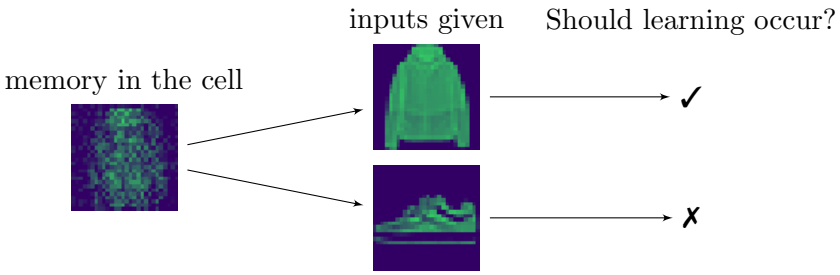
main.py

```
113   #------------------
114   for k in range(epoch):
115     debug_time.set("TREE")
116     sc.stdout(vector)
```

Now, before calling `intcyt`, we are going to set up a collection of parameters that will control the learning rate of our algorithm. These parameters depend on the type of data contained in our dataset. From the point of view of [1], these parameters help us define what is called the "gamma parameter", defined in [1, Sec. 2.3]. Recall that the formula for the gamma parameter is of the following form:

$$\gamma(c,a,j,u) = \begin{cases} 0 & \text{if "learning should not occur} \\ & \text{according to specific criteria";} \\ \text{see [1, Sec. 2.3]} & \text{otherwise.} \end{cases} \tag{2.2}$$

The collection of parameters that we are about to define allow us to give a meaning to the sentence "learning should not occur according to specific criteria". The idea is to take advantage of the interpretability of the data memorized by the cells of the super cell to determine whether these cells have learned any information from the data. If information has been learned, then we only want to update the content of the corresponding cells if the input is similar to their content and has a chance to make the memorized information more robust.



Because our data represent images, we employ a relatively simple approach, which measures the amount of contrast in the data. A strong contrast is likely to be linked to an abstraction of a concept rather than random data (as will be seen below).

To measure contrast in our data, we define three variables: `brightness`, `profiles` and `scores`. The variable `brightness` defines a series of brightness levels: the higher, the brighter. In our case, we will consider 5 levels of brightness, each expressed in percent with respect to the maximum value contained in the data: 10%, 25%, 50%, 75% and 90%. For instance, a random input tends to approximately have

- ▷ 90% of its pixels above 10% of the value of its brightest pixel;
- ▷ 25% of its pixels above 75% of the value of its brightest pixel;

- ▷ 50% of its pixels above 50% of the value of its brightest pixel;
- ▷ 75% of its pixels above 25% of the value of its brightest pixel;
- ▷ 10% of its pixels above 90% of the value of its brightest pixel.

In other words, for a random image, the rule of thumb is that $(100 - x)\%$ of the pixels is greater than or equal to $x\%$ of the value of its brightest pixel. For non-random images, the former percentage tend to be decreased. For instance, in the case of `MNIST`, we were able to notice that each data satisfied the following profile (on average):

- ▷ under 17.5% of its pixels were above 10% of the value of its brightest pixel;
- ▷ under 15.6% of its pixels were above 75% of the value of its brightest pixel;
- ▷ under 13.3% of its pixels were above 50% of the value of its brightest pixel;
- ▷ under 10.6% of its pixels were above 25% of the value of its brightest pixel;
- ▷ under 8.8% of its pixels were above 90% of the value of its brightest pixel.

In our implementation, we will define various contrast profiles corresponding to various learning stages (*e.g.* student and expert). These stages will be specified in terms of pairs of lower bounds and upper bounds and will be stored in the list `profiles`. For instance, a relation `profiles[i] = (0,.175)` means that the percentage of pixels above `brightness[i]` percent of the brightest pixel value should be between 0% and 17.5%.

In order to know whether it is reasonable to update the memory of a cell while it is learning, we use agreement levels. Here, we define the agreement of two vectors, say v and w, as the cosine of their angular distance. Alternatively, the agreement of v and w can be computed as the normalized scalar product of v and w, as shown below.

$$\mathsf{argeement}(v, w) = v \cdot w = \frac{\sum v_i w_i}{\|v\|\|w\|} = \mathsf{cos}(\theta)$$

Because, in our case, the components of v and w are non-negative, the agreement of v and w is a value between 0 and 1. Intuitively, this quantity can be seen as measuring a correlation between the two vectors v and w.

Now, we only want to update an organelle of a cell if the agreement level of the organelle with the input is high enough for a given contrast profile.

$$\texttt{contrast(organelle)} \checkmark \quad \longrightarrow \quad \mathsf{argeement}(\texttt{organelle}, \texttt{input}) \text{ good enough?}$$

To control the quality of agreements between organelles and inputs, we use the list `scores`. Specifically, this list will contain lower bounds above which an agreement level should be in order for the update of the organelle to be authorized. Technically, this means that an organelle will be modified through a gradient descent method if the following property is satisfied:

(P) : there exists an index `i` for which

1) the organelle satisfies the contrast profile `profiles[i]`;

2) the agreement of the organelle with the input is greater than or equal to `scores[i]`.

To conclude our discussion, the sentence "learning should not occur according to specific criteria" corresponds to the logical negation of the property (P).

If we look at the formula of the gamma parameter given in [1, Sec. 2.3], we still need to define two more values E and F, which appear in the case where (P) is true, as shown below.

$$\gamma(c, a, j, u) = \begin{cases} 0 & \text{if } \mathsf{not}(P) \\ \text{(a formula depending on } E \text{ and } F) & \text{otherwise.} \end{cases}$$

While the value E allows to increase the speed of the learning process, the value F allows us to slow down the learning rate of the organelles that possess a relatively low agreement with the input. Note that, in our case, these values where determined heuristically.

Enough explanation and let us now proceed to the code! We start with dataset `SVHN`, for which our method does not work as well as with the datasets `MNIST` and `fashion-MNIST`, mainly because of the variability of RGB codes. A possible correction for the `SVHN` data would be to adapt our contrast profile method to these RGB codes.

main.py

```
117     #------------------
118     #brightness:  intensity levels (length m)
119     #profiles:  intervals for intensity counts (length n*m)
120     #scores:  agreement scores for a given profile (length n)
121     if sys.argv[1] == "SVHN":
122       #------------------
123       brightness = [.1,.25,.5,.75,.9]
124       profiles = [[(0,.6),(0,.375),(0,.15),(0,.05),(0,.005)]] #expert
125       scores = [.82] #expert
126       E = 14.5
127       F = 25
```

Contrary to `SVHN`, the images stored in the `MNIST` dataset are bicolor. This makes the learning process of an image much more apprehensible for our contrast profiles. As a result, we were able to distinguish two learning stages in the evolution of the cells of IntCyt: a student phase and an expert phase. In the following lines of code, we can see that the expert profile has relatively low upper bounds.

main.py

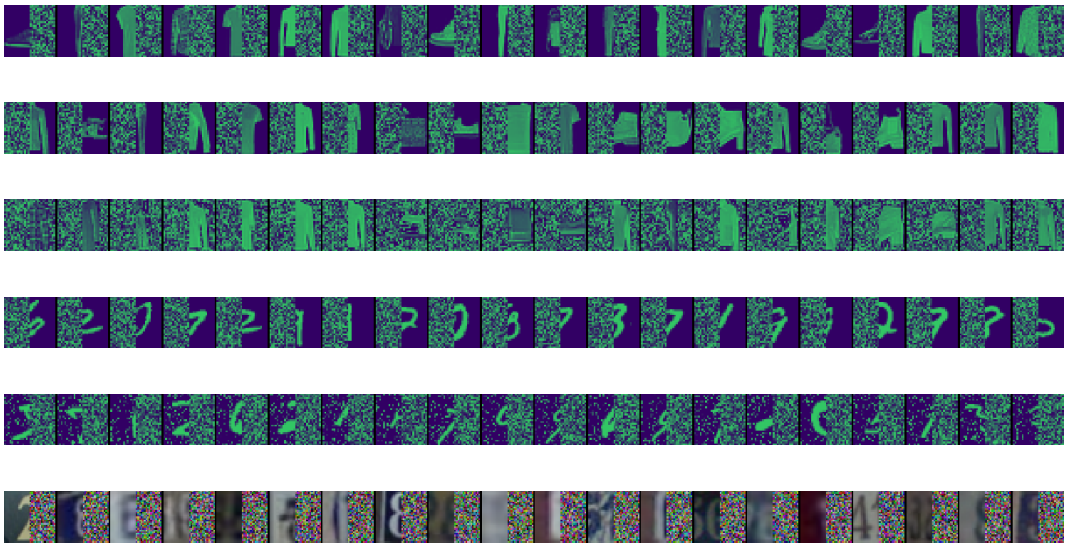
```
128     #------------------
129     if sys.argv[1] == "MNIST":
130       #------------------
131       brightness = [.1,.25,.5,.75,.9]
132       #the average profile for MNIST is [(0,.175), (0,.156), (0,.133),
    (0,.106), (0,.088)]
133       profiles = [[(0,.6),(0,.25),(0,1),(0,1),(0,.1)], #student
134                   [(0,.2),(0,.15),(0,.1),(0,.1),(0,.1)]] #expert
135       scores = [.7, #student
136                 .8] #expert
137       E = 12.5
138       F = 20
```

The `fashion-MNIST` dataset is very similar to the `MNIST` dataset, so it should not be surprising that we also have a student phase and an expert phase. However, the contrast profiles are a little bit different due to the nature of the data contained in the `fashion-MNIST` dataset, which involve greater amounts of bright pixels.

main.py

```
139     #------------------
140     if sys.argv[1] == "fashion-MNIST":
141       #------------------
142       brightness = [.1,.25,.5,.75,.9]
143       profiles = [[(0,.7),(0,.5),(0,.3),(0,.1),(0,.01)], #student
144                   [(0,.5),(0,.3),(0,.2),(0,.15),(0,.1)]] #expert
145       scores = [.5, #student
146                 .8] #expert
147       E = 13.5
148       F = 20
```

Before calling the function `intcyt`, let us extend the option `-load` of our launch command to two additional values `-load-selfsup-left` and `-load-selfsup-right`. These values will allow us to parameterize self-supervised challenges, as those shown in [1, Results]. Specifically, these options will instruct the script `main.py` to adapt the learning strategy of the gamma parameter to self-supervised challenges (this will be discussed in section 2.7 in more detail). Typical examples of such challenges would make the algorithm start with a cell whose organelles contain halves of images whose other halves are completed with white noise, as shown below. The goal for our algorithm would then be to reconstruct the images entirely.



As will be seen, we will generate such images through the script `challenge.py` by calling one of the following options: `-left`, `-right`, `-left-noisy` or `-right-noisy`. The generated images are then saved in the directory `result-load` in a file named `load_initial.gz`.

Because, in such circumstances, the main goal for the algorithm is to be able to reconstruct the missing half of the image, one may want to not alter the side of the image that contains information (unless this is desired by the user). For this purpose, we add the two options `-load-selfsup-left` and `-load-selfsup-right` to our launch command in order to specify which of the sides of the image should not be modified during the learning phase. These two options create to a list `selfsup` containing a parameterization of the area of the image that should not be altered. We do so by adding the following piece of code to the file `main.py`.

main.py

```
149     #------------------
150     selfsup = list()
151     if len(sys.argv) > 2 and sys.argv[2] = "-load-selfsup-right":
152       selfsup.append([image_size[1]/2, #middle of image
153                       image_size[1]-1, #right of image
154                       image_size[1]])  #width
155     elif len(sys.argv) > 2 and sys.argv[2] = "-load-selfsup-left":
156       selfsup.append([0,                  #left of image
157                       image_size[1]/2-1, #middle of image
158                       image_size[1]])    #width
```

Note that by not calling the options `-load-selfsup-left` or `-load-selfsup-right`, we let the variable `selfsup` be an empty list. As a result, the algorithm can alter both sides of the images during the learning process.

It is now time to use the function `intcyt` (section 5.1), which will constitute the heart of our learning algorithm. First, we create a variable `gamma_parameter` in which we stored the output of the function `usf.gamma` (section 3.1.4) applied to the contrast profile, as shown below. Then, we call the function `intcyt` on the variable `gamma_parameter` as well as the parameters defined before the epoch loop.

main.py

```
159     #------------------
160     gamma_parameter = usf.gamma(E,F,brightness,profiles,scores,*selfsup)
161     intcyt(operad,sc,epoch*i+k,events,vector,gamma_parameter,filtering)
```

Finally, we save the root cell, the organelles and the tree structure of the super cell in the files `save_roo.gz`, `save_org.gz` and `save_tre.gz`, respectively.

main.py

```
162     #------------------
163     #The sate of the super cell is saved in the memory
164     #------------------
165     #usf.print_root(sc,image_size,sys.stdout,option="display")
166     #usf.print_organelles(sc,image_size,sys.stdout,option="display")
167     #usf.print_tree(sc,image_size,sys.stdout,option="display")
168     usf.print_root(sc,image_size,fsave_roo,option="save")
169     usf.print_organelles(sc,image_size,fsave_org,option="save")
170     usf.print_tree(sc,image_size,fsave_tre,option="save")
171     fsave_roo.flush()
172     fsave_org.flush()
173     fsave_tre.flush()
```

We finish the code by closing of the opened file pointers, as shown below.

main.py

```
174 #------------------
175 fsave_roo.close()
176 fsave_org.close()
177 fsave_tre.close()
178 if sys.argv[1] in ["MNIST","fashion-MNIST"]:
179   fim.close()
180   ftr.close()
```

We are now done for the code of `main.py`. To conclude this section, let us summarize the different ways in which this script can be called. If we formalize the various options of

`main.py` through a formal grammar description, then the script `main.py` can be launched via the following command

```
> python main.py <dataset-name> <loading-option>
```

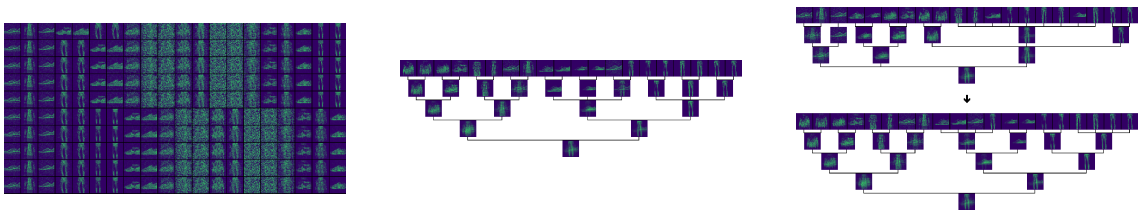
where we can replace the two tags with one of the following values:

```
<dataset-name>:
MNIST | fashion-MNIST | SVHN
<loading-option>:
-load | -load-selfsup-right | -load-selfsup-right | ε (empty)
```

Note that forgetting to specify the name of dataset will exit the program.

2.6. Visualizing the results

The goal of this section is to program a set of functions that will allow us to visualize the progress of our algorithm during the learning process. We will have three functions, which will show different degrees of detail (see the displays shown below).



Our first function, `visualize`, can show the evolution of the root or the leaves of the super cell. More specifically, for a list `query` of indices corresponding to the indices of images in a given dataset, the function displays a collection of vectors, which can be taken from either `save_roo.gz` or `save_org.gz`. Below, the variable `fload` is the file pointer reading the saved data (hence either `save_roo.gz` or `save_org.gz`), the variable `batch` is the number of vectors supposed to be read and `image_size` corresponds of the dimension of the images encoded by these vectors – it corresponds the same list `image_size` used in section 2.5.

visualize.py

```
4  #--------------------------------------------------------------------
5  def visualize(fload,batch,query,image_size):
6    memory = usf.get_memory(fload,batch,query)
7    image = usf.make_rgb_grid(memory,image_size)
8    fig, ax = plt.subplots(1)
9    #remove axis
10   ax.axis("off")
11   #display the image
12   ax.imshow(image)
13   plt.show()
```

Our second function, `visualize_tree`, combines the output of `visualize` with the tree structure of the super cell associated with the greatest index contained in `query`. This time, the variable `fload` is supposed to read the file `save_tre.gz`. The function `visualize_tree` starts with the following loop, which collects the leaves of all but the last tree returned by the function `usf.get_trees` (see section 3.1.11) and stores the last tree in a variable `tree`.

visualize.py

```
14 #-----------------------------------------------------------------------
15 def visualize_tree(fload,query,image_size):
16   trees = usf.get_trees(fload,query)
17   memory = list()
18   tree = list()
19   for i in range(len(trees)):
20     if i != len(trees)-1:
21       memory.append(trees[i][0])
22     else:
23       tree = trees[i]
```

We store the images of the leaves in the variable `image1` and we store the image of the last tree in `image2`.

visualize.py

```
24   image1 = usf.make_rgb_grid(memory,image_size)
25   image2 = usf.make_rgb_tree(tree,image_size)
```

We then concatenate the two resulting images as a list `image` and finish in the same as in `visualize`.

visualize.py

```
26   image = image1 + image2
27   fig, ax = plt.subplots(1)
28   #remove axis
29   ax.axis("off")
30   #display the image
31   ax.imshow(image)
32   plt.show()
```

Last but not least, our third function,`visualize_forest`, displays the tree structures of all the super cells associated with the indices contained in the list `query`.

The code of the function `visualize_forest` is very similar to that of `visualize_tree`.

visualize.py

```
33 #-----------------------------------------------------------------------
34 def visualize_forest(fload,query,image_size):
35   trees = usf.get_trees(fload,query)
36   image = list()
37   for i in range(len(trees)):
38     image = image + usf.make_rgb_tree(trees[i],image_size)
39     if i != len(trees)-1:
40       image = image + usf.make_arrow_panel(panel_width=len(image[0]),
   length=6)
41   fig, ax = plt.subplots(1)
42   #remove axis
43   ax.axis("off")
44   #display the image
45   ax.imshow(image)
46   plt.show()
```

As in `main.py`, the script `visualize.py` will be equipped with a collection of options. Specifically, we will define three types of options, which will allow us to define the arguments of the functions `visualize`, `visualize_tree` and `visualize_forest`. The launch command for `visualize.py` will be of the following form:

```
> python visualize.py <dataset-name> <display-option> <query-intervals>
```

where we can replace the three tags with one of the following values:

```
<dataset-name>:
MNIST | fashion-MNIST | SVHN
<display-option>:
-forest | -tree | ε (empty)
<query-intervals>:
i1 j1 i2 j2 ...  in jn (a list of non-negative integers where ik < jk)
```

Because the tag <display-option> can be empty, the first value of <query-intervals> can be contained by either sys.argv[2] or sys.argv[3]. As a result, we will use an index re-adjustment r to collect the potential arguments i_k and j_k so that these are contained in the system variables sys.argv[2*(k-1)+r] and sys.argv[2*(k-1)+r+1]. The value stored in r is determined as follows.

visualize.py

```
47 #-------------------------------------------------------------------------
48 if sys.argv[2][0] != "-":
49   r = 2
50 else:
51   r = 3
```

An example of a launch command for visualize.py is given below.

```
> python visualize.py fashion-MNIST -forest 200 203 50 51 100 101 0 1
```

As can be seen above, each pair of integer is made of successive integers. However, the pairs may not need to be given in an increasing order. In the piece of code given below, we use the list of integers associated with the tag <query-intervals> to construct the list query to be given to our functions. In the previous example, the list query would take the form [200,201,202,50,100,0].

visualize.py

```
52 #-------------------------------------------------------------------------
53 query = list()
54 for i in range((len(sys.argv)-2)/2):
55   query = query + range(int(sys.argv[2*i+r]),int(sys.argv[2*i+r+1]))
```

We now take care of the value of the tag <dataset-name>, through which we parametrize three variables image_size, batch_roo and batch_org.

The option SVHN gives the following parameters.

visualize.py

```
56 #-------------------------------------------------------------------------
57 #To visualize learning from SVHN dataset
58 if sys.argv[1] == "SVHN":
59   image_size = [32,32,3] #rgb
60   batch_roo = 1
61   batch_org = 20
```

Alternatively, we use the same parameters for either options MNIST and fashion-MNIST.

visualize.py

```
62 #----------------------------------------------------------------------
63 #To visualize learning from MNIST dataset
64 if sys.argv[1] in ["MNIST","fashion-MNIST"]:
65   image_size = [28,28,1] #bicolor
66   batch_roo = 1
67   batch_org = 20
```

Finally, we take care of the values of the tag <display-option> as follows. For no value given, we apply the function `visualize` to the data stored in `save_roo.gz` and `save_org.gz`. The result of such an operation displays the roots and the organelles of the super cell associated with the loop indices stored in the list `query`.

visualize.py

```
68 #----------------------------------------------------------------------
69 if sys.argv[2][0] != "-":
70   fload_roo = gzip.open("save_roo.gz","r")
71   fload_org = gzip.open("save_org.gz","r")
72   #--------------
73   visualize(fload_roo,batch_roo,query,image_size)
74   visualize(fload_org,batch_org,query,image_size)
75   #--------------
76   fload_roo.close()
77   fload_org.close()
```

If the option `-tree` is given, then we display the leaves of all the super cells associated with the loop indices stored in the list `query`, together with the tree structure of the last super cell.

visualize.py

```
78 #----------------------------------------------------------------------
79 elif sys.argv[2] == "-tree":
80   fload_tre = gzip.open("save_tre.gz","r")
81   #--------------
82   visualize_tree(fload_tre,query,image_size)
83   #--------------
84   fload_tre.close()
```

If the option `-forest` is given, then we display the tree structures of all the super cells associated with the loop indices stored in the list `query`.

visualize.py

```
85 #----------------------------------------------------------------------
86 elif sys.argv[2] == "-forest":
87   fload_tre = gzip.open("save_tre.gz","r")
88   #--------------
89   visualize_forest(fload_tre,query,image_size)
90   #--------------
91   fload_tre.close()
92 #----------------------------------------------------------------------
```

This finalizes the code of the file `visualize.py`. Before moving on to the code of our next script, `challenge.py`, we conclude the section by showing visualizations of outputs returned by the script `main.py` through the functions of the script `visualize.py`.

We begin with the dataset `SVHN`. Because we do not have any initialization for this dataset, we generate one through the script `main.py`. We start with the following command.

```
> python main.py SVHN
```

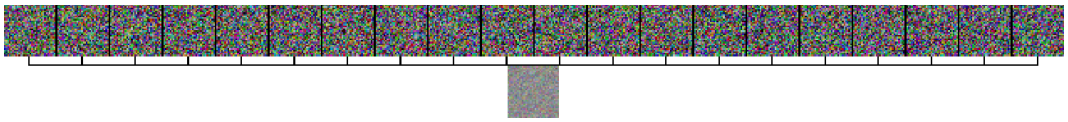
Right after taping the carriage return key ↵ on the keyboard, you should see, in the standard output, a display similar to the one shown below. The label [Allostasis 0] shown towards the end of the display indicates that the algorithm is currently at cycle 0.

```
[Learning data labeled as 1]

[TREE]
[0] -> Cell[0]oooooooooooooooooo [0]:0.7978860358 [1]:0.7938557942
[2]:0.8118207372 [3]:0.8014380039 [4]:0.8095886724 [5]:0.8055258661
[6]:0.8026621764 [7]:0.8046829853 [8]:0.7997212603 [9]:0.8068208694
[10]:0.7960182403 [11]:0.8028378799 [12]:0.7931610043 [13]:0.7953383775
[14]:0.8070709252 [15]:0.7935919636 [16]:0.8007175106 [17]:0.8096277577
[18]:0.7965840558 [19]:0.801800826

[Allostasis 0]
[brightness] 0.8675 0.7382 0.4902 0.2587 0.096
False
```

After some time, the algorithm will reach the label [Allostasis 1]. Form then on, we can start to visualize the past states of the super cell. For instance, to visualize the initialization of the super cell, we can launch the scrip `visualize.py` as follows.

```
> python visualize.py SVHN -tree 0 1
```

This has the result of creating a `matplotlib` window containing the following display.

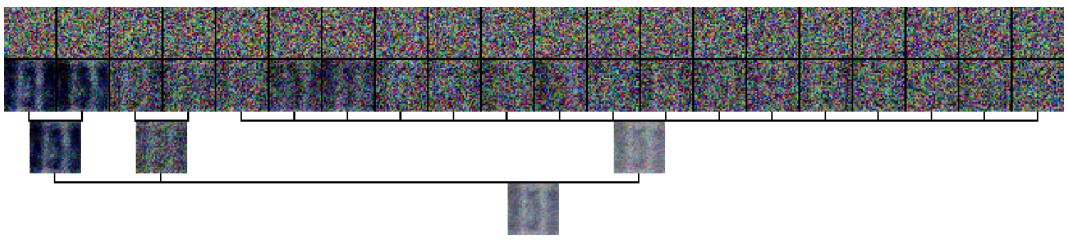


In the image above, the row of images forming the leaves of the tree corresponds to the information contained by the organelles of the cell while the image underneath the row represents the sum of all the organelles, which is formalized as the *content* of the cell in [1, Def. 1.21].

After the label [Allostasis 187] has passed, we can call the following command.

```
> python visualize.py SVHN -tree 0 1 186 187
```

The output associated with the previous command is shown below, where the top row contain the organelles of the super cell at cycle 0 and the tree, below it, shows the state and structure of the super cell at cycle 186.

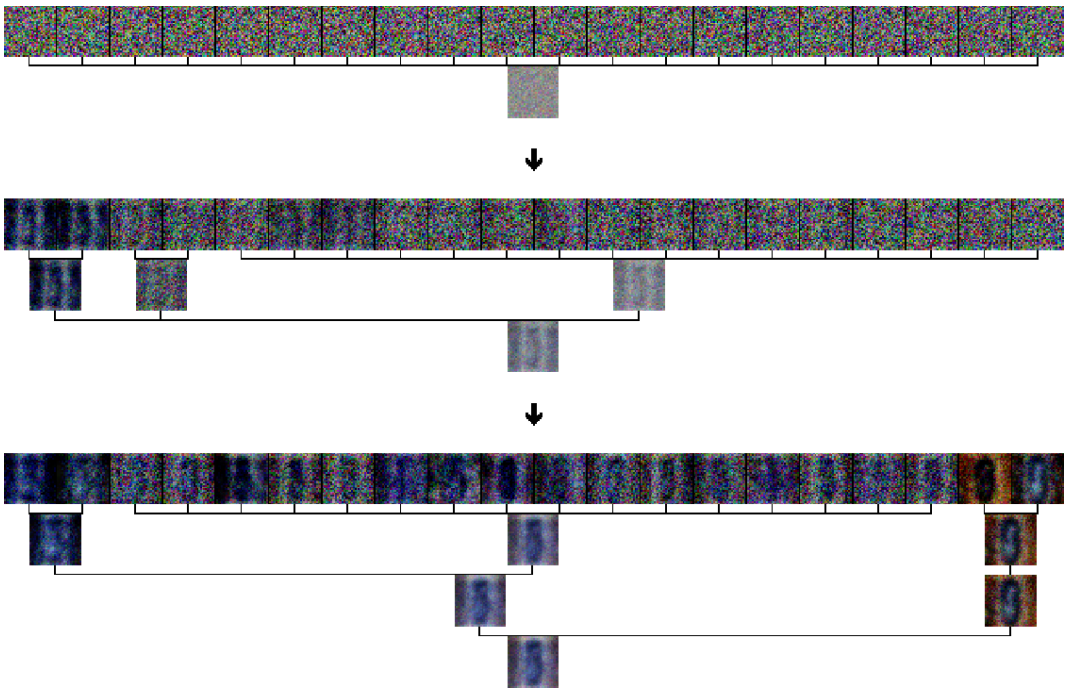


Even though we can distinguish either a 3 or a 5 in the leftmost leaves of the previous tree, our parameterization for `SVHN` is not optimal and needs to be adapted to a RGB code colors. Indeed, let us try to visualize the states of the super cell in the 1000's cycles to see

how the memory of the super cell has evolved. For instance, if we wait until cycle 1252 and use the following command, where we replace the option `-tree` with `-forest`,

```
> python visualize.py SVHN -forest 0 1 186 187 1251 1252
```

then our output should look approximately like the one shown below.



As can be seen, the concepts learned by the super cell are quite vague. However, to put things in context, the dataset `SVHN` contains a lot of blurry images too. This tells us more about what `intcyt` does: it tries to construct abstractions of the concepts contained in a dataset at a quality level that approximates that of its data.

Note that the organelles of the super cells (shown above) all seem to describe the same abstraction. Such a limited learning can be explained by the current parametrization of the function `usf.gamma` (section 3.1.4), which is not adapted to RGB code colors. The interested reader is invited look into the code of the module `useful.py` if they want to experiment better learning strategies for `SVHN`.

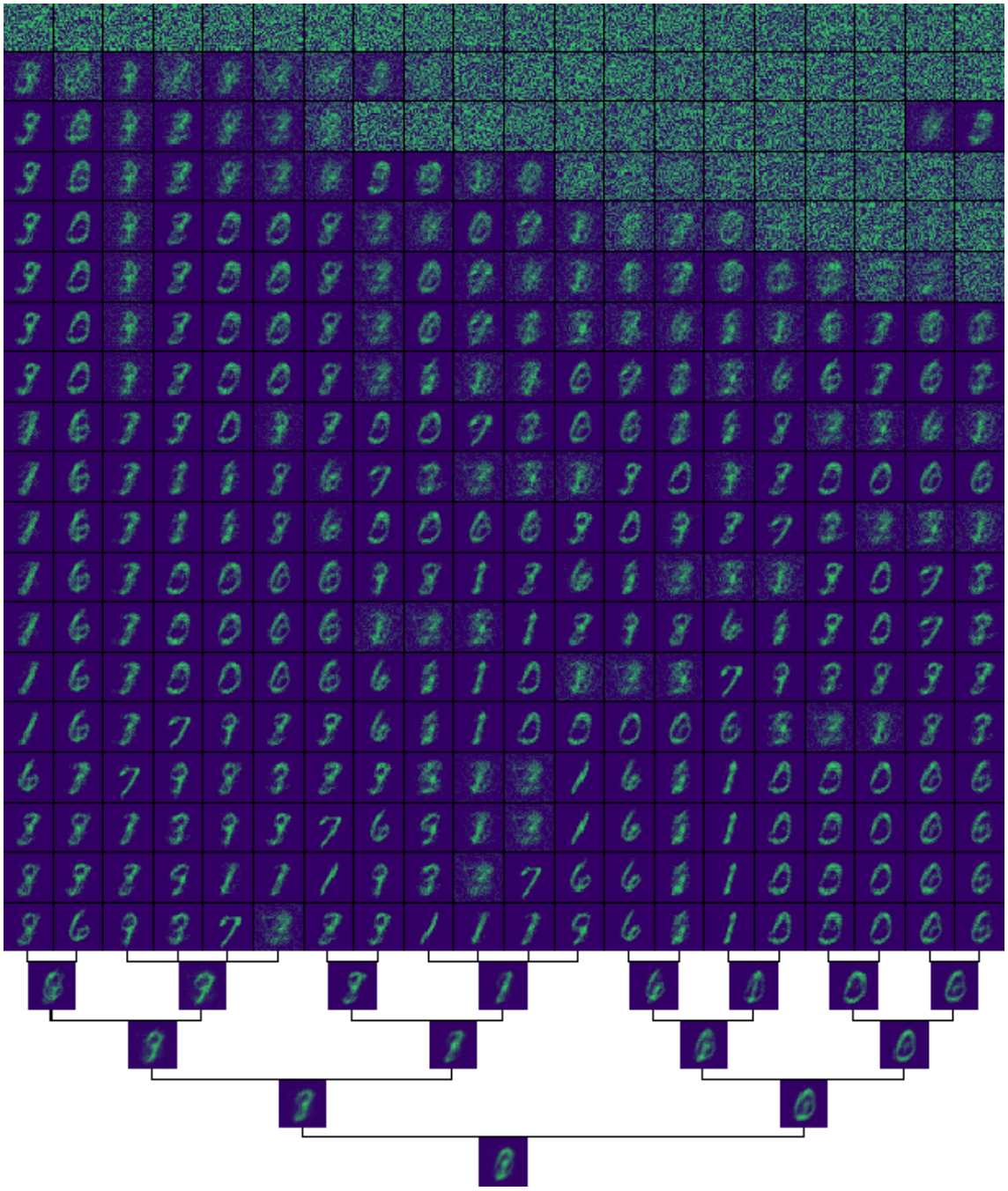
From now on, we shall focus on our two bicolor datasets, namely `MNIST` and `fashion-MNIST`. We start with the dataset `MNIST` and launch the script `main.py` with the following command.

```
> python main.py MNIST
```

After a few hundreds cycles, say 2001, we can call the following command to visualize the shape of the super cell at cycle 2000 and the evolution of its organelles.

```
> python visualize.py fashion-MNIST -tree 0 1 100 101 200 201 300 301 400
401 500 501 600 601 700 701 800 801 900 901 1000 1001 1100 1101 1200 1201
1300 1301 1400 1401 1500 1501 1700 1701 1900 1901 2000 2001
```

The returned output looks as follows in my case.

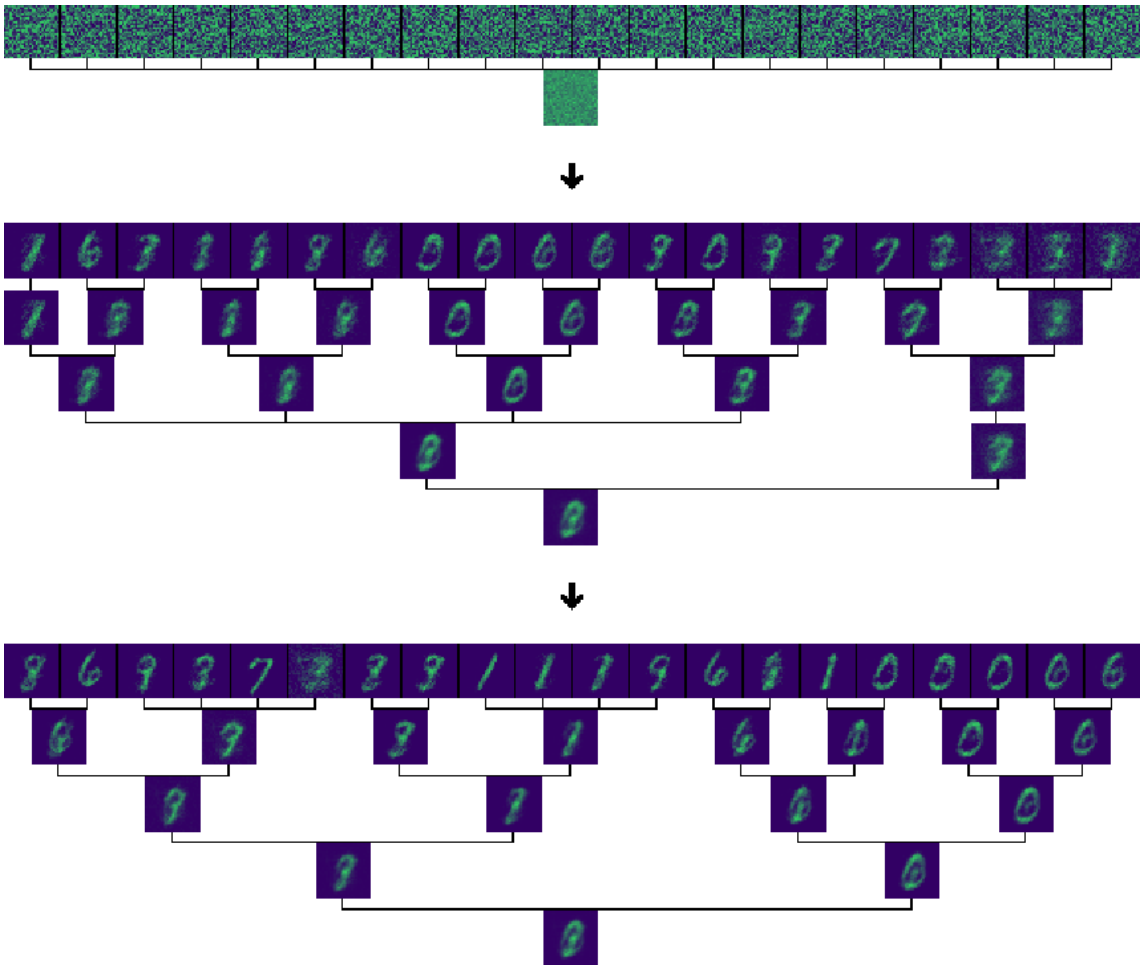


As can be seen, the algorithm first focuses on separating the information from the white noise, in the first cycles, and then moves on to gathering pieces of information that look similar together.

Alternatively, we can call the following command to understand how the architecture of the super cell evolved during the learning phase.

```
> python visualize.py MNIST -forest 0 1 1000 1001 2000 2001
```

In my case of my initialization, we can see that the architecture of the super cell has evolved quite a lot during the learning phase (see picture below). In particular, the super cell may have still been in the process of evolving at cycle 2001, which means that the super cell would/could have ended up being more organized than the ones shown below after a longer time.

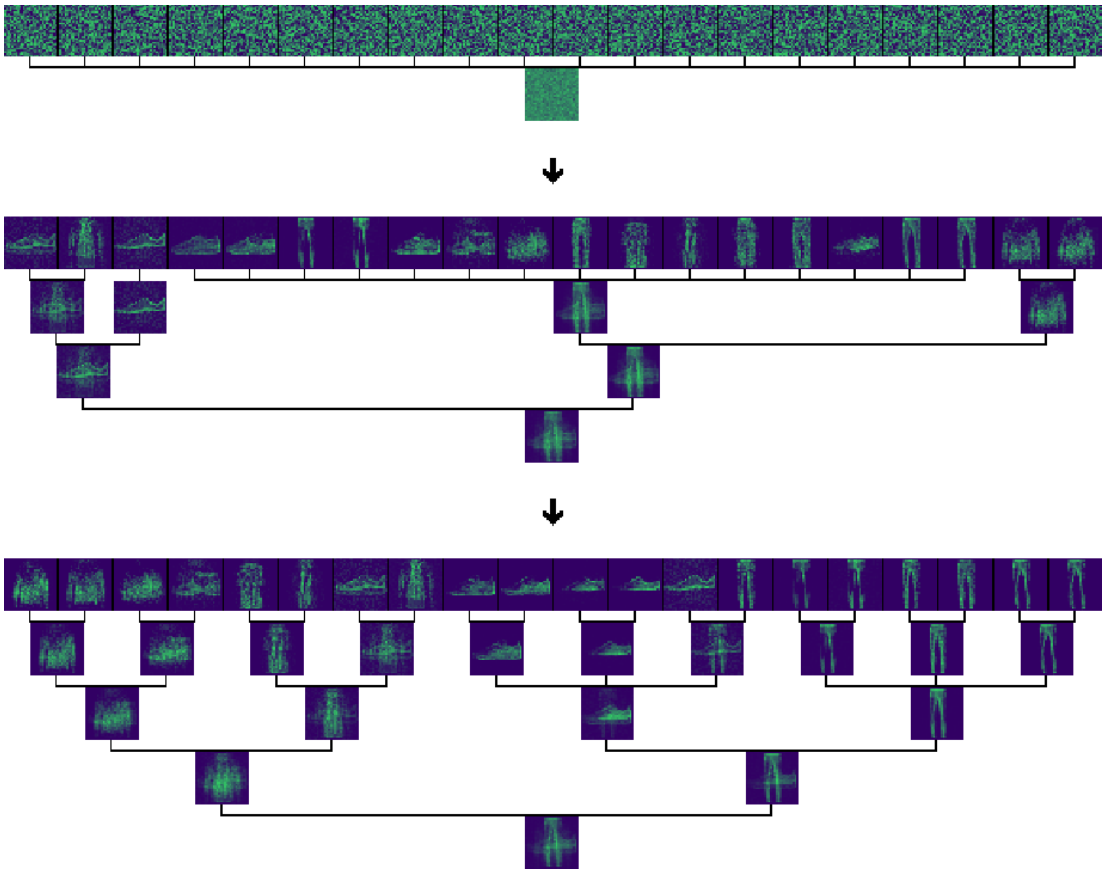


We proceed similarly for the dataset `fashion-MNIST`. We start by calling the script `main.py` as follows.

```
> python main.py fashion-MNIST
```

After a few hundred cycles, we can we call the script `visualize.py`. In my case, I will use the following command, which gives me the display shown below.

```
> python visualize.py fashion-MNIST -forest 0 1 400 401 938 939
```



In the following section, we will see how our script `main.py` performs on initializations that are not everywhere random and contains partial information regarding the dataset.

2.7. Self-supervision

The goal of the present section is to write a script that will generate initializations with halves of images taken from the datasets. Given the learning and abstraction abilities seen in section 2.6, we expect our algorithm to be able to reconstruct the missing halves. We will have 5 types of challenges, which we will call through the following options:

- `-right`: hides the left part of an image with white noise;

- `-right-noisy`: hides the left part of an image with white noise and fills the background of the image with similar white noise;

- `-left`: hides the right part of an image with white noise;
- `-left-noisy`: hides the right part of an image with white noise and fills the background of the image with similar white noise;

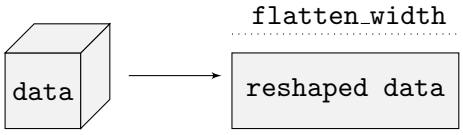
- ε (`empty`): takes the full image;

The code of our script will be saved in the file `challenge.py` and will be very similar to that of `main.py`. As in `main.py`, we start by opening the dataset files, which we can control by passing the options `MNIST`, `fashion-MNIST`, or `SVHN` to the launch command of `challenge.py`.

challenge.py

```
8  #-------------------------------------------------------------------------
9  #Loading the dataset for learning
10 #-------------------------------------------------------------------------
11 #Open the SVHN dataset
12 if len(sys.argv) > 1 and sys.argv[1] == "SVHN":
13   dic_svhn = sio.loadmat("data/train_32x32.mat")
14   #Access to the dictionary
15   dicim = dic_svhn["X"] #shape:  32, 32, 3, 73257
16   dictr = dic_svhn["y"] #shape:  73257, 1
17   image_size = [32,32,3] #height, width, depth
18 #------------------
19 #Open the MNIST dataset
20 elif len(sys.argv) > 1 and sys.argv[1] == "MNIST":
21   fim = gzip.open("data/train-images-idx3-ubyte.gz","r")
22   ftr = gzip.open("data/train-labels-idx1-ubyte.gz","r")
23   ftr.read(8)
24   fim.read(16)
25   image_size = [28,28,1] #height, width, depth
26 #------------------
27 #Open the fashion-MNIST dataset
28 elif len(sys.argv) > 1 and sys.argv[1] == "fashion-MNIST":
29   fim = gzip.open("data/t10k-images-idx3-ubyte.gz","r")
30   ftr = gzip.open("data/t10k-labels-idx1-ubyte.gz","r")
31   ftr.read(8)
32   fim.read(16)
33   image_size = [28,28,1] #height, width, depth
34   categories = ["t-shirt","trousers","pullover", \
35                 "dress","jacket","sandal","shirt", \
36                 "sneaker","bag","ankle-boot"]
37 else:
38   exit(0)
```

We will also need three parameters, which we call `ary`, `dim` and `flatten_width`, to control the dimensions of our initialization. The parameter `dim` contains the "volume" of every image in a given dataset, the parameter `flatten_width` contains the multiplication between the width and the depth of the images of the dataset (as shown below)



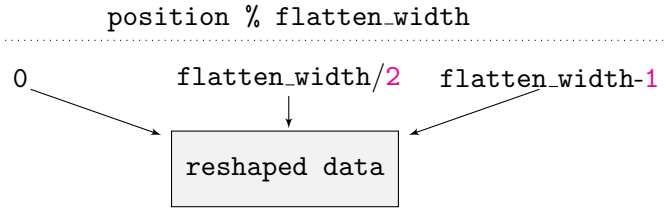
and `ary` is the number of organelles possessed by the super cell.

challenge.py
```
39 #--------------------------------------------------------------------
40 #Parameters
41 #--------------------------------------------------------------------
42 dim = image_size[0] * image_size[1] * image_size[2]
43 flatten_width = image_size[1] * image_size[2]
44 ary = 20
```

As previously said, we intend to initialize the organelles of our super cell with halves of images. These images will be picked randomly within the 1000 first images of the dataset. We implement this random picks through the following loop, which creates the list `init` containing the indices of those images to be used in the initialization.

challenge.py
```
45 #--------------------------------------------------------------------
46 #Randomly select data in the dataset.
47 #--------------------------------------------------------------------
48 init = list()
49 while len(init) < ary:
50   n = random.randint(0,999)
51   if not(n in init):
52     init.append(n)
53 init = sorted(init)
54 print init
```

We can classify our challenges in two groups: those that hide the left half of the images and those that hide the right half. Because we do not intend to alter the part of the image containing the information, we store, in a variable `random_init`, the position (modulo `flatten_width`) of the pixels that can be altered with white noise.



We do so by adding the following lines of code to `challenge.py`.

challenge.py
```
55 #--------------------------------------------------------------------
56 random_init = list()
57 if len(sys.argv) > 2 and sys.argv[2][:6] == "-right":
58   random_init.extend([0, flatten_width/2-1])
59 elif len(sys.argv) > 2 and sys.argv[2][:5] == "-left":
60   random_init.extend([flatten_width/2, flatten_width-1])
61 #--------------------------------------------------------------------
```

Before entering the main part of the code, we generate the file in which we want to store the initialization. We create it using the module `gzip` and call it `load_initial.gz` as follows.

challenge.py
```
62 #--------------------------------------------------------------------
63 #Save the randomly picked data in a file
64 #--------------------------------------------------------------------
65 fself = gzip.open("result-load/load_initial.gz","w")
```

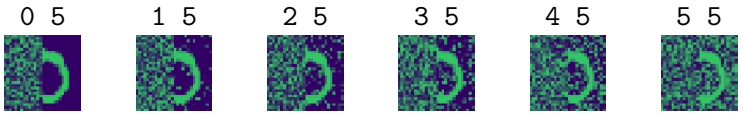
We are now ready to collect the images whose indices belong to the list `init` and alter them according to the options specified in the launch command, which will take the following form.

```
> python challenge.py <dataset-name> <initialization-option> <pair>
```

The different values for each of the tags is given below.

```
<dataset-name>:
MNIST | fashion-MNIST | SVHN
<initialization-option>:
-right | -left |
-right-noisy | -left-noisy
<pair>:
i j (a pair of non-negative integers) | ε (empty)
```

The tag `<pair>` is meant to refine the two options `-right-noisy` and `-left-noisy` by specifying the probability with which the white noise should be added to the half of the image that contains data. Specifically, if the tag `<pair>` is allocated two non-negative integers `i` and `j`, then the pixels of null intensity that are in the half containing the image will have a probability of `i/j` to be completed with white noise, as shown below.



We now want now to collect the images whose indices belong to the list `init`. To do so, we use a loop that goes through the first 1000 images of the datasets. The following piece of code is the same as the one we used in `main.py`.

challenge.py

```
66  for i in range(1000):
67    #------------------
68    #Get labels and inputs
69    #------------------
70    if sys.argv[1] == "SVHN":
71      label = dictr[i]
72      inputs = dicim[:,:,:,i].reshape(dim)
73  #------------------
74    if sys.argv[1] == "MNIST":
75      buf_lab = ftr.read(1)
76      buf_inp = fim.read(dim)
77      label = np.frombuffer(buf_lab, dtype=np.uint8).astype(np.int64)
78      inputs = np.frombuffer(buf_inp, dtype=np.uint8).astype(np.float32)
79  #------------------
80    if sys.argv[1] == "fashion-MNIST":
81      buf_lab = ftr.read(1)
82      buf_inp = fim.read(dim)
83      label = map(lambda x:  categories[x], np.frombuffer(buf_lab,
    dtype=np.uint8).astype(np.int64))
84      inputs = np.frombuffer(buf_inp, dtype=np.uint8).astype(np.float32)
```

The rest of the code is now dedicated to the situation in which the loop reads an image whose associated loop index belongs to the list `init`. First, we display its corresponding label on the standard output by using the function `debug_time.set`.

challenge.py

```
85  #------------------
86    if i in init:
87      #------------------
88      debug_time.set("Data picked:  " + ", ".join(map(str,label)))
89      #------------------
```

Second, if the list `random_init` is non-empty, then we construct the initialization according to the specification given in the launch command, as shown below.

challenge.py

```
90      if len(random_init) == 2:
91        for k in range(len(inputs)):
92          if random_init[0] <= k % flatten_width <= random_init[1]:
93            inputs[k] = random.randint(0,250)
94          elif len(sys.argv) > 2 and sys.argv[2] in ["-right-noisy",
    "-left-noisy"] and inputs[k] == 0:
95            if len(sys.argv) == 3:
96              inputs[k] = random.randint(0,250)
97            elif len(sys.argv) > 4:
98              if 1 <= random.randint(0,int(sys.argv[4])) <=
    int(sys.argv[3]):
99                inputs[k] = random.randint(0,250)
```

We finish the code by displaying the initialization on the standard output and saving it in the file `load_initial.gz`.

challenge.py

```
100     #------------------
101     linputs = inputs.tolist()
102     usf.print_data(linputs,image_size,sys.stdout,option = "display")
103     usf.print_data(linputs,image_size,fself,option = "save")
104     fself.write("\n")
105 #-------------------------------------------------------------------------
106 fself.close()
107 if sys.argv[1] in ["MNIST","fashion-MNIST"]:
108   fim.close()
109   ftr.close()
```

The rest of this section is dedicated to showing examples of outputs of `main.py` relative to initializations generated by the script `challenge.py`.

We start with `MNIST`. First, we generate a self-supervised challenge made of left halves of images by calling the following command.

```
> python challenge.py MNIST -left
```

In my case, I obtain the following initialization:

Before calling the script `main.py`, we shall change the contrast profile associated with `MNIST`. Indeed, note that the previous initialization contains valuable information about the data and it would makes sense to take advantage of this information to alter the halves of the images that contain white noise. As a result, our strategy will be to use the contrast profiles only on the left halves of the images. To do this properly, we want to adapt the contrast profiles associated with `MNIST` to these halves as best as possible. For the present challenge, we found that the following contrast profile work well.

main.py

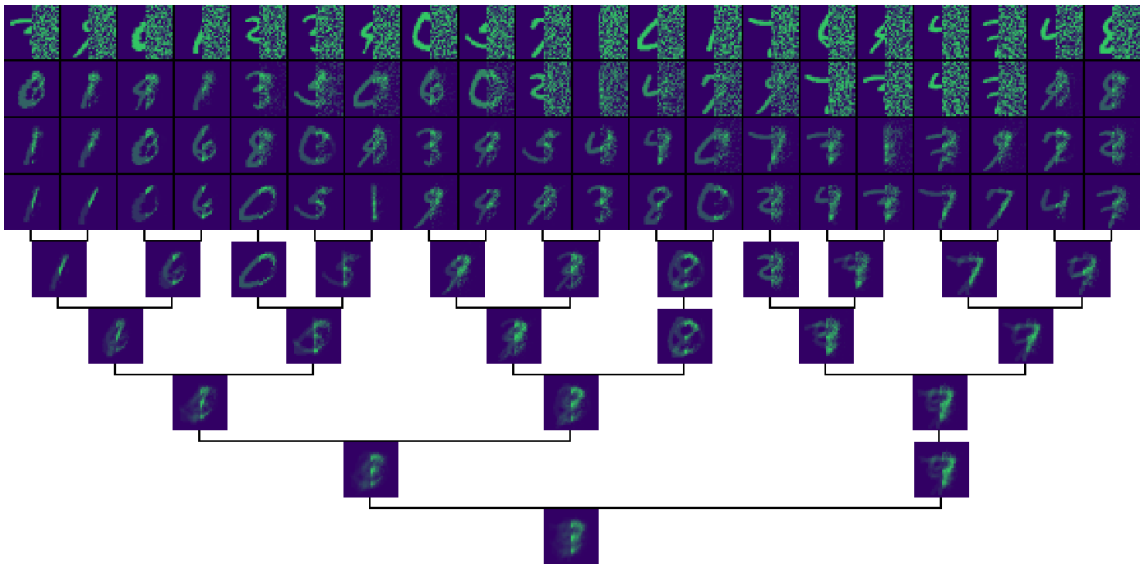
```
127     #------------------
128     if sys.argv[1] == "MNIST":
129       #------------------
130       brightness = [.1,.25,.5,.75,.9]
131       #the average profile for MNIST is [(0,.175), (0,.156), (0,.133),
    (0,.106), (0,.088)]
132       profiles = [[(0,.45),(0,.25),(0,.1),(0,.05),(0,.01)], #student
133                   [(0,.3),(0,.3),(0,.1),(0,.05),(0,.01)]] #expert
134       scores = [.7, #student
135                 .8] #expert
136       E = 14
137       F = 25
```

After making these changes in `main.py`, we start the learning phase through the following command, in which we use the option `-load-selfsup-left` to instruct the script to not alter the left halves of the images.

```
> python main.py MNIST -load-selfsup-left
```

After a few thousands cycles (in my case, 5001 cycles), I call the script `visualize.py` with the command shown below and I obtain the tree displayed after it.

```
> python visualize.py MNIST -tree 0 1 500 501 1000 1001 1359 1360 4579 4580
5000 5001
```



We can proceed similarly for `fashion-MNIST`. First, let us generate a new challenge as follows.

```
> python challenge.py fashion-MNIST -right
```

In my case, I obtain the following initialization.

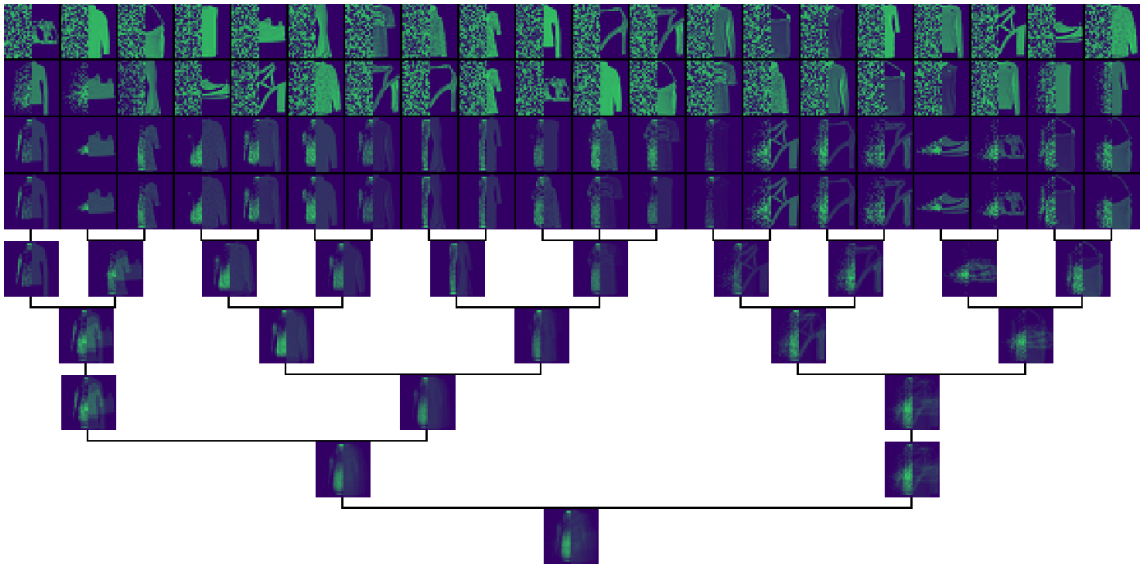
As with `MNIST`, we should also update the contrast profile of `fashion-MNIST`. For our current challenge, the following change suffices.

main.py

```
172       F = 22.5
```

After a few thousands cycles (in my case, 14490 cycles), I call the script `visualize.py` with the command shown below and I obtain the tree displayed after it.

```
python visualize.py fashion-MNIST -tree 0 1 850 851 11589 11590 14489 14490
```

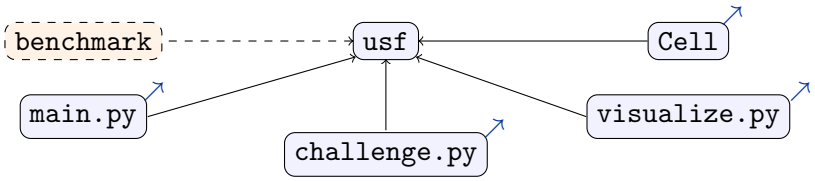


I will let the reader experiment on the other types of challenges. Note that this may require the modification of the contrast profiles for the corresponding dataset chosen.

Presentation of the module `useful.py`

3.1. Description of `usf` (class item)

3.1.1. Introduction. This section introduces the reader to the class item `usf`, which is a repository of functions used in the tutorial of section 2 as well as in the class `Cell` (section 4.1). The class item `usf` is also used in the benchmarking file attached with the library.



Note that `usf` is not a class, but a item of the non-importable class `_Useful`. The class `_Useful` is equipped with 5 types of methods, which are listed below:

▷ a set of 2 methods taking care of controling the learning rate of `intcyt` (section 5.1):
- `contrast`: indicates whether a vector satisfies a certain contrast profile;
- `gamma`: corresponds to the gamma parameter used in [1, Sec. 2.3].

▷ a set of 4 methods taking care of saving and displaying information stored in a super cell:
- `print_data`: saves or displays a vector;
- `print_root`: saves or displays the root of a super cell [1, Conv. 2.2];
- `print_organelles`: saves or displays the organelles of a super cell [1, Def. 2.7];
- `print_tree`: saves or displays the structure of a super cell [1, Conv. 2.2];

▷ a set of 4 methods loading information from saved data:
- `parse_image`: parses the components of a vector stored in a file;
- `get_memory`: loads a collection of vector data stored in a file;
- `get_trees`: loads a super cell structure stored in a file;
- `get_last_cycle`: returns the index of the last super cell stored in a file;

▷ a set of 6 methods displaying the evolution of a super cell from saved data:
- `join_images`: attach two images next to each other;
- `rgb_colormap`: returns an RGB code color for bicolor and RGB images;

• make_rgb_panel: displays a row of images representing memorized data in a super cell;

• make_rgb_grid: displays a grid of images representing memorized data in the organelles of a super cell;

• make_rgb_tree: displays a tree of images representing memorized data in a super cell;

• draw_arrow: displays an arrow going down.

▷ a set of 3 functions taking care of the combinatorics behind cell fusion and cel fission:

• zero_matrix: returns a square matrix initialized with zeros;

• join_fibers: computes the transitive closure of two partitions;

• cliques: returns one of the maximally weighted connected components of a weighted adjacency matrix.

3.1.2. Structure. The following tables give a preview of the class item usf. The table given below describes the various dependencies of the class item.

Dependencies	
Class type	Module section
_Useful	N/A
Statistics	
▷ Importable objects: 0	
▷ Non-importable objects: 0	
▷ Importable functions: 19	
▷ Non-importable functions: 0	

The following two tables give a description of the 16 importable functions of the class item. In the third column, we use the symbol ∼ to refer to a type that will be specified in the topmost section shown in the corresponding rightmost column.

Functions			
Name	Input types	Output types	Related sections
.contrast	- list(float) - list(list(float))	- fun: ∼ -> ∼	▷ section 3.1.3
.gamma	- float - float - list(float) - list(list(float * float)) - list(float) - list(list(float))	- fun: ∼ -> ∼	▷ section 3.1.4
.print_data	- list(float) - list(int) - file - string	- self	▷ section 3.1.5
.print_root	- SuperCell - list(int) - file - string	- self	▷ section 3.1.6
.print_organelles	- SuperCell - list(int) - file - string	- self	▷ section 3.1.7

In this second table, the type image refers to a sub-type of list(list(list(float))) consisting of lists of lists of RGB lists (lists of float of length 3).

.print_tree	- SuperCell - list(int) - file - string - int - int	- self	▷ section 3.1.8
.parse_image	- string - list(string) - list(float)	- list(string)	▷ section 3.1.9
.get_memory	- file - int - list(int)	- list(list(float))	▷ section 3.1.10
.get_trees	- file - list(int)	- list(list(float))	▷ section 3.1.11
.get_last_cycle	- file - int	- int	▷ section 3.1.12
.join_images	- image - image - int - int - bool	- image	▷ section 3.1.13
.rgb_colormap	- float - bool	- fun: ∼ -> ∼	▷ section 3.1.14
.make_rgb_panel	- list(list(float)) - list(int)	- image	▷ section 3.1.15
.make_rgb_grid	- list(list(list(float))) - list(int)	- image	▷ section 3.1.16
.make_rgb_tree	- list(list(float)) - list(int)	- image	▷ section 3.1.17
.draw_arrow	- int - int	- image	▷ section 3.1.18
.zero_matrix	- int	- list(list(int))	▷ section 3.1.19
.join_fibers	- list(list(int)) - list(list(int))	- list(list(int))	▷ section 3.1.20
.cliques	- list(list(int))	- list(list(int))	▷ section 3.1.21

3.1.3. Description of usf.contrast (function). This section describes the code and the functionalities of the function usf.contrast. The method is equipped with the following inputs.

.__init__		
Inputs	Types	Specifications
brightness	list(float)	necessary
profiles	list(list(float * float))	necessary

The method possesses one action, which we describe below through examples.

Action	
Condition	Always

Description	The method returns a function `contrast_profiles` that takes a `float` item `vector` and an optional `list(list(float))` item `challenge` and returns a `list(bool)` item `contrast_tests` whose coefficient `contrast_tests[i]` indicates whether the input `vector` *satisfies the contrast profile* defined by the list `profiles[i]` and the value `brightness[i]` (see the tutorial or the explanation below). To explain what this means, let us denote by `percents[j]` the percentage of indices `u` (ranging from `0` to `self.dimension`) for which
	1) the ratio `vector[u]/max(vector)` is greater than `brightness[j]`;
	2) the following equation holds (when `challenge` is non-empty):
	`challenge[0][0] <= u % challenge[0][2] <= challenge[0][1].`
	Then, the `bool` item `contrast_tests[i]` indicates whether there exists an index `j` for which the following inequality holds:
	`profiles[i][j][0] <= percents[j] <= profiles[i][j][1]`
	As a result, the output list `contrast_tests` indicates whether any of the contrast profiles are satisfied by the input `vector`.

In the following examples, we illustrate the use of the function `usf.contrast` with no input `challenge` given. Note that giving such an input would amount to the same type of behavior, except that some of the components of the lists contained in `vectors` would not be considered in the computation.

```
>>> brightness = [.25,.5,.75]
>>> profiles = [[(.0,.9),(.0,.5),(.0,.25)],[(.0,.4),(.0,.6),(.0,.5)]]
>>> vectors = [[1,2,5,3,7], [5,0,0,0,4],[25,51,8,1,52]]
>>> contrast_profiles = usf.contrast(brightness,profiles)
>>> for j in range(len(vectors)):
...  print "contrast profiles:  " + str(contrast_profiles(vectors[j]))
...  print "----------"
...
[brightness] 0.8 0.4 0.2
True False

contrast profiles:  [True, False]
----------
[brightness] 0.4 0.4 0.4
False True

contrast profiles:  [False, True]
----------
[brightness] 0.6 0.4 0.4
False False

contrast profiles:  [False, False]
----------
```

The grey messages displayed in the previous example appear automatically in the standard output. They show the brightness profiles associated with each of the lists of the input `vectors` and indicate whether these profiles satisfy the contrast profiles defined by the pair `brightness` and `profiles`. In the context of the previous example, the messages inform

us that the list vectors[0] satisfies the contrast profile profiles[0], the list vectors[1] satisfies the contrast profile profiles[1], and the list vectors[2] does not satisfy any of the contrast profiles of profiles.

3.1.4. Description of usf.gamma (function). This section describes the code and the functionalities of the function usf.gamma. The method is equipped with the following six inputs, including one that is optional.

.__init__		
Inputs	Types	Specifications
E	float	necessary
F	float	necessary
brightness	list(float)	necessary
profiles	list(list(float * float))	necessary
scores	list(float)	necessary
*challenge	list(list(float))	optional

The method possesses one action, which we describe below through examples.

Action	
Condition	Always
Description	The method returns a function gamma_parameter that plays the role of the "gamma parameter" discussed in [1, Sec. 2.3]. Specifically, the function gamma_parameter takes a Cell item c (see section 4.1.3) and a list(list(float)) item a and returns a list(list(float)) item gamma_parameter(c,a) whose coefficients gamma_parameter(c,a)[j][u] satisfies the following formula: $\begin{cases} 0 & \text{if } (*) \\ 10^{\mathtt{E}} \times \left(\dfrac{\mathtt{c.agreement(j,a[j],*challenge)}}{\mathtt{max(c.agreement(i,a[i],*challenge)\ |\ i)}} \right)^{\mathtt{F}} & \text{else.} \end{cases}$ where $(*)$ is the property that there exists an index i for which: 1) the j-th organelle of c satisfies the contrast profile define by the list profiles[i] and the value brightness[i], which means that the list returned by the function `self.contrast(brightness,profiles)(c.organelles[j],*challenge)` contains at least one True value (see section 3.1.3); 2) the agreement c.agreement(j,a[j],*challenge) (see section 4.1.16) is greater than or equal to scores[i].

In the following examples, we illustrate the use of the function usf.gamma with no input challenge given. Note that giving such an input would amount to the same type of behavior, except that some of the components of the organelles of the Cell item c (see section 4.1.3) would not be considered in the computation.

```
>>> E = 1
>>> F = 1
>>> brightness = [.25,.5,.75]
>>> profiles = [[(.0,.9),(.0,.5),(.0,.25)],[(.0,.4),(.0,.6),(.0,.5)]]
>>> scores = [.5,.8]
>>> gamma_parameter = usf.gamma(E,F,brightness,profiles,scores)
>>> c = Cell(dimension = 5, residual = 0.5, cytosol = [-2,3,5,0,0],
organelles = [[1,2,5,3,7], [5,0,0,0,4],[25,51,8,1,52]])
>>> a = [[70,9,5,7,58],[1,5,65,2,44],[8,7,87,5,100]]
>>> g = gamma_parameter(c,a)
[brightness] 0.8 0.4 0.2
True False

[brightness] 0.4 0.4 0.4
False True

[brightness] 0.6 0.4 0.4
False False
```

Above, the grey messages inform us that

- the first organelle of `c` satisfies the contrast profile defined by `profiles[0]`,
- the second organelle of `c` satisfies the contrast profile defined by `profiles[1]`,
- the third organelle of `c` does not satisfy any of the contrast profiles of `profiles`.

However, the previous data is only half of the information needed by `gamma_parameter` to determine the values of the output `g`. Specifically, the function `gamma_parameter` also tests whether the agreements of the organelles with their respective inputs are greater than or equal to the corresponding thresholds given in `scores`. If the agreement associated with the j-th organelle of `c` is less than the threshold `scores[j]`, then the elements of the j-th list of `g` are zero values.

We illustrate the previous discussion through the following display, in which we show the agreements and the values for the gamma parameters together.

```
>>> for j in range(len(g)):
...  print "agreement:  "+str(c.agreement(j,a[j]))
...  print "gammas:  "+str(g[j])
...
```

Below, the gamma parameter associated with the first organelle of `c` is equal to `10.0 * 1.0` because that organelle is associated with the maximum agreement, which also is greater than `scores[0]`.

```
agreement:  0.627367719768
gammas:  [10.0, 10.0, 10.0, 10.0, 10.0]
```

Now, the gamma parameter associated with the second organelle of `c` is equal to `10.0 * 0.0` because its associated agreement is less than `scores[1]`.

```
agreement:  0.359257831799
gammas:  [0.0, 0.0, 0.0, 0.0, 0.0]
```

Finally, the gamma parameter associated with the third organelle of `c` is equal to `10.0 * 0.9990995982390753` because that organelle does not satisfy any of the contrast profile and hence does not need to be filtered through an agreement test.

```
agreement:  0.626802836768
gammas:  [9.990995982390753, 9.990995982390753, 9.990995982390753,
9.990995982390753, 9.990995982390753]
```

3.1.5. Description of usf.print_data (function). Writing in progress – see cl_usf.py for more information.

3.1.6. Description of usf.print_root (function). Writing in progress – see cl_usf.py for more information.

3.1.7. Description of usf.print_organelles (function). Writing in progress – see cl_usf.py for more information.

3.1.8. Description of usf.print_tree (function). Writing in progress – see cl_usf.py for more information.

3.1.9. Description of usf.parse_image (function). Writing in progress – see cl_usf.py for more information.

3.1.10. Description of usf.get_memory (function). Writing in progress – see cl_usf.py for more information.

3.1.11. Description of usf.get_trees (function). Writing in progress – see cl_usf.py for more information.

3.1.12. Description of usf.get_last_cycle (function). Writing in progress – see cl_usf.py for more information.

3.1.13. Description of usf.join_images (function). Writing in progress – see cl_usf.py for more information.

3.1.14. Description of usf.rgb_colormap (function). Writing in progress – see cl_usf.py for more information.

3.1.15. Description of usf.make_rgb_panel (function). Writing in progress – see cl_usf.py for more information.

3.1.16. Description of usf.make_rgb_grid (function). Writing in progress – see cl_usf.py for more information.

3.1.17. Description of usf.make_rgb_tree (function). Writing in progress – see cl_usf.py for more information.

3.1.18. Description of usf.draw_arrow (function). Writing in progress – see cl_usf.py for more information.

3.1.19. Description of usf.zero_matrix (function). Writing in progress – see cl_usf.py for more information.

3.1.20. Description of usf.join_fibers (function). Writing in progress – see cl_usf.py for more information.

3.1.21. Description of usf.cliques (function). Writing in progress – see cl_usf.py for more information.

3.2. Description of debug_time (class item)

3.2.1. Introduction. This section introduces the reader to the class item debug_time, which gives an easy way to debug programs using this library (see examples in section 2).

3.2.2. Structure. The following tables give a preview of the class item usf. The table given below describes the various dependencies of the class item.

Dependencies	
Class type	Module section
_DebugTime	N/A
Statistics	
▷ Importable objects: 3	
▷ Non-importable objects: 0	
▷ Importable methods: 3	
▷ Non-importable methods: 0	

The following table gives a description of the 3 importable objects of the class:

Objects		
Name	Type	Related sections
.event_names	list(string)	▷ section 3.2.3
.iteration	int	▷ section 3.2.3
.global_time	string	▷ section 3.2.3

Finally, the following table gives a description of the 3 importable methods of the class:

Methods			
Name	Input types	Output types	Related sections
.__init__	- self	- self	▷ section 3.2.3
.set	- string	- self	▷ section 3.2.4
.call	- self	- self	▷ section 3.2.5

3.2.3. Description of debug_time.__init__ (function). Writing in progress – see cl_dbg.py for more information.

3.2.4. Description of debug_time.set (function). Writing in progress – see cl_dbg.py for more information.

3.2.5. Description of debug_time.call (function). Writing in progress – see cl_dbg.py for more information.

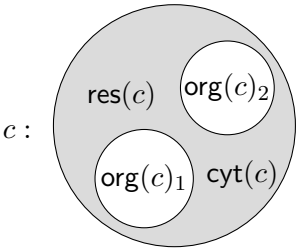
Chapter 4

Presentation of the module `celloperad.py`

4.1. Description of `Cell` (class)

4.1.1. Introduction. This section introduces the reader to the code of the class `Cell`, which possesses the following external dependencies.

The main goal of the class `Cell` is to model the features of a cell, as defined in [1, Def. 1.2]. Before presenting the features of the class, recall that, mathematically, a cell of some dimension N, equipped with n organelles, consists of a non-negative real number $\mathsf{res}(c)$, called the residual; a N-dimensional vector $\mathsf{cyt}(c) = (\mathsf{cyt}(c)_1, \dots, \mathsf{cyt}(c)_N)$ of real numbers, called the cytosolic content and a n-tuple $\mathsf{org}(c) = (\mathsf{org}(c)_1, \dots, \mathsf{org}(c)_n)$ of vectors in $\mathbb{R}_+^N$, where each vector $\mathsf{org}(c)_i$ is called the i-th organelles of c.



In this library, the class `Cell` is equipped with 9 objects, modeling various parameters pertaining to the previous definition, and 3 types of methods, which are listed below:

▷ a set of 3 methods meant to be used for testing and debugging:

- `check`: checks that the parameters of a cell are well-defined;
- `copy`: copies the data of a cell somewhere else in the memory;
- `stdout`: prints the list of parameters defining a cell on the standard output.

▷ a set of 9 methods meant to model the concepts developed in [1]:

- `__init__`: returns a cell for its associated set of parameters.
- `content`: returns the content $K(c)$ of a cell c [1, Def. 1.21].
- `compose`: computes an operadic composition of cells [1, Def. 1.6].
- `compose_all`: computes a simultaneous operadic composition of cells [1, Def. 1.14].

- `left`: returns the cell $\mathsf{left}(c)(\alpha, \kappa, \lambda)$, as defined in [1, Conv. 1.19].
- `right`: returns the list $\mathsf{right}(c)(\mu, \alpha, \kappa)$ of cells, as defined in [1, Conv. 1.19].
- `spontaneous_reaction`: returns the *cleaning* of a cell – see [1, Rem. 1.31 & Def 2.13].
- `action`: returns the action of a cell on a vector, as defined in [1, Def. 1.29].
- `algebra_operator`: returns the values of the algebra operator $U(c, d)(a)$ as expressed in [1, Prop. 1.35 (1.4)], given that certain fitting conditions are satisfied.

▷ and a set of 8 methods engineering the ideas of [1] in order to produce the learning algorithm described therein:

- `allostasis`: generalizes the formula of the allostatic differential $\partial_{j,v} U^2(c, d)/\partial(c, d)$ given in [1, Prop. 1.48] to a more practical operator.
- `agreement`: returns the k-th agreement of a cell on a vector [1, Def. 2.22].
- `merge`: merges a subset of the organelles of a cell.
- `divide`: decomposes a cell c into a pair (c_1, c_2) of cells such that $c = c_1 \otimes c_2$, as illustrated in [1, Conv. 1.50 & Ex. 1.51], provided that the cytosol of c is zero.
- `organelle_proportions`: returns the list of ratios $\mathsf{org}(c)_{n,u}/\mathcal{S}\mathsf{org}(c)_n$, which are used in the formula shown in [1, Th. 1.57].
- `content_proportions`: returns the list of ratios $\mathcal{S}\mathsf{org}(c)_n/(\sum_{k=1}^{n} \mathcal{S}\mathsf{org}(c)_k)$ appearing in the formula of [1, Prop. 1.54] provided that certain fitting conditions hold.
- `best_compartment`: returns the best partitioning of the organelles of a cell according to one of the criteria discussed in [1, Rem. 1.58].
- `proposed_clustering`: proposes an input cluster for the method `merge` or `divide`.

4.1.2. Structure. The following tables give a preview of the class `Cell`. The table given below describes the various dependencies of the class.

Dependencies	
Superclass ancestry	Module section
`object`	N/A
Statistics	
▷ Importable objects: 9	
▷ Non-importable objects: 0	
▷ Importable methods: 20	
▷ Non-importable methods: 0	

The following table gives a description of the 9 importable objects of the class.

Objects		
Name	Type	Related sections
`.dimension`	`int`	▷ section 4.1.3
`.residual`	`float`	▷ section 4.1.3
`.cytosol`	`list(float)`	▷ section 4.1.3
`.organelles`	`list(list(float))`	▷ section 4.1.3
`.K`	`list(float)`	▷ section 4.1.3
`.SK`	`float`	▷ section 4.1.3
`.Sorg`	`list(float)`	▷ section 4.1.3
`.well_defined`	`bool`	▷ section 4.1.3
`.well_defined_cytosol`	`list(bool)`	▷ section 4.1.3

Finally, the following table gives a description of the 20 importable methods of the class:

Methods			
Name	Input types	Output types	Related sections
`.__init__`	- int - float - list(float) - list(list(float))	- self	▷ section 4.1.3
`.check`	- self	- self	▷ section 4.1.4
`.copy`	- self	- Cell	▷ section 4.1.5
`.stdout`	- self	- self	▷ section 4.1.6
`.content`	- self	- list(float)	▷ section 4.1.7
`.compose`	- int - Cell	- Cell	▷ section 4.1.8
`.compose_all`	- list(Cell)	- Cell	▷ section 4.1.9
`.left`	- list(float) - list(float) - list(list(float))	- Cell	▷ section 4.1.10 ▷ section 4.1.11
`.right`	- list(float) - list(float) - list(float)	- Cell	▷ section 4.1.11 ▷ section 4.1.10
`.spontaneous_reaction`	- self	- self	▷ section 4.1.12 ▷ section 4.1.7 ▷ section 4.1.18 ▷ section 4.1.20
`.action`	- list(list(float))	- list(float)	▷ section 4.1.13
`.algebra_operator`	- list(list(float)) - list(float)	- list(float)	▷ section 4.1.14
`.allostasis`	- list(list(float)) - list(float) - int - int	- float	▷ section 4.1.15
`.agreement`	- int - list(float) - list(float)	- float	▷ section 4.1.16
`.merge`	- list(list(float)) - string	- self	▷ section 4.1.17
`.divide`	- list(list(float))	- Cell * Cell	▷ section 4.1.18
`.organelle_proportions`	- self	- list(list(float))	▷ section 4.1.19 ▷ section 4.1.21
`.content_proportions`	- self	- list(float)	▷ section 4.1.20 ▷ section 4.1.22
`.best_compartment`	- list(list(int))	- list(int)	▷ section 4.1.21 ▷ section 4.1.22
`.proposed_clustering`	- list(list(float)) - string - float	- list(int)	▷ section 4.1.22 ▷ section 4.1.21

4.1.3. Description of `.__init__` (method). This section describes the code and the functionalities of the method `.__init__`. The method is equipped with the following inputs.

`.__init__`		
Inputs	Types	Specifications
`dimension`	`int`	necessary
`residual`	`float`	necessary
`cytosol`	`list(float)`	necessary
`organelles`	`list(list(float))`	necessary

The method possesses one conditional action, which we describe below through sevaral examples.

Action	
Condition	If the length of the list `cytosol` and the lengths of the lists contained in `organelles` are all equal to `dimension`
Description	The method initializes the object `self.dimension` with the value of `dimension`; the object `self.residual` with the value of `residual`; the object `self.cytosol` with the list stored in `cytosol`; and the object `self.organelles` with the list stored in `organelles`. The method also initializes the object `self.K` with the *content* [1, Def. 1.21] of the cell, which also corresponds to the output of the method `self.content` (see section 4.1.7). The method stores in the object `self.SK` the sum `sum(self.K)` and stores in the object `self.Sorg` a list containing the sums `sum(self.organelles[i])` for every index `i`. Finally, the method initializes the objects `self.well_defined` and `self.well_defined_cytosol` with boolean values. The former indicates whether the value of `self.residual` as well as the sum `self.residual + sum(self.cytosol)`, and the values stored in every variable `self.organelles[i][u]` are non-negative. The latter indicates whether the values stored in every variable `self.cytosol[u]` are non-negative.

In the example given below, we define a `Cell` item through the constructor and we check that the arguments passed to the constructor are stored in the appropriate variables.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> print c.dimension
2
>>> print c.residual
0.5
>>> print c.cytosol
[-2, 3]
>>> print c.organelles
[[1, 2], [5, 0], [8, 7]]
```

The values stored in the objects `c.K`, `c.SK` and `c.Sorg` are quantities whose values are updated whenever the parameters of the cell change. This is to allow a quick access to their values instead of going through their re-computation. Specifically,

- `c.K` contains the content of the cell `c` (see below), which can also be computed by the method `c.content()` (see section 4.1.7). More specifically, the object `c.K` contains a list whose element `c.K[u]`, for any given `u` ranging from `0` to `self.dimension-1`, is the sum

$$\texttt{c.cytosol[u]} + \sum_{\texttt{i}} \texttt{c.organelles[i][u]}.$$

In [1], the quantity `c.K` corresponds to the quantity $K(c)$ introduced in [1, Def. 1.21];

- ▷ `c.SK` contains the sum `sum(c.K)` of the elements of the list `c.K`. The quantity `c.SK` corresponds to the quantity $\mathcal{S}K(c)$ used in [1, Def. 1.29];
- ▷ `c.Sorg` contains a list whose elements are the sums of each row of the matrix `c.organelles`, meaning that each `c.Sorg[u]` is the sum

$$\sum_{\texttt{i}} \texttt{c.organelles[i][u]}.$$

In [1], the quantity `c.Sorg` corresponds to the quantity $\mathcal{S}\texttt{org}(c)$ used in [1, Prop. 1.45].

```
>>> print c.K
[12, 12]
>>> print c.SK
24
>>> print c.Sorg
[3, 5, 15]
```

In the display given above, we show the values of `c.well_defined` and `c.well_defined_cytosol`. We can see that the cell `c` is well defined, but the first component of `c.cytosol` is negative, which may be an important piece of information if one wants to update the parameters of `c.cytosol` without changing the value of `c.well_defined`.

```
>>> print c.well_defined
True
>>> print c.well_defined_cytosol
[False, True]
```

4.1.4. Description of `.check` (method). This section describes the code and the functionalities of the method `.check`, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method prints, on the standard output, a list of boolean values indicating whether each of the values given by the object `self.residual`, the expression `self.residual + sum(self.cytosol)`, and the elements `self.cytosol[u]` and `self.organelles[i][u]` is non-negative.

Here is an example that illustrates the previous description.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-4,3], organelles =
[[1,2], [5,0], [8,7]])
>>> c.check()
residual:  True
residual + sum(cytosol):  False
-> cytosol[0]:  False
-> cytosol[1]:  True
organelles[0][0]:  True
organelles[0][1]:  True
organelles[1][0]:  True
organelles[1][1]:  True
organelles[2][0]:  True
organelles[2][1]:  True
```

4.1.5. Description of `.copy` (method). This section describes the code and the functionalities of the method `.copy`, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method allocates, somewhere else in memory, a new `Cell` item whose parameters are the same as `self`.

Below, we use the method `.stdout` (see section 4.1.6) to display the parameters of the cells created using `.copy`.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> c.stdout()
residual:  0.5
cytosol[0]:  -2
cytosol[1]:  3
1-th organelle:  [1, 2]
2-th organelle:  [5, 0]
3-th organelle:  [8, 7]
>>> d = c.copy()
>>> c.stdout()
residual:  0.5
cytosol[0]:  -2
cytosol[1]:  3
1-th organelle:  [1, 2]
2-th organelle:  [5, 0]
3-th organelle:  [8, 7]
```

4.1.6. Description of `.stdout` (method). This section describes the code and the functionalities of the method `.stdout`, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method prints the values stored in the variables `self.residual`, `self.cytosol[u]` and `self.organelles[i][u]` on the standard output.

As shown in the following example, we can display the parameters of a cell by calling the method `.stdout`.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> c.stdout()
residual:  0.5
cytosol[0]:  -2
cytosol[1]:  3
1-th organelle:  [1, 2]
2-th organelle:  [5, 0]
3-th organelle:  [8, 7]
```

4.1.7. Description of .content (method). This section describes the code and the functionalities of the method .content, which does not take any input. The method possesses one action, which we describe below through sevaral examples.

Action	
Condition	Always
Description	The method returns a list the_content, of length self.dimension, whose element the_content[u] is the sum of the value contained in self.cytosol[u] with the values contained in self.organelles[0][u], self.organelles[1][u], ... and self.organelles[self.dimension-1][u].

We illustrate the use of .content through the following three examples.

```
>>> c = Cell(dimension = 2, residual = 16.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> print c.content()
[12, 12]
>>> c = Cell(dimension = 2, residual = 16.5, cytosol = [0,0], organelles =
[[0,1], [1,0], [9,2]])
>>> print c.content()
[9, 4]
```

Note that the content of a Cell item will contain negative values if the values of the list .cytosol are negative and large enough.

```
>>> c = Cell(dimension = 2, residual = 16.5, cytosol = [-18,2], organelles
= [[0,1], [1,0], [9,2]])
>>> print c.content()
[-8, 5]
```

One way to prevent such a scenario is to make sure that the values contained in .cytosol do not go below a certain threshold. This can be done through the method

.spontaneous_reaction

(see section 4.1.12), which sets the values contained in .cytosol to 0, as shown below.

```
>>> c.spontaneous_reaction()
>>> print c.content()
[10, 3]
>>> c.stdout()
residual:  0.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [0, 1]
2-th organelle:  [1, 0]
3-th organelle:  [9, 2]
```

4.1.8. Description of `.compose` (method). This section describes the code and the functionalities of the method `.compose`. The method is equipped with two inputs.

`.compose`		
Inputs	Types	Specifications
`index`	`int`	necessary
`a_cell`	`Cell`	necessary

The method possesses one conditional action, which we describe below through an example.

Action 1	
Condition	If `a_cell.dimension` is equal to `self.dimension`
Description	The method returns the operadic composition of the `Cell` item `self` with the `Cell` item `a_cell` at the `index`-th organelle (see [1, Def. 1.6]), namely the cell whose dimension is `self.dimension`, whose residual is the sum `self.residual + a_cell.residual`, whose cytosol is the list containing the sums `self.cytosol[u] + a_cell.cytosol[u]` and whose lists of organelles is the list obtained from replacing the (1+`index`)-th index of the list `self.organelles` with the entire list of organelles contained in `a_cell.organelles`.

The following example shows how the method `.compose` can be used to compose cells at a given organelle. The idea is to mix the organelles and the cytosol of the "inner cell" with the organelles and the cytosol of the "outer cell".

```
>>> outer_cell = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3],
organelles = [[1,2], [5,0], [8,7]])
>>> inner_cell = Cell(dimension = 2, residual = 0.5, cytosol = [0,0],
organelles = [[0,1], [1,0], [9,2]])
>>> comp = outer_cell.compose(1,inner_cell)
```

Below, we can use the method `.stdout` to see that the organelles of the inner cell constitutes the organelles of the composite cell from the 2nd organelle to 4-th organelle.

```
>>> comp.stdout()
residual:  1.0
cytosol[1]:  -2
cytosol[2]:  3
1-th organelle:  [1, 2]
2-th organelle:  [0, 1]
3-th organelle:  [1, 0]
4-th organelle:  [9, 2]
5-th organelle:  [8, 7]
```

4.1.9. Description of `.compose_all` (method). This section describes the code and the functionalities of the method `.compose_all`. The method is equipped with the following input variable.

`.compose_all`		
Inputs	Types	Specifications
`cells`	`list(Cell)`	necessary

The method possesses one conditional action, which we describe below through an example.

Action 1	
Condition	If the length of the list `cells` is equal to `len(self.organelles)`
Description	The method returns the operadic composition of the `Cell` item `self` with each of the `Cell` items contained in `cells` for their corresponding indices in `cells`. The returned `Cell` item corresponds to a simultaneous composition of cells, as defined in [1, Def. 1.14]

Below, we show an example of a simultaneous composition of cells.

```
>>> outer_cell = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3],
organelles = [[1,2], [5,0], [8,7]])
>>> incell_1 = Cell(dimension = 2, residual = 0.5, cytosol = [0,0],
organelles = [[0,1], [1,0], [9,2]])
>>> incell_2 = Cell(dimension = 2, residual = 0.5, cytosol = [0,0],
organelles = [[10,1]])
>>> incell_3 = Cell(dimension = 2, residual = 0.5, cytosol = [0,0],
organelles = [[2,2],[22,0]])
>>> comp = outer_cell.compose_all([incell_1,incell_2,incell_3])
```

As shown below, the organelles of the "outer cell" were all replaced with the list of organelles of the "inner cells".

```
>>> comp.stdout()
residual:  2.0
cytosol[1]:  -2
cytosol[2]:  3
1-th organelle:  [0, 1]
2-th organelle:  [0, 1]
3-th organelle:  [9, 2]
4-th organelle:  [10, 1]
5-th organelle:  [2, 2]
6-th organelle:  [22, 0]
```

4.1.10. Description of `.left` (method). This section describes the code and the functionalities of the method `.left`. The method is equipped with the following input variables.

`.left`		
Inputs	Types	Specifications
`alpha_var`	`list(float)`	necessary
`kappa_var`	`list(list(float))`	necessary
`lambda_var`	`list(list(float))`	necessary

The method possesses one conditional action, which we describe below through an example.

Action	
Condition	If the lengths of the lists `alpha_var`, `kappa_var`, and `lambda_var` are equal to each other
Description	If we let c represents the `Cell` item `self` and we let α, κ and λ represent the three inputs lists, then the method returns the `Cell` item $\mathsf{left}(c)(\alpha,\kappa,\lambda)$, as defined in [1, Conv. 1.19]. This `Cell` item constitutes half of a solution for a factorization problem expressing `self` as a simultaneous composition of the form: $$c = \mathsf{left}(c)(\alpha,\kappa,\lambda) \circ \mathsf{right}(c)(\mu,\alpha,\kappa).$$ The other half $\mathsf{right}(c)(\mu,\alpha,\kappa)$ is accessible through the method `self.right` (see section 4.1.11) and returns a list of `Cell` items. The output of `self.left(alpha_var,kappa_var,lambda_var)` is a `Cell` item whose dimension is equal to `self.dimension`, whose residual is equal to the difference between `self.residual` and `sum(alpha_var)`, whose cytosol is the difference between `self.cytosol` the total sum of the coefficients of the matrix `kappa_var` and whose list of organelles is `lambda_var`.

The example given below uses the same `Cell` item as well as the same set of inputs `alpha_var` and `kappa_var` as those used in section 4.1.11, where we describe the other half of the factorization returned by the method `.right`.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> left = c.left([0,0.125],[[1,0],[0,2]],[[2,5],[0,7]])
>>> left.stdout()
residual:  0.375
cytosol[1]:  -3
cytosol[2]:  1
1-th organelle:  [2, 5]
2-th organelle:  [0, 7]
```

4.1.11. Description of `.right` (method). This section describes the code and the functionalities of the method `.right`. The method is equipped with the following input variables.

`.right`		
Inputs	Types	Specifications
`mu_var`	`list(float)`	necessary
`alpha_var`	`list(float)`	necessary
`kappa_var`	`list(list(float))`	necessary

The method possesses one conditional action, which we describe below through an example. Note that the first condition given in the following table is justified by the factorization theorem stated in [1, Th. 1.18].

Action	
Condition	If the sum `sum(mu_var)` is equal to the length of the list `self.organelles` and the lengths of the lists `lambda_var`, `alpha_var`, and `kappa_var` are equal to each other
Description	If we let c represents the `Cell` item `self` and we let μ, α and κ represent the three input lists, then the method returns the list $\mathsf{right}(c)(\mu,\alpha,\kappa)$ of `Cell` items, as defined in [1, Conv. 1.19]. This `Cell` item constitutes half of a solution for a factorization problem expressing `self` as a simultaneous composition of the form: $$c = \mathsf{left}(c)(\alpha,\kappa,\lambda) \circ \mathsf{right}(c)(\mu,\alpha,\kappa).$$ The other half $\mathsf{left}(c)(\alpha,\kappa,\lambda)$ is accessible through the method `self.left` (see section 4.1.10) and returns a `Cell` item. Each element `self.right(mu_var,alpha_var,kappa_var)[i]` is a `Cell` item whose dimension is equal to `self.dimension`, whose residual is equal to `alpha_var[i]`, whose cytosol is equal to the list `kappa_var[i]` and whose list of organelles is given by the sublist of `self.organelles` ranging from the index `L = sum(mu_var[:i])` to index `L+mu_var[i]-1`.

The example given below uses the same `Cell` item as well as the same set of inputs `alpha_var` and `kappa_var` as those used in section 4.1.10, where we describe the other half of the factorization returned by the method `.left`.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> right = c.right([1,2],[0,0.125],[[1,0],[0,2]])
>>> for r in right:
...     r.stdout()
...     print "--"
...
residual:  0
cytosol[1]:  1
cytosol[2]:  0
1-th organelle:  [1, 2]
--
residual:  0.125
cytosol[1]:  0
cytosol[2]:  2
1-th organelle:  [5, 0]
2-th organelle:  [8, 7]
--
```

4.1.12. Description of `.spontaneous_reaction` (method). This section describes the code and the functionalities of the method `.spontaneous_reaction`, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method returns the 'cleaning' [1, Def. 2.13] of the Cell item self. This cleaning is meant to simulate an overall chemical reaction occurring in the cytosol of the cell, as described in [1, Rem. 1.31]. Specifically, the method adds the value sum(self.cytosol) to self.residual while it subtracts it from self.SK. If the value of self.residual becomes negative after that change, then the function exits the program with an error message. In the case where no error message is returned, the method goes on and subtracts the value self.cytosol[u] from the value self.K[u] for every index u. Finally, the method sets the values of the list self.cytosol to 0.

The idea behind the "overall chemical reaction" computed by .spontaneous_reaction is to convert the positive values of the cytosol, which can be seen as available resources, into numbers that would compensate the negative values of the list .cytosol. These negative values can be seen as used or missing resources that needs to be compensated in order to re-establish equilibirum inside the cell. In the case where the "available resources" are not enough to compensate the "missing resources", we want to use the value stored in the object .residual as an alternative resource. This value can be interpreted as the energetic surplus of the system. The product of this reaction is the sum sum(self.cytosol), which can be seen as the energy remaining after the global reaction.

$$\texttt{residual+ positive\_cytosol} \to \texttt{sum(cytosol) + negative\_cytosol}$$

In the following example, we show that the method .spontaneous_reaction changes the values of the content .K (see section 4.1.3), its sum .SK and the value of the object .residual.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> print c.SK
24
>>> print c.K
[12, 12]
>>> c.spontaneous_reaction()
>>> c.stdout()
residual:  1.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [1, 2]
2-th organelle:  [5, 0]
3-th organelle:  [8, 7]
>>> print c.SK
23
>>> print c.K
[14, 9]
```

4.1.13. Description of .action (method). This section describes the code and the functionalities of the method .action. The method is equipped with the following input variable.

.action		
Inputs	Types	Specifications
matrix	list(list(float))	necessary

The method possesses one conditional action, which we describe below through an example.

Action	
Condition	If the length of matrix is equal to len(self.organelles) and the length of each lists in matrix is equal to self.dimension
Description	The method returns the action of the Cell item self on the matrix, as defined in [1, Def. 1.29]. More specifically, the method returns a list the_action of length self.dimension whose element the_action[u] is the sum of the values (self.organelles[i][u]/self.SK) * matrix[i][u] over every index i ranging from 0 to len(self.organelles)-1. By definition of the object self.SK (see section 4.1.3), the ratio self.organelles[i][u]/self.SK is smaller than 1 when sum(self.cytosol) is positive. In this case, we can interpret the output the_action as a vector of conditional expected values (see the formula given in [1, Def. 1.29]).

The following example shows how to use the method .action.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> a = [[70,9],[1,5],[5,81]]
>>> print c.action(a)
[4.791666666666666, 24.375]
```

4.1.14. Description of .algebra_operator (method). This section describes the code and the functionalities of the method .algebra_operator. The method is equipped with the following input variable.

.algebra_operator		
Inputs	Types	Specifications
matrix	list(list(float))	necessary

The method possesses one conditional action, which we describe below through an example.

Action	
Condition	If the length of matrix is equal to len(self.organelles) and the length of each lists in matrix is equal to self.dimension
Description	If we let c represent self and we let a represent the input matrix, the method returns the value of the algebra operator $U(c,d)(a)$ [1, Def. 1.33], where d is inferred from the organelles of c. More specifically, we use the formula of [1, Prop. 1.35 (1.4)], for which we replace each coefficient $(d_k \cdot a_k)_u$ shown therein with the element matrix[k][u]. In other words, the output of the method .algebra_operator is the sum of the terms (dividend[k]/self.SK) * matrix[k][u], over every index k ranging from 0 to len(self.organelles)-1, where dividend[k] is equal to (self.Sorg[k]-self.organelles[k][u]).

The following example shows how to use the method .algebra_operator.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> a = [[70,9],[1,5],[5,81]]
>>> print c.algebra_operator(a)
[7.291666666666666, 28.416666666666668]
```

As explained in the description above, the method `.algebra_operator` returns the values of a formula that is more general than the one given [1, Prop. 1.35 (1.4)]. To recover the formula given therein, we would need to give to the method `.algebra_operator`, the outputs of the method `.action` for a list of cells `d[1]`, ..., `d[len(self.organelles)]`. For instance, the method `.allostasis` (section 4.2.12) associated with the class `SuperCell` uses the method `.algebra_operator` in this way.

4.1.15. Description of `.allostasis` (method). This section describes the code and the functionalities of the method `.allostasis`. The method is equipped with the following input variables.

`.allostasis`		
Inputs	Types	Specifications
`matrix`	`list(list(float))`	necessary
`weight`	`list(float)`	necessary
`org_index`	`int`	necessary
`dim_index`	`int`	necessary

The method possesses one conditional action, which we describe below through an example.

Action	
Condition	If the length of `matrix` is equal to `len(self.organelles)` and the length of the list `matrix[org_index]` is equal to `self.dimension`
Description	If we let c represent `self`, we let a represent the input `matrix` and we let j and v denote the inputs `org_index` and `dim_index`, the method returns the value of the "allostatic differential" $\partial_{j,v}U(c,a)/\partial(c,d)(a)$ [1, Def. 1.47], where d is inferred from the organelles of c. More specifically, we use the formula given in [1, Prop. 1.48], for which we replace each coefficient $U(c,d)(a)_u$ shown in the formula therein with the element `weight[u]`. In other words, the output of the method `.allostasis` is the sum of the terms `- (ratio[u] / self.SK) * (term1 - term2[u])`, where `ratio[u]` is equal to the ratio `self.organelles[org_index][u]/self.Sorg[org_index]`, where `term1` is equal to the multiplication `matrix[org_index][dim_index] * weight[dim_index]` and where `term2[u]` is equal to the multiplication `matrix[org_index][u] * weight[u]` over every index `u` ranging from `0` to `self.dimension-1`.

In the following example, we illustrate the use of the method `.allostasis` in the case where the input variable `weight` is the vector $U(c,d)(a)_u$. In other words, the vector `weight` contains the output of the function `c.algebra_operator(a)` (see section 4.1.14). This vector corresponds to the list of values that one is supposed to use with `.allostasis` in order to satisfy the formula given in [1, Prop. 1.48].

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> a = [[70,9],[1,5],[5,81]]
>>> for j in range(len(c.organelles)):
...     for v in range(c.dimension):
...       print (j, v), c.allostasis(a,c.algebra_operator(a),j,v)
(0, 0) -7.07407407407
(0, 1) 3.53703703704
(1, 0) -0.0
(1, 1) -5.61631944444
(2, 0) 44.047337963
(2, 1) -50.3398148148
```

4.1.16. Description of `.agreement` (method). This section describes the code and the functionalities of the method `.agreement`. The method is equipped with the following three input variables, including one that is optional.

`.agreement`		
Inputs	Types	Specifications
`index`	`int`	necessary
`vector`	`list(float)`	necessary
`*challenge`	`list(float)`	optional

The method possesses two actions, which we describe below through sevaral examples.

Action 1	
Condition	If `challenge` is empty (absent from the list of given inputs)
Description	The method returns the agreement of the underlying `Cell` item `self` with the input `vector`, as defined in [1, Def. 2.22]. In other words, the method computes the normalized scalar product of the vectors `self.organelles[index]` and `vector`. When the list `vector` only contains non-negative values, the output of the method is a `float` item between `0.0` and `1.0`.

The following example shows how to use the method `.agreement`.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> a = [[70,9],[1,5],[5,81]]
>>> for j in range(len(c.organelles)):
...     print j,"-->",c.agreement(j,a[j])
...
0 --> 0.557621357192
1 --> 0.196116135138
2 --> 0.703620697651
```

We now describe the second action of the method `.agreement`.

Action 2	
Condition	If `challenge` is given and contains a unique element (meant to be a list of length 3 or more, containing `int` values)
Description	The method returns the agreement of the underlying `Cell` item `self` with the list `v` of length `len(self.dimension)` such that `v[u]` is equal to the coefficient `vector[u]` if the following condition is satisfied `challenge[0][0] <= u % challenge[0][2] <= challenge[0][1]` and `v[u]` is equal to 0 otherwise.

The following example shows how to use the method `.agreement`.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> a = [[70,9],[1,5],[5,81]]
>>> challenge1 = []
>>> for j in range(len(c.organelles)):
...     print j,"-->",c.agreement(j,a[j],*challenge1)
...
0 --> 0.557621357192
1 --> 0.196116135138
2 --> 0.703620697651
>>> challenge2 = [[0,0,2]]
>>> for j in range(len(c.organelles)):
...     print j,"-->",c.agreement(j,a[j],*challenge2)
...
0 --> 1.0
1 --> 1.0
2 --> 1.0
>>> challenge3 = [[1,1,2]]
>>> for j in range(len(c.organelles)):
...     print j,"-->",c.agreement(j,a[j],*challenge3)
...
0 --> 1.0
1 --> 0
2 --> 1.0
```

4.1.17. Description of `.merge` (method). This section describes the code and the functionalities of the method `.merge`. The method is equipped with the following two inputs, including one that is optional.

`.merge`		
Inputs	Types	Specifications
`list_of_organelles`	`list(list(float))`	necessary
`order = "order-sorted"`	`string`	optional

The method possesses one action, which we describe below through sevaral examples.

Action	
Condition	Always
Description	The method merges the organelles of `self` whose indices are in `list_of_organelles`. The organelles are merged into a unique organelle, which, after the merging, can be found at the index `min(list_of_organelles)`. The method gives the option to terminate faster if the list `list_of_organelles` is already sorted. We can do so by passing the string `"sorted"` to the second input variable `order`.

The following two examples show how to use the method `.merge`.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7], [4,27]])
>>> c.merge([0,2],order = "sorted")
>>> c.stdout()
residual:  0.5
cytosol[1]:  -2
cytosol[2]:  3
1-th organelle:  [9, 9]
2-th organelle:  [5, 0]
3-th organelle:  [4, 27]
```

Note that the method directly acts on the underlying `Cell` item `self`, meaning that the original item is lost after application of `.merge`.

```
>>> c.merge([2,1])
>>> c.stdout()
residual:  0.5
cytosol[1]:  -2
cytosol[2]:  3
1-th organelle:  [9, 9]
2-th organelle:  [9, 27]
```

4.1.18. Description of `.divide` (method). This section describes the code and the functionalities of the method `.divide`. The method is equipped with the following two input variables, including one that is optional.

`.divide`		
Inputs	Types	Specifications
`list_of_organelles`	`list(list(float))`	necessary
`order = "order-sorted"`	`string`	optional

The method possesses one conditional action, which we describe below through an example.

Action	
Condition	If the elements of the list `self.cytosol` are all zero values
Description	The method divides `self` into two `Cell` items `c1` and `c2` where `c1` contains all the organelles of `self` whose indices are in `list_of_organelles` and `c2` contains all the other organelles of `self`. The residual of both cells `c1` and `c2` is equal to half of `self.residual` and their cytosols are encoded by lists of zero values. The method gives the option to terminate faster if the list `list_of_organelles` is already sorted. We can do so by giving the string `"sorted"` to the second input variable `order`.

The following example shows how to use the method `.divide`. Note that the method will output an error message if the cytosol of the cell is not made of zero values. As shown below,

we can change the cytosol to a list of zero values by using the method .spontaneous_reaction (see section 4.1.12).

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7], [4,27]])
>>> c1, c2 = c.divide([0,2],order = "order-sorted")
Error:  in Cell.divide:  cytosol is not zero -- cannot divide
>>> c.spontaneous_reaction()
>>> c1, c2 = c.divide([0,2],order = "order-sorted")
>>> c1.stdout()
residual:  0.75
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [1, 2]
2-th organelle:  [8, 7]
>>> c2.stdout()
residual:  0.75
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [5, 0]
2-th organelle:  [4, 27]
```

4.1.19. Description of .organelle_proportions (method). This section describes the code and the functionalities of the method .organelle_proportions, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method outputs a list(list(float)) item prop whose element prop[i][u] is the ratio self.organelles[i][u]/self.Sorg[i].

The following example shows what the outputs of the method .organelle_proportions look like for a given cell.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> prop = c.organelle_proportions()
>>> for i in range(len(prop)):
...     print prop[i]
...
[0.3333333333333333, 0.6666666666666666]
[1.0, 0.0]
[0.5333333333333333, 0.4666666666666667]
[0.12903225806451613, 0.8709677419354839]
```

4.1.20. Description of .content_proportions (method). This section describes the code and the functionalities of the method .content_proportions, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method outputs a list(list(float)) item prop whose element prop[i] is the ratio self.Sorg[i]/sum(self.Sorg). This type of ratios corresponds to the type of ratios shown in [1, Prop. 1.54] provided that certain fitting conditions hold. Specifically, if the organelles of the Cell item self were equal to the contents of a collection of cells $d_1, d_2, \ldots, d_n$ and if the cytosol of self was only made of zero values, then the ratio prop[i] returned by the method .content_proportions would correspond to the ratio $$K(d_i)/K(d_1 \otimes d_2 \otimes \cdots \otimes d_n).$$ Since the tensoring of cells is associative, the previous type of ratios corresponds to the type of ratios used in [1, Prop. 1.54]. This correspondence between the outputs of .content_proportions and the previous ratios is used by some of the methods associated with the class SuperCell (see section 4.2). Very often, these methods use .content_proportions with the method .spontaneous_reaction in order to clear the cytosol of the underlying cell and make the previous correspondence hold.

The following example shows what the outputs of the method .content_proportions look like for a given cell.

```
>>> c = Cell(dimension = 2, residual = 0.5, cytosol = [-2,3], organelles =
[[1,2], [5,0], [8,7]])
>>> prop = c.content_proportions()
>>> for i in range(len(prop)):
...     print prop[i]
...
0.0555555555556
0.0925925925926
0.277777777778
0.574074074074
```

4.1.21. Description of .best_compartment (method). This section describes the code and the functionalities of the method .best_compartment. The method is equipped with the following input variable.

.best_compartment		
Inputs	Types	Specifications
cliques	list(list(int))	necessary

The method possesses one action, which we describe below through sevaral examples.

Action	
Condition	Always
Description	The method `.best_compartment` implements the selection criterion described in [1, Def. 2.32]. The goal of this criterion is to choose among all the lists of the input variable `cliques` a list that contains indices of organelles whose gathering would theoretically minimize the values of the algebra operator (section 4.1.14). As described in [1, Def. 2.32], the idea is to return one of the lists `cliques[k]` for which a certain associated sum `result_k` of terms of the form (4.1) `(dividend1 * divisor2)/float(dividend2 * divisor1)` is maximal. More specifically, if we let `compl[k]` denote the complement of `cliques[k]` in `range(len(self.organelles))`, then we compute, for every index `u` ranging from `0` to `self.dimension-1`, the following quantities: ▷ `dividend1 = sum(self.organelles[i][u] for i in cliques[k])` ▷ `divisor1 = sum(self.Sorg[i] for i in cliques[k])` ▷ `dividend2 = sum(self.organelles[i][u] for i in compl[k])` ▷ `divisor2 = sum(self.Sorg[i] for i in compl[k])` and we add ratio (4.1) to the variable `result_k` (initially equal to 0) whenever ratio (4.1) is greater than `1`. We then use the resulting value as a score to assess which of the list of organelles of `cliques` should be compartmentalized in a new cell in order to prominently minimize the values of the algebra operator (section 4.1.14). To better understand the previous statement, first observe that the ratios `dividend1/divisor1` and `dividend2/divisor2` correspond to the ratios that the method `.organelle_proportions` (section 4.1.19) would return if `self` was a `Cell` item with two organelles such that: 1) one organelle is encoded by the vector sum of those organelles whose indices are in `cliques[k]` 2) the other organelle is the sum of all the remaining organelles of `self`. Our interest in these two ratios lies in the statement of [1, Th. 1.57] and its interpretation given in [1, Rem. 1.58]. More specifically, the method is to be used when one wants to separate the organelles of `self` within two (potentially temporary) cells d_1 and d_2. The indices contained in the list `cliques[k]` are the indices of those organelles of `self` contained in the cell d_1 while the indices in `compl[k]` are the indices of those organelles of `self` contained in the cell d_2. In addition, if the two cells d_1 and d_2 were assumed to *fit* [1, Def. 1.23] the organelles of some third cell c – meaning that the content of d_1 (section 4.1.7) equals the vector $\texttt{org}(c)_1$ and the content of d_2 equals the vector $\texttt{org}(c)_1$ – then the method `.best_compartment` can be understood as follows:

Description	(i) it first computes the sum of real values resulting from the quotient of the quantity $\mathsf{org}(c)_{1,u}/\mathcal{S}\mathsf{org}(c)_1$ over the quantity $\mathsf{org}(c)_{2,u}/\mathcal{S}\mathsf{org}(c)_2$ whenever inequality (4.2) is satisfied for the index u; (4.2) $$\frac{\mathsf{org}(c)_{1,u}}{\mathcal{S}\mathsf{org}(c)_1} > \frac{\mathsf{org}(c)_{2,u}}{\mathcal{S}\mathsf{org}(c)_2};$$ (ii) it then returns one of the lists `cliques[k]` whose associated sum of quotients, computed at step (i), is maximal. Thus, the method is looking for a list `cliques[k]` for which inequality (4.2) seems to prominently hold over the list of indices u. The output of the method `.best_compartment` is used by the method `.proposed_clustering` (section 4.1.22) in order to know which of the proposed list `cliques[k]` is the best suited for creating a new compartment within the cell.

Below, we give four examples illustrating the use of the method `.best_compartment`.

```
>>> c = Cell(dimension = 3,residual = 0.5,cytosol = [-2,3,0],organelles =
[[1,10,1],[1,1,10],[10,1,1],[20,1,1],[1,20,1]])
>>> print c.best_compartment([[0,1],[0,3],[1,2],[1,3],[2,3]])
[1, 2]
>>> print c.best_compartment([[0,1,3],[1,2,3],[2,3]])
[2, 3]
>>> c = Cell(dimension = 3,residual = 0.5,cytosol = [-2,3,0],organelles =
[[1,10,1],[1,1,10],[10,1,1],[20,1,1],[1,20,1]])
>>> print c.best_compartment([[0,4],[1,4],[2,4],[3,4]])
[0, 4]
>>> print c.best_compartment([[0,3],[0,4],[0,1],[0,2]])
[0, 4]
>>> print c.best_compartment([[2,3],[2,1],[2,4],[2,0]])
[2, 3]
```

4.1.22. Description of `.proposed_clustering` (method). This section describes the code and the functionalities of the method `.proposed_clustering`. The method is equipped with the following three input variables, including one that is optional.

`.proposed_clustering`		
Inputs	Types	Specifications
`matrix`	`list(list(float))`	necessary
`option`	`string`	necessary
`filtering = 1.5`	`float`	optional

The method possesses one conditional action, which we describe below through sevaral examples.

Action	
Condition	If the length of `matrix` is equal to `len(self.organelles)` and the lengths of the lists contained in `matrix` are equal to `self.dimension`
Description	The method implements the clustering algorithm discussed throughout [1, Sec. 2.5]. Depending on the value of the input `option` (which corresponds to the parameter ε in [1, Sec. 2.5]), the method computes the lists of indices `i` for which the values `matrix[i][u]` are either greater or less (by a factor equal to the value of `filtering`) than the value $$\texttt{barycenter[u]} = \sum_{\texttt{k=0}}^{n} \texttt{matrix[k][u]} * \texttt{prop[k]}$$ where the list `prop` corresponds to the output of the method `self.content_proportions` (see section 4.1.20) and n denotes the integer `len(self.organelles)`. Note that, because each weight `prop[k]` can be viewed as a probability, the resulting list `barycenter` can be interpreted as a barycenter of the lists `matrix[k]`; see [1, Rem. 1.55] for further explanation. In more detail, the method goes through the following steps. First, it computes a `list(list(float))` item encoding a weighted adjacency $(n \times n)$-matrix `graph` whose coefficient `graph[i][j]` counts the number of indices `u`, ranging from `0` to `self.dimension-1`, for which the two values `matrix[i][u]` and `matrix[j][u]` are (1) either greater than the multiplication `filtering * barycenter[u]` if the input `option` is equal to the string `"division"`; (2) or less than the multiplication `filtering * barycenter[u]` if the input `option` is equal to the string `"merging"`. Here, the reader following the development of [1] may have noticed that the factor `filtering` corresponds to the factor ν used from [1, Def. 2.29] to [1, Def. 2.32]. If `graph` is the zero matrix, then the method `.proposed_clustering` returns the empty list. Otherwise, the method passes the matrix `graph` to the method `usf.cliques` (section 3.1.21), which returns a list `cliques` of the connected components of `graph` with maximal weight. In this case, the method `.proposed_clustering` returns the output of the function `self.best_compartment(cliques)` (see section 4.1.21).

In the spirit of [1, Rem. 1.58], the goal of the method `.proposed_clustering` is to find a set of organelles (specified by their indices) whose gathering in a new `Cell` item will decrease the values of `self.algebra_operator` (see section 4.1.14).

We illustrate the use of the method `.proposed_clustering` in the following examples, in which the method returns the indices of the organelles meant to be separated from the other organelles.

We start with an example illustrating the use of the option `"merging"` together with the value `filtering = 1`. In this case, the method `.proposed_clustering` corresponds to the fusion algorithm of [1, Sec. 2.5] for the parameters $\varepsilon = -$ and $\nu = 1$.

```
>>> c = Cell(dimension = 2,residual = 0.5,cytosol = [-2,3],organelles =
[[1,2],[5,0],[8,7],[4,27]])
>>> a = [[70,9],[1,5],[5,1],[12,45]]
>>> print "maximal clique = " + str(c.proposed_clustering(a,"merging",
filtering=1))
```

```
Searching cliques in the following graph:
[0, 1, 0, 1]
[0, 0, 1, 2]
[0, 0, 0, 1]
[0, 0, 0, 0]
Maximal weight = 2
Edges with maximal weight = [[1, 3]]
maximal clique = [1, 3]
```

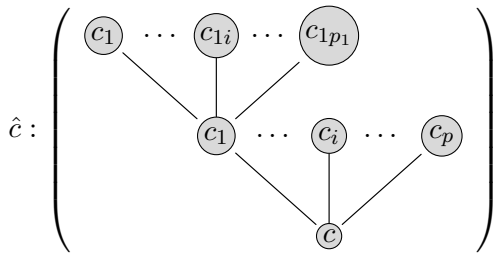
Note that, contrary to the method `best_compartment` (section 4.1.21), both the values of the organelles and the values of the input influence the choice of the output of the method `.proposed_clustering`. This is illustrated below for the option `"division"` and the value `filtering = 1`. In this case, the method `proposed_clustering` corresponds to the fission algorithm of [1, Sec. 2.5] for the parameters $\varepsilon = +$ and $\nu = 1$.

```
>>> c = Cell(dimension = 3,residual = 0.5,cytosol = [-2,3,0],organelles =
[[1,10,1],[1,1,10],[10,1,1],[20,1,1],[1,20,1]])
>>> a = [[1,10,1],[1,1,10],[10,1,1],[20,1,1],[1,20,1]]
>>> print "maximal clique = " + str(c.proposed_clustering(a,"division",
filtering=1))
Searching cliques in the following graph:
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 0]
[0, 0, 0, 1, 0]
[0, 0, 0, 0, 0]
[0, 0, 0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[0, 4], [2, 3]]
maximal clique = [0, 4]
>>> a = [[1,10,1],[1,1,10],[10,1,1],[20,1,1],[1,20,10]]
>>> print "maximal clique = " + str(c.proposed_clustering(a,"division",
filtering=1))
Searching cliques in the following graph:
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 1]
[0, 0, 0, 1, 0]
[0, 0, 0, 0, 0]
[0, 0, 0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[0, 4], [1, 4], [2, 3]]
maximal clique = [0, 1, 4]
>>> a = [[1,10,1],[1,1,10],[10,1,1],[20,1,1],[10,20,10]]
>>> print "maximal clique = " + str(c.proposed_clustering(a,"division",
filtering=1))
Searching cliques in the following graph:
[0, 0, 0, 0, 1]
[0, 0, 0, 1, 0]
```

```
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[0, 4], [2, 3], [2, 4], [3, 4]]
maximal clique = [0, 2, 3, 4]
>>> a = [[1,10,1],[1,1,10],[10,1,1],[20,1,1],[15,20,10]]
>>> print "maximal clique = " + str(c.proposed_clustering(a,"division",
filtering=1))
Searching cliques in the following graph:
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 0]
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[0, 4], [1, 4], [3, 4]]
maximal clique = [0, 1, 3, 4]
```

4.2. Description of SuperCell (class)

4.2.1. Introduction. This section introduces the reader to the code of the class SuperCell whose main goal is to model the features of a super cell, as defined in [1, Def. 2.1]. Before presenting the features of the class, recall that, mathematically, a super cell of some dimension N, of some height q and equipped with n organelles, consists of a tree structure labeled by cells of dimension N. In this respect, the collection of cells $c, c_1, \ldots, c_p, c_{11}, \ldots$ defining a super cell $\hat{c}$ are either junctions, meaning nodes possessing child cells, or leaves, meaning nodes without children (see [1, Conv. 2.2 & Def. 2.3]).



Except for the root cell, shown above at the bottom of the tree, every other cell has a parent cell. Other than the root and the leaves, all cells of a super cell are similar in structure. This similarity allows us to construct our methods as recursive extensions of simpler methods that only act on the *basal junction* of the super cell, namely the root and its junction. In this library, the class SuperCell is equipped with 8 objects, related to the various results of [1, Sec. 2], as well as 3 types of methods, which are listed below:

▷ a set of 2 methods meant to be used for initializing the tree structure of a super cell:

- `set_level`: increments the levels of each super cell/cell by a given value;
- `reset_depth`: recomputes the depth of each super cell/cell within a given super cell;

▷ a single debugging method:

- `stdout`: displays the tree structure of a super cell on the standard output;

▷ a set of 14 methods meant to implement the algorithmic steps of [1, Sec. 2]:

- `__init__`: returns a super cell for its associated set of parameters;
- `compress`: returns the total and recursive composition of all the cells of a super cell;

- `action`: returns the action of a super cell on a vector, as defined in [1, Def. 2.9];
- `base`: returns the basal pruning of the super cell, as defined in [1, Def. 2.10];
- `compute_variables`: computes parameters for the operations right and left; as defined in [1, Conv. 1.19];
- `homeostasis`: solve a homeostasis problem for the basal pruning of a super cell; for more information about this operation, see [1, Def. 1.39];
- `allostasis`: implements the algorithmic step of [1, Sec. 2.3];
- `spontaneous_reaction`: returns the cleaning of the super cell – see [1, Def. 2.16];
- `tensor_pre_action`: computes a barycenter of pre-actions – this is explained in more detail in [1, Rem 1.55 & Sec. 2.5];
- `merge_base`: merges the child super cells of the basal junction of a super cell, as described in [1, Sec. 2.5];
- `divide_base`: divides the child super cells of the root of a super cell, as described in [1, Sec. 2.5];
- `fusion`: implements the algorithmic step of [1, Sec. 2.5];
- `fission`: implements the algorithmic step of [1, Sec. 2.5];
- `compose`: implements the algorithmic step of [1, Sec. 2.4].

4.2.2. Structure. The following tables give a preview of the class `Cell`. The table given below describes the various dependencies of the class.

Dependencies	
Superclass ancestry	Module section
`object`	N/A
Statistics	
▷ Importable objects: 7	
▷ Non-importable objects: 0	
▷ Importable methods: 17	
▷ Non-importable methods: 2	

The following table gives a description of the 7 importable objects of the class.

Objects		
Name	Type	Related sections
`.depth`	`int`	▷ section 4.2.3
`.level`	`int`	▷ section 4.2.3
`.cell`	`Cell`	▷ section 4.2.3
`.is_leaf`	`bool`	▷ section 4.2.3
`.compose_state`	`bool`	▷ section 4.2.3
`.pre_action`	`list(float)`	▷ section 4.2.3
`.innercells`	`list(SuperCell)`	▷ section 4.2.3

Finally, the following table gives a description of the 17 importable methods of the class. In the second column, we use the symbol ∼ to refer to a type that is specified in the topmost section shown in the corresponding rightmost column.

Methods			
Name	Input types	Output types	Related sections
`.__init__`	- `Cell` - `list(SuperCell)`	- `self`	▷ section 4.2.3
`.set_level`	- `int`	- `self`	▷ section 4.2.4
`.reset_depth`	- `self`	- `self`	▷ section 4.2.5
`.stdout`	- `list(float)`	- `self`	▷ section 4.2.6
`.compress`	- `self`	- `Cell`	▷ section 4.2.7
`.action`	- `list(float)` - `fun: ∼ -> ∼` - `string`	- `list(float)`	▷ section 4.2.8
`.base`	- `fun: ∼ -> ∼`	- `SuperCell`	▷ section 4.2.9
`.compute_variables`	- `list(list(float))`	- `list(list(float))`	▷ section 4.2.10
`.homeostasis`	- `list(list(float))`	- `self`	▷ section 4.2.11
`.allostasis`	- `list(float)` - `fun: ∼ -> ∼` - `fun: ∼ -> ∼`	- `self`	▷ section 4.2.12 ▷ section 4.2.11
`.spontaneous_reaction`	- `list(float)` - `fun: ∼ -> ∼`	- `self`	▷ section 4.2.13
`.tensor_pre_action`	- `self`	- `self`	▷ section 4.2.14
`.merge_base`	- `list(list(float))` - `fun: ∼ -> ∼` - `string`	- `self`	▷ section 4.2.15 ▷ section 4.2.17
`.divide_base`	- `list(list(float))` - `fun: ∼ -> ∼` - `string`	- `self`	▷ section 4.2.16 ▷ section 4.2.18
`.fusion`	- `list(float)` - `Operad`	- `self`	▷ section 4.2.17
`.fission`	- `list(float)` - `Operad` - `float`	- `self`	▷ section 4.2.18 ▷ section 4.2.19
`.compose`	- `fun: ∼ -> ∼`	- `self`	▷ section 4.2.19

4.2.3. Description of `.__init__` (method). This section describes the code and the functionalities of the method `.__init__`. The method is equipped with the following two input variables, including one that is optional.

`.__init__`		
Inputs	Types	Specifications
`cell`	`Cell`	necessary
`*innercells`	`list(SuperCell)`	optional

The method possesses one action, which we describe below through sevaral examples.

Action	
Condition	Always
Description	The idea behind the method is to construct a tree structure encoding a super cell in the sense of [1, Conv. 2.2 & Def. 2.3]. The cell encoding the root of the tree is stored in `self.cell` while the list containing the children of a parent cell are stored in the object `self.innercells`. The method goes as follows. First, the method initializes the object `self.level` to zero; the object `self.compose_false` to `False`; and the object `self.pre_action` to an empty list. The method also gives the value contained in the variable `cell` to the object `self.cell` and stores the Boolean value of the logical test `(len(innercells) == 0) or (innercells[0] == [])` in `self.is_leaf`. Note that a super cell may or may not have an object `innercells`. If the value of `self.is_leaf` is `True`, then the object `.innercells` is not allocated and the user cannot access the object. On the other hand, if the value of `self.is_leaf` is `False`, then the object exists and contains the item stored in `innercells[0]`, which is supposed to be a list of `SuperCell` items. Lastly, the method calls the function `.set_level(1)` on every `SuperCell` item of `self.innercells`. This has the consequence of incrementing the value of all the objects `.level` by `1` throughout the hierarchical structure of each `SuperCell` item. The method also gives to the object `self.depth` the value `max_depth+1`, where the term `max_depth` represents the maximum of the values stored in the objects `.depth` throughout the hierarchical structures of all the `SuperCell` items of `self.innercells`

In the examples given below, we define various `SuperCell` items through the constructor and we check that the arguments passed to the constructor are stored in the appropriate variables. First, recall that the value of the object `.is_leaf` is `True` whenever a single input is given to the constructor or whenever the second input is an empty list.

```
>>> c1 = Cell(2,0.5,[0,0],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[0,0],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[0,0],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> print sc1.depth, sc1.level, sc1.is_leaf, sc1.compose_state
0 0 True False
>>> print sc1.pre_action
[]
>>> sc1.cell.stdout()
residual:  0.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [1, 2]
2-th organelle:  [5, 1]
3-th organelle:  [1, 8]
>>> sc2 = SuperCell(c2,[])
>>> print sc2.depth, sc2.level, sc2.is_leaf, sc2.compose_state
0 0 True False
>>> print sc2.pre_action
[]
```

```
>>> sc2.cell.stdout()
residual:  0.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [2, 0]
2-th organelle:  [0, 7]
3-th organelle:  [4, 2]
```

While the object .pre_action is initialized as an empty list, it can be filled by several methods of the class SuperCell to compute the expected signal and specialized signal of the super cell (see [1, Def. 2.12]). As suggested by its name, the object .pre_action refers to the *pre-action* of the underlying super cell, as defined in [1, Def. 2.9]. As a result, passing the value contained in the object .pre_action to the method .cell.action outputs the action of the super cell. Following [1, Def. 2.12], we also use the objects .pre_action to store the *expected signals* and *specialized signals* associated with the super cell – these signals are, by definition, pre-actions for particular shapes of inputs. The type of signals stored in each object .pre_action depends on the method previously called. For instance, the methods .action (see secton 4.2.8) and .allostasis (see section 4.2.12) can be used to fill the objects .pre_action with their corresponding expected signals. On the other hand, the methods .action (see secton 4.2.8) and .spontaneous_reaction (see section 4.2.13) can be used to fill the objects .pre_action with their corresponding specialized signals.

When the methods of the class SuperCell are used in accordance with the instructions of this documentation, the organelles of the Cell item contained in the object .cell should be equal to the contents of the directly-accessible child Cell items stored in .innercells (for the corresponding indices). Note that some SuperCell item do not possess the object .innercells, namely those SuperCell items whose object .is_leaf contains the value True – we refer to these cells as *leaves* [1, Conv. 2.2 & Def. 2.3]. To equip a SuperCell item with an object .innercells, it suffices to pass a list of SuperCell item to the second argument of the constructor, as shown below.

```
>>> sc = SuperCell(c,[sc1,sc2])
>>> print sc.depth, sc.level, sc.is_leaf, sc.compose_state
1 0 False False
>>> print sc.pre_action
[] 17 1000000000000000
>>> sc.cell.stdout()
residual:  0.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [8, 5]
2-th organelle:  [4, 5]
```

4.2.4. Description of .set_level (method). This section describes the code and the functionalities of the method .set_level. The method is equipped with the following input variable.

.set_level		
Inputs	Types	Specifications
level	list(SuperCell)	necessary

The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method passes the value contained in the input `level` to the object `self.level` and uses the function `.set_level(level+1)` on every `SuperCell` item contained in the list `self.innercells`. For a well-defined super cell whose root cell is at level `0`, this is equivalent to shifting the values of each object `.level` present in the hierarchical structure of the super cell by the value `level-1`

The following example shows how to use the method `.set_level`.

```
>>> c1 = Cell(2,0.5,[0,0],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[0,0],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[0,0],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> print sc.level, sc1.level, sc2.level
0 1 1
>>> sc.set_level(3)
>>> print sc.level, sc1.level, sc2.level
3 4 4
```

4.2.5. Description of `.reset_depth` (method). This section describes the code and the functionalities of the method `.reset_depth`, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method resets the values of the objects `.depth` for all the `SuperCell` items contained in the hierarchical structure of `self`. The reset is done recursively as follows: (1) if `self` is a leaf, then the value `0` is stored in `self.depth` (2) if `self` is a not leaf, then the method calls the function `.reset_depth()` for every `SuperCell` items in the list `self.innercells` and the object `self.depth` is given the value `max_depth+1` where the term `max_depth` is the maximum of the values of the objects `.depth` present in the hierarchical structures of the `SuperCell` items contained in the list `self.innercells`

The following example shows how to use the method `.reset_depth`.

```
>>> c1 = Cell(2,0.5,[0,0],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[0,0],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[0,0],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> sc.depth = 4
>>> sc1.depth = 4
>>> print sc.depth, print sc1.depth, print sc2.depth
4 4 0
>>> sc.reset_depth()
>>> print sc.depth, print sc1.depth, print sc2.depth
1 0 0
```

4.2.6. Description of `.stdout` (method). This section describes the code and the functionalities of the method `.stdout`. The method is equipped with the following input variable, which is optional.

`.stdout`		
Inputs	Types	Specifications
`*vector`	`list(SuperCell)`	optional

The method possesses two actions, which we describe below through sevaral examples.

Action 1	
Condition	If `*vector` is empty
Description	The method displays the tree structure of `self` on the standard output. Every line of the display looks as follows `....[lvl] -> Cell[res]{ooo...o}` and represents a `Cell` item belonging to the tree structure of `self`. The integer `lvl` shows the level of the `Cell` item while the integer `res` is the integer truncation of its residual value (section 4.1.3). Each symbol `o` represents an organelle of the underlying `Cell` item. Conventionally, the lines associated with the children of a parent cell are always displayed below the line associated with the parent cell. Finally, the method colors in purple the cells for which the associated object `.compose_state` is `True` in purple (for examples, see section 4.2.15 and section 4.2.16).

The following example shows how to use the method `.stdout` with no input.

```
>>> c1 = Cell(2,0.5,[0,0],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[0,0],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[0,0],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> sc.stdout()
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{ooo}
.[1] -> Cell[0]{ooo}
```

We now describe the second action.

Action 2	
Condition	If *vector is a list of length equal to self.dimension
Description	The method displays the tree structure of self on the standard output. Every line of the display can take two forms: either the form seen in Action 1, or the following form ....[lvl] -> Cell[res]{ooo...o} [num]: agr ... [num]: agr which represents a Cell item for which the object .is_leaf contains the value True. As with Action 1, the integers lvl and res correspond to the level of the Cell item and the integer truncation of its residual value, respectively. The list of terms [num]: agr shows the list of outputs agr returned by the functions self.cell.agreement(num,vector[0]) (see section 4.1.16) where num is the index of the organelle of the underlying Cell item. Conventionally, the lines representing the children of a parent cell are always displayed below the line associated with the parent cell. Finally, the method colors in purple the cells for which the associated object .compose_state is True in purple (for examples, see section 4.2.15 and section 4.2.16).

The following example shows how to use the method .stdout with an input. We will consider the same setting as in the previous example.

```
>>> sc.stdout([1,10])
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{ooo} [0]:0.9344877349 [1]:0.292714272 [2]:0.9996953077
.[1] -> Cell[0]{ooo} [0]:0.099503719 [1]:0.9950371902 [2]:0.5339929913
```

4.2.7. Description of .compress (method). This section describes the code and the functionalities of the method .compress, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method returns the Cell item resulting from composing (see section 4.1.8) all the cells present in the hierarchical structure of self (recursively from the leaves to the root).

The following example illustrates how to use the method .compress. In particular, we use the methods .stdout associated with the class Cell (see section 4.1.6) and the class SuperCell (see section 4.2.6).

```
>>> c1 = Cell(2,0.5,[0,0],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[0,0],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[0,0],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> sc.stdout([1,10])
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{ooo} [0]:0.9344877349 [1]:0.292714272 [2]:0.9996953077
.[1] -> Cell[0]{ooo} [0]:0.099503719 [1]:0.9950371902 [2]:0.5339929913
```

```
>>> c = sc.compress()
>>> c.stdout()
residual:  1.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [1, 2]
2-th organelle:  [5, 1]
3-th organelle:  [1, 8]
4-th organelle:  [2, 0]
5-th organelle:  [0, 7]
6-th organelle:  [4, 2]
>>> d = SuperCell(c)
>>> d.stdout([1,10])
[0] -> Cell[1]{oooooo} [0]:0.9344877349 [1]:0.292714272 [2]:0.9996953077
[3]:0.099503719 [4]:0.9950371902 [5]:0.5339929913
```

4.2.8. Description of `.action` (method). This section describes the code and the functionalities of the method `.action`. The method is equipped with the following three input variables, including one that is optional.

`.action`		
Inputs	Types	Specifications
`vector`	`list(SuperCell)`	necessary
`identity`	`fun: list(float) -> Cell`	necessary
`option = "expected"`	`string`	optional

The method possesses two actions, which we describe below through sevaral examples.

Action 1	
Condition	The input variable `option` contains the string `"specialized"`
Description	The method returns the action associated with the "specialized signal" [1, Def. 2.12] of the super cell `self` on the input `vector` relative to the function `identity`. To do so, the method first stores the recursive collection of specialized signals in the corresponding objects `.pre_action`. Each list `self.pre_action` is constructed through the following recursive process: (where every index `i` ranges from `0` to `len(self.cell.organelles)-1`): (1) If `self.is_leaf` is `True`, then the element `self.pre_action[i]` is given the action of the cell `identity(self.cell.organelles[i])` on `vector` (see section 4.1.13); (2) If `self.is_leaf` is `False`, then the element `self.pre_action[i]` is given the action of the super cell `self.innercells[i]` on `vector` relative to the function `identity`. Then, the method `self.action` returns a `list` item that corresponds to the output of the function `self.cell.action` on the list `self.pre_action`.

In the following two examples, we use the method `.stdout` (see section 4.2.6) with the constructor of the class `Operad` (see section 4.3.3), for a dimension equal to 2, and its associated method `.identity` of `Operad` (see section 4.3.4).

```
>>> c1 = Cell(2,0.5,[0,0],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[0,0],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[0,0],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> sc.stdout([1,10])
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{ooo} [0]:0.9344877349 [1]:0.292714272 [2]:0.9996953077
.[1] -> Cell[0]{ooo} [0]:0.099503719 [1]:0.9950371902 [2]:0.5339929913
>>> operad = Operad(2)
>>> print sc.action([1,10],operad.identity,"specialized")
[0.14971941638608305, 2.248877665544332]
```

In the following example, we see that the method `.compress` (see section 4.2.7) can change the output of the method `.action`, as shown below.

```
>>> c = sc.compress()
>>> d = SuperCell(c)
>>> d.stdout([1,10])
[0] -> Cell[1]{oooooo} [0]:0.9344877349 [1]:0.292714272 [2]:0.9996953077
[3]:0.099503719 [4]:0.9950371902 [5]:0.5339929913
>>> print d.action([1,10],operad.identity,"specialized")
[0.28114478114478114, 4.9326599326599325]
```

We now describe the second action of the method.

Action 2	
Condition	The input variable `option` is not specified and/or contains a string that is not `"specialized"`
Description	The method returns the action associated with the "expected signal" [1, Def. 2.12] of super cell `self` on the input `vector` relative to the function `identity`. To do so, the method first stores the recursive collection of expected signals associated with the cells of the super cell in the corresponding objects `.pre_action`. Each list `self.pre_action` is constructed through the following recursive process: (where every index `i` ranges from `0` to `len(self.cell.organelles)-1`): (1) If `self.is_leaf` is `True`, then the element `self.pre_action[i]` stores the list `vector` (see section 4.1.13); (2) If `self.is_leaf` is `False`, then the element `self.pre_action[i]` is given the action of the super cell `self.innercells[i]` on `vector` relative to the function `identity`. Then, the method `self.action` returns a list item that corresponds to the output of the function `self.cell.action` on the list `self.pre_action`.

The following example uses the same items as those used to illustrate Action 1. As in the previous example, we compare the action of a super cell and its 'compressed' version.

```
>>> print sc.action([1,10],operad.identity)
[0.2141414141414142, 2.7525252525252526]
>>> print d.action([1,10],operad.identity)
[0.3939393939393939, 6.060606060606061]
```

4.2.9. Description of `.base` (method). This section describes the code and the functionalities of the method `.base`. The method is equipped with the following input variable.

.base		
Inputs	Types	Specifications
identity	fun: list(float) -> Cell	necessary

The method possesses one action, which we describe below through sevaral examples.

Action	
Condition	Always
Description	The method returns the basal pruning of the tree structure of self (see [1, Def. 2.10]), namely the super cell that only consists of the root cell of self and its associated children (formal or not). This means that the output is either the truncation of the tree structure of self at level 1 or the formal extension of self into a SuperCell item of height 1 if self is a leaf. More specifically, the method outputs a SuperCell item whose object .cell is equal to the Cell item in self.cell and whose object .innercells is of the following form: (1) If self.is_leaf is True, then .innercells[i] is the leaf super cell SuperCell(identity(self.cell.organelles[i])) for every index i ranging from 0 to len(self.innercells)-1. (2) If self.is_leaf is False, then .innercells[i] is the leaf super cell SuperCell(self.innercells[i].cell) for every index i ranging from 0 to len(self.innercells)-1.

The following example illustrates how to use the method .base. We make use of the method .stdout (see section 4.2.6), which we use to compare the input with the output of the method .base. Note that our examples usess the constructor of the class Operad (see section 4.3.3), for a dimension equal to 2, and its associated method .identity of Operad (see section 4.3.4). First, we give an example where the method .base returns the formal extension of a leaf into a SuperCell of height 1 by replacing its organelles with identity cells.

```
>>> c1 = Cell(2,0.5,[0,0],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[0,0],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[0,0],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> operad = Operad(2)
>>> f = sc1.base(operad.identity)
>>> f.stdout()
[0] -> Cell[0]{ooo}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
```

We now illustrate the case where the method .base truncates the tree structure of a super cell at level 1. For simplicity, we use the method .copy, described in section 4.1.5, to build a 2-level super cell sd as follows.

```
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> d = c.copy()
>>> c3= c2.copy()
>>> sc3 = SuperCell(c3)
>>> sd = SuperCell(d,[sc,sc3])
```

```
>>> sd.stdout()
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{oo}
..[2] -> Cell[0]{ooo}
..[2] -> Cell[0]{ooo}
.[1] -> Cell[0]{ooo}
```

The truncation of `sd` by the method `.base` is shown below through the method `.stdout` (section 4.2.6).

```
>>> se = sd.base(operad.identity)
>>> se.stdout()
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{oo}
.[1] -> Cell[0]{ooo}
```

4.2.10. Description of `.compute_variables` (method). This section describes the code and the functionalities of the method `.compute_variables`. The method is equipped with the following input variable.

`.compute_variables`		
Inputs	Types	Specifications
`gradient_descent`	`list(list(float))`	necessary

The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method returns four lists `mu_var`, `alpha_var`, `kappa_var`, and `lambda_var` corresponding to the tuples μ, α, κ and λ needed to defined the cell $\mathsf{left}(c)(\alpha, \kappa, \lambda)$ and the collection $\mathsf{right}(c)(\mu, \alpha, \kappa)$ (see [1, Conv. 1.19], section 4.1.10 and section 4.1.11). In particular, these four lists correspond to the type of lists used to define and solve the homeostasis problem induced by λ (see [1, Def. 1.39] and/or the description below) First, the method stores in `mu_var` the list of values `self.innercells[i].cell.residual` for every index `i` ranging from `0` to `len(self.cell.organelles)` and constructs the list `alpha_var` as the list of integers `len(self.innercells[i].cell.organelles)` for every index `i` ranging from `0` to `len(self.cell.organelles)`. Before explaining the the method constructs the two lists `lambda_var` and `kappa_var`, it is worth mentioning that the latter is the solution of the homeostasis problem induced by the former (see [1, Def. 1.39]). In other words, the list `lambda_var` is to define the organelles of a re-factorization of the basal junction of `self` (see 4.2.9) while the list `kappa_var` contains the new cytosols for the child cells of the resulting junction.

Description	In fact, the coefficient `lambda_var[i][u]` is expected to be relatively close to the value `self.cell.organelles[i][u]`. The amount by which `self.cell.organelles[i][u]` differs from corresponds to the value contained in `gradient_descent[i][u]`, which is expected to be small compared to `self.cell.organelles[i][u]` (as with any gradient-descent-based method). If the value contained in `gradient_descent[i][u]` is negative (implying that the cell $\mathsf{left}(c)(\alpha,\kappa,\lambda)$ is not well-defined: meaning that the associated object `.well_defined` is `False`), then the method `.compute_variables` changes the value of `gradient_descent[i][u]` to `0`. Then, the method computes `lambda_var` as the list containing the difference
	`self.cell.organelles[i][u] - gradient_descent[i][u]`
	for every pair `(i,u)` of valid indices. The modification of `gradient_descent` is important for the method `.homeostasis` (see section 4.2.11) in order to create cells $\mathsf{left}(c)(\alpha,\kappa,\lambda)$ and $\mathsf{right}(c)(\mu,\alpha,\kappa)$ that are well-defined .
	Regarding `kappa_var`, each coefficient `kappa_var[i]` correspond to a list computing according to the vector formula of [1, Def. 1.41]. Specifically, this means that each coefficient `kappa_var[i][u]` contains the value
	`lambda_var[i][u]`
	`- self.innercells[i].cell.K[u]`
	`+ self.innercells[i].cell.cytosol[u]`
	for every index `u` ranging from `0` to `self`.dimension-`1`.

The following example illustrates how to use the method `.compute_variables`. In particular, we make use of the method `.base` (see section 4.2.9), which allows us to interpret a leaf `SuperCell` item (see section 4.2.3) as a tree of cells of height 1, and we the method `.identity` associated with the class `Operad`.

```
>>> c = Cell(3,0.5,[12,5,8],[[7,2,1],[10,5,1],[1,7,8],[1,2,5]])
>>> sc = SuperCell(c)
>>> operad = Operad(3)
>>> base = sc.base(operad.identity)
>>> gradient_descent = [[.1,3,.1],[.1,.2,.1],[.1,.05,.2],[-2,.1,.1]]
>>> mu_var, alpha_var, kappa_var, lambda_var = base.compute_variables(
gradient_descent)
>>> print mu_var
[1, 1, 1, 1]
>>> print alpha_var
[0, 0, 0, 0]
>>> print kappa_var
[[-0.09999999999999964, 0, -0.09999999999999998], [-0.09999999999999964,
-0.20000000000000018, -0.09999999999999998], [-0.09999999999999998,
-0.04999999999999982, -0.20000000000000018], [2, -0.10000000000000009,
-0.09999999999999964]]
>>> print lambda_var
[[6.9, 2, 0.9], [9.9, 4.8, 0.9], [0.9, 6.95, 7.8], [3, 1.9, 4.9]]
```

4.2.11. Description of `.homeostasis` (method). This section describes the code and the functionalities of the method `.homeostasis`. The method is equipped with the following input variables.

.homeostasis		
Inputs	Types	Specifications
gradient_descent	list(list(float))	necessary
identity	fun: list(float) -> Cell	necessary

The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method finds a re-factorization, in the sense of [1, Def. 1.39], for the basal junction [1, Def. 2.10] of the tree structure of self [1, Conv. 2.2]. To do so, the method loops on the outputs of the method .homeostasis until its outputs generate a well-defined cell factorization. More specifically, the method stores the basal junction of self in a variable cd by using the function self.base(identity) (see section 4.2.9). Then, the method uses the function cd.compute_variables(gradient_descent) to compute candidate parameters μ, α, κ and λ that allow us to re-factorize the junction cd into a junction consisting of the root cell $\mathsf{left}(c,d)(\alpha,\kappa,\lambda)$ and the list of child cells $\mathsf{right}(c,d)(\mu,\alpha,\kappa)$, as defined in [1, Conv. 1.19]). Recall that the data $\mathsf{left}(c,d)(\alpha,\kappa,\lambda)$ and $\mathsf{right}(c,d)(\mu,\alpha,\kappa)$ can be obtained through the methods left (section 4.1.10) and right (section 4.1.11). The other role of cd.compute_variables is to find the invalid perturbations values of gradient_descent and to set them to 0. The method .homeostasis then re-computes (if necessary) the solutions $\mathsf{left}(c,d)(\alpha,\kappa,\lambda)$ and $\mathsf{right}(c,d)(\mu,\alpha,\kappa)$ until they all define well-defined Cell items. When the cells present in the tree structure of self (and in particular the cells making the junction cd) are well-defined, the method is guaranteed to terminate (Indeed, if gradient_descent is only made of zeros, then the junction cd is a valid output for .homeosasis).

The following example illustrates how to use the method .homeostasis. We make use of the class Operad (see section 4.3.3) and its associated method .identity (see section 4.3.4).

```
>>> c = Cell(3,0.5,[12,5,8],[[7,2,1],[10,5,1],[1,7,8],[1,2,5]])
>>> sc = SuperCell(c)
>>> operad = Operad(3)
>>> sc.cell.stdout()
residual:  0.5
cytosol[1]:  12
cytosol[2]:  5
cytosol[3]:  8
1-th organelle:  [7, 2, 1]
2-th organelle:  [10, 5, 1]
3-th organelle:  [1, 7, 8]
4-th organelle:  [1, 2, 5]
>>> gradient_descent = [[.1,3,.1],[.1,.2,.1],[.1,.05,.2],[-2,.1,.1]]
>>> sc.homeostasis(gradient_descent,operad.identity)
>>> sc.cell.stdout()
residual:  0.5
```

```
cytosol[1]:  10.3
cytosol[2]:  5.35
cytosol[3]:  8.5
1-th organelle:  [6.9, 2, 0.9]
2-th organelle:  [9.9, 4.8, 0.9]
3-th organelle:  [0.9, 6.95, 7.8]
4-th organelle:  [3, 1.9, 4.9]
```

4.2.12. Description of `.allostasis` (method). This section describes the code and the functionalities of the method `.allostasis`. The method is equipped with the following input variables.

.allostasis		
Inputs	Types	Specifications
`vector`	`list(float)`	necessary
`identity`	`fun: list(float) -> Cell`	necessary
`gamma`	`fun: Cell * list(list(float)) -> list(list(float))`	necessary

The method possesses one action, which we describe below through an example.

Action	
Condition	Always

Description	The method computes the algorithmic step described in [1, Sec. 2.3]. Recall that this step consists in mimicking a gradient-descent-like optimization of the parameters of the super cell `self` in order to minimize the values of the algebra operators (section 4.1.14) associated with each cells present in the hierarchical structure of `self`.
	The method first stores the "expected signals" [1, Def. 2.12] of `self` relative to the list `vector` in the corresponding objects `.pre_action` (also, see section 4.2.8).
	Then, for each cell in the hierarchical structure of `self` accessible via each object `.cell` (section 4.2.3), the method computes the allostatic differential [1, Def. 1.47] through the method `.allostasis` (section 4.1.15), namely the value
	`dU_de = self.cell.algebra_operator(self.pre_action).`
	The method then uses the allostatic differential `dU_de` and the function `gamma` to compute the allostatic matrix [1, Def. 2.18] associated with `self.cell`: this is done by creating a `list(list(float))` item `gradient_descent` whose coefficient `gradient_descent[i][u]` is the multiplication
	`gamma(self.cell,i,self.pre_action)[i][u] * dU_de`
	for every index `i` ranging from `0` to `len(self.cell.organelles)-1` and every index `u` ranging from `0` to `self.cell.dimension-1`. Finally, the matrix `gradient_descent` is given to the method `self.homeostasis` (section 4.2.11) together with the input `identity` in order to make each junction of `self` 'reach homeostasis' (In the sense of [1, Def. 2.11]).

The following example illustrates how to use the method `.homeostasis`. We make use of the class `Operad` (see section 4.3.3), its associated method `.identity` (see section 4.3.4) and the function `usf.gamma` (see section 3.1.4), which we pass to the input parameter `gamma` .

We start our examples with a super cell that possess the same paramters as those used in the examples of section 3.1.3 and section 3.1.4, except for the amount given to the object

.residual. Note that a higher value for .residual allows the method .allostasis to update more parameters as it is less likely to produce ill-defined re-factorizations of the super cell through the use of the method .homeostasis (see [1, Def. 2.15], section 4.2.10, and section 4.2.11 for more information on well-definedness and the re-factorization process).

```
>>> operad = Operad(5)
>>> c = Cell(dimension = 5, residual = 1000, cytosol = [-2,3,5,0,0],
organelles = [[1,2,5,3,7], [5,0,0,0,4],[25,51,8,1,52]])
>>> sc = SuperCell(c)
>>> sc.cell.stdout()
residual:  1000
cytosol[1]:  -2
cytosol[2]:  3
cytosol[3]:  5
cytosol[4]:  0
cytosol[5]:  0
1-th organelle:  [1, 2, 5, 3, 7]
2-th organelle:  [5, 0, 0, 0, 4]
3-th organelle:  [25, 51, 8, 1, 52]
```

We now use the function usf.gamma (section 3.1.4) to generate a "gamma parameter" for the method .allostasis.

```
>>> brightness = [.25,.5,.75]
>>> profiles = [[(.0,.9),(.0,.5),(.0,.25)],[(.0,.4),(.0,.6),(.0,.5)]]
>>> scores = [.5,.8]
>>> gamma = usf.gamma(3,20,brightness,profiles,scores)
>>> sc.allostasis([10,1,2,5,15],operad.identity,gamma)
[brightness] 0.8 0.4 0.2
True False

[brightness] 0.4 0.4 0.4
False True

[brightness] 0.6 0.4 0.4
False False

[Gamma parameters][0]
79.6021925779
1000.0
23.2126583827
[Allostasis matrix][1]
6.26672163138
323.214148404
2.41792613144
[Allostasis matrix][2]
-8.36162731541
-36.2360630527
-0.427461634702
```

The displays appearing after the green labels tell us about the average values of the gamma parameters and the average values of the coefficients of the allostatic matrix. The values displayed after the label [Allostasis matrix][2] are the average values of the values selected by the method .homeostasis for a valid update of the parameters of the super cell.

In our case, calling the method .allostasis has updated the super cell as follows.

```
>>> sc.cell.stdout()
residual:  1000
cytosol[1]:  -11.6441450451
cytosol[2]:  11.8732941391
cytosol[3]:  5
cytosol[4]:  0
cytosol[5]:  -224.354909108
1-th organelle:  [8.92395297628549, 2, 5, 3, 40.884183600753644]
2-th organelle:  [5, 0, 0, 0, 185.18031526336028]
3-th organelle:  [26.720192068820307, 42.12670586090116, 8, 1,
61.29041024378717]
```

After the update, we can see that the organelles of the super cell are more specialized in certain dimensions, which can make the next update more difficult for random inputs. We illustrate this in the next example, in which the organelles of the super cell all satisfy one of the contrast profiles associated with the function usf.gamma, but do not pass the agreement test (see section 3.1.3 and section 3.1.4 for more detail on contrast profiles and agreement tests).

```
>>> sc.allostasis([3,12,20,15,1],operad.identity,gamma)
[brightness] 0.2 0.2 0.2
True True

[brightness] 0.2 0.2 0.2
True True

[brightness] 0.6 0.4 0.2
True False

[Gamma parameters][0]
0.0
0.0
0.0
[Allostasis matrix][1]
0
0
0
[Allostasis matrix][2]
0
0
0
```

As is shown below, the parameters of the super cell have not changed.

```
>>> sc.cell.stdout()
residual:  1000
cytosol[1]:  -11.6441450451
cytosol[2]:  11.8732941391
cytosol[3]:  5
cytosol[4]:  0
cytosol[5]:  -224.354909108
1-th organelle:  [8.92395297628549, 2, 5, 3, 40.884183600753644]
2-th organelle:  [5, 0, 0, 0, 185.18031526336028]
```

```
3-th organelle:  [26.720192068820307, 42.12670586090116, 8, 1,
61.29041024378717]
```

Now, we give another example showing what happens when the super cell does not have enough "energy" in its object .residual. We use the same parameters as those used in the first example given above, except for the value give to .residual, which is set to 200.

```
>>> c = Cell(dimension = 5, residual = 200, cytosol = [-2,3,5,0,0],
organelles = [[1,2,5,3,7], [5,0,0,0,4],[25,51,8,1,52]])
>>> sc = SuperCell(c)
>>> sc.cell.stdout()
residual:  200
cytosol[1]:  -2
cytosol[2]:  3
cytosol[3]:  5
cytosol[4]:  0
cytosol[5]:  0
1-th organelle:  [1, 2, 5, 3, 7]
2-th organelle:  [5, 0, 0, 0, 4]
3-th organelle:  [25, 51, 8, 1, 52]
```

We now call the method .allostasis again. Because we have not changed the organelles of the super cell, we obtain the same displays regarding the brightness profiles satisfied by these organelles.

```
>>> gamma = usf.gamma(3,20,brightness,profiles,scores)
>>> sc.allostasis([10,1,2,5,15],operad.identity,gamma)
[brightness] 0.8 0.4 0.2
True False

[brightness] 0.4 0.4 0.4
False True

[brightness] 0.6 0.4 0.4
False False

[Gamma parameters][0]
79.6021925779
1000.0
23.2126583827
```

As can be seen, the result of applying the method .allostasis for such the new value of .residual has the consequence of canceling the expected updates for the first and second organelles (see the average updates after the label [Allostasis matrix][2] below)

```
[Allostasis matrix][1]
6.26672163138
323.214148404
2.41792613144
[Allostasis matrix][2]
0
0
1.77465882782
```

As shown below, the parameters of the super cell have been changed accordingly.

```
>>> sc.cell.stdout()
residual:  200
cytosol[1]:  -2
cytosol[2]:  11.8732941391
cytosol[3]:  5
cytosol[4]:  0
cytosol[5]:  0
1-th organelle:  [1, 2, 5, 3, 7]
2-th organelle:  [5, 0, 0, 0, 4]
3-th organelle:  [25, 42.12670586090116, 8, 1, 52]
```

4.2.13. Description of `.spontaneous_reaction` (method). This section describes the code and the functionalities of the method `.spontaneous_reaction`. The method is equipped with the following input variables.

`.spontaneous_reaction`		
Inputs	Types	Specifications
`vector`	`list(float)`	necessary
`identity`	`fun: list(float) -> Cell`	necessary

The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The present method extends the method `.spontaneous_reaction` defined for `Cell` items (section 4.1.12) to `SuperCell` items. In addition, the method carries out two other tasks: it stores the specialized signals [1, Def. 2.12] of `self` generated by the input `vector` in the corresponding objects `pre_action` (also, see section 4.2.8) and it implements the 'cleaning' operation described in [1, Def. 2.16], which means that it makes the `SuperCell` item `self` reach homeostasis (see [1, Def. 2.11 & Rem. 2.17]). Here, 'reaching homeostatis' means that the content of any `Cell` item of the form `*.innercells[i].cell`, where `*` represents a `SuperCell` item in the hierarchical structure of `self`, equals the list contained in the object `*.cell.organelles[i]` (see [1, Def. 2.16: item 2.3]). To do so, the method calls the function `*.cell.spontaneous_reaction()` in every super cell `*` present in the hierarchical structure of `self`, and then stores the specialized signals generated by the input `vector` in the corresponding objects `*.pre_action`. After each computation of a specialized signal, the method uses the parameters of the updated child super cells (stored in `.innercells`) to compute the value of the objects `.cell.organelles`, `*.cell.Sorg`, `*.cell.Sorg` and `*.cell.SK` (section 4.1.3). In addition, the method uses the assignments `*.cell.organelles[i] = *.innercells[i].cell.K` throughout the hierarchical structure of `self` to put the returned `SuperCell` item `self` in a homeostatic state (see [1, Def. 2.11 & Rem. 2.17]).

The following example shows the action of the method `.spontaneous_reaction` on a `SuperCell` item. As can be seen, the cytosol of the three cell `c1`, `c2` and `c` are turned into lists of zeros and the residuals are augmented accordingly (see section 4.1.12).

```
>>> c1 = Cell(2,0.5,[4,2],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[1,2],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[8,7],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> operad = Operad(2)
>>> sc.stdout([4,5])
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{ooo} [0]:0.977802414 [1]:0.7657048647 [2]:0.8523227286
.[1] -> Cell[0]{ooo} [0]:0.6246950475 [1]:0.7808688094 [2]:0.90795938
>>> sc.spontaneous_reaction([4,5],operad.identity)
>>> sc.cell.stdout()
residual:  15.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [7, 11]
2-th organelle:  [6, 9]
```

We can display the description of the child super cells of `cs` to see that the cytosolic content have been cleaned up and that the objects `.residual` have been filled with the sum of their associated cytosolic contents.

```
>>> sc.innercells[0].cell.stdout()
residual:  6.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [1, 2]
2-th organelle:  [5, 1]
3-th organelle:  [1, 8]
>>> sc.innercells[1].cell.stdout()
residual:  3.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [2, 0]
2-th organelle:  [0, 7]
3-th organelle:  [4, 2]
```

4.2.14. Description of `.tensor_pre_action` (method). This section describes the code and the functionalities of the method `.tensor_pre_action`, which does not take any input. The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	In the same way as [1, Prop. 1.54] computes a barycenter of pre-actions (see [1, Rem. 1.55]), the present method computes the barycenter of the pre-actions associated with the basal junction of `self`, where we take the barycentric weights to be the outputs of the function `self.cell.content_proportions()` (see section 4.1.20). Specifically, the output of the method is a `list(float)` item, call it `barycenter`, of length `self.cell.dimension`, whose element `barycenter[u]` is the sum of the terms `self.pre_action[i][u] * prop[i]` in which `prop[i]` is the `i`-th output of the function `self.cell.content_proportions()`, namely the ratio `self.cell.Sorg[i]/float(self.cell.SK)`, over every index `i` ranging from `0` to `len(self.cell.organelles)-1`.

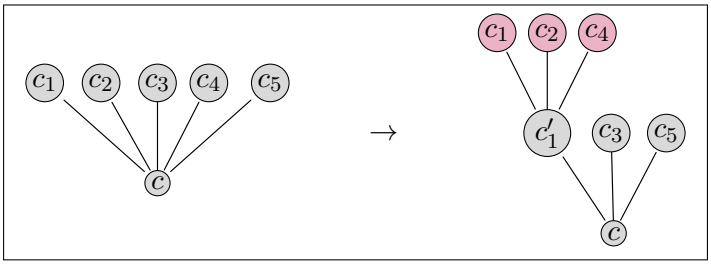
The following example shows how to use the method `.tensor_pre_action`. Note that to use this method, we need to pre-fill the objects `.pre_action` of the super cell with lists of values. Ideally, these lists would correspond to one of the two types of signals associated with the super cell, namely either its expected signals or its specialized signals (see [1, Def. 2.12]). Below, we use the method `spontaneous_reaction` to fill the objects `.pre_action` with specialized signals. We use the same items as those used in section 4.2.13.

```
>>> c1 = Cell(2,0.5,[4,2],[[1,2],[5,1],[1,8]])
>>> c2 = Cell(2,0.5,[1,2],[[2,0],[0,7],[4,2]])
>>> c = Cell(2,0.5,[8,7],[[8,5],[4,5]])
>>> sc1 = SuperCell(c1)
>>> sc2 = SuperCell(c2,[])
>>> sc = SuperCell(c,[sc1,sc2])
>>> operad = Operad(2)
>>> sc.stdout([4,5])
[0] -> Cell[0]{oo}
.[1] -> Cell[0]{ooo} [0]:0.977802414 [1]:0.7657048647 [2]:0.8523227286
.[1] -> Cell[0]{ooo} [0]:0.6246950475 [1]:0.7808688094 [2]:0.90795938
>>> sc.spontaneous_reaction([4,5],operad.identity)
>>> print sc.pre_action
[[1.0246913580246915, 2.391975308641975], [1.2444444444444445,
2.555555555555556]]
>>> print sc.tensor_pre_action()
[1.1245791245791246, 2.4663299663299663]
```

4.2.15. Description of `.merge_base` (method). This section describes the code and the functionalities of the method `.merge_base`. The method is equipped with the following three input variables, including one that is optional.

`.merge_base`		
Inputs	Types	Specifications
`list_of_organelles`	`list(list(float))`	necessary
`tensor`	`fun: list(SuperCell) -> SuperCell`	necessary
`order = "non-sorted"`	`string`	optional

The method possesses one action, which we describe below through sevaral examples.

Action	
Condition	Always
Description	The method .merge_base implements the operation described in [1, Def. 2.26]. The idea is to extend the method .merge (section 4.1.17) associated with the class Cell to the basal junction of self (see section 4.2.9). Put simply, the method merges a subset of the organelles of the root cell of self into a single organelle and uses the input function tensor to distribute the child super cells, stored in self.innercells, accordingly (see picture below). Note that .merge_base does not act on leaf super cells (see section 4.2.3).  Now, to be more specific, the subset of indices of the organelles of self to be merged is given by the list list_of_organelles. Similarly to the method .merge, the list list_of_organelles is sorted before use if the input variable order does not contain the string "sorted". After this sorting step, the method merges the corresponding organelles of self.cell by calling the function self.cell.merge(list_of_organelles,"sorted"). The method then makes sure that the merging of these organelles is consistent with the whole tree structure of self. This is done by creating two new lists merged_innercells and new_innercells for the merged and untouched organelles. The method fills the list merge_innercells with all the SuperCell items of the form self.innercells[i] for which the index i belongs to list_of_organelles. If we denote by j the smallest index of list_of_organelles, then the element new_innercells[j] is given the SuperCell item tensor(merged_innercells). For any other index, the list new_innercells contains the super cells of the form self.innercells[i] whose index i, ranging from 0 to len(self.innercells)-1, is not in list_of_organelles. The method also fills the list new_innercells[j].pre_action in the same way as the list new_innercells was filled, but where we replace the list self.innercells with the list self.pre_action. Finally, the method .merge_base terminates with the following actions: (1) it sets the level of new_innercells[j] to self.level+1 by calling the method .set_level(self.level+1) (section 4.2.4). (2) it assigns the list of super cells new_innercells to self.innercells; (3) it recomputes self.pre_action as the output of the function new_innercells[j].tensor_pre_action() (see section 4.2.14);

The following example illustrates the use of the method .merge_base with the methods .pseudo_tensor (section 4.3.7) and .merging_tensor (section 4.3.8) associated with the class Operad. In addition, we use the method .action (section 4.2.8) to pre-fill each object pre_action with a non-empty list of length 2, for every super cell present in the hierarchical structure of the super cell sc.

```
>>> c = Cell(2,0.5,[4,2],[[1,2],[5,1],[1,8],[4,4],[0,7]])
>>> operad = Operad(2)
>>> children = list()
>>> for i in range(5):
...     children.append(SuperCell(operad.identity(c.organelles[i])))
>>> sc = SuperCell(c,children)
>>> sc.action([0,0],"specialized")
>>> sc.stdout()
[0] -> Cell[0]{ooooo}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
```

Below, we use `.merging_tensor`, which sets the objects `.compose_state` of each merged super cell to `True`, as shown by the purple display of the method `.stdout`.

```
>>> sc.merge_base([0,1,3],operad.merging_tensor,"sorted")
>>> sc.stdout()
[0] -> Cell[0]{ooo}
.[1] -> Cell[0]{ooo}
..[2] -> Cell[0]{o}
..[2] -> Cell[0]{o}
..[2] -> Cell[0]{o}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
```

Alternatively, we can use the method `.pseudo_tensor`, which does not change the value of the objects `.compose_state`. Below, we give the output of the previous code if we used the method `.pseudo_tensor` instead of `.merging_tensor`.

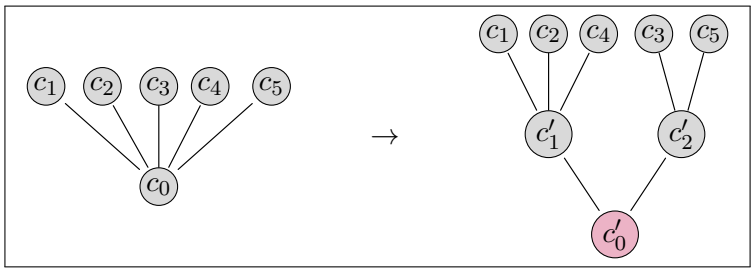
```
>>> sc.merge_base([0,1,3],operad.merging_tensor,"sorted")
>>> sc.stdout()
[0] -> Cell[0]{ooo}
.[1] -> Cell[0]{ooo}
..[2] -> Cell[0]{o}
..[2] -> Cell[0]{o}
..[2] -> Cell[0]{o}
.[1] -> Cell[0]{o}
.[1] -> Cell[0]{o}
```

4.2.16. Description of `.divide_base` (method). This section describes the code and the functionalities of the method `.divide_base`. The method is equipped with the following input variables, including one that is optional.

`.divide_base`		
Inputs	Types	Specifications
`list_of_organelles`	`list(list(float))`	necessary
`tensor`	`fun: list(SuperCell) -> SuperCell`	necessary
`order = "non-sorted"`	`string`	optional

The method possesses one action, which we describe below through sevaral examples.

Action	
Condition	Always
Description	The method .divide_base implements the operation described in [1, Def. 2.25]. The idea is to extend the method .divide (section 4.1.18) associated with the class Cell to the basal junction of self (see section 4.2.9). Put simply, the method separates a subset of the organelles of the root cell of self from its complement subset in two different cells and uses the input function tensor to distribute the child super cells, stored in self.innercells, accordingly (see picture below).



Now, to be more specific, the subset of indices of the organelles of self to be isolated from the other organelles is given by the list list_of_organelles. The method isolates the corresponding organelles in different cells c_1 and c_2 by calling the function

```
self.cell.divide(list_of_organelles).
```

The method then makes sure that the merging of these organelles is consistent with the whole tree structure of self. This is done by creating two new lists new_innercells_1 and new_innercells_2 of child super cells for the newly generated cells c_1 and c_2. The list new_innercells_1 contains the super cells of the form self.innercells[i] whose index i, ranging from 0 to len(self.innercells)-1, is in list_of_organelles, while the list new_innercells_2 contains the super cells of the form self.innercells[i] whose index i is not in list_of_organelles. The resulting super cells are defined in the obvious way as follows:

```
sc_1 = SuperCell(c_1,new_innercells_1)
sc_2 = SuperCell(c_2,new_innercells_2).
```

The method fills up the lists sc1.pre_action and sc2.pre_action in the same way as the lists new_innercells_1 and new_innercells_1 are filled, but where we replace the lists self.innercells_1 and self.innercells_2 with the lists self.pre_action.
Finally, the method divide_base computes self.pre_action as the list of length 2 containing the outputs of the function sc_1.tensor_pre_action() and sc_2.tensor_pre_action() (see section 4.2.14);

The following example illustrates the use of the method .divide_base with the methods .pseudo_tensor (section 4.3.7) and .dividing_tensor (section 4.3.9) associated with the class Operad. In addition, we use the method .spontaneous_reaction (section 4.2.13) to store in each object .cytosol a list of zero values (as required by the method .divide (section 4.1.18) and pre-fill each object pre_action with a non-empty list of length 2, for every super cell present in the hierarchical structure of the super cell sc.

```
>>> c = Cell(2,0.5,[4,2],[[1,2],[5,1],[1,8],[4,4],[0,7]])
>>> operad = Operad(2)
>>> sc = SuperCell(c)
>>> sc.spontaneous_reaction([0,0],operad.identity)
>>> sc.stdout()
[0] -> Cell[6]{ooooo}
```

Below, we use the method `.dividing_tensor` for the input `tensor` associated with the method `.divid_top`. This has the consequence of setting the objects `.compose_state` of each divided super cell to `True`, as indicated by the purple display returned by the method `.stdout`.

```
>>> sc.divide_base([0,1,3],operad.dividing_tensor)
>>> sc.stdout()
[0] -> Cell[0]{oo}
.[1] -> Cell[3]{ooo}
.[1] -> Cell[3]{oo}
```

Alternatively, we can use the method `.pseudo_tensor`, which does not change the value of the objects `.compose_state`. Below, we give the output of the previous code if we used the method `.pseudo_tensor` instead of `.merging_tensor`.

```
>>> sc.divide_base([0,1,3],operad.pseudo_tensor)
>>> sc.stdout()
[0] -> Cell[0]{oo}
.[1] -> Cell[3]{ooo}
.[1] -> Cell[3]{oo}
```

4.2.17. Description of `.fusion` (method). This section describes the code and the functionalities of the method `.fusion`. The method is equipped with the following input variables, including one that is optional.

`.fusion`		
Inputs	Types	Specifications
`vector`	`list(float)`	necessary
`operad`	`Operad`	necessary
`filtering = 1.5`	`float`	optional

The method possesses one action, which we describe below through an example.

Action	
Condition	Always

Description	The method implements the algorithmic step described in [1, Sec. 2.5]. It mainly consists in recursively applying the method `.merge_base` (section 4.2.15) on all the non-leaf cells of `self` (see [1, Conv. 2.2 & Def. 2.3]) – leaf cells are excluded to keep the number of organelles of the super cell constant (in the sense of [1, Def. 2.7]). To do so, the method first calls the function
	`self.spontaneous_reaction(vector,operad.identity)`
	(see section 4.2.13) to clean every super cell present in the hierarchical structure of `self` from its cytosolic content. Then, the method computes a list `mer` of candidate organelles to be merged within each super cell by calling the function
	`*.cell.proposed_clustering(*.pre_action,"merging",filtering)`
	(see section 4.1.22), where `*` denotes any super cell present in the hierarchical structure of `self`. If the list `mer` is empty or includes all the organelles, then the fusion event is canceled. Otherwise, the method calls the function `self.merge_base(mer,operad.merging_tensor)`, which merges the organelles of whose indices belong to the list `mer`. Note that the merging is done relative to the method `.merging_tensor`, which is associated with the input `operad` (see section 4.2.15 and section 4.3.8).
	Finally, the method ues the function `*.reset_depth()` to reset the depth of every super cell in the hierarchical structure of `self`.

The following example illustrates the use of the method `.fusion` with the class `Operad`.

```
>>> c = Cell(2,0.5,[4,2],[[1,2],[5,1],[1,8],[4,4],[0,7]])
>>> operad = Operad(2)
>>> c1 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[10,5]]))
>>> c2 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[35,2]]))
>>> c3 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[100,5]]))
>>> c4 = SuperCell(Cell(2,0.5,[1,1],[[1,15],[0,25],[40,12]]))
>>> c5 = SuperCell(Cell(2,0.5,[1,1],[[80,1],[0,2],[27,1]]))
>>> sc = SuperCell(c,[c1,c2,c3,c4,c5])
>>> sc.stdout([10,50])
[0] -> Cell[6]{oooooo}
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2448393108
.[1] -> Cell[2]{ooo} [0]:0.9914542955 [1]:0.9805806756 [2]:0.4696129729
.[1] -> Cell[2]{ooo} [0]:0.2083571163 [1]:0.9805806756 [2]:0.232274682
>>> sc.fusion([10,50],operad)
```

```
Searching cliques in the following graph:
[0, 2, 2, 1, 2]
[0, 0, 2, 1, 2]
[0, 0, 0, 1, 2]
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 0]
Maximal weight = 2
Edges with maximal weight = [[0, 1], [0, 2], [0, 4], [1, 2], [1, 4], [2,
4]]
Merging occurring due to organelle(s):  [0, 1, 2, 4] at level = 0
>>> sc.stdout([10,50])
[0] -> Cell[6]{oo}
.[1] -> Cell[0]{oooo}
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2448393108
..[2] -> Cell[2]{ooo} [0]:0.2083571163 [1]:0.9805806756 [2]:0.232274682
.[1] -> Cell[2]{ooo} [0]:0.9914542955 [1]:0.9805806756 [2]:0.4696129729
>>> sc.innercells[0].innercells[0].cell.stdout()
residual:  2.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [10, 1]
2-th organelle:  [40, 2]
3-th organelle:  [10, 5]
>>> sc.innercells[0].innercells[1].cell.stdout()
residual:  2.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [10, 1]
2-th organelle:  [40, 2]
3-th organelle:  [35, 2]
>>> sc.innercells[0].innercells[2].cell.stdout()
residual:  2.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [10, 1]
2-th organelle:  [40, 2]
3-th organelle:  [100, 5]
>>> sc.innercells[0].innercells[3].cell.stdout()
residual:  2.5
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [80, 1]
2-th organelle:  [0, 2]
3-th organelle:  [27, 1]
```

4.2.18. Description of `.fission` (method). This section describes the code and the functionalities of the method `.fission`. The method is equipped with the following input variables, including one that is optional.

.fission		
Inputs	Types	Specifications
vector	list(float)	necessary
operad	Operad	necessary
filtering = 1.5	float	optional

The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method implements the algorithmic step described in [1, Sec. 2.5]. It mainly consists in recursively applying the method .divide_base (section 4.2.16) on all the cells of self – including leaf cells [1, Conv. 2.2 & Def. 2.3]. To do so, the method first calls the function self.spontaneous_reaction(vector,operad.identity) (see section 4.2.13) to clean every super cell present in the hierarchical structure of self from its cytosolic content. Then, the method computes a list div of candidate organelles to be isolated from the other organelles within each super cell by calling the function *.cell.proposed_clustering(*.pre_action,"division",filtering) (see section 4.1.22), where * denotes any super cell in the hierarchical structure of self. If the list div is empty or includes the indices of all the organelles, then the fission event is canceled. Otherwise, the method calls the function self.divide_base(div,operad.dividing_tensor), which isolates the organelles whose indices belong to the list div. Note that the division is done relative to the method .dividing_tensor, which is associated with the input operad (see section 4.2.16 and section 4.3.9). Finally, the method uses the function *.reset_depth()s to reset the depth of every super cell in the hierarchical structure of self.

The following example illustrates the use of the method .fission with the class Operad.

```
>>> c = Cell(2,0.5,[4,2],[[1,2],[5,1],[1,8],[4,4],[0,7]])
>>> operad = Operad(2)
>>> c1 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[10,5]]))
>>> c2 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[35,2]]))
>>> c3 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[100,5]]))
>>> c4 = SuperCell(Cell(2,0.5,[1,1],[[1,15],[0,25],[40,12]]))
>>> c5 = SuperCell(Cell(2,0.5,[1,1],[[80,1],[0,2],[27,1]]))
>>> sc = SuperCell(c,[c1,c2,c3,c4,c5])
>>> sc.stdout([10,50])
[0] -> Cell[6]{ooo}
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2448393108
.[1] -> Cell[2]{ooo} [0]:0.9914542955 [1]:0.9805806756 [2]:0.4696129729
.[1] -> Cell[2]{ooo} [0]:0.2083571163 [1]:0.9805806756 [2]:0.232274682
>>> sc.fission([10,50],operad)
```

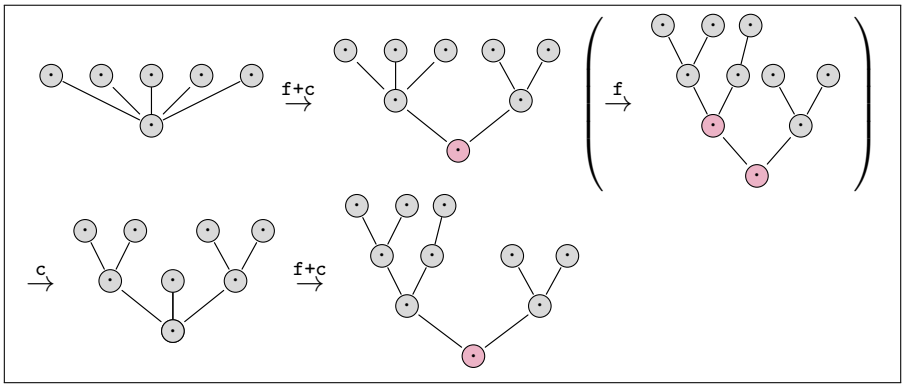
```
Warning:  in SuperCell._fission:  total fission canceled at level 1
Warning:  in SuperCell._fission:  total fission canceled at level 1
Warning:  in SuperCell._fission:  total fission canceled at level 1
Searching cliques in the following graph:
[0, 1, 0]
[0, 0, 0]
[0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[0, 1]]
Division occurring due to organelle(s):  [0, 1] at level = 1
Warning:  in SuperCell._fission:  total fission canceled at level 1
Searching cliques in the following graph:
[0, 0, 0, 0, 0]
[0, 0, 0, 0, 1]
[0, 0, 0, 1, 0]
[0, 0, 0, 0, 0]
[0, 0, 0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[1, 4], [2, 3]]
Division occurring due to organelle(s):  [2, 3] at level = 0
>>> sc.stdout([10,50])
[0] -> Cell[0]{oo}
.[1] -> Cell[3]{oo}
..[2] -> Cell[2]{ooo} [0]:0.9904048953 [1]:0.9835249384 [2]:0.7321129014
..[2] -> Cell[0]{oo}
...[3] -> Cell[1]{oo} [0]:0.9914542955 [1]:0.9805806756
...[3] -> Cell[1]{o} [0]:0.4696129729
.[1] -> Cell[3]{ooo}
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
..[2] -> Cell[2]{ooo} [0]:0.2083571163 [1]:0.9805806756 [2]:0.232274682
>>> sc.innercells[0].innercells[0].cell.stdout()
residual:  1.25
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [1, 17]
2-th organelle:  [1, 64]
3-th organelle:  [25, 18]
>>> sc.innercells[0].innercells[1].innercells[0].cell.stdout()
residual:  1.25
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [1, 15]
2-th organelle:  [0, 25]
>>> sc.innercells[0].innercells[1].innercells[1].cell.stdout()
residual:  1.25
cytosol[1]:  0
cytosol[2]:  0
1-th organelle:  [40, 12]
```

4.2.19. Description of `.compose` (method). This section describes the code and the functionalities of the method `.compose`. The method is equipped with the following input variable.

`.compose`		
Inputs	Types	Specifications
`identity`	`fun: list(float) -> Cell`	necessary

The method possesses one action, which we describe below through an example.

Action	
Condition	Always
Description	The method implements the algorithmic step described in [1, Sec. 2.4] – the idea is to compose, within their respective parent cells, every super cell whose object `.compose_state` contains `True`. An important feature of the method is to proceed in a way that does not break the super cell structure (which is possible – see section [1, Sec. 2.4]). Before describing the method is details, we can broadly describe the method as follows: it uses the function `*.cell.compose(k,c)` for every parent cell `*` and child cell `c` whose associated object `.compose_state` contains `True` (see section 4.1.8). During this composition process, the method also takes care of preserving the association between the pre-actions and their corresponding super cells. More specifically, the method proceed as follows: (1) if `self.is_leaf` contains the value `True`, then the method returns `self`. (2) if `self.is_leaf` contains the value `False`, then the method checks whether all super cells in the object `self.innercells` are such that their associated objects `.is_leaf` and `.compose_state` contain the value `True`. (2.1) If this is the case, then `self.innercells` only contains leaves (section 4.2.3) and the method composes all these leaf `SuperCell` within `self`, making the resulting `SuperCell` item `self` a leaf. (2.2) Otherwise, the method composes the cells associated with the super cells of the list `self.innercells` within `self` by making sure to equip each leaf `SuperCell` of `self.innercells` with formal child super cells consisting of the super cells `SuperCell(identity(comp_i.cell.organelles[j]))` where `comp_i` is the output of the recursive call of the method `.compose(identity)` for the leaf super cell `self.innercells[i]`.

Description	Note that because the root cell of the underlying tree structure of `self` does not have a parent cell, the composition of the root cell never occurs, which usually has the consequence of making the hierarchical structure of `self` grow over time. The growth of the tree caused by these exceptions is illustrated below in the context of a series of calls of the method `.fission` (section 4.2.18) directly followed by calls of the method `.compose`. We display in brackets the outputs of the method `.fission` if they are different from the outputs of the method `.compose`. 

The following example combines the examples used in section 4.2.17 and section 4.2.18. We first construct a super cell of level 2 that possesses internal super cells whose objects `.compose_state` are `True`.

```
>>> c = Cell(2,0.5,[4,2],[[1,2],[5,1],[1,8],[4,4],[0,7]])
>>> operad = Operad(2)
>>> c1 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[10,5]]))
>>> c2 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[35,2]]))
>>> c3 = SuperCell(Cell(2,0.5,[1,1],[[10,1],[40,2],[100,5]]))
>>> c4 = SuperCell(Cell(2,0.5,[1,1],[[1,15],[0,25],[40,12]]))
>>> c5 = SuperCell(Cell(2,0.5,[1,1],[[80,1],[0,2],[27,1]]))
>>> sc = SuperCell(c,[c1,c2,c3,c4,c5])
>>> sc.stdout([10,50])
[0] -> Cell[6]{ooo}
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
.[1] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2448393108
.[1] -> Cell[2]{ooo} [0]:0.9914542955 [1]:0.9805806756 [2]:0.4696129729
.[1] -> Cell[2]{ooo} [0]:0.2083571163 [1]:0.9805806756 [2]:0.232274682
>>> sc.fusion([10,50],operad)
Searching cliques in the following graph:
[0, 2, 2, 1, 2]
[0, 0, 2, 1, 2]
[0, 0, 0, 1, 2]
[0, 0, 0, 0, 1]
[0, 0, 0, 0, 0]
Maximal weight = 2
Edges with maximal weight = [[0, 1], [0, 2], [0, 4], [1, 2], [1, 4], [2,
4]]
Merging occurring due to organelle(s):  [0, 1, 2, 4] at level = 0
>>> sc.stdout([10,50])
```

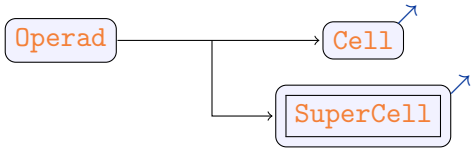
```
[0] -> Cell[6]{oo}
.[1] -> Cell[0]{oooo}
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
..[2] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2448393108
..[2] -> Cell[2]{ooo} [0]:0.2083571163 [1]:0.9805806756 [2]:0.232274682
.[1] -> Cell[2]{ooo} [0]:0.9914542955 [1]:0.9805806756 [2]:0.4696129729
>>> sc.fission([10,50],operad)
Warning:  in SuperCell._fission:  total fission canceled at level 2
Warning:  in SuperCell._fission:  total fission canceled at level 2
Warning:  in SuperCell._fission:  total fission canceled at level 2
Warning:  in SuperCell._fission:  total fission canceled at level 2
[0, 0, 0, 1]
[0, 0, 0, 0]
[0, 0, 0, 0]
[0, 0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[0, 3]]
Division occurring due to organelle(s):  [0, 3] at level = 1
Searching cliques in the following graph:
[0, 1, 0]
[0, 0, 0]
[0, 0, 0]
Maximal weight = 1
Edges with maximal weight = [[0, 1]]
Division occurring due to organelle(s):  [0, 1] at level = 1
Warning:  in SuperCell._fission:  total fission canceled at level 0
>>> sc.stdout([10,50])
[0] -> Cell[6]{oo}
.[1] -> Cell[0]{oo}
..[2] -> Cell[0]{oo}
...[3] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
...[3] -> Cell[2]{ooo} [0]:0.2083571163 [1]:0.9805806756 [2]:0.232274682
..[2] -> Cell[0]{oo}
...[3] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
...[3] -> Cell[2]{ooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2448393108
.[1] -> Cell[0]{oo}
..[2] -> Cell[1]{oo} [0]:0.9914542955 [1]:0.9805806756
..[2] -> Cell[1]{o} [0]:0.4696129729
```

We now show the action of the method `.compose()` on the super cell `cs` – note that the output is a 1-level tree structure, which corresponds to the same type of structure we started with (see the first display `cs.stdout([10,50])`).

```
>>> sc.compose(operad.identity)
>>> sc.stdout([10,50])
[0] -> Cell[6]{oooo}
.[1] -> Cell[5]{oooooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.6139406135
[3]:0.2083571163 [4]:0.9805806756 [5]:0.232274682
.[1] -> Cell[5]{oooooo} [0]:0.292714272 [1]:0.2448393108 [2]:0.2517386496
[3]:0.292714272 [4]:0.2448393108 [5]:0.2448393108
.[1] -> Cell[1]{oo} [0]:0.9914542955 [1]:0.9805806756
.[1] -> Cell[1]{o} [0]:0.4696129729
```

4.3. Description of `Operad` (class)

4.3.1. Introduction. This section introduces the reader to the code of the class `Operad`, which possesses the following external dependencies.



The main goal of the class `Operad` is to model the features of the colored operad described in [1, Sec. 3]. Before presenting the features of the class, recall that, mathematically, this colored operad can be defined as the map $\mathcal{O}_n^N : (\mathbb{R}_+^N)^n \times \mathbb{R}_+^N \to \mathbf{Set}$ sending every tuple $(x_1, \dots, x_n, y)$ in $(\mathbb{R}_+^N)^n \times \mathbb{R}_+^N$ to the set $\mathbb{R}$. Every element 0 in a set of the form $\mathcal{O}_1^N(a, a) = \mathbb{R}$ is called the *identity* on a and the sum operation of the form

$$\mathcal{O}_n^N(x_1, \dots, x_n, y) \times \prod_{i=1}^{n} \mathcal{O}_{m_i}^N(z_{i,1}, \dots, z_{i,m_i}, x_i) \to \mathcal{O}_{m_1+\dots+m_n}^N(z_{1,1}, \dots, z_{n,m_n}, y)$$

is called a *composition*. In addition, the operad is equipped with tensor operations given by the addition operations of the following form:

$$\otimes : \mathcal{O}_n^N(x_1, \dots, x_n, y) \times \mathcal{O}_m^N(x'_1, \dots, x'_m, y') \to \mathcal{O}_{n+m}^N(x_1, \dots, x_n, x'_1, \dots, x'_m, y + y').$$

In this library, the class `Operad` is equipped with 1 object, recording the dimension N of the objects of the operad, and 2 types of methods, which are listed below:

▷ a set of 3 methods meant to generate cells and super cells:

- `__init__`: initializes the dimension of the objects of the operad;
- `identity`: creates an identity cell, as defined in [1, Def. 1.9]);
- `generate`: generate a super cell with random values (section 4.2).

▷ a set of 4 methods giving a variety of tensor structures [1, Sec. 1.7]:

- `tensor`: returns a tensor of cells, as defined in [1, Conv. 1.50 & Ex. 1.51] .
- `pseudo_tensor`: returns the non-composed version of a tensor (see [1, Ex. 1.52]).
- `merging_tensor`: updates the objects `.compose_state` associated with the child cells of the root of a super cell according to [1, Def. 2.26].
- `dividing_tensor`: updates the object `.compose_state` associated with the root of a super cell according to [1, Def. 2.25].

4.3.2. Structure. The following tables give a preview of the class `Operad`. The table given below describes the various dependencies of the class.

Dependencies	
Superclass ancestry	Module section
`object`	N/A
Statistics	
▷ Importable objects: 1 ▷ Non-importable objects: 0 ▷ Importable methods: 7 ▷ Non-importable methods: 0	

The following table gives a description of the single importable object of the class.

Objects		
Name	Type	Related sections
`.dimension`	`int`	▷ section 4.3.3

Finally, the following table gives a description of the 7 importable methods of the class:

Methods			
Name	Input types	Output types	Related sections
`.__init__`	- `int`	- `Cell`	▷ section 4.3.3
`.identity`	- `list(float)`	- `Cell`	▷ section 4.3.4
`.tensor`	- `list(Cell)`	- `Cell`	▷ section 4.3.6
`.pseudo_tensor`	- `list(SuperCell)`	- `SuperCell`	▷ section 4.3.7
`.merging_tensor`	- `list(SuperCell)`	- `SuperCell`	▷ section 4.3.8
`.dividing_tensor`	- `list(SuperCell)`	- `SuperCell`	▷ section 4.3.9
`.generate`	- `int` - `int` - `fun: void -> float`	- `SuperCell`	▷ section 4.3.3

4.3.3. Description of `.__init__` (method). Writing in progress – see `cl_ope.py` for more information.

4.3.4. Description of `.identity` (method). Writing in progress – see `cl_ope.py` for more information.

4.3.5. Description of `.generate` (method). Writing in progress – see `cl_ope.py` for more information.

4.3.6. Description of `.tensor` (method). Writing in progress – see `cl_ope.py` for more information.

4.3.7. Description of `.pseudo_tensor` (method). Writing in progress – see `cl_ope.py` for more information.

4.3.8. Description of `.merging_tensor` (method). Writing in progress – see `cl_ope.py` for more information.

4.3.9. Description of `.dividing_tensor` (method). Writing in progress – see `cl_ope.py` for more information.

Presentation of the module `cellint.py`

5.1. Description of `intcyt` (function)

This section describes the code of the function `intcyt`. The function is equipped with the following input variable, where we denote by α a polymophic type and we use the symbol `X` as a shortcut for the type `list(list(float))`.

`intcyt`		
Inputs	Types	Specifications
`operad`	`list(Operad)`	necessary
`supercell`	`list(SuperCell)`	necessary
`index`	`list(int)`	necessary
`events`	`list(`α`)`	necessary
`vector`	`list(float)`	necessary
`gamma`	`fun: Cell * X -> X`	necessary
`filtering = [1.5]*2`	`list(int * int)`	optional

The function possesses one action, which is discussed in the tutorial of section 2.

Action 1	
Condition	Always
Description	This function implements the algorithm of [1, Sec. 2] – see section 2 of this documentation for a detailed description.

Bibliography

[1] R. Tuyeras, L. Z. Agudelo, Soumya P. Ram, *et al.* (2020), *Cellular intelligence: reaching dynamic specialization through non-equilibrium compartmentalization*, **Supplementary text**.

[2] R. Tuyeras, L. Z. Agudelo, Soumya P. Ram, *et al.* (2020), *Cellular intelligence: reaching dynamic specialization through non-equilibrium compartmentalization*, **Main text**.

[3] L. Agudelo, R. Tuyeras, *et al.*, (2020), *Stress resilience controlled by transcriptional condensate.*