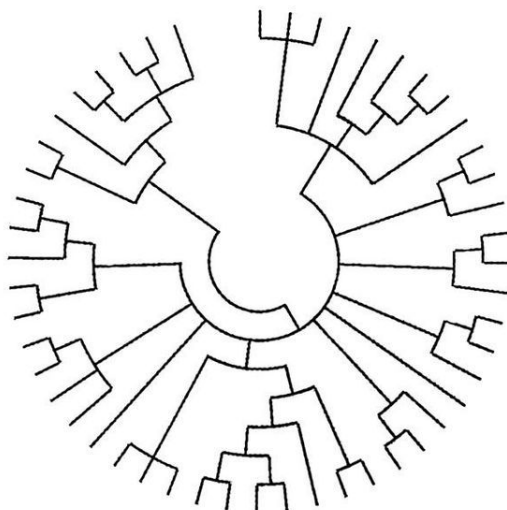


DOCUMENTATION FOR THE PYTHON LIBRARY PEDIGRAD.PY

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VERSION 1.2



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Introduction

1.1. About pedigrad and Pedigrad.py

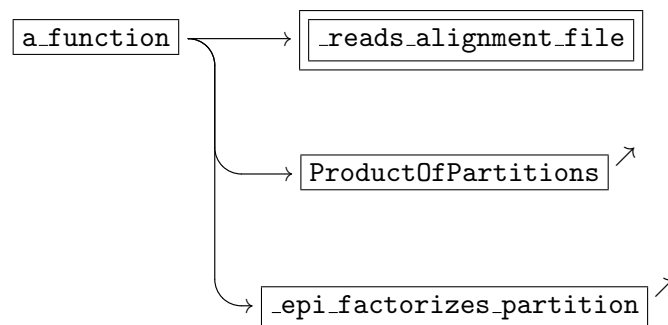
Pedigrad is a mathematical tool that was initially created to model various mechanisms of genetics (see [5]). Mathematically, pedigrad is defined as a functor sending the cones of a certain type of limit sketch to cones in a given category of values. Pedigrad can encode different aspects of biology depending on their ‘categories of values’ and associated cones. So far, the python library `Pedigrad.py` only includes pedigrad taking their values in the category of partitions whose cones are product cones (see [4]).

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 `Pedigrad.py` as well as a description of the (importable and non-importable) functions of its sub-modules

- `PartitionCategory.py` (see Chapter 3)
- `SegmentCategory.py` (see Chapter 4)
- `PedigradCategory.py` (see Chapter 5)
- `AsciiTree.py` (see Chapter 6)

A description of a function will always start with a dependency flow chart as given below if the function depends on other procedures.



A double box indicates that the function does not have any dependencies while an arrow on the top-right corner of a box means that the function belongs to another module of the library.

Also, the python code will always be specified in text editor mode as follows.

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

A console mode is also used for most of the examples (see below).

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

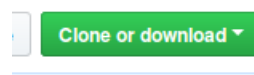
1.3. Acknowledgments

I would like to thank Maxim Wolf and Carles Boix for interesting discussions about DNA and genetics. I would also like to thank Maxim Wolf for answering many of my questions and giving me some of his time.

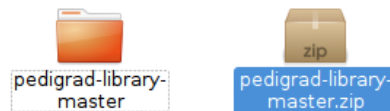
Tutorial

2.1. Installation and preparation

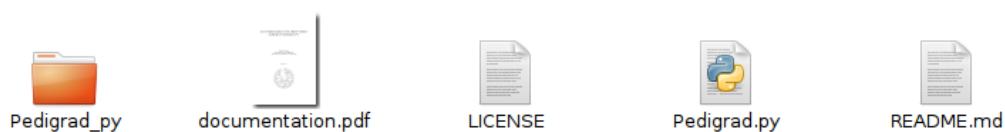
To install the library, first download the package by clicking on the green button on the right of the screen at <https://github.com/remytuyeras/pedigrad-library>.



The downloaded package should be a compressed file named `pedigrad-library-master.zip`. Create a new directory in which you can copy and extract the compressed file using your favorite extraction application.



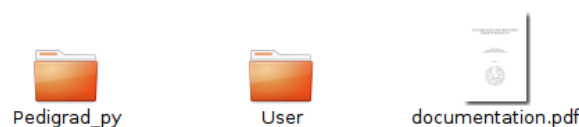
Enter the extracted directory whose inside should look as follows.



In this tutorial, and in general, the use of the library `Pedigrad` will require the creation of three files:

- ▷ a sequence alignment file (usually with an extension `.fa` or `.fasta`);
- ▷ a file in which a pre-ordered set is specified (preferably with an extension `.yaml`);
- ▷ a python file in which the user uses the library (the extension is obviously `.py`).

To do this properly, create a new directory in `pedigrad-library-master`, call it `User`, and copy the file `Pedigrad.py` in `User`.



Open the file `Pedigrad.py` that you copied in `User`. Once inside, you will be able to see several instances of the function

```
sys.path.insert(0,—)
```

in which paths appear in the second argument. Add the text `../` at the beginning of every path passed to the function `sys.path.insert(0,—)`, as shown below¹.

```
1#-----
2import sys
3sys.path.insert(0, 'Pedigrad_py/PartitionCategory/')
4from PartitionCategory import *
5
6#print_partition(partition): standard output
7
8#EquivalenceRelation: .classes, .range, .closure, .quoti
9
10#product_of_partitions(partition1,partition2): list
11
12#coproduct_of_partitions(partition1,partition2): list
13
14#MorphismOfPartitions: .arrow, .source, .target
15
16#homset_is_inhabited(source,target): Boolean
17
18#-----
19import sys
20sys.path.insert(0, 'Pedigrad_py/SegmentCategory/')
21from SegmentCategory import *
22
23#SegmentObject: .colors, .topology
24
25#CategoryOfSegments: .domain, .mask, .preorder
26
27#-----
28import sys
29sys.path.insert(0, 'Pedigrad_py/PedigradCategory/')
30from PedigradCategory import *
```

```
1#-----
2import sys
3sys.path.insert(0, '../Pedigrad_py/PartitionCategory/')
4from PartitionCategory import *
5
6#print_partition(partition): standard output
7
8#EquivalenceRelation: .classes, .range, .closure, .quoti
9
10#product_of_partitions(partition1,partition2): list
11
12#coproduct_of_partitions(partition1,partition2): list
13
14#MorphismOfPartitions: .arrow, .source, .target
15
16#homset_is_inhabited(source,target): Boolean
17
18#-----
19import sys
20sys.path.insert(0, '../Pedigrad_py/SegmentCategory/')
21from SegmentCategory import *
22
23#SegmentObject: .colors, .topology
24
25#CategoryOfSegments: .domain, .mask, .preorder
26
27#-----
28import sys
29sys.path.insert(0, '../Pedigrad_py/PedigradCategory/')
30from PedigradCategory import *
```

Once the paths are all updated, create, in the directory `User`, three new files with the names `align.fa`, `main.py` and `omega.yml`.



align.fa



main.py



omega.yml



Pedigrad.py

Open the file `main.py` and insert the following piece of code.


```
1 from Pedigrad import *
```

We are now ready to use the library – proceed to section 2.2.

2.2. Sequence alignments

Open the file named `align.fa` and paste the sequence alignment to be studied.

```
1 >Human
2 ATGTCAGACTGCTACACGGAGCTGGAGAAGGCAGTCATTGTCTGGTGGAAAACTTCTACAAATATGTGT
3 CTAAGTACAGCCTGGTCAAGAACAAAGATCAGCAAGAGCAGCTTCCGCGAGATGCTCCAGAAAGAGCTGAA
4 CCACATGCTGTGCGACACAGGGAACCGGAAGGCTGCGGATAAGCTCATCCAGAACCTGGATGCCAATCAT
5 GATGGGCGCATCAGCTTCGATGAGTACTGGACCTTGATAGGCGGCATACCGGCCCATCGCCAAACTCA
6 TCCATGAGCAGGAGCAGCAGAGCAGCAGCTAG
7 >Chimp
8 ATGTCAGACTGCTACACGGAGCTGGAGAAGGCAGTCATTGTCTGGTGGAAAACTTCTACAAATATGTGT
9 CTAAGTACAGCCTGGTCAAGAACAAAGATCAGCAAGAGCAGCTTCCGCGAGATGCTCCAGAAAGAGCTGAA
10 CCACATGCTGTGCGACACAGGGAACCGGAAGGCTGCGGATAAGCTCATCCAGAACCTGGATGCCAATCAT
11 GATGGGCGCATCAGCTTCGATGAGTACTGGACCTTGATAGGCGGCATACCGGCCCATCGCCAAACTCA
12 TCCGTGAGCAGGAGCAGCAGAGCAGCAGCTAG
13 >Mouse_Lemur
14 ATGGCGGACTGCTACACGGAGCTGGAGAAGGCGGTCGTTGTCTGGTGGAAAACTTCTACAAATACGTGT
15 CTAAGCAGCAGCTGGTCAAGAACAAAGATCAGCAAGAGCAGCTTCCGCAAGATGCTCCAGAAAGAGCTGAA
16 CCATATGCTGACGACGACGCGGGAACCGCAAGGCTGCAGACAAGCTCATCCAGAACCTGGATGCCAACAC
```

The name of the taxa should always be preceded by the symbol `>` and followed by a new line character (obtained by using the return key ). The DNA sequence associated with the taxon should then be displayed. Note that the sequence can contain new line characters, but cannot contain the character `>`.

¹Note that the highlight mode of my text editor is different from the one used in this documentation.

For this tutorial, we shall consider the following alignment, in which the noticeable mutations are colored in red.

```

                                align.fa
1 >Alice
2 ATGGGAATCCTCGAACCACCTTATCGCGCGTAATCTGGAATCGATTGATCAAGGTACGTTGGCGAAAGGTAG
3 >Bob
4 ATGGGCATCCTCAAGCCTTTTAACGCTGGTAATCTAGGAGTCGATCGAGCAAGCTACGATGGCTAAAGTTAG
5 >Carles
6 ATGGGCATCCTCAATCCCTTTAACGCGGGTAATCTCGGATTCGATCGAGCAAGCTACGTTGGCGAAAGTTAG
7 >Doug
8 ATGGGCATCCTCTAGCCATTTATCGCCAGTAATCTTGCATTCGATGGATCAAGGTACGTTGGCAAAAGTTAG
9 >Eric
10 ATGGGAATCCTCTAGCCCTTTATCGCCCGTAATCTAGAATTCGATAGATCAAGGTACGATGGCTATAGCTAG
11 >Fred
12 ATGGGAATCCTCGACCCACTTAGCGCGTGTAATCTGGAAGTCGATTGAACAAGGTACGTTGGCCAGAGGTAG
11 >Gary
12 ATGGGAATCCTCAAAACCGTTATCGCTCGTAATCTAGGATTCGATAGACCAAGGTACGATGGCAAAAGCTAG
13 >Haley
14 ATGGGCATCCTCGACCCAAATTATCGCTCGTAATCTTGCAATCGATAGATCAAGTTACGTTGGCAAAAGTTAG

```

Copy the previous text and paste it in file named `align.fa`. Then, open the file named `main.py` and add the following piece of code.

```

3 align = readalignment_file("align.fa", READ_DNA)
4 for i in range(len(align[0])):
5     print(str(i)+": " +str(align[0][i]))
6 print("----")
7 for i in range(len(align[1])):
8     print(str(i)+": " +str(align[1][i]))

```

Save and compile `main.py` – you should obtain the following result in the console.

```

0: Alice
1: Bob
2: Carles
3: Doug
4: Eric
5: Fred
6: Gary
7: Haley
----
0: ['A', 'T', 'G', 'G', 'G', 'A', 'A', 'T', 'C', 'C', 'T', 'C', 'G', 'A',
'A', 'C', 'C', 'A', 'C', 'T', 'T', 'A', 'T', 'C', 'G', 'C', 'G', 'T', 'A', 'A', 'T', 'C', 'T', 'G', 'G', 'A', 'A', 'T', 'C', 'G', 'A', 'T', 'T', 'G', 'A', 'T', 'C', 'A', 'A', 'G', 'G', 'T', 'A', 'C', 'G', 'T', 'T', 'G', 'G', 'C', 'G', 'A', 'A', 'A', 'G', 'G', 'T', 'A', 'G']
1: ['A', 'T', 'G', 'G', 'G', 'C', 'A', 'T', 'C', 'C', 'T', 'C', 'A', 'A', 'G', 'C', 'C', 'T', 'T', 'T', 'A', 'A', 'C', 'G', 'C', 'T', 'G', 'G', 'T', 'A', 'A', 'T', 'C', 'T', 'A', 'G', 'G', 'A', 'G', 'T', 'C', 'G', 'A', 'T', 'C', 'G', 'A', 'G', 'C', 'A', 'A', 'G', 'C', 'T', 'A', 'C', 'G', 'A', 'T', 'G', 'G', 'C', 'T', 'A', 'A', 'A', 'G', 'T', 'T', 'A', 'G']

```

```

2: ['A', 'T', 'G', 'G', 'G', 'C', 'A', 'T', 'C', 'C', 'T', 'C', 'A', 'A',
   'T', 'C', 'C', 'C', 'T', 'T', 'T', 'A', 'A', 'C', 'G', 'C', 'G', 'G', 'G',
   'T', 'A', 'A', 'T', 'C', 'T', 'C', 'G', 'G', 'A', 'T', 'T', 'C', 'G', 'A',
   'T', 'C', 'G', 'A', 'G', 'C', 'A', 'A', 'G', 'C', 'T', 'A', 'C', 'G', 'G',
   'T', 'G', 'G', 'C', 'G', 'A', 'A', 'A', 'G', 'T', 'T', 'A', 'G']
3: ['A', 'T', 'G', 'G', 'G', 'C', 'A', 'T', 'C', 'C', 'T', 'C', 'T', 'A',
   'G', 'C', 'C', 'A', 'T', 'T', 'T', 'A', 'T', 'C', 'G', 'C', 'C', 'A', 'G',
   'T', 'A', 'A', 'T', 'C', 'T', 'T', 'G', 'C', 'A', 'T', 'T', 'C', 'G', 'A',
   'T', 'G', 'G', 'A', 'T', 'C', 'A', 'A', 'G', 'G', 'T', 'A', 'C', 'G', 'T',
   'T', 'G', 'G', 'C', 'A', 'A', 'A', 'A', 'G', 'T', 'T', 'A', 'G']
4: ['A', 'T', 'G', 'G', 'G', 'A', 'A', 'T', 'C', 'C', 'T', 'C', 'T', 'A',
   'G', 'C', 'C', 'C', 'T', 'T', 'T', 'A', 'T', 'C', 'G', 'C', 'C', 'C', 'G',
   'T', 'A', 'A', 'T', 'C', 'T', 'A', 'G', 'A', 'A', 'T', 'T', 'C', 'G', 'A',
   'T', 'A', 'G', 'A', 'T', 'C', 'A', 'A', 'G', 'G', 'T', 'A', 'C', 'G', 'A',
   'T', 'G', 'G', 'C', 'T', 'A', 'T', 'A', 'G', 'C', 'T', 'A', 'G']
5: ['A', 'T', 'G', 'G', 'G', 'A', 'A', 'T', 'C', 'C', 'T', 'C', 'G', 'A',
   'C', 'C', 'C', 'A', 'C', 'T', 'T', 'A', 'G', 'C', 'G', 'C', 'G', 'T', 'G',
   'T', 'A', 'A', 'T', 'C', 'T', 'G', 'G', 'A', 'A', 'G', 'T', 'C', 'G', 'A',
   'T', 'T', 'G', 'A', 'A', 'C', 'A', 'A', 'G', 'G', 'T', 'A', 'C', 'G', 'T',
   'T', 'G', 'G', 'C', 'C', 'A', 'G', 'A', 'G', 'G', 'T', 'A', 'G']
6: ['A', 'T', 'G', 'G', 'G', 'A', 'A', 'T', 'C', 'C', 'T', 'C', 'A', 'A',
   'A', 'C', 'C', 'C', 'G', 'T', 'T', 'A', 'T', 'C', 'G', 'C', 'T', 'C', 'G',
   'T', 'A', 'A', 'T', 'C', 'T', 'A', 'G', 'G', 'A', 'T', 'T', 'C', 'G', 'A',
   'T', 'A', 'G', 'A', 'C', 'C', 'A', 'A', 'G', 'G', 'T', 'A', 'C', 'G', 'A',
   'T', 'G', 'G', 'C', 'A', 'A', 'A', 'A', 'G', 'C', 'T', 'A', 'G']
7: ['A', 'T', 'G', 'G', 'G', 'C', 'A', 'T', 'C', 'C', 'T', 'C', 'G', 'A',
   'C', 'C', 'C', 'A', 'A', 'T', 'T', 'A', 'T', 'C', 'G', 'C', 'T', 'C', 'G',
   'T', 'A', 'A', 'T', 'C', 'T', 'T', 'G', 'C', 'A', 'A', 'T', 'C', 'G', 'A',
   'T', 'A', 'G', 'A', 'T', 'C', 'A', 'A', 'G', 'T', 'T', 'A', 'C', 'G', 'T',
   'T', 'G', 'G', 'C', 'A', 'A', 'A', 'A', 'G', 'T', 'T', 'A', 'G']

```

As can be seen, the procedure `read_alignment_file` can be used to collect the name of the taxa and the DNA sequence of each of them in the form of lists. See section 5.1 for a detailed description of this function.

Note that the lists contained in `align[1]` contain all the nucleotides of the alignment, even those that do not present any mutation. To only select the columns that present mutations, one can use the procedure `column_is_trivial` (see section 5.4).

For illustration, replace the current code contained in the file `main.py` with the following piece of code.

```

1 from Pedigrad import *
2
3 align = read_alignment_file("align.fa", READ_DNA)
4
5 positions = list()
6 transpose = list()
7 for i in range(len(align[1][0])):
8     column = list()
9     for j in range(len(align[1])):
10         column.append(align[1][j][i])
11     if not(column_is_trivial(column, [])):

```

```

12     transpose.append(column)
13     positions.append(i)
14
15 for i in range(len(transpose)):
16     print(str(i+1) + ") at position " + str(positions[i])+" : " +
           str(transpose[i]))

```

Now, save and compile `main.py` – you should obtain the following result in the console.

```

1) at position 5:  ['A', 'C', 'C', 'C', 'A', 'A', 'A', 'C']
2) at position 12: ['G', 'A', 'A', 'T', 'T', 'G', 'A', 'G']
3) at position 14: ['A', 'G', 'T', 'G', 'G', 'C', 'A', 'C']
4) at position 17: ['A', 'T', 'C', 'A', 'C', 'A', 'C', 'A']
5) at position 18: ['C', 'T', 'T', 'T', 'T', 'C', 'G', 'A']
6) at position 22: ['T', 'A', 'A', 'T', 'T', 'G', 'T', 'T']
7) at position 26: ['G', 'T', 'G', 'C', 'C', 'G', 'T', 'T']
8) at position 27: ['C', 'G', 'G', 'A', 'C', 'T', 'C', 'C']
9) at position 35: ['G', 'A', 'C', 'T', 'A', 'G', 'A', 'T']
10) at position 37: ['A', 'G', 'G', 'C', 'A', 'A', 'G', 'C']
11) at position 39: ['C', 'G', 'T', 'T', 'T', 'G', 'T', 'A']
12) at position 45: ['T', 'C', 'C', 'G', 'A', 'T', 'A', 'A']
13) at position 48: ['T', 'G', 'G', 'T', 'T', 'A', 'C', 'T']
14) at position 53: ['G', 'C', 'C', 'G', 'G', 'G', 'G', 'T']
15) at position 58: ['T', 'A', 'G', 'T', 'A', 'T', 'A', 'T']
16) at position 63: ['G', 'T', 'G', 'A', 'T', 'C', 'A', 'A']
17) at position 65: ['A', 'A', 'A', 'A', 'T', 'G', 'A', 'A']
18) at position 68: ['G', 'T', 'T', 'T', 'C', 'G', 'C', 'T']

```

We are now ready to proceed to the next section of the tutorial.

2.3. Categories of partitions

The lists contained in the variable `transpose` (see section 2.2) are what could be seen as *labeled partitions* in the sense of [4]. While the partitioning induced by these so-called ‘labeled partitions’ can be displayed via the debug function `print_partition`, the ‘labels’ are those characters ‘A’, ‘C’, ‘G’ and ‘T’ shown in the last console display of section 2.2.

To see the partitioning induced by the elements of `transpose`, the code of `main.py` should be updated as follows (after line 16).

```

17     print_partition(transpose[i])
18     print('')

```

Compiling the new code of `main.py` now provides the following display.

```

1) at position 5:  ['A', 'C', 'C', 'C', 'A', 'A', 'A', 'C']
[[0, 4, 5, 6], [1, 2, 3, 7]]

2) at position 12: ['G', 'A', 'A', 'T', 'T', 'G', 'A', 'G']
[[0, 5, 7], [1, 2, 6], [3, 4]]

3) at position 14: ['A', 'G', 'T', 'G', 'G', 'C', 'A', 'C']
[[0, 6], [1, 3, 4], [2], [5, 7]]

4) at position 17: ['A', 'T', 'C', 'A', 'C', 'A', 'C', 'A']

```

[[0, 3, 5, 7], [1], [2, 4, 6]]

5) at position 18: ['C', 'T', 'T', 'T', 'T', 'C', 'G', 'A']
[[0, 5], [1, 2, 3, 4], [6], [7]]

6) at position 22: ['T', 'A', 'A', 'T', 'T', 'G', 'T', 'T']
[[0, 3, 4, 6, 7], [1, 2], [5]]

7) at position 26: ['G', 'T', 'G', 'C', 'C', 'G', 'T', 'T']
[[0, 2, 5], [1, 6, 7], [3, 4]]

8) at position 27: ['C', 'G', 'G', 'A', 'C', 'T', 'C', 'C']
[[0, 4, 6, 7], [1, 2], [3], [5]]

9) at position 35: ['G', 'A', 'C', 'T', 'A', 'G', 'A', 'T']
[[0, 5], [1, 4, 6], [2], [3, 7]]

10) at position 37: ['A', 'G', 'G', 'C', 'A', 'A', 'G', 'C']
[[0, 4, 5], [1, 2, 6], [3, 7]]

11) at position 39: ['C', 'G', 'T', 'T', 'T', 'G', 'T', 'A']
[[0], [1, 5], [2, 3, 4, 6], [7]]

12) at position 45: ['T', 'C', 'C', 'G', 'A', 'T', 'A', 'A']
[[0, 5], [1, 2], [3], [4, 6, 7]]

13) at position 48: ['T', 'G', 'G', 'T', 'T', 'A', 'C', 'T']
[[0, 3, 4, 7], [1, 2], [5], [6]]

14) at position 53: ['G', 'C', 'C', 'G', 'G', 'G', 'G', 'T']
[[0, 3, 4, 5, 6], [1, 2], [7]]

15) at position 58: ['T', 'A', 'G', 'T', 'A', 'T', 'A', 'T']
[[0, 3, 5, 7], [1, 4, 6], [2]]

16) at position 63: ['G', 'T', 'G', 'A', 'T', 'C', 'A', 'A']
[[0, 2], [1, 4], [3, 6, 7], [5]]

17) at position 65: ['A', 'A', 'A', 'A', 'T', 'G', 'A', 'A']
[[0, 1, 2, 3, 6, 7], [4], [5]]

18) at position 68: ['G', 'T', 'T', 'T', 'C', 'G', 'C', 'T']
[[0, 5], [1, 2, 3, 7], [4, 6]]

The indices that appear in the previous partitions (ranging from 0 to 7) represent the taxa given in the sequence alignment – each taxon is represented by its index in the list `align[0]` (see the beginning of section 2.2).

We are now going to combine the partitions contained in `transpose`. As will be seen, the resulting combinations refine the partitioning of the input partitions. The refinement is

done by using the procedure

```
product_of_partitions(−, −),
```

which returns the categorical product of two input labeled partitions. As explained in [4], such a product can be computed in the category of *unlabeled partitions*, which can be seen as labeled partitions whose labels satisfy a particular labeling system.

To see how this works, update the code of `main.py`, from line 15 to line 18, as follows.

```
15 hypothesis = [transpose[0]]
16 for i in range(len(transpose)-1):
17     hypothesis.append(product_of_partitions(hypothesis[i], transpose[i+1]))
18
19 for i in range(len(hypothesis)):
20     print(str(i+1) + "-th partition :" + str(hypothesis[i]))
21     print('')
```

Compiling `main.py` should now give the following display on the console.

```
1-th partition :['A', 'C', 'C', 'C', 'A', 'A', 'A', 'C']
[[0, 4, 5, 6], [1, 2, 3, 7]]
```

```
2-th partition :[0, 1, 1, 2, 3, 0, 4, 5]
[[0, 5], [1, 2], [3], [4], [6], [7]]
```

```
3-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
4-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
5-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
6-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
7-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
8-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
9-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
10-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
11-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```
12-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

```

13-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]

14-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]

15-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]

16-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]

17-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]

18-th partition :[0, 1, 2, 3, 4, 5, 6, 7]
[[0], [1], [2], [3], [4], [5], [6], [7]]

```

While the first partition keeps the labels coming from the sequence alignment (this is can explained by line 15, in the code of `main.py`), the other partitions were relabeled according to the labeling system of unlabeled partitions.

Also, as can be seen, the successive refinements quickly reach the partition of the following form (categorically, this is an initial partition).

```
[[0], [1], [2], [3], [4], [5], [6], [7]]
```

This shows that refining the partitions induced by a sequence alignment requires an analytic step, which will be made available via the methods of a **Pedigrad** item (see section 2.7).

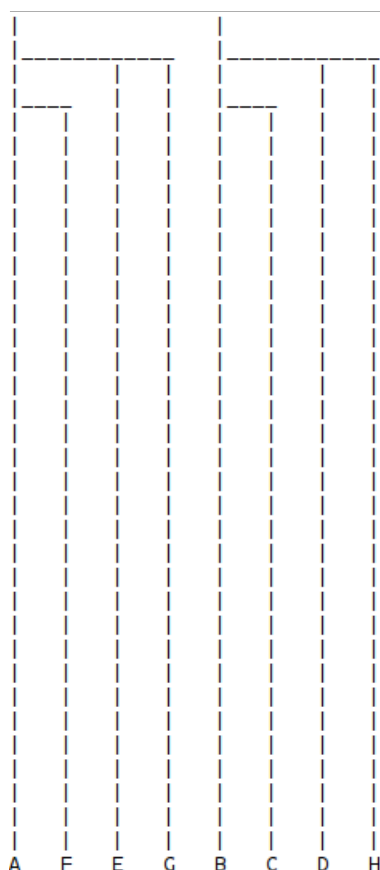
Before moving on to the analytical part of this tutorial, we show, in section 2.4, how the previous list of partitions can be more efficiently displayed as an evolutionary tree. This type of tree construction can be identified as the type of construction used in the cladistic literature (see [2, Chapter 1 & 8] and [6, 3, 1]) to infer the phylogeny of a group of taxa.

2.4. Displaying evolutionary trees

Instead of being displayed as a long sequence of lists, the last console display of section 2.3 could also be displayed as an evolutionary tree. This type of display can be obtained via the procedure `print_evolutionary_tree` (see Chapter 6 and section 6.5 for more detail). In this case, the code of `main.py` would need to be replaced, from line 19 to line 21, with the following piece of code.

```
19 print_evolutionary_tree(hypothesis)
```

Compiling `main.py` would result in the display of the following evolutionary tree.



2.5. Pre-ordered sets

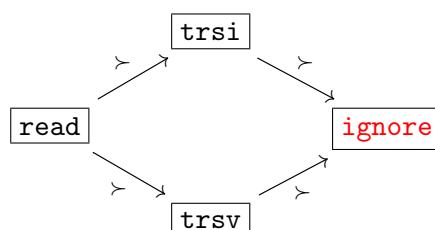
From this section on, the present tutorial aims at using the methods described in [4] to compute the phylogeny of our sequence alignment. The analysis starts by defining the semantics in which we want to work. This is done by defining a pre-order structure on a set of ‘colors’.

To start with, open the file named `omega.yml` and copy the following lines of code.

```

                                omega.yml
1 !obj:
2   - read #color to read a nucleotide as-is
3   - trsi #color to read a transition (mutation)
4   - trsv #color to read a transversion (mutation)
5 rel:
6   - read > trsi;
7   - read > trsv;
```

The previous lines defines a pre-ordered set with four elements and four generating relations as follows.



The element called `ignore`, which does not appear in the code entered in `omega.yml`, is specified via the symbol `!`, appearing right before the key word `obj`. This symbol `!` formally

adds an minimum element to the pre-ordered set of `omega.yml`. This minimum element will later allow us to use blanks in the specification of segments (see section 4.1 for more detail).

2.6. Categories of segments

In this section, we use the pre-order structure defined in section 2.5 to model the evolutionary histories of our taxa directly from the point of view of the DNA strands.

To do so, we need use what is called a *category of quasi-homologous segments* (see [5, 4]). The definition of such a mathematical tool, usually denoted as $\text{Seg}(\Omega, n)$, depends on a pre-ordered set Ω and an non-negative integer n , which stands for the length of the DNA strands in the sequence alignment under study. To define this object in the present library, one primarily needs to use the class `SegmentCategory` (section 4.4). Other classes can be used, but since these turn out to be subclasses of the class `SegmentCategory`, it seems to be more appropriate to focus on `SegmentCategory` for the present section. To call an instance of `SegmentCategory`, replace the current code of `main.py`, between line 15 to line 19, with the following lines.

```
15 Seg = CategoryOfSegments("omega.yml", len(align[1][0]))
```

The content of `main.py` should look as follows².

```
1 from Pedigrad import *
2
3 align = read_alignment_file("align.fa", READ_DNA)
4
5 positions = list()
6 transpose = list()
7 for i in range(len(align[1][0])):
8     column = list()
9     for j in range(len(align[1])):
10         column.append(align[1][j][i])
11     if not(column_is_trivial(column, [])):
12         transpose.append(column)
13         positions.append(i)
14
15 Seg = CategoryOfSegments("omega.yml", len(align[1][0]))
16
```

The variable `Seg` can now be used to generate a history of genetic events by using the set of ‘colors’ `read`, `trsi` and `trsv` defined in `omega.yml`. Specifically, a genetic event is represented by what is called a *segment* in [4], which is to say an object in the category $\text{Seg}(\Omega, n)$. Segments are usually represented as partitioned sequences of colored nodes as follows.

$(\circ\circ\circ)(\bullet\bullet)(\bullet)(\bullet\bullet)(\bullet)(\bullet)(\bullet\bullet)(\bullet\bullet\bullet)(\bullet\bullet)(\bullet)(\circ\circ\circ)$

○ = ignore

● = trsi

● = trsv

● = read

As can be seen, the colors of the segments stand for elements of the pre-ordered structure given in `omega.yml`. From the user’s point of view, the previous segments can be specified by the following regular expression.

```
[(3,2,1,'read'), (5,1,1,'trsi'), (6,2,1,'read'), (8,1,1,'trsi'),
(9,1,1,'trsv'), (11,2,1,'read'), (13,3,1,'read'), (16,2,1,'read'),
(17,1,1,'trsv')]
```

²Once again, note that the highlight mode of my text editor is different from the one used in this documentation.

Each quadruple given in the previous list represents a colored patch of the segment. The specification of such a patch follows the following syntax:

(start_position, number_of_nodes, number_of_times_repeated, the_color)

where

- ▷ `start_position` is the index at which the patch starts in the segment;
- ▷ `number_of_nodes` is the length of the patch (i.e. the number of nodes);
- ▷ `number_of_times_repeated` is the number of times the patch is successively repeated (see below);

[(2,3,5,'read')] = (○○)(●●●)(●●●)(●●●)(●●●)(●●●)

- ▷ `the_color` is the the reading state at which the patch is set;

In terms of structure, a segment is more than a regular expression (as given above). It is in fact recorded in the form of a `SegmentObject` item (see section 4.3), where `SegmentObject` is a class equipped with two objects: `.topology` and `.colors` (see below).

A regular expression can be turned into a `SegmentObject` item by using the object `.segment` of the class `SegmentCategory` (see section 4.4.4), as shown below.

```
s = Seg.segment([(3,2,1,'read'), (5,1,1,'trsi'), (6,2,1,'read'),
(8,1,1,'trsi'), (9,1,1,'trsv'), (11,2,1,'read'), (13,3,1,'read'),
(16,2,1,'read'), (17,1,1,'trsv')])
```

For the sake of illustration, add the following piece of code to `main.py`. This will give us two lists of segments that we can use to test our next functions.

```
17 history1 = list()
18 history2 = list()
19 for i in range(len(transpose)):
20     if i % 3 != 0:
21         history1.append(Seg.segment([(positions[i],1,1,'read')]))
22     if not(i % 5 in [0,2]):
23         history2.append(Seg.segment([(positions[i],1,1,'read')]))
```

The user can display the two lists `history1` and `history2` by using the following lines of code.

```
25 for i in range(len(history1)):
26     print(history1[i].topology,history1[i].colors)
17 print("----")
28 for i in range(len(history1)):
29     print(history1[i].topology,history1[i].colors)
```

Compiling `main.py` should give the following display in the console.

```
[(12, 12)], ['read']
[(14, 14)], ['read']
[(18, 18)], ['read']
[(22, 22)], ['read']
[(27, 27)], ['read']
[(35, 35)], ['read']
[(39, 39)], ['read']
[(45, 45)], ['read']
[(53, 53)], ['read']
```

```

((58, 58)], ['read'])
((65, 65)], ['read'])
((68, 68)], ['read'])
---
((12, 12)], ['read'])
((17, 17)], ['read'])
((18, 18)], ['read'])
((26, 26)], ['read'])
((35, 35)], ['read'])
((37, 37)], ['read'])
((45, 45)], ['read'])
((53, 53)], ['read'])
((58, 58)], ['read'])
((65, 65)], ['read'])

```

Our goal is now to compare genetic events in order to assess their relevance. We should therefore be at least able to say if two segments are equal. Thus, let us add the following piece of code to `main.py`.

```

31 def segments_are_equal(segment1, segment2):
32     return (segment1.topology == segment2.topology) and (segment1.colors ==
    segment2.colors)

```

This function can be quickly tested with the following lines of code.

```

34 print(segments_are_equal(history1[0], history2[0]))
35 print(segments_are_equal(history1[1], history2[1]))

```

The resulting output should look as follows in the console.

```

True
False

```

This last line of code suggests that we could compare the two lists `history1` and `history2` by comparing their matching segments. To do so, add the following piece of code to the file `main.py`.

```

37 def count_uniformity(ground, list_of_agreements):
38     list_of_counts = list()
39     for i in range(len(ground)):
40         list_of_counts.append(0)
41     for i in range(len(list_of_agreements)):
42         for segment in list_of_agreements[i]:
43             for j in range(len(ground)):
44                 if segments_are_equal(ground[j], segment):
45                     list_of_counts[j] = list_of_counts[j] + 1
46     return list_of_counts

```

The function `count_uniformity` uses the variable `ground` as a base to record the occurrences of a segment. The idea is that `ground` contains all the segments containing a patch of length 1 at the positions contained in the list `positions`. The comparison of the two lists `history1` and `history2` is then done via the following lines of code.

```

48 ground = list()
49 for i in range(len(transpose)):
50     ground.append(Seg.segment([(positions[i],1,1,'read')]))
51
52 count = count_uniformity(ground,[history1,history2])
53 for i in range(len(ground)):
54     print(ground[i].topology,ground[i].colors,count[i])

```

Compiling the file `main.py` should now add the following display in the console.

```

((5, 5)], ['read'], 0)
((12, 12)], ['read'], 2)
((14, 14)], ['read'], 1)
((17, 17)], ['read'], 1)
((18, 18)], ['read'], 2)
((22, 22)], ['read'], 1)
((26, 26)], ['read'], 1)
((27, 27)], ['read'], 1)
((35, 35)], ['read'], 2)
((37, 37)], ['read'], 1)
((39, 39)], ['read'], 1)
((45, 45)], ['read'], 2)
((48, 48)], ['read'], 0)
((53, 53)], ['read'], 2)
((58, 58)], ['read'], 2)
((63, 63)], ['read'], 0)
((65, 65)], ['read'], 2)
((68, 68)], ['read'], 1)

```

Each integer given on the right-hand side of each line is the number of times the segment (given on the left) appears in `history1` and `history2`. These numbers can now be used to compare the two lists `history1` and `history2`.

For instance, let us add the lines of code given below to `main.py`. This piece of code defines a function that computes the intersection of `history1` and `history2` by only selecting the segments that appear twice.

```

56 def intersection_of_agreements(ground,list_of_agreements):
57     if len(list_of_agreements) == 0:
58         return []
59     else:
60         list_of_counts = count_uniformity(ground,list_of_agreements)
61         the_intersection = list()
62         for i in range(len(list_of_counts)):
63             if list_of_counts[i] == len(list_of_agreements):
64                 the_intersection.append(ground[i])
65         return the_intersection

```

To test the function `intersection_of_agreements`, add the following code to the file `main.py`.

```

67 intersection = intersection_of_agreements(ground,[history1,history2])
68 for i in range(len(intersection)):
69     print(intersection[i].topology,intersection[i].colors)

```

Save and compile – you obtain the following additional display in the console.

```
((12, 12), ['read'])
((18, 18), ['read'])
((35, 35), ['read'])
((45, 45), ['read'])
((53, 53), ['read'])
((58, 58), ['read'])
((65, 65), ['read'])
```

2.7. Categories of pedigrees

Presentation of the module PartitionCategory.py

3.1. Description of `_image_of_partition`

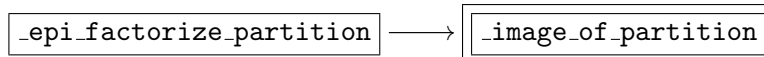
The function `_image_of_partition` takes a list of elements and returns the list of its elements without repetition in the order in which they can be accessed from the left to the right.

```
1 def _image_of_partition(partition):
2     """ the source code of this function can be found in iop.py """
3     return the_image
```

This corresponds to returning the image object of the underlying partition of the list.

```
>>> print(_image_of_partition([3,3,2,1,1,2,4,5,6,5,2,6]))
[3, 2, 1, 4, 5, 6]
>>> print(_image_of_partition(['A',4,'C','C','G',4,0,0,1,'a','A']))
['A', 4, 'C', 'G', 0, 1, 'a']
```

3.2. Description of `_epi_factorize_partition`



The function `_epi_factorize_partition` relabels the elements of a list with non-negative integers. It starts with the integer 0 and attributes a new label by increasing the previously attributed label by 1. The first element of the list always receives the label 0 and the highest integer used in the relabeling equals the length of the image (section 3.1) of the list decreased by 1.

```
1 def _epi_factorize_partition(partition):
2     """ the source code of this function can be found in efp.py """
3     return epimorphism
```

Even though a list already encodes an epimorphism, the goal of the function

`_epi_factorize_partition`

is to return a canonical *choice* of epimorphism.

$$S \xrightarrow[e(f)]{\quad} \text{Im}(f) \xrightarrow[\cong]{\quad} K$$

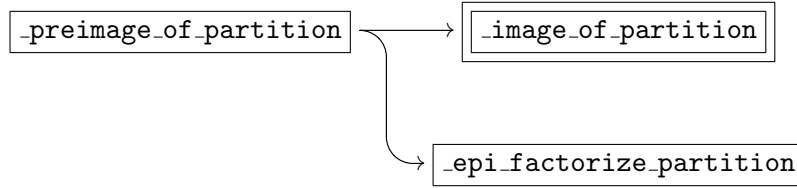
f

This choice ensures that two partitions characterized by the same set of universal properties are *equal* as python lists. In [4], this type of construction is formulated in terms of ‘epi-skeletal’ structure for the object S (see the diagram above).

```
>>> p = [3,3,2,1,1,2,4,5,6,5,2,6]
>>> print(_epi_factorize_partition(p))
[0, 0, 1, 2, 2, 1, 3, 4, 5, 4, 1, 5]
>>> im = _image_of_partition(p)
>>> print(_epi_factorize_partition(im))
[0, 1, 2, 3, 4, 5]
>>> print(_epi_factorize_partition(['A',4,'C','C','G',4,0,0,1,'a','A']))
[0, 1, 2, 2, 3, 1, 4, 4, 5, 6, 0]
```

Note that the function does not literally relabel the input list, but allocates a new space in the memory to store the relabeled list.

3.3. Description of `_preimage_of_partition`



The function `_preimage_of_partition` takes a list and returns the list of the lists of indices that index the same element.

```
1 def _preimage_of_partition(partition):
2     """ the source code of this function can be found in piop.py """
3     return the_preimage
```

From the point of view of partitions, the returned list `the_preimage` (see code above) is the preimage of the underlying epimorphism $f : S \rightarrow K$ of the input `partition`, where the preimage of f is defined as the K -indexed set of the fibers of the epimorphism.

$$\text{Prelm}(f) = \{f^{-1}(k)\}_{k \in K}$$

Note that, from an implementation viewpoint, the set K might not be equipped with an obvious order relation, which makes it difficult to define the preimage of $f : S \rightarrow K$ as a python list. To rectify this flaw, the preimage is computed with respect to the canonical epimorphism $e(f) : S \rightarrow \text{Im}(f)$ whose codomain is equipped with the natural order on integers (see section 3.2).

$$\text{Prelm}(f) := \{e(f)^{-1}(k)\}_{k \in \text{Im}(f)}$$

```
>>> p = ['a','a',2,2,3,3,'a']
>>> print(_preimage_of_partition(p))
[[0, 1, 6], [2, 3], [4, 5]]
>>> print(_epi_factorize_partition(p))
[0, 0, 1, 1, 2, 2, 0]
```

```
>>> p = [2,1,0,6,5,4,2,1,0]
>>> print(_preimage_of_partition(p))
[[0, 6], [1, 7], [2, 8], [3], [4], [5]]
>>> print(_epi_factorize_partition(p))
[0, 1, 2, 3, 4, 5, 0, 1, 2]
```

In the first example given above:

- the list [0,1,6] is the fiber of the element 'a' and its index in the preimage is 0;
- the list [2,3] is the fiber of the element 2 and its index in the preimage is 1;
- the list [4,5] is the fiber of the element 3 and its index in the preimage is 2.

The preimage will always orders its fibers with respect to the order in which the elements of the input list appear.

3.4. Description of `print_partition`

`print_partition` \longrightarrow `_preimage_of_partition`

The function `print_partition` is a debug function that takes a list of elements and prints its preimage on the standard output (i.e. the console).

```
1 def print_partition(partition):
2     print(_preimage_of_partition(partition))
```

See section 3.3 for examples.

3.5. Description of `_join_preimages_of_partitions`

`_join_preimages_of_partitions` \longrightarrow `_image_of_partition`

The function `_join_preimages_of_partitions` takes two lists of lists of indices (the indices can be repeated and should only be non-negative integers) and returns the list of the maximal unions of internal lists that intersect within the concatenation of the two input lists (see the examples below).

```
1 def _join_preimages_of_partitions(preimage1,preimage2):
2     """ the source code of this function can be found in jpop.py """
3     return the_join
```

For instance, the two input lists `preimage1` and `preimage2` could be two outputs of the procedure

`_preimage_of_partition(-,-)`

for two input lists of the same length. From the point of view of partitions, this would amount to computing the coproduct of two partitions and taking its pre-image. Since a category of partitions can be seen as a partially ordered set, such a coproduct is also the *join* of the two partitions.

For illustration, if we consider the following two lists of lists of indices

```
>>> p1 = [[0, 3], [1, 4], [2]]
>>> p2 = [[0, 1], [2], [3], [4]]
```

we can notice that

- the internal list [0,3] of `p1` intersects with the internal lists [0,1] and [3] in `p2`;
- the internal list [0,1] of `p1` intersects with the internal lists [1,4] and [1] in `p2`;

- the internal list [1,4] of p1 intersects with the internal list [4] in p2;

and

- the internal list [2] of p1 only intersects with the internal list [2] in p2,

so that we have

```
>>> print(_join_preimages_of_partitions(p1,p2))
[[1, 4, 0, 3], [2]]
```

In terms of implementation, the program

(3.1) `_join_preimages_of_partitions(p1,p2)`

considers each internal list of p1 and searches for the lists of p2 that intersect it. If an intersection is found between two internal lists, it merges the two internal lists in p1 and empties that of p2 (the list is emptied and *not* removed in order to preserve a coherent indexing of the elements of p2). The function continues until all the possible intersections have been checked.

Here is a detail of what program (3.1) does with respect to the earlier example:

The element 0 of [0,3] is searched in the list [0,1] of p2;

The element 0 is found;

The lists [0,3] and [0,1] are merged in p1 and [0,1] is emptied from p2 as follows:

```
p1 = [[0, 3, 1], [1, 4], [2]]
p2 = [[], [2], [3], [4]]
```

The element 0 has now been found in p2 and does not need to be searched again (breaks)

The element 3 of [0, 3] is searched in the list [] of p2;

The element 3 is not found (continues);

The element 3 of [0, 3] is searched in the list [2] of p2;

The element 3 is not found (continues);

The element 3 of [0, 3] is searched in the list [3] of p2;

The element 3 is found;

The lists [0,3] and [3] are merged in p1 and [3] is emptied from p2 as follows:

```
p1 = [[0, 3, 1], [1, 4], [2]]
p2 = [[], [2], [], [4]]
```

The element 3 has now been found in p2 and does not need to be searched again (breaks)

All elements of the initial list [0, 3] have been searched.

The first lists of p1 is appended to p2 in order to ensure the transitive computation of the maximal unions through the next iterations.

The list [0, 3, 1] of p1 is emptied as follows:

```
p1 = [[], [1, 4], [2]]
p2 = [[], [2], [], [4], [0, 3, 1]]
```

Repeat the previous procedure with respect to the list [1, 4] of p1. We obtain the following pair:

```
p1 = [[], [], [2]]
p2 = [[], [2], [], [], [], [1, 4, 0, 3]]
```

Repeat the previous procedure with respect to the remaining list [2] of p1. We obtain the following pair:

```
p1 = [[], [], []]
p2 = [[], [], [], [], [], [1, 4, 0, 3], [2]]
```

The function stops because there is no more list to process in `p1`. The output is all the non-empty lists of `p2`; i.e. `[[1, 4, 0, 3], [2]]`

Note that, because of the iterative nature of the previous algorithm, the procedure

```
_join_preimages_of_partitions(-)
```

does not necessarily presents its output in the same way as the procedure

```
_preimage_of_partition(-)
```

does. For instance, while the index 0 will always be contained in the first list of the output of `_preimage_of_partition`, it might not be contained in the first list of the output of `_join_preimages_of_partitions` as illustrated below.

```
>>> l = _preimage_of_partition([1,2,4,5,1,2,3,2,2,1,3])
>>> print(l)
[[0, 4, 9], [1, 5, 7, 8], [2], [3], [6, 10]]
>>> m = _preimage_of_partition([1,2,5,4,2,2,5,6,5,7,8])
>>> print(m)
[[0], [1, 4, 5], [2, 6, 8], [3], [7], [9], [10]]
>>> print(_join_preimages_of_partitions(l,m))
[[3], [6, 10, 2, 1, 5, 7, 8, 0, 4, 9]]
```

Interestingly, the procedure `_join_preimages_of_partitions` can also be used to compute the intersection-free closure of a set of sets, as shown below.

```
>>> a = [[1,0,2,1,3,2,5,4,6],[15,15,18,0,13],[7,11,12,22],[23,12]]
>>> closure_of_a = _join_preimages_of_partitions(a,a)
>>> print(closure_of_a)
[[15, 18, 0, 13, 1, 2, 3, 5, 4, 6], [23, 12, 7, 11, 22]]
```

3.6. Description of *EquivalenceRelation* (class)

`EquivalenceRelation` \longrightarrow `_join_preimages_of_partitions`

The class `EquivalenceRelation` possesses two objects, namely

- `.classes` (list of lists);
- `.range` (integer);

and three methods, namely

- `__init__` (constructor);
- `.closure`;
- `.quotient`.

The constructor `__init__` takes between 1 and 2 arguments: the first argument should either be an empty list or a list of lists of indices (i.e. non-negative integers) and the second argument, which is optional when the first argument is not an empty list, should be an integer that is greater than or equal to the maximum index contained in the first input, if it exists.

```

1 class EquivalenceRelation:
2     #The objects of the class are:
3     #.classes (list of lists);
4     #.range (integer);
5     #The following constructor takes between 1 and 2 arguments,
6     #the first one being a list and the second being an integer.
7     def __init__(self,*args):
8         """ the source code of this constructor can be found in cl.er.py """
9     def closure(self):
10         self.classes = _join_preimages_of_partitions(self.classes,
11 self.classes)
12     def quotient(self):
13         """ the source code of this function can be found in cl.er.py """
14         return the_quotient

```

If the first input is not empty, then it is stored in the object `.classes` while the object `.range` receives:

- either the second input, when this second input is given;
- or the maximum index contained in the first input when no second input is given.

```

>>> eq1 = EquivalenceRelation([[0,1,2,9],[7,3,8,6],[4,9,5]])
>>> print(eq1.classes)
[[0, 1, 2, 9], [7, 3, 8, 6], [4, 9, 5]]
>>> print(eq1.range)
9
>>> eq2 = EquivalenceRelation([[0,1,2,9],[7,3,8,7],[9,15]],18)
>>> print(eq2.classes)
[[0, 1, 2, 9], [7, 3, 8, 7], [9, 15]]
>>> print(eq2.range)
18

```

If the first input is empty, then the second argument is required. In this case, the object `.classes` receive the lists containing all the singleton lists containing the integers from 0 to the integer given in the second argument, which is, for its part, stored in the object `.range`.

```

>>> eq3 = EquivalenceRelation([],5)
>>> print(eq3.classes)
[[0], [1], [2], [3], [4], [5]]

```

The method `.closure()` replaces the content of the object `.classes` with the transitive closure of its classes. After this procedure, the object `.classes` describes an actual equivalence relation (modulo the singleton equivalence classes, which do not need to be specified for obvious reasons).

```

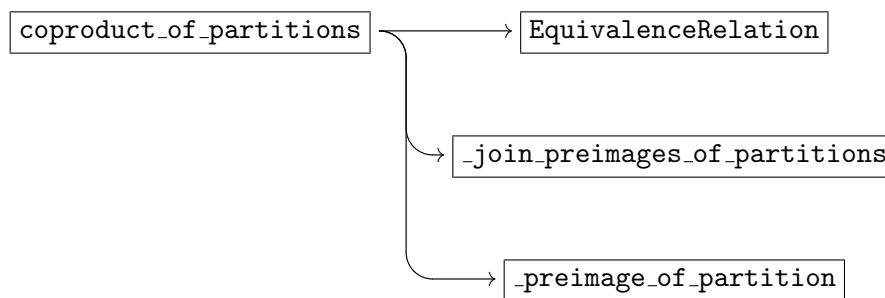
>>> eq1.closure()
>>> print(eq1.classes)
[[7, 3, 8, 6], [4, 9, 5, 0, 1, 2]]
>>> eq2.closure()
>>> print(eq2.classes)
[[7, 3, 8], [9, 15, 0, 1, 2]]

```

The method `.quotient()` returns a list of integers whose length is equal to the integer contained in the object `.range` decreased by 1 and whose non-trivial fibers are those contained in the object `.classes` after a call of the method `.closure()`.

```
>>> print(eq1.quotient())
[1, 1, 1, 0, 1, 1, 0, 0, 0, 1]
>>> print(eq2.quotient())
[1, 1, 1, 0, 2, 3, 4, 0, 0, 1, 5, 6, 7, 8, 9, 1, 10, 11, 12]
```

3.7. Description of coproduct_of_partitions



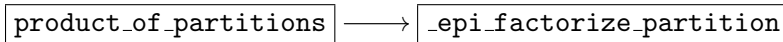
The function `coproduct_of_partitions` takes two lists of the same length and returns their coproduct (or join) as partitions. Specifically, the procedure outputs the quotient of the join of their preimages. If the two input lists do not have the same length, then an error message is outputted and the program is aborted.

```
1 def coproduct_of_partitions(partition1,partition2):
2     if len(partition1) == len(partition2):
3         #Returns the coproduct of two partitions as the quotient of the
4         #equivalence relation induced by the join of the preimages
5         #of the two partitions.
6         the_join = EquivalenceRelation(_join_preimages_of_partitions(
7             _preimage_of_partition(partition1),_preimage_of_partition(partition2)))
8         return the_join.quotient()
9     else:
10        print("Error:  in coproduct_of_partitions:  lengths do not match.")
11        exit()
```

Note that the outputs of the procedure `coproduct_of_partitions` do not necessarily belong to the set of outputs of the procedure `_epi_factorize_partition`. The reason comes from the way in which the procedure `_join_preimages_of_partitions` is implemented (see the end of section 3.5).

```
>>> l = [1,2,4,5,1,2,3,2,2,1,3]
>>> m = [1,2,5,4,2,2,5,6,5,7,8]
>>> c = coproduct_of_partitions(l,m)
>>> print(c)
[1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1]
>>> print(_epi_factorize_partition(c))
[0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0]
```

3.8. Description of `product_of_partitions`



The function `product_of_partitions` takes two lists and returns a list that is the relabeling of the zipping of the two lists (i.e. the list of pairs of elements with corresponding indices in each of the input lists) via the procedure `_epi_factorize_partition`.

```

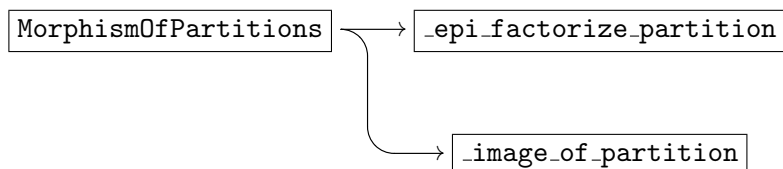
1 def product_of_partitions(partition1,partition2):
2     #The following line checks if the product of the two lists is possible.
3     if len(partition1) == len(partition2):
4         #Constructs the list of pairs of element with the
5         #same index in the two lists, and then relabels
6         #the pairs using _epi_factorize_partition.
7         return _epi_factorize_partition(zip(partition1,partition2))
8     else:
9         print("Error:  in product_of_partitions:  lengths do not match.")
10    exit()
  
```

The function outputs an error if the two input lists do not have the same length.

```

>>> product_of_partitions([1,1,1,1,2,3],[‘a’,‘b’,‘c’,‘c’,‘c’,‘c’])
[0, 1, 2, 2, 3, 4]
>>> product_of_partitions([1,1,1,1,2],[‘a’,‘b’,‘c’,‘c’,‘c’,‘c’])
Error:  in product_of_partitions:  lengths do not match.
  
```

3.9. Description of `MorphismOfPartitions` (class)



The class `MorphismOfPartitions` possesses three objects, namely

- `.arrow` (list)
- `.source` (list)
- `.target` (list)

and a constructor `__init__`. The constructor `__init__` takes two lists and stores, in the object `.arrow`, a list that describes, if it exists, the (unique) morphism of partitions from the first list (seen as a partition) to the second list (seen as a partition). The canonical epimorphisms associated with the partitions of the first and second input lists (see section 3.2) are stored in the objects `.source` and `.target`, respectively.

```

1 class MorphismOfPartitions:
2     #The objects of the class are:
3     #.arrow (list);
4     #.source (list);
5     #.target (list).
6     def __init__(self,source,target):
7         """ the source code of this constructor can be found in cl.mop.py """
  
```

If we suppose that the two input lists are labeled in the same way as the procedure

```
_epi_factorize_partition
```

would (re)label them, then the list that is to be contained in the object `.arrow` is the zipping of the two lists, as illustrated in the following example.

Consider the following lists.

```
>>> p1 = [0,1,2,3,3,4,5]
>>> p2 = [0,1,2,3,3,3,1]
```

Their zipping is as follows:

```
>>> p3 = zip(p1,p2)
>>> print(p3)
[(0, 0), (1, 1), (2, 2), (3, 3), (3, 3), (4, 3), (5, 1)]
```

The image of the zipping is then as follows:

```
>>> p4 = _image_of_partition(p3)
>>> print(p4)
[(0, 0), (1, 1), (2, 2), (3, 3), (4, 3), (5, 1)]
```

We can see that for each pair (x,y) in `p4`, every component x is mapped to a unique image y so that `p4` defines the *graph* of the morphism of partitions between `p1` and `p2`. The constructor `__init__` then outputs the list recapturing the previous graph.

```
>>> m = MorphismOfPartitions(p1,p2)
>>> print(m.arrow)
[0, 1, 2, 3, 3, 1]
```

If there exists no morphism from the first input list to the second input list, then the function outputs an error message.

For example, if we modify `p2` as follows

```
>>> p2 = [0,1,2,3,6,3,1]
```

then the image of the zipping of `p1` and `p2` is as follows:

```
>>> p4 = _image_of_partition(zip(p1,p2))
>>> print(p4)
[(0, 0), (1, 1), (2, 2), (3, 3), (3, 6), (4, 3), (5, 1)]
```

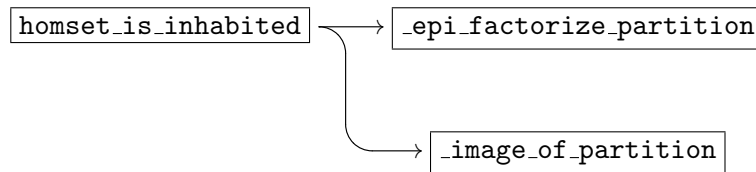
As can be seen, the argument 3 is ‘mapped’ to two different images, namely 3 and 6. In this case, the constructor `__init__` exits the program with an error message.

Here is a complete example summarizing the previous explanation.

```
>>> m = MorphismOfPartitions([1,6,5,3,3,4,2],[1,2,5,4,4,4,2])
>>> print(m.source)
[0, 1, 2, 3, 3, 4, 5]
>>> print(m.target)
[0, 1, 2, 3, 3, 3, 1]
>>> print(m.arrow)
[0, 1, 2, 3, 3, 1]
>>> m = MorphismOfPartitions([1,6,5,3,3,4,2],[1,2,5,4,6,4,2])
Error: in MorphismOfPartitions.__init__: source and target are not
compatible.
```

Note that the function of section 3.10 can be used to avoid the earlier error message.

3.10. Description of `homset_is_inhabited`



The function `homset_is_inhabited` takes two lists and returns a Boolean value indicating whether there exists a morphism of partitions from the underlying partition of the first input list to the underlying partition of the second input list.

```

1 def homset_is_inhabited(source,target):
2     """ the source code of this function can be found in hii.py """
3     return flag
  
```

The way this function is implemented is very similar to the way the constructor of `MorphismOfPartitions` is implemented (see section 3.9).

```

>>> p1 = [0,1,2,3,3,4,5]
>>> p2 = [0,1,2,3,3,3,1]
>>> homset_is_inhabited(p1,p2)
True
>>> p2 = [0,1,2,3,6,3,1]
>>> homset_is_inhabited(p1,p2)
False
  
```

Presentation of the module

SegmentCategory.py

4.1. Description of `_read_pre_order`

The function `_read_pre_order` takes the name of a file (called `name_of_file`) and returns a Boolean value and a list of lists.

```
1 def _read_pre_order(name_of_file):
2     """ the source code of this function can be found in rpo.py """
3     return (flag_zero_obj, the_pre_order)
```

The input file is supposed to contain some specific code lines that describe a pre-ordered set. The code follows a certain syntax that will be detailed in this section. Because this syntax is compatible with the yaml grammar, these pre-ordered sets will usually be specified with the extension `.yaml` in our examples. Here is an example of such a file.

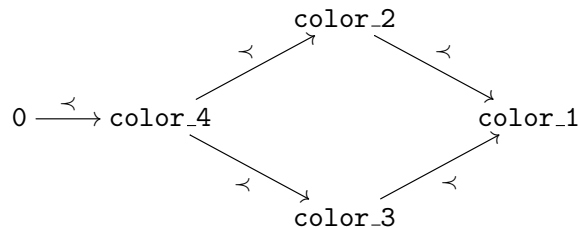
`Omega.yaml`

```
1 #This is an example of pre-ordered set.
2
3 !obj:
4 - color_1 #object for color 1
5 - color_2 #object for color 2
6 - color_3 #object for color 3
7 - color_4 #object for color 4
8
9 rel: #these are generating relations for the preorder.
10 - color_1 > color_2, color_3;
11 - color_1 > color_3, color_1;
12 - color_3 > color_4;
13 - color_2 > color_4;
```

Diagrammatically, this pre-ordered set can be described by the graph given below, whose square commutes. We will see below why there is an additional object 0 that is not specified

in the yaml file.

(4.1)



4.1.1. Comments. Comments are allowed and are specified as in python and in yaml, which is to say by the character #.

4.1.2. Objects. The set of elements of the pre-ordered set should always be specified in terms of a list of words succeeding one of the key words ‘obj:’ or ‘!obj:’ as shown below.

```
obj: [name1] [separator] [name2] [separator] (etc.)
!obj: [name1] [separator] [name2] [separator] (etc.)
```

The labels [name1] and [name2] stand for words that should only be made of the characters 0-9, @, A-Z, _ and a-z while the label [separator] stands for any character that is not in this list of characters. Repetitions of names are taken care by the parser, which ignores all repetitions. The following specification of objects is equivalent to that given in *Omega.yaml*.

Objects.yaml

```
1 #Note that we now use different types of separator.
2 !obj: color_1 ;
3 ,, color_2 ; color_1 ;
4 --> color_3. !color_4 *
```

While the key word **obj:** is only supposed to present the list of the elements of the pre-ordered set, the key word **!obj:** should only be used to formally *add* a formal initial object (i.e. a minimum element) to the pre-ordered set. This element was represented by 0 in diagram (4.1).

4.1.3. Relations. The pre-order relations of the set should be specified after the key word **rel:** by a list of phrases satisfying the following syntax.

```
[dominant_object]>[predecessor1] [separator] [predecessor2] [separator] (etc.);
```

Such a line means that [dominant_object] is greater than or equal to all the elements listed after the symbol ‘>’. The list of predecessors stops at the symbol ‘;’. Note that the symbol ‘;’ can be omitted for the last line of the file. The following specification of relations is equivalent to that given in *Omega.yaml*.

Omega_bis.yaml

```
1 #The pre-ordered set can be very compact.
2 !obj: 1 2 3 4
3 rel: 1>2,3 ; 3>4 ; 2>4
```

The labels [dominant_object] and [predecessor(*n*)] stand for words that should only be made of the characters 0-9, @, A-Z, _ and a-z while the label [separator] stands for any character that is not in this list of characters.

4.1.4. Output. Finally, the output of the function `_read_pre_order` is a pair

(flag_zero_obj, the_pre_order)

whose first component `flag_zero_obj` is a Boolean value specifying by **False** or **True** whether the word `obj:` (**False**) or `!obj:` (**True**) was used to define the list of objects and whose

second component `the_pre_order` is a list of lists giving the *non-transitive* down-closures of the elements of the pre-ordered set in the order in which these were given in the input file.

Specifically, a list in the list `the_pre_order` will always start with the element of which it is supposed to give the down-closure, as shown below.

[dominant_object, predecessor1, predecessor2, (etc.)]

For instance, the output of our previous example `Omega.yml` is as follows.

```
>>> omega = _read_pre_order("Omega.yml")
>>> print("Formal initial object: "+str(omega[0]))
Formal initial object: True
>>> for i in range(len(omega[1])):
...     print(omega[1][i])
['color_1', 'color_2', 'color_3']
['color_2', 'color_4']
['color_3', 'color_4']
['color_4']
```

4.2. Description of `_transitive_closure`

The function `_transitive_closure` takes a list of lists (called `down_closure`) and returns another list of lists whose pointer is the same as that given in the input (i.e. the input is therefore modified by the function to make the output).

```
1 def _transitive_closure(down_closure):
2     """ the source code of this function can be found in tc.py """
3     return down_closure
```

The input `down_closure` is supposed to take the form of a list of the (potentially) non-transitive down-closures of the elements of a given pre-ordered set. In other words, the input `down_closure` should take the same form as that taken by the second outputs of the procedure `_read_pre_order(-)` (see section 4.1). Specifically, the down-closure of an element `dominant_object` is the unique list of `down_closure` starting with this element (see below).

[dominant_object, predecessor1, predecessor2, (etc.)]

The output `down_closure` is then the list of the transitive down-closures of the elements of that pre-ordered set.

Here is an example with the procedure `_read_pre_order`. Let us consider the following pre-order specification.

`Omega.yml`

```
1 #This is a non-transitive presentation of a pre-ordered set.
2
3 #The list of the elements of the set (without the formal minimum).
4 !obj:  1 2 3 4 5 6
5
6 #The list of the non-trivial (generating) relations.
7 rel:   1 > 2; 2 > 3; 3 > 5; 5 > 6;
```

As shown below, we can see that the output of the procedure `_read_pre_order` does not include the transitive relation $1 > 2 > 3$ in the down-closure of 1. On the other hand, the relation $1 > 3$ does appear in the down-closure of 1 even it is not specified in `Omega.yml`.

```
>>> preorder = _read_pre_order("Omega.yml")
>>> print("Formal initial object: "+str(preorder[0]))
>>> for i in range(len(preorder[1])):
...     print(preorder[1][i])
['1', '2']
['2', '3']
['3', '5']
['4']
['5', '6']
['6']
>>> omega = _transitive_closure(preorder[1])
>>> for i in range(len(omega)):
...     print(omega[i])
['1', '2', '3', '5', '6']
['2', '3', '5', '6']
['3', '5', '6']
['4']
['5', '6']
['6']
```

4.3. Description of SegmentObject (class)

The class `SegmentObject` possesses two objects, namely

- `.topology` (list of 2-tuples);
- `.colors` (list of indices),

and two methods, namely

- `__init__` (constructor)
- `.patch`

The idea of behind the two objects `.colors` and `.topology` is that they contain all the needed information to define a mathematical segment, that is to say a pair (t, c) where t is the *topology*, usually encoded by an order preserving surjection, and c is the *coloring map*, usually encoded by a function going to a pre-ordered set.

```
1 class SegmentObject:
2     #The objects of the class are:
3     #.topology (list of 2-tuples);
4     #.colors (list of indices);
5     def __init__(self, topology, colors):
6         """ the source code of this constructor can be found in cl_so.py """
7     def patch(self, position):
8         """ the source code of this function can be found in cl_so.py """
9     return the_index
```

The constructor `__init__` takes two lists, specifically a lists of indices and a list of pairs of increasing indices, and allocate them in the object `.colors` and `.topology`, respectively

For instance, we could first define an uncolored topology of the form

$$(\circ\circ\circ)(\circ\circ\circ)(\circ\circ\circ)(\circ\circ\circ)(\circ\circ\circ)$$

by using the list `t` defined below.

```
>>> t = list()
>>> for i in range(5):
...     t = t + [(3*i,3*i+2)]
```

Then, we could add colors to this topology, say to form the following Boolean segment.

(ooo)(●●●)(●●●)(ooo)(ooo)

In this case, the colors would be specified by a list of colors whose length is equal to `len(t)` and the associated segment would be defined via the constructor `__init__` as follows.

```
>>> c = [0,1,1,0,0]
>>> s = SegmentObject(t,c)
```

For its part, the method `.patch` takes an integer and returns the index of the first pair (a,b) of `.topology` that bounds the integer, that is to say that the input integer is greater than or equal to the first component a and also is less than or equal to the second component b . If no such index exists, then the procedure returns `-1`.

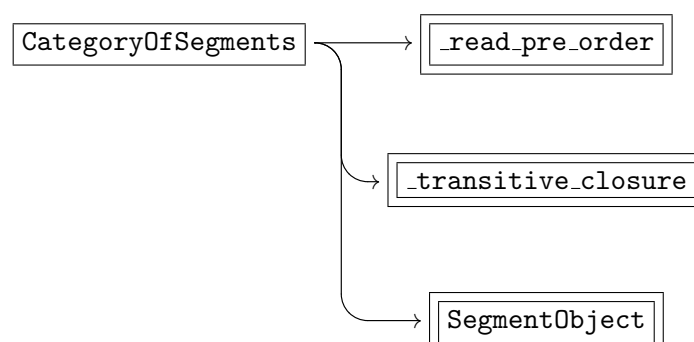
For example, we can use the method `.patch` to recover all the information contained in our previous segment `s`, as illustrated below.

```
>>> for i in range(15):
...     print("Position "+str(i)+" belongs to "+str(s.topology[s.patch(i)])+"
...           and its color is "+str(s.colors[s.patch(i)]))
```

Position 0 belongs to (0, 2) and its color is 0
Position 1 belongs to (0, 2) and its color is 0
Position 2 belongs to (0, 2) and its color is 0
Position 3 belongs to (3, 5) and its color is 1
Position 4 belongs to (3, 5) and its color is 1
Position 5 belongs to (3, 5) and its color is 1
Position 6 belongs to (6, 8) and its color is 1
Position 7 belongs to (6, 8) and its color is 1
Position 8 belongs to (6, 8) and its color is 1
Position 9 belongs to (9, 11) and its color is 0
Position 10 belongs to (9, 11) and its color is 0
Position 11 belongs to (9, 11) and its color is 0
Position 12 belongs to (12, 14) and its color is 0
Position 13 belongs to (12, 14) and its color is 0
Position 14 belongs to (12, 14) and its color is 0

Finally, note that the pre-ordered set that is usually associated with a segment (t, c) can be specified through the class `CategoryOfSegments` defined in section 4.4.

4.4. Description of *CategoryOfSegments* (class)



The class `CategoryOfSegments` possesses three objects, namely

- `.domain` (integer)
- `.mask` (Boolean)
- `.preorder` (list of lists)

and five methods, namely

- `__init__` (constructor)
- `.can_switch_to`
- `.homset_is_inhabited`
- `.topology`
- `.segment`

In addition, the class `CategoryOfSegments` may be used as a super class (this is allowed by an argument `object`; see below). In this library, the class `CategoryOfSegments` is the paren of the classes `LocalAnalysis` and `Pedigrad` (see section 5.3 and section 5.5).

```
1 class CategoryOfSegments(object):
2     #The objects of the class are:
3     #.domain (integer);
4     #.mask (Boolean);
5     #.preorder (list of lists);
```

The three objects `.domain`, `.mask`, and `.preorder` give all the needed information to specify a category of quasi-homologous segments $\mathbf{Seg}(\Omega | n)$ (as defined in [5, 4]) for some pre-ordered set (Ω, \preceq) and non-negative integer n . Specifically, the object

- `.domain` contains the integer n defining what is called the *domain* [5, 4] of the segments of $\mathbf{Seg}(\Omega | n)$, which can informally be identified as the length of the segments;
- `.mask` indicates whether the pre-ordered set (Ω, \preceq) contains a formal initial object (i.e. a minimum element), which is usually used as an ‘ignore’ state or a mask;
- `.preorder` contains the down-closure of all the elements of the pre-ordered set Ω . This type of data corresponds to the type of data outputted by the following procedure composition (see section 4.2 and section 4.1)

`_transitive_closure(_read_pre_order(-)[1])`

```
6 def __init__(self, name_of_file, length_of_segments):
7     """ the source code of this constructor can be found in cl.cos.py """
```

For its part, the constructor `__init__` takes two inputs, namely the name of file that contains a pre-order structure and an integer, and stores

- the integer in the object `.domain`;
- a Boolean value specifying whether the pre-order structure comprises a formal initial object in `.mask`;
- the down-closures of the elements of the pre-order in `.preorder`.

The other methods of the class are very ‘categorical’, in the sense that they either answers question that are relevant to the category structure of $\mathbf{Seg}(\Omega | n)$ or provide items that would be directly accessible from its structure.

```

8  def can_switch_to(self,color1,color2):
9  """ the source code of this function can be found in cl.cos.py """
10     return (color2 in self.preorder[i])
11  def homset_is_inhabited(self,source,target):
12  """ the source code of this function can be found in cl.cos.py """
13     return flag
14  def topology(self,expression):
15  """ the source code of this function can be found in cl.cos.py """
16     return the_topology
17  def segment(self,expression):
18  """ the source code of this function can be found in cl.cos.py """
19     return the_segment

```

4.4.1. Comparing colors. The method `.can_switch_to` takes two strings that are meant to be names of elements in the pre-ordered set and returns a Boolean value indicating whether the first string is greater than or equal to the second one with respect to the pre-order structure.

For illustration, consider the following pre-order specification.

```

                                omega.yml
1  !obj:  0 1 2
2  rel:   2 > 1; 0 > 2

```

We can then use the method `.can_switch_to` to verify whether a certain a pre-order relation holds as follows.

```

>>> Seg = CategoryOfSegments("omega.yml",50)
>>> print(Seg.can_switch_to("2","1"))
True
>>> print(Seg.can_switch_to("1","2"))
False
>>> print(Seg.can_switch_to("1","1"))
True
>>> print(Seg.can_switch_to("0","1"))
True

```

4.4.2. Hom-sets. The method `.homset_is_inhabited` takes two `SegmentObject` items (see section 4.3) and returns a Boolean value specifying if there is a morphism from the first one to the second one. Theoretically, this function parses the two segments as if the object `.mask` was set to the value `True`, in which case the topologies of the segments may lack some patches, which are then assumed to have the color of the formal initial object of the pre-ordered set (Ω, \preceq) (see section 4.4.4).

The following example uses the method `.segment`, which is described in section 4.4.4.

```

>>> Seg = CategoryOfSegments("omega.yml",50)
>>> s1 = Seg.segment([(0,3,10,"1"),(30,6,2,"2")])
>>> s2 = Seg.segment([(0,6,7,"1")])
>>> print(Seg.homset_is_inhabited(s1,s2))
True
>>> s1 = Seg.segment([(0,3,10,"1"),(30,7,2,"2")])
>>> s2 = Seg.segment([(0,6,7,"1")])
>>> print(Seg.homset_is_inhabited(s1,s2))

```

False

4.4.3. Constructing a topology. The method `.topology` takes a list of 3-tuples and returns a list of 2-tuples. The input list is meant to encode a regular expression that describes the topology of a segment. The 3-tuples contained by the input list specifies

- where a patch starts;
- how long the patch is;
- how many such patches are repeated successively.

Specifically, the input satisfies the following syntax:

`[(start_position, length_of_patch, number_of_such_patches), (etc.)]`

Also, note that the start positions of the 3-tuples contained in the regular expression need to be given in an increasing order. For instance, a topology of the form

$$(ooo)(ooo)(oooo)(ooo)(ooo)(ooo)(ooo)$$

would be encoded by the following lists of 3-tuples:

`[(0, 3, 2), (6, 4, 1), (10, 3, 4)]`

However, as is shown, the expression given below is not a valid example.

```
>>> Seg = CategoryOfSegments("omega.yml",22)
>>> expr = [(10, 3, 4), (6, 4, 1), (0, 3, 2)]
>>> s = Seg.topology(expr)
```

Error: in `CategoryOfSegments.topology`: expression is not well-formed

The output of the procedure is the implementation of the regular expression into a topology (a list of 2-tuples). The 2-tuples contained in the output are the start and end positions of each patch. For instance, the output that would be produced for our first example (given above) would be as follows.

`[(0, 2), (3, 5), (6, 9), (10, 12), (13, 15), (16, 18), (19, 21)]`

Also, depending on whether the object `.mask` is `True` or `False`, the regular expression either needs to cover the whole topology or only needs to give a few relevant patches whose color might not be that of the initial object of the pre-order structure.

- 1) If `.mask` contains `True`, then only a few patches can be specified so that the remaining patches of the topology are implicit. For instance, the expression `[(5,3,1)]` can specify either one of the following topologies when `.domain` is equal to 15.

(4.2)

$$(ooooo)(ooo)(oooooooo) \quad (o)(o)(o)(o)(o)(ooo)(o)(o)(o)(o)(o)(o)$$

In practice, it is always recommended to associate the implicit part of the topology with the ‘mask’ color – given by the initial object of (Ω, \preceq) .

```
>>> Seg = CategoryOfSegments("omega.yml",15)
>>> expr = [(5,3,1)]
>>> s = Seg.topology(expr)
>>> print(s)
[(5, 7)]
```

- 2) If `.mask` contains `False`, then all the patches of the topology must be specified so that the only way to specify the topology given on the left-hand side of (4.2) is to give the following expression.

```
>>> expr = [(0,5,1), (5,3,1), (8,7,1)]
>>> s = Seg.topology(expr)
>>> print(s)
[(0, 4), (5, 7), (8, 14)]
```

4.4.4. Constructing a segment. The method `.segment` takes is very similar to the procedure `.topology`. It takes a list of 4-tuples and returns a `SegmentObject` item. The input list is meant to encode a regular expression that describes the segment. The 4-tuples contained by the input list specifies

- where a patch starts;
- how long the patch is;
- how many such patches are repeated successively;
- the color name (or state) associated with the group of patches.

Specifically, the input satisfies the following syntax:

```
[(start_position, length_of_patch, number_of_such_patches, color), (etc.) ]
```

Also, note that the start positions of the 4-tuples contained in the regular expression need to be given in an increasing order. For instance, a segment of the form

(000)(000)(1111)(222)(222)(222)(222)

would be encoded by the following lists of 3-tuples:

```
[(0,3,2,'0'), (6,4,1,'1'), (10,3,4,'2')]
```

However, as is shown, the expression given below is not a valid example.

```
>>> expr = [(10,3,4,'2'), (6,4,1,'1'), (0,3,2,'0')]
>>> s = Seg.segment(expr)
Error: in CategoryOfSegments.segment: expression is not well-formed
```

In addition, the color names associated with the patches of the segment must be elements of the pre-order structure specified in the object `.preorder`.

```
>>> Seg = CategoryOfSegments("omega.yml",22)
>>> expr = [(0,3,2,'0'), (6,4,1,'1'), (10,3,4,"red")]
>>> s = Seg.segment(expr)
Error: in CategoryOfSegments.segment: color 'red' not found in .preorder
```

The output of the procedure is the implementation of the regular expression into a `SegmentObject` item. For instance, the segment that would be produced for our first example (given above) would be given by the following pair of lists.

```
topology = [(0, 2), (3, 5), (6, 9), (10, 12), (13, 15), (16, 18), (19, 21)]
colors = ['0', '0', '1', '2', '2', '2', '2']
```

Also, depending on whether the object `.mask` is `True` or `False`, the regular expression either needs to cover the whole segment or only needs to give a few relevant patches whose color is not that of the initial object potentially specified in the pre-order structure.

- 1) If `.mask` contains `True`, then only a few patches can be specified so that the remaining patches of the segment have an implicit topology. For instance, the expression

$[(5,3,1, '1')]$ can specify either one of the following segments when `.domain` is equal to 15.

(4.3)

$(\circ\circ\circ\circ\circ)(\bullet\bullet\bullet)(\circ\circ\circ\circ\circ\circ\circ) \quad (\circ)(\circ)(\circ)(\circ)(\circ)(\bullet\bullet\bullet)(\circ)(\circ)(\circ)(\circ)(\circ)(\circ)(\circ)$

Note that, in practice, this polymorphism is never taken into account as it is always associated with the ‘mask’ color – given by the initial object of (Ω, \preceq) .

```
>>> Seg = CategoryOfSegments("omega.yml", 15)
>>> expr = [(5,3,1, '1')]
>>> s = Seg.segment(expr)
>>> print(s.topology)
[(5, 7)]
>>> print(s.colors)
['1']
```

- 2) If `.mask` contains `False`, then all the patches of the topology must be specified so that the only way to specify the topology given on the left-hand side of (4.3) is to give an expression as follows.

```
>>> expr = [(0,5,1, '0'), (5,3,1, '1'), (8,7,1, '0')]
>>> s = Seg.segment(expr)
>>> print(s.topology)
[(0, 4), (5, 7), (8, 14)]
>>> print(s.colors)
['0', '1', '0']
```

Presentation of the module PedigradCategory.py

5.1. Description of read_alignment_file

The function `read_alignment_file` takes the name of a file and an integer and returns a pair of lists.

```
1 def read_alignment_file(name_of_file,reading_mode):
2     """ the source code of this function can be found in raf.py """
3     return (names,alignment)
```

The input file is given in terms of a string and should be as given in the following example, where `This is a text` is a text that does not contain the character '>'.

Align.fa

```
1 >Name of taxon1
2 This is a text
3
4 >Name of taxon2
5 This is a
6 text
```

The second input `reading_mode` specifies whether the text specifically contains a DNA sequence or any regular text. In the former case, the value of `reading_mode` must be 1, which will imply that all lower case letters `a`, `c`, `g` and `t` are read as upper case letters `A`, `C`, `G` and `T`. The global variable `READ_DNA` can be used for this purpose.

```
>>> READ_DNA
1
```

The output `names` is a list of strings containing the names placed after the character '>' in the input file while the output `alignment` is a list of lists of characters that spell each text displayed after the names saved in `names`.

As can be seen in the example given below, the index of a name in `names` corresponds to the index of its associated text in `alignment`.

```
>>> output = read_alignment_file("Align.fa",READ_DNA)
>>> for i in range(len(output[0])):
...     print(str(i)+":  "+str(output[0][i]))
0:  Name of taxon1
1:  Name of taxon2
>>> for i in range(len(output[1])):
...     print(str(i)+":  "+str(output[1][i]))
0:  ['T', 'h', 'i', 's', ' ', 'i', 's', ' ', 'A', ' ', 'T', 'e', 'x', 'T']
1:  ['T', 'h', 'i', 's', ' ', 'i', 's', ' ', 'A', 'T', 'e', 'x', 'T']
```

5.2. Description of ID_to_EQ

The function `ID_to_EQ` takes a string and returns a list of lists, which describes an equivalence relation whose equivalence classes (the internal lists) can be used during the parsing of a sequence alignment to identify certain molecular patches together.

```
1 def ID_to_EQ(name_ID):
2     """ the source code of this function can be found in ite.py """
3     return N21_EQ
4     else:
5         print("Error:  in ID_to_EQ: name_ID is not recognized")
5         exit()
```

The function `ID_to_EQ` is meant to be used with two sets of global variables. One sets consists of strings that define the valid inputs of `ID_to_EQ` while the other set consists of the possible outputs of `ID_to_EQ`, which are lists of lists that are

- either already equipped with specific equivalence classes describing a well-known evolution model (transition mutations, codon translation, etc.)
- or empty so that they can be ‘edited’ (see below).

We now give three examples of global variables that are associated with pre-determined equivalence classes, the first one being the trivial one, which is to say that it will involve no other identification than the reflexive ones (i.e. the identities).

```
>>> ID_to_EQ(NUCL_ID)
[[]]
```

Using the previous equivalence relation implies that the characters of a sequence alignment are read as-is (see section 5.3 for more details).

The next equivalence relation describes transition mutations ($A \leftrightarrow G$ and $C \leftrightarrow T$), which commonly occur on the nucleotides of DNA strands. These are often silent mutations so that one sometimes reasonably wants to identify `A` with `G` and `C` with `T`.

```
>>> ID_to_EQ(TRAN_ID)
[['A', 'G'], ['C', 'T']]
```

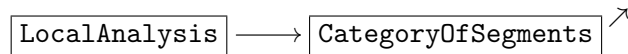
The last equivalence relation contains the equivalence classes induced by the codon table, that is to say those codons coding for the same amino acids.

```
>>> ID_to_EQ(AMIN_ID)
[['TTT', 'TTC'], ['TTA', 'TTG'], ['CTT', 'CTC', 'CTA', 'CTG'], ['TCT',
'TCC', 'TCA', 'TCG', 'AGT', 'AGC'], ['TAT', 'TAC'], ['CAT', 'CAC'], ['CAA',
'CAG'], ['TGT', 'TGC'], ['CGT', 'CGC', 'CGA', 'CGG'], ['ATT', 'ATC', 'ATA'],
['GTT', 'GTC', 'GTA', 'GTG'], ['ACT', 'ACC', 'ACA', 'ACG'], ['GCT', 'GCC',
'GCA', 'GCG'], ['AAT', 'AAC'], ['AAA', 'AAG'], ['GAT', 'GAC'], ['GAA',
'GAG'], ['AGA', 'AGG'], ['GGT', 'GGC', 'GGA', 'GGG']]
```

The user can also design its own equivalence relation (up to 21) via the (empty) global variables `N01_EQ`, `N02_EQ`, ..., `N21_EQ`, which are associated with the global strings `N01_ID`, `N02_ID`, ..., `N21_ID`. The way an equivalence relation can be used with its associated string will be explained in section 5.3.

```
>>> print(N05_ID)
n5
>>> print(ID_to_EQ(N05_ID))
[]
>>> N05_EQ.append(["A", "G"])
>>> print(N05_EQ)
[['A', 'G']]
>>> print(ID_to_EQ(N05_ID))
[['A', 'G']]
>>> N04_EQ.extend(["AC", "TC"], ["CC", "TC"]))
>>> print(ID_to_EQ(N04_ID))
[['AC', 'TC'], ['CC', 'TC']]
```

5.3. Description of LocalAnalysis (subclass)



The class `LocalAnalysis` is a subclass of `CategoryOfSegments` (section 4.4) that possesses three objects, namely

- `.equiv` (list of strings)
- `.base` (list of `SegmentObject` items)

and one method, namely a constructor `__init__`.

```
1 class LocalAnalysis(CategoryOfSegments):
2     #The objects of the class are:
3     #.equiv (list of strings);
4     #.base (list of SegmentObjects);
5     def __init__(self, analysis_mode, *args):
6     """ the source code of this constructor can be found in cl_la.py """
```

The idea behind the class `LocalAnalysis` is to specify the shape of a local analysis [4] via the two objects `.equiv` and `.base`. It is however important to understand that a `LocalAnalysis` item does not strictly define a local analysis in the sense of [4] because it is not associated with a sequence alignment yet. The sequence alignment is only meant to be specified at the level of a `Pedigree` item (section 5.5).

In other words, the present structure only specifies the schema of a local analysis, by describing its pattern of construction, rather than the associated functor $L : B \rightarrow \mathbf{Lpnt}(S)$

induced from the data of a sequence alignment. Even though the domain B is contained in the object `.base`, the mapping rules are not properly defined. Instead, one specifies, in the object `.equiv`, recipes for these mapping rules. Such a pattern specification is then used, in section 5.5, to generate what is regarded as a pedigrad [5, 4].

The constructor `__init__` of `LocalAnalysis` takes between 4 and 5 arguments and uses them to initialize the objects of the class according to certain pre-determined or personalized patterns. The first argument taken by `__init__` is always a string. However, the form of its second and third arguments may vary depending on the string contained in the first argument. On the other hand, the last two arguments always keep the same form, namely a string and an integer, which are given to the constructor of `CategoryOfSegments` to initialize the (super) objects `.domain`, `.mask`, and `.preorder` (see section 4.4)

More specifically, the first argument of `__init__` is meant to be part of a set of global variables containing strings, which are all displayed below.

```

EXPR_MODE = 'exp'
SEGM_MODE = 'seg'
NUCL_MODE = 'nu'
TRAN_MODE = 'tr'
TRNO_MODE = 'tr0nu'
TRN1_MODE = 'tr1nu'
TRN2_MODE = 'tr2nu'
AMNO_MODE = 'aa0'
AMN1_MODE = 'aa1'
AMN2_MODE = 'aa2'
AMIN_MODE = 'aa'

```

Depending on the string contained in the first argument, the constructor `__init__` may take four or five arguments. In addition, the second and third arguments may also take different forms.

The procedures `__init__(NUCL_MODE, -)` and `__init__(TRAN_MODE, -)` take three arguments whose last two arguments should be as described above, namely a string and an integer meant to be fed to the method `__init__` of `CategoryOfSegments`. For its part, the first argument should be a string that is the name of an element in the pre-order structure stored in the object `.preorder`.

The following example illustrates the two types of local analysis schemas that are obtained from the global variables `NUCL_MODE` and `TRAN_MODE`. The pre-order structure `omega.yml` used below is that given in section 4.4.1.

```

>>> Loc = LocalAnalysis(NUCL_MODE, '1', "omega.yml", 10)
>>> print(Loc.domain)
10
>>> print(Loc.mask)
True
>>> print(Loc.preorder)
[['0', '2', '1'], ['1'], ['2', '1']]
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))

```

```

segment 0: [(0, 0)] ['1'] ---> nu
segment 1: [(1, 1)] ['1'] ---> nu
segment 2: [(2, 2)] ['1'] ---> nu
segment 3: [(3, 3)] ['1'] ---> nu
segment 4: [(4, 4)] ['1'] ---> nu
segment 5: [(5, 5)] ['1'] ---> nu
segment 6: [(6, 6)] ['1'] ---> nu
segment 7: [(7, 7)] ['1'] ---> nu
segment 8: [(8, 8)] ['1'] ---> nu
segment 9: [(9, 9)] ['1'] ---> nu
>>> Loc = LocalAnalysis(TRAN_MODE, '2', "omega.yml", 10)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(0, 0)] ['2'] ---> tr
segment 1: [(1, 1)] ['2'] ---> tr
segment 2: [(2, 2)] ['2'] ---> tr
segment 3: [(3, 3)] ['2'] ---> tr
segment 4: [(4, 4)] ['2'] ---> tr
segment 5: [(5, 5)] ['2'] ---> tr
segment 6: [(6, 6)] ['2'] ---> tr
segment 7: [(7, 7)] ['2'] ---> tr
segment 8: [(8, 8)] ['2'] ---> tr
segment 9: [(9, 9)] ['2'] ---> tr

```

From the point of view of the function `ID_to_EQ` (see section 5.2), the previous two procedures specify how the images of the local analyses should be ‘quotiented’ via the strings contained in the object `.equiv`. Specifically, the type of local analysis returned by

```
...__init__(NUCL_MODE, -)
```

is meant to read the columns of a sequence alignment without identification between the characters while the type of local analysis returned by `...__init__(TRAN_MODE, -)` is meant to identify A with G and C with T.

```

>>> Loc = LocalAnalysis(NUCL_MODE, '1', "omega.yml", 10)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(ID_to_EQ(Loc.equiv[i])))
segment 0: [(0, 0)] ['1'] ---> [[]]
segment 1: [(1, 1)] ['1'] ---> [[]]
segment 2: [(2, 2)] ['1'] ---> [[]]
segment 3: [(3, 3)] ['1'] ---> [[]]
segment 4: [(4, 4)] ['1'] ---> [[]]
segment 5: [(5, 5)] ['1'] ---> [[]]
segment 6: [(6, 6)] ['1'] ---> [[]]
segment 7: [(7, 7)] ['1'] ---> [[]]
segment 8: [(8, 8)] ['1'] ---> [[]]
segment 9: [(9, 9)] ['1'] ---> [[]]
>>> Loc = LocalAnalysis(TRAN_MODE, '2', "omega.yml", 10)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(ID_to_EQ(Loc.equiv[i])))

```

```

segment 0: [(0, 0)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 1: [(1, 1)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 2: [(2, 2)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 3: [(3, 3)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 4: [(4, 4)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 5: [(5, 5)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 6: [(6, 6)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 7: [(7, 7)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 8: [(8, 8)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 9: [(9, 9)] ['2'] ---> [['A', 'G'], ['C', 'T']]

```

The three procedures

```

__init__(TRN0_MODE, -), __init__(TRN1_MODE, -) and __init__(TRN2_MODE, -)

```

take three arguments whose last two arguments are as described above, namely a string and an integer meant to be fed to the method `__init__` of `CategoryOfSegments`. For its part, the first argument should be a list of two strings that are the names of elements in the pre-order structure stored in the object `.preorder`.

```

>>> Loc = LocalAnalysis(TRN0_MODE, ['2', '1'], "omega.yml", 10)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(0, 0)] ['2'] ---> tr
segment 1: [(1, 1)] ['1'] ---> nu
segment 2: [(2, 2)] ['1'] ---> nu
segment 3: [(3, 3)] ['2'] ---> tr
segment 4: [(4, 4)] ['1'] ---> nu
segment 5: [(5, 5)] ['1'] ---> nu
segment 6: [(6, 6)] ['2'] ---> tr
segment 7: [(7, 7)] ['1'] ---> nu
segment 8: [(8, 8)] ['1'] ---> nu
segment 9: [(9, 9)] ['2'] ---> tr
>>> Loc = LocalAnalysis(TRN2_MODE, ['2', '1'], "omega.yml", 10)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(0, 0)] ['1'] ---> nu
segment 1: [(1, 1)] ['1'] ---> nu
segment 2: [(2, 2)] ['2'] ---> tr
segment 3: [(3, 3)] ['1'] ---> nu
segment 4: [(4, 4)] ['1'] ---> nu
segment 5: [(5, 5)] ['2'] ---> tr
segment 6: [(6, 6)] ['1'] ---> nu
segment 7: [(7, 7)] ['1'] ---> nu
segment 8: [(8, 8)] ['2'] ---> tr
segment 9: [(9, 9)] ['1'] ---> nu

```

From the point of view of the function `ID.to_EQ` (see section 5.2), a procedure of the form

```

__init__(TRNX_MODE, -)

```

generates a local analysis that is meant to identify A with G and C with T on every column whose position is X modulo 3 and that is meant to read the other columns as-is.

```
>>> Loc = LocalAnalysis(TRN0_MODE,['2','1'], "omega.yml",10)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(ID_to_EQ(Loc.equiv[i])))
segment 0: [(0, 0)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 1: [(1, 1)] ['1'] ---> [[]]
segment 2: [(2, 2)] ['1'] ---> [[]]
segment 3: [(3, 3)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 4: [(4, 4)] ['1'] ---> [[]]
segment 5: [(5, 5)] ['1'] ---> [[]]
segment 6: [(6, 6)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 7: [(7, 7)] ['1'] ---> [[]]
segment 8: [(8, 8)] ['1'] ---> [[]]
segment 9: [(9, 9)] ['2'] ---> [['A', 'G'], ['C', 'T']]
>>> Loc = LocalAnalysis(TRN2_MODE,['2','1'], "omega.yml",10)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(ID_to_EQ(Loc.equiv[i])))
segment 0: [(0, 0)] ['1'] ---> [[]]
segment 1: [(1, 1)] ['1'] ---> [[]]
segment 2: [(2, 2)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 3: [(3, 3)] ['1'] ---> [[]]
segment 4: [(4, 4)] ['1'] ---> [[]]
segment 5: [(5, 5)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 6: [(6, 6)] ['1'] ---> [[]]
segment 7: [(7, 7)] ['1'] ---> [[]]
segment 8: [(8, 8)] ['2'] ---> [['A', 'G'], ['C', 'T']]
segment 9: [(9, 9)] ['1'] ---> [[]]
```

The three procedures

```
.__init__(AMN0_MODE,-), .__init__(AMN1_MODE,-) and .__init__(AMN2_MODE,-)
```

take three arguments whose last two arguments are as described above, namely a string and an integer meant to be fed to the method `.__init__` of `CategoryOfSegments`. For its part, the first argument should be a string that is the name of an element in the pre-order structure stored in the object `.preorder`.

```
>>> Loc = LocalAnalysis(AMN0_MODE,'1', "omega.yml",21)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(0, 2)] ['1'] ---> aa
segment 1: [(3, 5)] ['1'] ---> aa
segment 2: [(6, 8)] ['1'] ---> aa
segment 3: [(9, 11)] ['1'] ---> aa
segment 4: [(12, 14)] ['1'] ---> aa
segment 5: [(15, 17)] ['1'] ---> aa
segment 6: [(18, 20)] ['1'] ---> aa
```

```
>>> Loc = LocalAnalysis(AMN1_MODE, '1', "omega.yml", 21)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(1, 3)] ['1'] ---> aa
segment 1: [(4, 6)] ['1'] ---> aa
segment 2: [(7, 9)] ['1'] ---> aa
segment 3: [(10, 12)] ['1'] ---> aa
segment 4: [(13, 15)] ['1'] ---> aa
segment 5: [(16, 18)] ['1'] ---> aa
>>> Loc = LocalAnalysis(AMN2_MODE, '1', "omega.yml", 21)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(2, 4)] ['1'] ---> aa
segment 1: [(5, 7)] ['1'] ---> aa
segment 2: [(8, 10)] ['1'] ---> aa
segment 3: [(11, 13)] ['1'] ---> aa
segment 4: [(14, 16)] ['1'] ---> aa
segment 5: [(17, 19)] ['1'] ---> aa
```

From the point of view of the function `ID.to_EQ` (see section 5.2), a procedure of the form

```
...__init__(AMNX_MODE, -)
```

generates a local analysis that reads the codons of a sequence alignment with the assumption that the codon topology starts at position `X` and identifies them according to the codon translation table.

```
>>> Loc = LocalAnalysis(AMN2_MODE, '1', "omega.yml", 21)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(ID.to_EQ(Loc.equiv[i])))
segment 0: [(2, 4)] ['1'] ---> [['TTT', 'TTC'], ['TTA', 'TTG'], ['CTT',
'CTC', 'CTA', 'CTG'], ['TCT', 'TCC', 'TCA', 'TCG', 'AGT', 'AGC'], ['TAT',
'TAC'], ['CAT', 'CAC'], ['CAA', 'CAG'], ['TGT', 'TGC'], ['CGT', 'CGC',
'CGA', 'CGG'], ['ATT', 'ATC', 'ATA'], ['GTT', 'GTC', 'GTA', 'GTG'], ['ACT',
'ACC', 'ACA', 'ACG'], ['GCT', 'GCC', 'GCA', 'GCG'], ['AAT', 'AAC'], ['AAA',
'AAG'], ['GAT', 'GAC'], ['GAA', 'GAG'], ['AGA', 'AGG'], ['GGT', 'GGC',
'GGA', 'GGG']]
segment 1: [(5, 7)] ['1'] ---> [['TTT', 'TTC'], ['TTA', 'TTG'], ['CTT',
'CTC', 'CTA', 'CTG'], ['TCT', 'TCC', 'TCA', 'TCG', 'AGT', 'AGC'], ['TAT',
'TAC'], ['CAT', 'CAC'], ['CAA', 'CAG'], ['TGT', 'TGC'], ['CGT', 'CGC',
'CGA', 'CGG'], ['ATT', 'ATC', 'ATA'], ['GTT', 'GTC', 'GTA', 'GTG'], ['ACT',
'ACC', 'ACA', 'ACG'], ['GCT', 'GCC', 'GCA', 'GCG'], ['AAT', 'AAC'], ['AAA',
'AAG'], ['GAT', 'GAC'], ['GAA', 'GAG'], ['AGA', 'AGG'], ['GGT', 'GGC',
'GGA', 'GGG']]
```



```

segment 2: [(8, 10)] ['1'] ---> [['TTT', 'TTC'], ['TTA', 'TTG'], ['CTT',
'CTC', 'CTA', 'CTG'], ['TCT', 'TCC', 'TCA', 'TCG', 'AGT', 'AGC'], ['TAT',
'TAC'], ['CAT', 'CAC'], ['CAA', 'CAG'], ['TGT', 'TGC'], ['CGT', 'CGC',
'CGA', 'CGG'], ['ATT', 'ATC', 'ATA'], ['GTT', 'GTC', 'GTA', 'GTG'], ['ACT',
'ACC', 'ACA', 'ACG'], ['GCT', 'GCC', 'GCA', 'GCG'], ['AAT', 'AAC'], ['AAA',
'AAG'], ['GAT', 'GAC'], ['GAA', 'GAG'], ['AGA', 'AGG'], ['GGT', 'GGC',
'GGA', 'GGG']]
segment 3: [(11, 13)] ['1'] ---> [['TTT', 'TTC'], ['TTA', 'TTG'], ['CTT',
'CTC', 'CTA', 'CTG'], ['TCT', 'TCC', 'TCA', 'TCG', 'AGT', 'AGC'], ['TAT',
'TAC'], ['CAT', 'CAC'], ['CAA', 'CAG'], ['TGT', 'TGC'], ['CGT', 'CGC',
'CGA', 'CGG'], ['ATT', 'ATC', 'ATA'], ['GTT', 'GTC', 'GTA', 'GTG'], ['ACT',
'ACC', 'ACA', 'ACG'], ['GCT', 'GCC', 'GCA', 'GCG'], ['AAT', 'AAC'], ['AAA',
'AAG'], ['GAT', 'GAC'], ['GAA', 'GAG'], ['AGA', 'AGG'], ['GGT', 'GGC',
'GGA', 'GGG']]
segment 4: [(14, 16)] ['1'] ---> [['TTT', 'TTC'], ['TTA', 'TTG'], ['CTT',
'CTC', 'CTA', 'CTG'], ['TCT', 'TCC', 'TCA', 'TCG', 'AGT', 'AGC'], ['TAT',
'TAC'], ['CAT', 'CAC'], ['CAA', 'CAG'], ['TGT', 'TGC'], ['CGT', 'CGC',
'CGA', 'CGG'], ['ATT', 'ATC', 'ATA'], ['GTT', 'GTC', 'GTA', 'GTG'], ['ACT',
'ACC', 'ACA', 'ACG'], ['GCT', 'GCC', 'GCA', 'GCG'], ['AAT', 'AAC'], ['AAA',
'AAG'], ['GAT', 'GAC'], ['GAA', 'GAG'], ['AGA', 'AGG'], ['GGT', 'GGC',
'GGA', 'GGG']]
segment 5: [(17, 19)] ['1'] ---> [['TTT', 'TTC'], ['TTA', 'TTG'], ['CTT',
'CTC', 'CTA', 'CTG'], ['TCT', 'TCC', 'TCA', 'TCG', 'AGT', 'AGC'], ['TAT',
'TAC'], ['CAT', 'CAC'], ['CAA', 'CAG'], ['TGT', 'TGC'], ['CGT', 'CGC',
'CGA', 'CGG'], ['ATT', 'ATC', 'ATA'], ['GTT', 'GTC', 'GTA', 'GTG'], ['ACT',
'ACC', 'ACA', 'ACG'], ['GCT', 'GCC', 'GCA', 'GCG'], ['AAT', 'AAC'], ['AAA',
'AAG'], ['GAT', 'GAC'], ['GAA', 'GAG'], ['AGA', 'AGG'], ['GGT', 'GGC',
'GGA', 'GGG']]

```

The procedure `...init__(AMIN_MODE,-)`, takes three arguments whose last two arguments are as described above, namely a string and an integer meant to be fed to the method `...init__` of `CategoryOfSegments`. For its part, the first argument should be a list of three strings that are the names of elements in the pre-order structure stored in the object `.preorder`. From the point of view of the function `ID_to_EQ` (see section 5.2), the procedure

```
...init__(AMIN_MODE,-)
```

generates a local analysis that reads all the codons of the sequence and identifies them according to the codon translation table.

```

>>> Loc =LocalAnalysis(AMIN_MODE,['0','1','2'], "omega.yml",21)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
          str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(0, 2)] ['0'] ---> aa
segment 1: [(3, 5)] ['0'] ---> aa
segment 2: [(6, 8)] ['0'] ---> aa
segment 3: [(9, 11)] ['0'] ---> aa
segment 4: [(12, 14)] ['0'] ---> aa
segment 5: [(15, 17)] ['0'] ---> aa
segment 6: [(18, 20)] ['0'] ---> aa

```

```

segment 7: [(1, 3)] ['1'] ---> aa
segment 8: [(4, 6)] ['1'] ---> aa
segment 9: [(7, 9)] ['1'] ---> aa
segment 10: [(10, 12)] ['1'] ---> aa
segment 11: [(13, 15)] ['1'] ---> aa
segment 12: [(16, 18)] ['1'] ---> aa
segment 13: [(2, 4)] ['2'] ---> aa
segment 14: [(5, 7)] ['2'] ---> aa
segment 15: [(8, 10)] ['2'] ---> aa
segment 16: [(11, 13)] ['2'] ---> aa
segment 17: [(14, 16)] ['2'] ---> aa
segment 18: [(17, 19)] ['2'] ---> aa

```

Finally the user can design their own local analysis by using the procedures

```
...init__(EXPR_MODE,—) and ...init__(SEGM_MODE,—),
```

which take four more arguments as described below:

- the first argument of `...init__(EXPR_MODE,—)` should be a list of regular expressions specifying `SegmentObject` items (section 4.3). This list is then turned into a list of `SegmentObject` items, which is to be stored in the object `.base`;
- the first argument of `...init__(SEGM_MODE,—)` should be a list of `SegmentObject` items (section 4.3), which is to be stored in the object `.base`;
- the second argument should be a list of strings, which is to be stored in the object `.equiv`. More specifically, the strings should be among those contained in the global variables `NUCL_ID`, `TRAN_ID`, `AMIN_ID`, `N01_ID`, `N02_ID`, ..., and `N21_ID`;
- and, as mentioned many times above, the last two arguments should be a string and an integer, which are to be passed to the method `...init__` of `CategoryOfSegments` (see section 4.4).

Below, we show two examples of how the previous two procedures can be used. Note how these examples use the (empty) global variables `N01_EQ` and `N02_EQ` (see section 5.2).

```

>>> N01_EQ.append(["A","G"])
>>> N02_EQ.extend(["AC","TC"],["CC","TC"])
>>> base = [[(5,1,1,'1')], [(6,2,1,'2')], [(8,1,1,'1')], [(9,2,2,'2')]]
>>> equiv = [N01_ID, N02_ID, N01_ID, N02_ID, N02_ID]
>>> Loc = LocalAnalysis(EXPR_MODE,base,equiv,"omega.yml",21)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
...           str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(5, 5)] ['1'] ---> n1
segment 1: [(6, 7)] ['2'] ---> n2
segment 2: [(8, 8)] ['1'] ---> n1
segment 3: [(9, 10), (11, 12)] ['2', '2'] ---> n2
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
...           str(Loc.base[i].colors) + " ---> " + str(ID_to_EQ(Loc.equiv[i])))
segment 0: [(5, 5)] ['1'] ---> [['A', 'G']]
segment 1: [(6, 7)] ['2'] ---> [['AC', 'TC'], ['CC', 'TC']]
segment 2: [(8, 8)] ['1'] ---> [['A', 'G']]
segment 3: [(9, 10), (11, 12)] ['2', '2'] ---> [['AC', 'TC'], ['CC', 'TC']]

```

Alternatively, the procedure `__init__(SEGM_MODE, -)` would require to have a pre-defined environment in which `SegmentObject` items can be defined. Note the difference between the previous lines of codes and the following ones, which use the class `CategoryOfSegments`.

```
>>> N01_EQ.append(["A", "G"])
>>> N02_EQ.extend(["AC", "TC"], ["CC", "TC"])
>>> Seg = CategoryOfSegments("omega.yml", 21)
>>> base = [Seg.segment([(5, 1, 1, '1')]), Seg.segment([(6, 2, 1, '2')]),
            Seg.segment([(8, 1, 1, '1')]), Seg.segment([(9, 2, 2, '2')])]
>>> equiv = [N01_ID, N02_ID, N01_ID, N02_ID, N02_ID]
>>> Loc = LocalAnalysis(SEGM_MODE, base, equiv, "omega.yml", 21)
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
            str(Loc.base[i].colors) + " ---> " + str(Loc.equiv[i]))
segment 0: [(5, 5)] ['1'] ---> n1
segment 1: [(6, 7)] ['2'] ---> n2
segment 2: [(8, 8)] ['1'] ---> n1
segment 3: [(9, 10), (11, 12)] ['2', '2'] ---> n2
>>> for i in range(len(Loc.base)):
...     print("segment " + str(i) + ": " + str(Loc.base[i].topology) + " " +
            str(Loc.base[i].colors) + " ---> " + str(ID_to_EQ(Loc.equiv[i])))
segment 0: [(5, 5)] ['1'] ---> [['A', 'G']]
segment 1: [(6, 7)] ['2'] ---> [['AC', 'TC'], ['CC', 'TC']]
segment 2: [(8, 8)] ['1'] ---> [['A', 'G']]
segment 3: [(9, 10), (11, 12)] ['2', '2'] ---> [['AC', 'TC'], ['CC', 'TC']]
```

5.4. Description of `column_is_trivial`

The function `column_is_trivial` takes two lists of elements and returns `True` if, apart from the elements in the second input list, the first input list contains copies of a unique element; returns `False` if, apart from the elements in the second input list, the first input list contains at least two different elements.

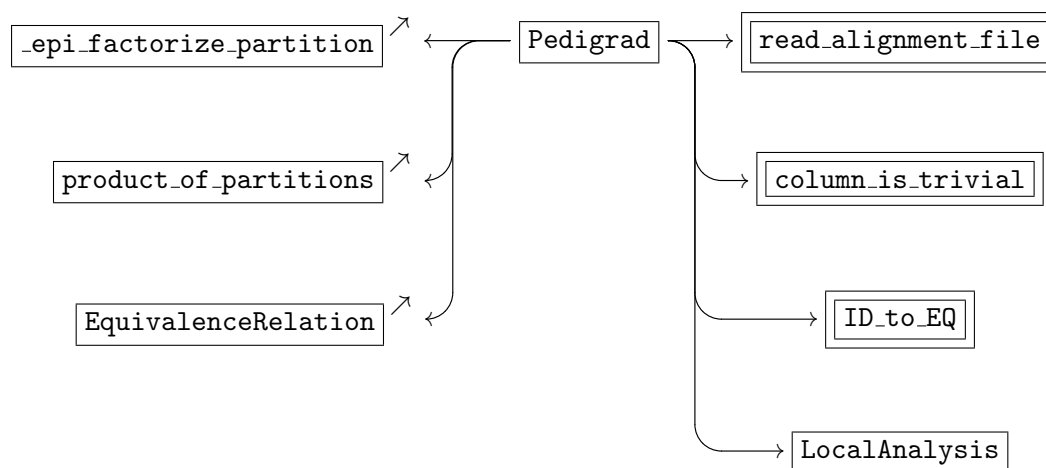
```
1 def column_is_trivial(column, exceptions):
2     """ the source code of this function can be found in cit.py """
3     return flag
```

As will be seen later in other functions, there are often special characters that need to be handled differently from the other characters. For instance, the character `'.'` is often used in alignments to mean that a character is actually missing. These special characters sometimes need to be ignored in the analysis.

```
>>> p = ['e', 'e', 'e', 'e', 'e']
>>> print(column_is_trivial(p, []))
True
>>> p = ['e', 'e', 'a', 'a', 'e']
>>> print(column_is_trivial(p, []))
False
>>> p = [0, '.', 0, 0, '.', 0, 1, 0]
>>> print(column_is_trivial(p, ['.']))
False
>>> print(column_is_trivial(p, ['.'], 1))
```

True

5.5. Description of Pedigrad (subclass)



The class `Pedigrad` is a subclass of `LocalAnalysis` (section 5.3) that possesses two objects, namely

- `.local` (list of lists)
- `.taxa` (list)

and two methods, namely

- `__init__` (constructor)
- `.partition`
- `.reduce`
- `.agree`

The constructor `__init__` takes from 5 to 6 arguments, which are meant to be used with the function `read_alignment_file` and the constructor of `LocalAnalysis`. More specifically, the constructor of `Pedigrad` usually takes

- the name of a file and an integer, given to the function `read_alignment_file`;
- a list of arguments, given to the constructor of `LocalAnalysis`.

```

1 class Pedigrad(LocalAnalysis):
2     #The objects of the class are:
3     #.local (list);
4     #.taxa (list).
5     def __init__(self,name_of_file,reading_mode,*args):
6         """ the source code of this constructor can be found in cl.ped.py """
  
```

The list of arguments `*args` (shown above) usually contains those arguments that would be given to the constructor of `LocalAnalysis` (see `__init__` in section 5.3), except for the last argument, which does not need to be given if

- the name of the file is the name of an existing file;
- the name of the file is empty (see the examples given later).

For illustration, we will use the preorder structure `omega.yml` given in section 4.4.1 and the following alignment file.

```

Align.fa
1 > A
2 aaaaaaaaaaf
3 > B
4 bbbbbbbbf
5 > C
6 ccccccccf
7 > D
8 ddddddddf
9 > E
10 eeeeeeeef

```

The following lines of code illustrate the syntax with which an instance of `Pedigrad` can be constructed and compares it to that used to construct an instance of `LocalAnalysis`.

```

>>> P = Pedigrad("align.fa",not(READ_DNA),TRN2_MODE,['2','1'],"omega.yml")
>>> L = LocalAnalysis(TRN2_MODE,['2','1'],"omega.yml",500)
>>> P = Pedigrad("align.fa",not(READ_DNA),AMNO_MODE,'1',"omega.yml")
>>> L = LocalAnalysis(AMNO_MODE,'1',"omega.yml",500)
>>> P = Pedigrad("",not(READ_DNA),TRN2_MODE,['2','1'],"omega.yml")
TypeError: __init__() takes exactly 3 arguments (2 given)
>>> P = Pedigrad("",not(READ_DNA),TRN2_MODE,['2','1'],"omega.yml",500)

```

If the name of the file that is passed to the constructor, in its first argument, is not empty, then the first two arguments are passed to the procedure `read_alignment_file(-,-)` and the constructor proceeds to the initialization of the objects `.local`, `.taxa` and `.base` as follows:

- it stores the first output of `read_alignment_file` in the object `.taxa`;
- it appends the remaining lists of arguments with the length of the second output of `read_alignment_file` and gives the resulting tuples of arguments to the constructor of `LocalAnalysis` (see below).

```

super(Pedigrad, self).__init__(*args+(len(alignment[0]),))

```

Once the object `.base` of the super class has been (pre-)initialized by this process, the `SegmentObject` items that it contains are used to parse the sequence alignment. The parsed data is then stored in the object `.local` as follows:

- ▷ For every patch (x,y) occurring in the topology of i -th segment contained `.base`, the characters appearing from position x to position y , in the sequence alignment, are collected for each line of the sequence alignment (i.e. each list of characters contained in the second output of `read_alignment_file`) and put together to form a list of strings;
- ▷ This list of strings is then relabeled with respect to the indices of the lists of equivalence classes that should have been among the arguments meant to be given to the constructor of `LocalAnalysis`;
- ▷ If the relabeled list of strings is not trivial according to the procedure

```
column_is_trivial(-,[]),
```

then it is stored at position i in the object `.local`;

- ▷ If the lists of strings happens to be trivial, then it is not stored and the associated segment is removed from the object `.base` (thus shifting the indexing).

```
>>> print(NUCL_EQ)
[[]]
>>> P = Pedigrad("align.fa",not(READ_DNA),NUCL_MODE,'2',"omega.yml")
>>> print(P.taxa)
[' A', ' B', ' C', ' D', ' E']
>>> print(P.domain,len(P.base),len(P.local))
(10, 9, 9)
>>> for i in range(len(P.base)):
...     print("segment " + str(i) + ": " + str(P.base[i].topology) + ",
...           "+str(P.base[i].colors) + " ---> " + str(P.local[i]))
segment 0: [(0, 0)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 1: [(1, 1)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 2: [(2, 2)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 3: [(3, 3)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 4: [(4, 4)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 5: [(5, 5)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 6: [(6, 6)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 7: [(7, 7)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 8: [(8, 8)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
```

When the `SegmentObject` items of the base only contain patches of length 1 and the equivalence classes are empty (as above), then the list of lists stored in `.local` corresponds to the transpose of the sequence alignment (when seen as a matrix), up to removal of those columns (in the alignment) that only contain the same character.

Below, we give several other examples, some of which present bases whose `SegmentObject` items contain patches of length greater than 1.

Our first example illustrates how the lists of strings contained in the object `.local` are relabeled when the equivalence class contained in `NUCL_EQ` is replaced with non-trivial ones.

```
>>> NUCL_EQ.remove([])
>>> NUCL_EQ.extend(['e'],['d'],['c'],['b'],['a'])
>>> print(NUCL_EQ)
[['e'], ['d'], ['c'], ['b'], ['a']]
>>> P = Pedigrad("align.fa",not(READ_DNA),NUCL_MODE,'2',"omega.yml")
>>> for i in range(len(P.base)):
...     print("segment " + str(i) + ": " + str(P.base[i].topology) + ",
...           "+str(P.base[i].colors) + " ---> " + str(P.local[i]))
segment 0: [(0, 0)], ['2'] ---> [4, 3, 2, 1, 0]
segment 1: [(1, 1)], ['2'] ---> [4, 3, 2, 1, 0]
segment 2: [(2, 2)], ['2'] ---> [4, 3, 2, 1, 0]
segment 3: [(3, 3)], ['2'] ---> [4, 3, 2, 1, 0]
segment 4: [(4, 4)], ['2'] ---> [4, 3, 2, 1, 0]
segment 5: [(5, 5)], ['2'] ---> [4, 3, 2, 1, 0]
segment 6: [(6, 6)], ['2'] ---> [4, 3, 2, 1, 0]
segment 7: [(7, 7)], ['2'] ---> [4, 3, 2, 1, 0]
segment 8: [(8, 8)], ['2'] ---> [4, 3, 2, 1, 0]
```

This second example is similar to the previous one, but the relabelling only occurs where the lists of strings contained in the object `.local` are detected. Note that the following example uses the modified version `NUCL_EQ` designed in the previous example.

```
>>> print(NUCL_EQ)
[['e'], ['d'], ['c'], ['b'], ['a']]
>>> print(TRAN_EQ)
[['A', 'G'], ['C', 'T']]
>>> P = Pedigrad("align.fa",not(READ_DNA),TRN2_MODE,['2','1',"omega.yml"])
>>> for i in range(len(P.base)):
...     print("segment " + str(i) + ": " + str(P.base[i].topology) + ",
...           "+str(P.base[i].colors) + " ---> " + str(P.local[i]))
segment 0: [(0, 0)], ['1'] ---> [4, 3, 2, 1, 0]
segment 1: [(1, 1)], ['1'] ---> [4, 3, 2, 1, 0]
segment 2: [(2, 2)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 3: [(3, 3)], ['1'] ---> [4, 3, 2, 1, 0]
segment 4: [(4, 4)], ['1'] ---> [4, 3, 2, 1, 0]
segment 5: [(5, 5)], ['2'] ---> ['a', 'b', 'c', 'd', 'e']
segment 6: [(6, 6)], ['1'] ---> [4, 3, 2, 1, 0]
segment 7: [(7, 7)], ['1'] ---> [4, 3, 2, 1, 0]
```

We finish with the following example, in which the local analysis is designed by the user.

```
>>> N01_EQ.extend(['aaa','eee'],[['bbb']])
>>> alignment = read_alignment_file("align.fa",not(READ_DNA))
>>> domain = len(alignment[1][0])
>>> base = list()
>>> equiv = list()
>>> for i in range(domain/3):
...     base.append([(3*i,3,1,'1')])
...     equiv.append(N01_ID)
>>> P = Pedigrad("align.fa",not(READ_DNA),EXPR_MODE,base,equiv,"omega.yml")
>>> print(P.domain,len(P.base),len(P.local))
(10, 3, 3)
>>> for i in range(len(P.base)):
...     print("segment " + str(i) + ": " + str(P.base[i].topology) + ",
...           "+str(P.base[i].colors) + " ---> " + str(P.local[i]))
segment 0: [(0, 2)], ['1'] ---> [0, 1, 'ccc', 'ddd', 0]
segment 1: [(3, 5)], ['1'] ---> [0, 1, 'ccc', 'ddd', 0]
segment 2: [(6, 8)], ['1'] ---> [0, 1, 'ccc', 'ddd', 0]
```

If the name of the file passed to the constructor, in its first argument, is empty, then the objects `.local` and `.taxa` are initialized with empty lists while the other objects `.equiv`, `.base`, `.domain`, `.mask` and `.preorder` are initialized via the constructor of the class `LocalAnalysis`.

Let us now focus on the other methods of the class, which recover usual or canonical operations on pedigrees.

```
7 def partition(self,*args):
8     """ the source code of this constructor can be found in cl_ped.py """
9     return the_image
10 def reduce(self,equivalence,*args):
11     """ the source code of this constructor can be found in cl_ped.py """
12     return new_pedigrad
13 def agree(self,ground,pulling_condition):
14     """ the source code of this constructor can be found in cl_ped.py """
15     return agreeing_segments
```

5.5.1. Partition. The method `.partition` takes

- either no argument;
- or the regular expression of `SegmentObject` item and a string (specifically `EXPR_MODE`);
- or a `SegmentObject` item and a string (specifically `SEGM_MODE`).

If no argument is given, then the procedure returns a terminal partition. Otherwise, the procedure returns (see the formula below) the image of the right Kan extension $\mathbb{R}L$ [4, Definition 4.29] of the underlying local analysis $L : B \rightarrow \mathbf{Lprt}(S)$ on the segment τ given as input.

$$\mathbb{R}L(\tau) = \prod_{v \in B} \prod_{\mathbf{Seg}(\Omega|n)(\tau, v)} L^b(v)$$

This image is obtained from the product of those partitions, in the object `.local`, whose indices correspond to the indices of those segments v , in the object `.base`, toward which there is a morphism of segments from the input `SegmentObject` item τ .

$$\mathbf{Seg}(\Omega|n)(\tau, v) \neq \emptyset$$

For illustration, let us change the sequence alignment to the following one.

<code>Align.fa</code>
1 > A
2 CCCAGTTAG
3 > B
4 CCGATATAA
5 > C
6 GGCTTATAG
7 > D
8 GGCGTATAG
9 > E
10 ACCATATAA

For simplicity, we shall suppose that the global variable is as initially provided by the library `NUCL_EQ` (empty) and we shall consider the following pedigrad.

```
>>> print(NUCL_EQ)
[[]]
>>> P = Pedigrad("align.fa", not(READ_DNA), NUCL_MODE, '2', "omega.yml")
>>> for i in range(len(P.base)):
...     print("segment " + str(i) + ": " + str(P.base[i].topology) + ",
...           "+str(P.base[i].colors) + " ---> " + str(P.local[i]))
segment 0: [(0, 0)], ['2'] ---> ['C', 'C', 'G', 'G', 'A']
segment 1: [(1, 1)], ['2'] ---> ['C', 'C', 'G', 'G', 'C']
segment 2: [(2, 2)], ['2'] ---> ['C', 'G', 'C', 'C', 'C']
segment 3: [(3, 3)], ['2'] ---> ['A', 'A', 'T', 'G', 'A']
segment 4: [(4, 4)], ['2'] ---> ['G', 'T', 'T', 'T', 'T']
segment 5: [(5, 5)], ['2'] ---> ['T', 'A', 'A', 'A', 'A']
segment 6: [(8, 8)], ['2'] ---> ['G', 'A', 'G', 'G', 'A']
```

First, recall that if no argument is given to the procedure `.partition`, then the procedure returns the terminal partition, whose (unique) value is chosen to be 0.

```
>>> print(P.partition())
[0, 0, 0, 0, 0]
```

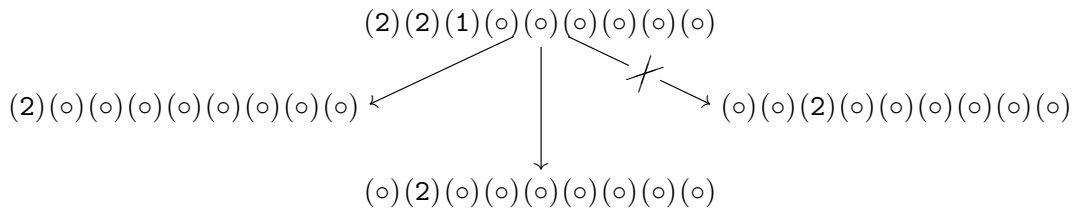
Let us now look at the outputs of the procedure `partition` when the regular expression of a segment is given as an input. For instance, suppose that one wants to compute the image of the following segment via the previously specified pedigrad.

$$(5.1) \quad (2)(2)(1)(\circ)(\circ)(\circ)(\circ)(\circ)(\circ)$$

This would be encoded by the following specification.

```
>>> print(P.partition([(0,1,1,'2'),(1,1,1,'2'),(2,1,1,'1')],EXPR.MODE))
[0, 0, 1, 1, 2]
```

Recall that the earlier output is the product of those partitions, in `.local`, whose indices correspond to the indices of those segments, in `.base`, toward which there is a morphism of segment from the input `SegmentObject` item.



This calculation is made more explicit in the following lines of code, in which the segments of the base are given by the regular expressions `[(0,1,1,'2')]`, `[(1,1,1,'2')]`, and `[(2,1,1,'2')]`.

```
>>> s1 = P.segment([(0,1,1,'2'),(1,1,1,'2'),(2,1,1,'1')])
>>> s2 = P.segment([(0,1,1,'2')])
>>> print(P.homset_is_inhabited(s1,s2))
True
>>> s3 = P.segment([(1,1,1,'2')])
>>> print(P.homset_is_inhabited(s1,s3))
True
>>> s4 = P.segment([(2,1,1,'2')])
>>> print(P.homset_is_inhabited(s1,s4))
False
>>> p1 = P.partition(s1,SEGM.MODE)
>>> p2 = P.partition(s2,SEGM.MODE)
>>> print(product_of_partitions(p1,p2))
[0, 0, 1, 1, 2]
```

For the sake of comparison, we can now compute the image of the following segment.

$$(5.2) \quad (2)(2)(2)(\circ)(\circ)(\circ)(\circ)(\circ)(\circ)$$

```
>>> print(P.partition([(0,1,1,'2'),(1,1,1,'2'),(2,1,1,'2')],EXPR.MODE))
[0, 1, 2, 2, 3]
```

The difference between the image of segment (5.1) and that of segment (5.2) comes from non-triviality if the following image.

```
>>> print(P.partition([(2,1,1,'2')],EXPR.MODE))
[0, 1, 0, 0, 0]
```

5.5.2. Reduce. The method `.reduce` takes from 2 to 3 arguments and returns a *Pedigrad* item that is a reduction of the ambient pedigrad (the `self` object) in the sense of [4] (see below for more detail). Specifically, the method `.reduce` takes:

- an *EquivalenceRelation* item (see section 3.6);
- an integer;
- and if the previous integer is equal to 1, a list of elements.

The second input can be specified via the global variable `REMOVE`, which contains the integer 1, as shown below.

```
>>> print(REMOVE,not(REMOVE))
(1, False)
```

If the second input is `not 1`, then the procedure returns the reduced pedigrad [4] whose ‘images’ (i.e. the outputs of the method `.partition`) are equal to the categorical products of the images of the ambient pedigrad (for the same segment) with the underlying partition of the *EquivalenceRelation* item passed to the function (see below).

$$\begin{array}{ccccc} & & \mathbb{R}(L) \times u & & \\ & \searrow & & \nearrow & \\ \text{Seg}(\Omega | n) & \xrightarrow{\cong} & \text{Seg}(\Omega | n) \times \mathbf{1} & \xrightarrow{(\mathbb{R}(L), u)} & \text{Uprt}(S) \times \text{Uprt}(S) & \xrightarrow{\times} & \text{Uprt}(S) \end{array}$$

The following two examples consider the *Pedigrad* item defined in section 5.5.1. Note that the partitions displayed in the two pair of loops are exactly the same for the same indices.

```
>>> u = EquivalenceRelation([ [0,1,2,3] ],4)
>>> Pxu = P.reduce(u,not(REMOVE))
>>> for i in range(len(Pxu.base)):
...     print("segment "+str(i)+": "+str(Pxu.base[i].topology)+"
...           "+str(Pxu.base[i].colors)+" ---> "+str(Pxu.local[i]))
segment 0: [(0, 0)] ['2'] ---> [0, 0, 1, 1, 2]
segment 1: [(1, 1)] ['2'] ---> [0, 0, 1, 1, 2]
segment 2: [(2, 2)] ['2'] ---> [0, 1, 0, 0, 2]
segment 3: [(3, 3)] ['2'] ---> [0, 0, 1, 2, 3]
segment 4: [(4, 4)] ['2'] ---> [0, 1, 1, 1, 2]
segment 5: [(5, 5)] ['2'] ---> [0, 1, 1, 1, 2]
segment 6: [(8, 8)] ['2'] ---> [0, 1, 0, 0, 2]
>>> for i in range(len(Pxu.base)):
...     print(str(i) + ") compare to the product..... " + str(
...           product_of_partitions(P.local[i],u.quotient()))
0) compare to the product..... [0, 0, 1, 1, 2]
1) compare to the product..... [0, 0, 1, 1, 2]
2) compare to the product..... [0, 1, 0, 0, 2]
3) compare to the product..... [0, 0, 1, 2, 3]
4) compare to the product..... [0, 1, 1, 1, 2]
5) compare to the product..... [0, 1, 1, 1, 2]
6) compare to the product..... [0, 1, 0, 0, 2]
```

Here is another example where the equivalence relation is divided into two classes. This division changes the partitions contained in `Pxu.local`.

```
>>> u = EquivalenceRelation([[0,1],[2,3]],4)
>>> Pxu = P.reduce(u,not(REMOVE))
>>> for i in range(len(Pxu.base)):
...     print("segment "+str(i)+": "+str(Pxu.base[i].topology)+"
...           "+str(Pxu.base[i].colors)+" ---> "+str(Pxu.local[i]))
segment 0: [(0, 0)] ['2'] ---> [0, 0, 1, 1, 2]
segment 1: [(1, 1)] ['2'] ---> [0, 0, 1, 1, 2]
segment 2: [(2, 2)] ['2'] ---> [0, 1, 2, 2, 3]
segment 3: [(3, 3)] ['2'] ---> [0, 0, 1, 2, 3]
segment 4: [(4, 4)] ['2'] ---> [0, 1, 2, 2, 3]
segment 5: [(5, 5)] ['2'] ---> [0, 1, 2, 2, 3]
segment 6: [(8, 8)] ['2'] ---> [0, 1, 2, 2, 3]
>>> for i in range(len(Pxu.base)):
...     print(str(i) + ") compare to the product..... " + str(
...         product_of_partitions(P.local[i],u.quotient()))
0) compare to the product..... [0, 0, 1, 1, 2]
1) compare to the product..... [0, 0, 1, 1, 2]
2) compare to the product..... [0, 1, 2, 2, 3]
3) compare to the product..... [0, 0, 1, 2, 3]
4) compare to the product..... [0, 1, 2, 2, 3]
5) compare to the product..... [0, 1, 2, 2, 3]
6) compare to the product..... [0, 1, 2, 2, 3]
```

This means that the partitions of the returned pedigrad will gather, via the same images (or, equivalently, within the same fibers), those integers that:

- are in non-trivial classes of the first input (i.e. the `RelationEquivalence` item);
- and are gathered together in the corresponding partitions of the ambient pedigrad;

and isolate (within singleton fibers) those integers that:

- are in trivial classes of the first input (i.e. the `RelationEquivalence` item);
- or are not present in the classes of the first input;

If the second input is equal to 1 (i.e. equal to `REMOVE`), then the procedure returns the same images as those returned in the case where the second input is not 1, *except for* those images that originate from patches of the sequence alignment whose rows indexed by indices in the first input are elements of the third output, in which case these images are all equal to the terminal partition (see below).

For illustration, let us suppose that our sequence alignment file `Align.fa` now contains some missing characters, as shown below.

Align.fa

```

1 > A
2 CCCAGTTAG
3 > B
4 CCGA..TAA
5 > C
6 GGCTTATAG
7 > D
8 GGCGTATAG
9 > E
10 ACCATATAA

```

Our next example now ignores the segments containing positions associated with missing characters. Specifically, these segments are eliminated from the base because the list of characters ['.'] is passed in the third argument of `.reduce`.

```

>>> u = EquivalenceRelation([0,1,2,3],4)
>>> Pxu = P.reduce(u,REMOVE,['.'])
>>> for i in range(len(Pxu.base)):
...     print("segment "+str(i)+": "+str(Pxu.base[i].topology)+"
...           "+str(Pxu.base[i].colors)+" ---> "+str(Pxu.local[i]))
segment 0: [(0, 0)] ['2'] ---> [0, 0, 1, 1, 2]
segment 1: [(1, 1)] ['2'] ---> [0, 0, 1, 1, 2]
segment 2: [(2, 2)] ['2'] ---> [0, 1, 0, 0, 2]
segment 3: [(3, 3)] ['2'] ---> [0, 0, 1, 2, 3]
segment 4: [(8, 8)] ['2'] ---> [0, 1, 0, 0, 2]
>>> for i in range(len(Pxu.base)):
...     print(str(i) + ") compare to the product..... " + str(
...           product_of_partitions(P.local[i],u.quotient()))
0) compare to the product..... [0, 0, 1, 1, 2]
1) compare to the product..... [0, 0, 1, 1, 2]
2) compare to the product..... [0, 1, 0, 0, 2]
3) compare to the product..... [0, 0, 1, 2, 3]
4) compare to the product..... [0, 1, 2, 2, 3]

```

Here is another example where the equivalence relation is divided into two classes. This division changes the partitions contained in `Pxu.local`.

```

>>> u = EquivalenceRelation([0,1],[2,3],4)
>>> Pxu = P.reduce(u,REMOVE,['.'])
>>> for i in range(len(Pxu.base)):
...     print("segment "+str(i)+": "+str(Pxu.base[i].topology)+"
...           "+str(Pxu.base[i].colors)+" ---> "+str(Pxu.local[i]))
segment 0: [(0, 0)] ['2'] ---> [0, 0, 1, 1, 2]
segment 1: [(1, 1)] ['2'] ---> [0, 0, 1, 1, 2]
segment 2: [(2, 2)] ['2'] ---> [0, 1, 2, 2, 3]
segment 3: [(3, 3)] ['2'] ---> [0, 0, 1, 2, 3]
segment 6: [(8, 8)] ['2'] ---> [0, 1, 2, 2, 3]
>>> for i in range(len(Pxu.base)):
...     print(str(i) + ") compare to the product..... " + str(
...           product_of_partitions(P.local[i],u.quotient()))

```

```

0) compare to the product..... [0, 0, 1, 1, 2]
1) compare to the product..... [0, 0, 1, 1, 2]
2) compare to the product..... [0, 1, 2, 2, 3]
3) compare to the product..... [0, 0, 1, 2, 3]
4) compare to the product..... [0, 1, 2, 2, 3]

```

We can check that the missing segments are associated with terminal partitions.

```

>>> print(Pxu.partition([(5,1,1,'2')],EXPR_MODE))
[0, 0, 0, 0, 0]
>>> print(Pxu.partition([(6,1,1,'2')],EXPR_MODE))
[0, 0, 0, 0, 0]

```

Note that when the option `REMOVE` is used, the base of the local analysis that generate the reduced pedigrad is modified so that the (partial) pedigrad that is produced is not $\mathbb{R}(L) \times u$ where L is the ambient local analysis, but a pedigrad of the form $\mathbb{R}(L \circ \iota) \times u$ where $L \circ \iota$ is a restriction of the local analysis L .

5.5.3. Agree. The method `.agree` takes a list of `SegmentObject` items and a list of non-negative integers (i.e. a partition) and returns all those segments contained in the first input whose images are equal to the second input. Categorically, this corresponds to pulling back what can be seen as the restriction of the pedigrad on the first input, say G , along the obvious functor $\mathbf{1} \rightarrow \mathbf{Uprt}(S)$ determined by the second input.

$$\begin{array}{ccc}
 \text{Agree}(u) & \dashrightarrow & G \\
 \downarrow & & \downarrow \subseteq \\
 & & \text{Seg}(\Omega | n) \\
 & & \downarrow \mathbb{R}(L) \\
 \mathbf{1} & \xrightarrow{u} & \mathbf{Uprt}(S)
 \end{array}$$

For illustration, let us consider the pedigrad defined in section 5.5.1. For convenience, we here recall the alignment file used thereof. The **red**, **purple** and **blue** characters are related to the examples given below. The **gray** characters are characters that are not included in the object `.base` of the `Pedigrad` item (see the beginning of section 5.5).

```

Align.fa
1 > A
2 CCCAGTTAG
3 > B
4 CCGATATAA
5 > C
6 GGCTTATAG
7 > D
8 GGCGTATAG
9 > E
10 ACCATATAA

```

The following example uses the method `.agree` to collect all the positions of the alignment that have matching characters between taxon A and taxon B (see the red characters above).

```

>>> u = EquivalenceRelation([[0,1]],4)
[0, 0, 1, 2, 3]

```

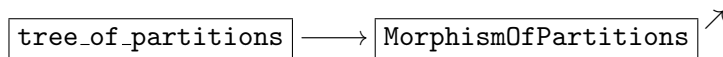
```
>>> Pxu = P.reduce(u,not(REMOVE))
>>> agreement = Pxu.agree(Pxu.base,u.quotient())
>>> for seg in agreement:
...     print("P("+str(seg.topology)+") = "+str(Pxu.partition(seg,SEGM_MODE)))
P([(0, 0)]) = [0, 0, 1, 2, 3]
P([(1, 1)]) = [0, 0, 1, 2, 3]
P([(3, 3)]) = [0, 0, 1, 2, 3]
```

We finish this section by giving the same types of example for taxon B with C (see green characters) and D with E (see blue characters).

```
>>> u = EquivalenceRelation([[1,2]],4)
[1, 0, 0, 2, 3]
>>> Pxu = P.reduce(u,not(REMOVE))
>>> agreement = Pxu.agree(Pxu.base,u.quotient())
>>> for seg in agreement:
...     print("P("+str(seg.topology)+") = "+str(Pxu.partition(seg,SEGM_MODE)))
P([(4, 4)]) = [0, 1, 1, 2, 3]
P([(5, 5)]) = [0, 1, 1, 2, 3]
>>> u = EquivalenceRelation([[3,4]],4)
[1, 2, 3, 0, 0]
>>> Pxu = P.reduce(u,not(REMOVE))
>>> agreement = Pxu.agree(Pxu.base,u.quotient())
>>> for seg in agreement:
...     print("P("+str(seg.topology)+") = "+str(Pxu.partition(seg,SEGM_MODE)))
P([(2, 2)]) = [0, 1, 2, 3, 3]
P([(4, 4)]) = [0, 1, 2, 3, 3]
P([(5, 5)]) = [0, 1, 2, 3, 3]
```

Presentation of the module AsciiTree.py

6.1. Description of tree_of_partitions



The function `tree_of_partitions` takes a list of partitions that can successively be related by morphisms of partitions and returns the actual lists of morphisms of partitions between these.

```

1 def tree_of_partitions(partitions):
2     """ the source code of this function can be found in top.py """
3     return the_tree
  
```

The input list should always start with the target of the first arrow, then present its source, which should also be the target of the next arrow, etc.

```

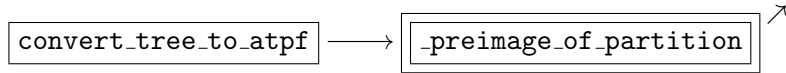
>>> l = [[0,0,0,0,0,0], [0,0,0,0,0,1], [0,0,2,2,2,1], [0,0,3,1,1,2],
         [0,1,2,3,4,5]]
>>> tree = tree_of_partitions(l)
>>> for i in range(len(tree)):
...     print(tree[len(tree)-1-i].source)
...     print("  |\n  | "+"arrow num "+str(len(tree)-i) + ": " + str(
        tree[len(tree)-1-i].arrow) + "\n  |\n  V")
...     print(tree[0].target)
[0, 1, 2, 3, 4, 5]
|
| arrow num 4:  [0, 0, 1, 2, 2, 3]
|
V
[0, 0, 1, 2, 2, 3]
|
| arrow num 3:  [0, 1, 1, 2]
|
V
  
```

```

[0, 0, 1, 1, 1, 2]
|
| arrow num 2:  [0, 0, 1]
|
V
[0, 0, 0, 0, 0, 1]
|
| arrow num 1:  [0, 0]
|
V
[0, 0, 0, 0, 0, 0]

```

6.2. Description of `convert_tree_to_atpf`

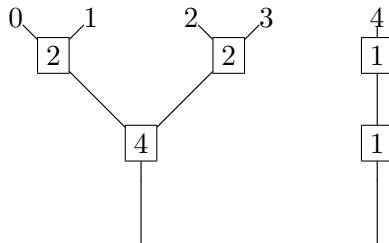


The function `convert_tree_to_atpf` takes a list of morphisms of partitions (as returned by the procedure `tree_of_partitions`) and converts it into its associated ascii tree pre-format (abbrev. atpf), which is defined as any ATPF term that be can constructed from the following double grammar rules.

The grammar terms	and their associated weights
$\text{ATPF} := [\text{Tree}_1, \text{Tree}_2, \dots, \text{Tree}_k];$	
$\text{Tree} := (\text{weight}(\text{Tree}), [\text{Tree}_1, \text{Tree}_2, \dots, \text{Tree}_k]),$	$\text{weight}(\text{Tree}) := \sum_i \text{weight}(\text{Tree}_i);$
$\text{Tree} := (\text{weight}(\text{Tree}), [\text{Leaf}_1, \text{Leaf}_2, \dots, \text{Leaf}_k]),$	$\text{weight}(\text{Tree}) := \sum_i \text{weight}(\text{Leaf}_i);$
$\text{Leaf} := (\text{weight}(\text{Leaf}), l), \text{ where } l \text{ is a list}$	$\text{weight}(\text{Leaf}) := \text{len}(l);$

The idea behind such construction is to give access to the number of leaves contained in each fork of a tree. This type of information will later be used to display trees with ascii characters on the console. For illustration, the following line gives an example of an atpf that describes the forest displayed below it.

```
atpf = [(4, [(2, [0, 1]), (2, [2, 3])]), (1, [(1, [4])])]
```



Note that the number of levels in the trees can be linked to what one could call the *depth* of the bracketing structure in the atpf. Specifically, we define the *depth* of an atpf according to the following recursive equations, relative to the definition of the terms given above.

```

depth(ATPF) := max{depth(Treei) | i = 1, ..., k};
depth(Tree) := max{depth(Treei) | i = 1, ..., k} + 1;
depth(Tree) := max{depth(Leafi) | i = 1, ..., k} + 1;
depth(Leaf) := 1;

```


The procedure `convert_tree_to_atpf` then returns a list and an integer, where the list is the atpf of the input (i.e. of the tree) and the integer is equal to the depth of the atpf, which is equal to `len(tree)+1`.

```
1 def _convert_tree_to_atpf(tree):
2     """ the source code of this function can be found in ctt.py """
3     return (the_atpf, len(tree)+1)
```

Since the depth is only returned for parsing purposes (see section 6.3 and section 6.4), the main task of the procedure `convert_tree_to_atpf` is to compute the atpf associated with the input list of composable morphisms of partitions by considering the successive preimages of each morphisms of partitions contained in the list.

For illustration, consider the following list of partitions:

```
>>> a = [0,1,0,0,0,0]
>>> b = [0,2,0,0,0,1]
>>> c = [0,4,2,3,3,5]
```

This list induces an obvious sequence of morphisms of partitions that can be constructed by the procedure `tree_of_partitions` (see section 6.1).

Since the lengths of these partitions is 6, the atpf will induce a higher level bracketing of the elements of the list `[0,1,2,3,4,5]`. To start with, one considers the preimage of the last partition `c` whose preimage is given by the following list of lists:

```
>>> _preimage_of_partition(c)
[[0], [1], [2], [3, 4], [5]]
```

To start constructing the atpf, we follow the recursive definition of the grammar of atpfs (given above) by taking the lists `[0]`, `[1, 2]`, `[3, 4]`, and `[5]` to be the initial values of the recursion so that the first level of the atpf is given by the following list, in which the red numbers are the weight of the list terms (see grammar rule for `Leaf`).

```
the_atpf = [(1, [0]), (1, [1]), (1, [2]), (2, [3, 4]), (1, [5])]
```

For the next level, we need to compute the preimage of the arrow encoding the morphism of partitions $c \rightarrow b$. Specifically, the arrow of the morphism $c \rightarrow b$ is as follows (when `c` and `b` are relabeled as `[0,1,2,3,3,4]` and `[0,1,0,0,0,2]`, respectively).

```
>>> f = MorphismsOfPartitions(c,b)
>>> for i in range(len(f.arrow)):
...     print("f: "+str(i)+" |-> "+str(f.arrow[i]))
f: 0 |-> 0
f: 1 |-> 1
f: 2 |-> 0
f: 3 |-> 0
f: 4 |-> 2
```

Since `b` has three elements in its image, the morphism f ($c \rightarrow b$) possesses three fibers, which are given by the following list of lists:

```
>>> fiber = _preimage_of_partition(f.arrow)
>>> print(fiber)
[[0, 2, 3], [1], [4]]
```

Following the atpf grammar, we now need to replace

```

fiber[0][0] with the_atpf[0] where fiber[0][0] = 0
fiber[0][1] with the_atpf[2] where fiber[0][0] = 2
fiber[0][2] with the_atpf[3] where fiber[0][0] = 3
fiber[1][0] with the_atpf[1] where fiber[0][0] = 1
fiber[2][0] with the_atpf[4] where fiber[0][0] = 4

```

so that the fiber is turned into the following list.

```

fiber = [[(1, [0]), (1, [2])], (2, [3, 4]), [(1, [1])], [(1, [5])]

```

To complete the construction of the next level of the atpf, there remains to compute the weight for each internal list. Precisely, we can see that

- the weight of [(1, [0]), (1, [2]), (2, [3, 4])] is $1+1+2 = 4$;
- the weight of [(1, [1])] is 1;
- the weight of [(1, [5])] is 1.

We then equip each list with its weight by using tuples, as shown below.

```

the_atpf = [(4, [(1, [0]), (1, [2]), (2, [3, 4])]), (1, [(1, [1])]), (1, [(1, [5])])]

```

We then repeat the previous procedure with, this time, the fiber of the morphism $b \rightarrow a$ and the earlier list so that the final atpf is of the following form.

```

the_atpf = [(5, [(4, [(1, [0]), (1, [2]), (2, [3, 4])]), (1, [(1, [5])])]), (1, [(1, [(1, [1])])])]

```

6.3. Description of `convert_atpf_to_atf`

The function `convert_atpf_to_atf` takes an atpf and its depth (see section 6.2) and returns the associated ascii tree format (abbrev. atf), which is a modified version of an atpf in which one subtracts all the weights by the rightmost weight of the next level, as shown by the following grammar rules

```

ATPF := [Tree1, Tree2, ..., Treek];
Tree := ((weight(Tree), weight(Tree) - weight(Treek)), [Tree1, Tree2, ..., Treek]);
Tree := ((weight(Tree), weight(Tree) - weight(Treek)), [Leaf1, Leaf2, ..., Leafk]);
Leaf := ((weight(Leaf), 0), l), where l is a list;

```

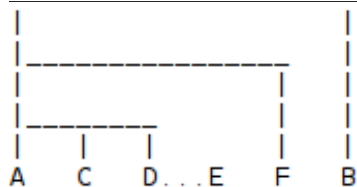
Note that this function uses the depth of the atpf in order to differentiate between the leaves and the intermediate levels of the tree, which require two different types of treatment.

```

1 def convert_atpf_to_atf(atpf, depth):
2     """ the source code of this function can be found in cata.py """
3     return the_atf

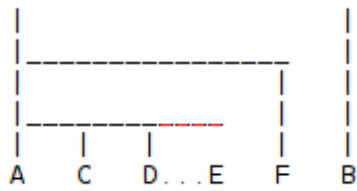
```

The reason for this is that the procedure `print_atf` is to display ascii trees whose trunks are on the left of the screen, as show below.



Subtracting the rightmost weights of the atpf from the weight placed below it, in the tree, allows `print_atf` (see section 6.4) to know when it needs to stop printing the horizontal level of the tree. Intuitively, the following pictures shows what atpf would look like without

conversion into an atf, where the red underscore symbols sticking out toward the right are symbolize the amount of weight subtracted in the atf.



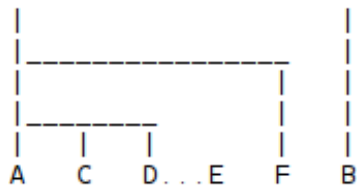
6.4. Description of `print_atf`

The function `print_atf` takes an atf and its depth and prints the ascii tree associated with the atf on the standard output.

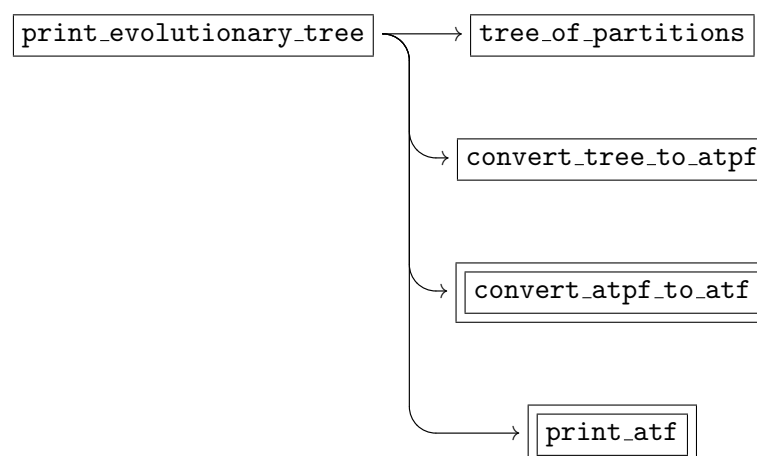
```
1 def print_atf(atf,depth):
2     """ the source code of this function can be found in patf.py """
```

The following example shows how `print_atf` can be combined with the procedures `convert_tree_to_atpf` and `convert_atpf_to_atf`.

```
>>> l = [[0,1,0,0,0,0], [0,2,0,0,0,1], [0,4,2,3,3,5]]
>>> tree = tree_of_partitions(l)
>>> atpf = convert_tree_to_atpf(tree)
>>> atf = convert_atpf_to_atf(*atpf)
>>> print_atf(atf,atpf[1])
```



6.5. Description of `print_evolutionary_tree`



The function `print_evolutionary_tree` takes a list of partitions between which a sequence of composable morphisms exists and returns the tree encoded by this sequence of morphisms.

```
1 def print_evolutionary_tree(atf,depth):
2     #Returns a sequence of morphisms of partitions.
3     tree = tree_of_partitions(partitions)
4     #Returns an ascii tree pre-format and its depth.
5     atpf = convert_tree_to_atpf(tree)
6     #Returns the ascii tree format of the atpf.
7     atf = convert_atpf_to_atf(*atpf)
8     #Prints the atf on the standard output.
9     print_atf(atf,atpf[1])
```

Bibliography

- [1] G. F. Estabrook, F. R. McMorris, (1980), *When is one estimate of evolutionary relationships a refinement of another?*, Journal of Mathematical Biology, Volume 10, Issue 4, pp 367–373.
- [2] J. Felsenstein, (2003), *Inferring Phylogenies*, Sinauer Associates, Sunderland, Massachusetts.
- [3] W. J. Le Quesne, (1 June 1969), *A method of selection of characters in numerical taxonomy*, Systematic Zoology, Volume 18, Issue 2, pp 201–205.
- [4] R. Tuyéras, *Categorical approach to tree inference*, [arXiv:????](#)
- [5] R. Tuyéras, *Category Theory for Genetics*, [arXiv:1708.05255](#)
- [6] E.O. Wilson, (1965), *A consistency test for phylogenies based on contemporaneous species*, Systematic Zoology, Volume: 14, pp 214–220.