**Morty v1.0**

**M**easurements **o**f Dive**r**si**ty**

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**1. Introduction**

**1.1. Overview**

Morty is a Python library for measuring the *alpha* (intragroup) and/or *beta* (inter-group) diversity of a *metacommunity* composed of two constituent *subcommunities*. Morty was initially developed to handle the very large communities represented by a person’s B- and T-cell repertoires (Arora and Arnaout, 2020), but can be used to measure alpha and beta diversity for any large or complex system.

**1.2. Background and Terminology**

*1.2.1. Diversity Indices*

At its core, diversity is simply a count: for example, a count of the number of unique species present in a population. However, in many situations a more accurate or useful representation of the population can be had by selectively upweight the more common species relative to the rarer ones (in a sense, to be “less distracted” by rare species). Hill’s framework (Hill, 1973) makes it simple to control this weighting through the *viewpoint parameter,* *q*: the investigator can set *q*=0 to perform a count with no upweighting, or set *q* to 0, 1, 2, …, ∞ (or any fractional value) to measure diversity with different weights. The resulting *diversity indices* are written *qD* and read "D-q" (e.g., *0D* is read as "D-zero"), and have simple and natural relationships to e.g. Shannon entropy (*q*=1), the Gini-Simpson index (*q*=2), the Berger-Parker index (*q*=∞), and others. These indices are also called *D numbers*, *Hill numbers*, or *effective numbers* (as in, for example, the "effective-number" form of Shannon entropy). The reader is referred to the Wikipedia [entry](https://en.wikipedia.org/wiki/Diversity_index) on diversity indices for further discussion.

*1.2.2 Diversity with Similarity*

In addition to using *q* to upweight higher-frequency species, it is often also useful to consider the *similarity* between pairs of species in measuring diversity. The idea here is that an ecosystem consisting of, say, 100 very different animal and plant species seems intuitively more diverse than an ecosystem that consists of 100 lichens; incorporating similarity allows *D*-number measures to reflect this intuition.

In the implementation here, this is done by constructing a similarity matrix, ***Z***, whose axes are the species and whose entries are the pairwise similarity between each pair of species, with 0 being completely unique and 1 being completely similar. Note that ignoring similarity is the same as setting ***Z*** to the identity matrix, ***I***  (i.e., ones on the diagonal and zero everywhere else). The result is a set of *D-*numbers for *similarity classes*, or *class diversity*, which we write *qDS* (Leinster and Cobbold’s *qD****Z***) instead of *qD*, where the *S* subscript denotes "with similarity." When comparing to *qDS*, *qD* can be considered *species* or *raw diversity*. The reader is referred to the work of Leinster and Cobbold and of Reeve *et al.* for development and details of the mathematical framework that we implement here (Leinster and Cobbold, 2012; Reeve et al., 2014).

Especially when ignoring similarity, diversity measured on samples from complex systems can substantially underestimate the diversity in the overall system from which the sample was taken. Morty corrects for this error using Recon (software available separately on GitHub; see below). Therefore, installation of Recon is required in order to use Morty. Including similarity decreases the effective number, decreasing the likelihood of error, especially for larger samples. The reader is referred to Kaplinsky and Arnaout for more details on Recon (Kaplinsky and Arnaout, 2016).

*1.2.3 Subcommunities and Metacommunities*

A *community* is a collection of individuals of different species. Each species *i* is present at a given frequency, *pi*. Morty calculates diveristy of individual communities and between pairs of communities. The two communities are referred to as *subcommunities*, and the two subcommunities together are referred to as a *metacommunity*. (In principle one can compare diversity among any number of subcommunities, but currently Morty is written for pairs.)

One chooses the subcommunities and the metacommunity based on the question at hand. For example, in immunology, we often have immune repertoires from two different individuals and desire some measure of the diversity within each repertoire, and of the overlap between them. In this case, each repertoire is a subcommunityand the two subcommunities together form the metacommunity, and our measures will be the alpha diversity of each subcommunity and the beta diversity between them. Note that alpha and beta diversity are independent of each other and therefore can be measured independently of each other (Jost, 2007).

There are different ways one can measure beta diversity (Chiu et al., 2014; Jost, 2007; Reeve et al., 2014). Following Reeve et al. 2014, Morty outputs how *representative* of the metacommunity each subcommunity is; if two subcommunities of equal size have nothing in common, then each constitutes half of the diversity of the metacommunity, and the normalized *representativeness* of each subcommunity for the metacommunity is 0.5. The normalized representativeness of subcommunity 1 for the metacommunity is written 1 ("rho-bar 1"), and that of subcommunity 2 is 2. Note that generally, 1≠2. Morty also outputs their average, .

In addition, also following Reeve et al., Morty outputs 1 ("beta-bar 1") and 2, which are the reciprocals of 1 and 2. The average of 1 and 2  is . The *i* values are interpreted as the effective number of distinct subcommunities "like" subcommunity *i* that the metacommunity contains. In the example above in which 1=0.5, 1=2, meaning that the metacommunity effectively contains two subcommunities like subcommunity 1. (As another example, if the U.S. state of California is subcommunity 1 and the United States is the metacommunity, 1 would indicate effectively how many distinct California-equivalents the United States comprises.) Thus, is the average effective number of distinct subcommunities present in the metacommunity.

**1.3. Features**

Morty was built to compare pairs of repertoires, communities composed of very large numbers of species (made up of different amino-acid sequences) (Arora and Arnaout, 2020). Because large numbers of species means a similarity matrix ***Z*** that is potentially too large to store or load into memory, Morty includes the ability to generate the similarity matrix ***Z*** on the fly for calculating both alpha and beta diversities, as described in 1.2.

**1.4. Citing Morty**

Please cite Arora, R., and Arnaout, R. (2020). Private Antibody Repertoires Are Public. BioRxiv 2020.06.18.159699.

**2. Installation**

**2.1. Availability**

Morty is publicly available on Github (https://github.com/ArnaoutLab/morty) subject to the terms in the license (Section 5).

**2.2. Requirements**

Morty requires:

* Python 3 (tested using Python version 3.8; earlier versions of Python 3 should work but have not been tested)
* The numpy, Cython and Levenshtein python libraries (which can be installed using standard methods, e.g. pip)
* simlib (written by us), which can be compiled from similib.pyx using setup.py (provided as part of this GitHub repository) using the command:

python3 setup.py build\_ext --inplace

In addition, measuring alpha diversity without similarity (***Z***=***I***) requires:

* recon\_v3.0.py, which is available on GitHub (<https://github.com/ArnaoutLab/Recon>)
* The scipy python library (which can be installed using standard methods, e.g. pip)

**2.3. Supported Platforms**

Morty has been tested on Macintosh OS X versions Mojave (10.14.6) and Catalina (10.15.5).

**2.4. Latest Version**

As of this writing, the latest version of Morty is 1.0.

**3. Operation**

This section describes the various modes for running Morty. It can be run to generate alpha diversity for one community, or beta diversity of two subcommunities (which together constitute the metacommunity).

**3.1 Alpha Diversity (-mo, --mode alpha)**

*3.1.1. Description*

Given a subcommunity in a text file as an input, -mo alpha outputs alpha diversity values for this subcommunity. The output includes both class (*qDS*) and species (*qD*) alpha-diversity values.

The user can provide their own pre-calculated similarity matrix, formatted in numpy format (.npy) or as a .csv file. Alternatively, the user can specify a python function to calculate similarity matrix on the fly using Morty (see §3.3.2 for details and §3.4.2.1 for example). If no similarity matrix or such function is provided, Morty will assume the species are protein sequences (strings written using the standard 20-amino-acid alphabet), and will calculate similarity using a multiplicatively independent model in which each single edit-distance difference between two species carries a cost *c* (recall the initial motivation behind Morty was calculating similarity in immune repertoires (Arora et al., 2018)).

*3.1.2. Usage*

python3 morty.py --mode alpha --input\_files "filename.txt" --master\_output\_dir output\_path --recon\_files "filename\_for\_recon.txt" --community\_names "subcommunity\_name" [-qs [0.,1.,...] -v]

*3.1.3. Input*

Morty takes filename.txt as input, passed using the -if/--input\_files command-line parameter. The filename must be enclosed between quotes. Each input file should consist of two columns, delimited by a tab character (\t). Rows must be delimited by a newline character (\n). The first column must contain the name of the species (or some other species data), and the second column an integer count giving the frequency of that species. Thus, each row should have the form:

species\tcount\n

(Here, \t and \n denote the tab and newline characters, respectively.) Note, if a species appears multiple times in the file, the frequencies will be added, not overwritten.

The input file to get the Recon estimate filename\_for\_recon.txt can be specified using the command line option -rf/--recon\_files. This may or may not be same as filename.txt.

*3.1.4. Output*

Calling Morty according to the command in §3.1.2 will append results to a master output file, specified by -ma/--master\_filename\_alpha which by default is alpha\_diversity\_master\_file.txt and is found in master\_output\_dir. If no such file exists, one will be created.

Each time Morty is run in alpha mode, its output is appended to this master output file, with one new line for each subcommunity. This output contains information in the following order, with each piece of information separated by a tab (\t):

1. A unique run\_id code that identifies the run (i.e., the specific instance of Morty’s execution)
2. Type of diversity being calculated (alpha in the case of alpha diversity)
3. Name of the subcommunity for which the alpha diversity is calculated (taken from filename in the list of filenames following the -if parameter, if no repertoire names are provided using the -cn/--community\_names parameter)
4. A tuple of two dictionaries (in standard Python input syntax), one for species diversities (*qD*) and one for class diversities (*qDS*). The dictionary keys are the *q* values and the dictionary values of are the corresponding *qD* (first dictionary) or *qDS* (second dictionary) alpha-diversity values
5. Timestamp at which the code was run
6. A copy of the command that was run (for easy future reference)

**3.2. Beta Diversity (-mo, --mode beta)**

*3.2.1 Description*

For two subcommunities that constitute a metacommunity, -mo/--mode beta outputs the following beta diversity values: (rho\_bar), (beta\_bar), (R\_bar) and (B\_bar). Note that two different values of rho\_bar and beta\_bar will be calculated—1 and 2, and 1 and 2—since there are two subcommunities being considered (see §1.2). For each of the above, values according to species (*qD*) and class diversity (*qDS*) measures will be calculated, for the *q* values indicated.

*3.2.2. Usage*

python3 morty.py --mode beta --input\_files "filename1.txt,filename2.txt" --master\_output\_dir output\_path --community\_names "subcommunity1\_name,subcommunity2\_name" [--list\_of\_qs [0.,1.,...] --verbose]

*3.2.3. Input*

Input files and formatting are as in §3.1.3. The only difference is that beta diversity expects two input files and their corresponding community names.

*3.2.4. Output*

Calling Morty according to the command in §3.2.2 will append results to a master output file, specified by -mb/--master\_filename\_beta which by default is beta\_diversity\_master\_file.txt and is found in master\_output\_dir. If no such file exists, one will be created.

Output is added to the output file line by line. Six new lines in total will be added for a single run in beta mode, with lines in the following order: B\_bar, R\_bar, beta\_bar for subcommunity 1, beta\_bar for subcommunity 2, rho\_bar for subcommunity 1, and rho\_bar for subcommunity 2. In turn, analogous to the output when run in alpha mode (§3.1.4), each line contains information in the following order, separated by a tab character:

1. A unique run\_id code that identifies the run
2. Type of beta diversity (B\_bar, R\_bar, etc.)
3. Names of the subcommunities. For beta\_bar and rho\_bar, the resulting diversity values are measured from the perspective of the subcommunity that is mentioned first
4. A tuple of two dictionaries (in standard Python syntax), one for species diversities (*qD*) and one for class diversities (*qDS*). The dictionary keys are the *q* values and the dictionary values of are the corresponding *qD* (first dictionary) or *qDS* (second dictionary) alpha-diversity values
5. Timestamp at which the code was run
6. The command that was run (for easy reference)

**3.3. Run Parameters**

*3.3.1 Required parameters*

|  |  |
| --- | --- |
| -mo, --mode | Options are alpha or beta |
| -if, --input\_files | One input file name/path for --mode alpha, and two input filenames/path for --mode beta where the filenames are separated by a comma. These files correspond to communities and contain species information and its count, in the format defined in §3.4.1. |
| -cn, --community\_names | Name of the subcommunities, separated by a comma. Order should match --input\_files. |
| -mod, --master\_output\_dir | User’s local directory where the alpha and beta master output files will be written. |

*3.3.2. Optional parameters*

|  |  |
| --- | --- |
| -qs, --list\_of\_qs | List of *q* values for which diversity is to be calculated. The default is [0., 0.5, 1., 1.5, 2., 2.5, 3., 3.5, 4., 4.5, 5., 5.5, 6., 6.5, 7., 7.5, 8., 8.5, 9., 9.5, 10., inf] Note the format: the *q*-values must be contained within square brackets (like a python list) and passed as strings (i.e. with quotes). |
| -Z, --user\_similarity\_matrix\_file | A numpy ([.npy format](https://numpy.org/doc/stable/reference/generated/numpy.lib.format.html)) or a comma-separated (.csv format) file that contains the user’s pre-calculated similarity matrix. The user must supply a text file that contains the column/row header by using the -uq/--unique\_species\_user parameter (see examples in §3.4.2 for implementation). The user must ensure that the order of the species is identical in both the column and the row header such that the diagonal of the similarity matrix is the same. This is should be an all-against-all square matrix. Note that the default is none and in this default setting, Morty will calculate the similarity matrix (see §3.1.1). |
| -uq, --unique\_species\_user | A text file that contains the name of the species, separated by \n, in the order that is used for constructing a similarity matrix, using -Z/--user\_similarity\_matrix\_file. The order of the species in this text file must be the order of the items in both the row and column dimensions. See §3.4.2 for examples. |
| -ZF, --user\_similarity\_function | A comma-separated string of length of 2 in the following order: (1) name of the user-defined python function that the to calculate all-against-all similarity, and (2) path to the .py file from which the python function will be imported. It is the user’s responsibility to ensure that the python function must accept only the list of unique species as an input, which is the column and row header of the similarity matrix, and return only the complete similarity matrix. See §3.4.2 for examples.  Note that the default is “get\_similarity\_matrix,path/to/get\_fast\_similarity.py” which has been optimized for immune repertoire amino acid sequences (see §3.1.1). |
| -v, --verbose | Turn on verbose output. |

**3.4 Examples**This section will demonstrate usage of various command-line options on some use-cases of Morty using example data. Note that when Morty is run (irrespective of the mode), both types of diversity metric—with and without similarity (also referred to as “class” and “species/raw” diversity)—are calculated. The example commands for data generation and Morty execution can also be found in morty/example.ipynb  
  
Note: Example data files generated here should exist in Example/ for a fresh download. Running this code will overwrite them.  
  
*3.4.1 Run Morty using default similarity function.*By default, Morty will use the similarity function written for amino-acid sequences used in Arora *et al.* 2018 and Arora & Arnaout 2020.   
  
Generate community input files with data resembling amino-acid sequences:  
**with** open("Examples/immune\_test\_1\_species\_to\_count.txt", "w") **as** f, open("Examples/immune\_test\_2\_species\_to\_count.txt", "w") **as** g, open("Examples/immune\_test\_3\_species\_to\_count.txt", "w") **as** h:

f.write("CARPQST\t1\n")

f.write("CARPQSP\t1")

g.write("CARPQST\t1\n")

g.write("MALMNN\t1")

h.write("WFALPCV\t1\n")

h.write("EEIYREEEEE\t1")  
  
Run alpha diversity on one of these communities:  
  
Command:  
python3 morty.py -cn 'immune\_test\_1' -mo alpha -if 'Examples/immune\_test\_1\_species\_to\_count.txt' -qs '[0., 1., 2., inf]' -rf 'Examples/immune\_test\_1\_species\_to\_count.txt' --master\_output\_dir 'Examples'  
  
Screen output:  
2020-08-14 07:50:13

run\_id: TptRd

Similarity matrix will be generated by:

Function: get\_similarity\_matrix

Imported from: /Users/rohitarora/Documents/GitHub/morty/get\_fast\_similarity.py

Output for run TptRd written to: Examples/alpha\_diversity\_master\_file.txt

2020-08-14 07:50:14  
  
The results of this run can either be viewed in real time by using --verbose option when running the command, or looking for the run\_id tmO6T in Examples/alpha\_diversity\_master\_file.txt. For a quick look, simply use grep.  
  
Command:  
grep TptRd Examples/alpha\_diversity\_master\_file.txt

Screen output:  
TptRd alpha immune\_test\_1 ({'0.0Ds': '1.325e+00', '1.0Ds': '1.325e+00', '2.0Ds': '1.325e+00', 'infDs': '1.325e+00'}, {'0.0D': '8.100e+01', '1.0D': '8.100e+01', '2.0D': '8.100e+01', 'infD': '8.100e+01'}) 2020-08-14 07:50:13 python morty.py -cn immune\_test\_1 -mo alpha -if Examples/immune\_test\_1\_species\_to\_count.txt -qs [0., 1., 2., inf] -rf Examples/immune\_test\_1\_species\_to\_count.txt --master\_output\_dir Examples

In this community, the two species look very similar (per this similarity metric), and therefore the effective diversity with similarity is closer to 1. This value is closer to 2, as the species are more dissimilar. User is encouraged to repeat this example with the remaining two example community data files.  
  
Now, we run beta diversity on pairs of these communities.  
  
Command:  
python3 morty.py -cn 'immune\_test\_1,immune\_test\_2' -mo beta -if "Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_2\_species\_to\_count.txt" -qs '[0.0]' --verbose --master\_output\_dir 'Examples'  
  
Screen output:  
2020-08-14 08:08:12

run\_id: BmIWe

Similarity matrix will be generated by:

Function: get\_similarity\_matrix

Imported from: /Users/rohitarora/Documents/GitHub/morty/get\_fast\_similarity.py

Output for run BmIWe written to: Examples/beta\_diversity\_master\_file.txt

2020-08-14 08:08:12  
  
As discussed above, results of this run can be viewed in real time by using the --verbose option in the command or by using grep:  
  
Command:  
grep BmIWe Examples/beta\_diversity\_master\_file.txt

Screen output:

BmIWe B\_bar immune\_test\_1 immune\_test\_2 {'0.0Ds': '1.230e+00', '0.0D': '1.333e+00'} 2020-08-14 08:08:12 python morty.py -cn immune\_test\_1,immune\_test\_2 -mo beta -if Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_2\_species\_to\_count.txt -qs [0.0] --master\_output\_dir Examples

BmIWe R\_bar immune\_test\_1 immune\_test\_2 {'0.0Ds': '8.177e-01', '0.0D': '7.500e-01'} 2020-08-14 08:08:12 python morty.py -cn immune\_test\_1,immune\_test\_2 -mo beta -if Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_2\_species\_to\_count.txt -qs [0.0] --master\_output\_dir Examples

BmIWe beta\_bar immune\_test\_1 immune\_test\_2 {'0.0Ds': '1.323e+00', '0.0D': '1.333e+00'} 2020-08-14 08:08:12 python morty.py -cn immune\_test\_1,immune\_test\_2 -mo beta -if Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_2\_species\_to\_count.txt -qs [0.0] --master\_output\_dir Examples

BmIWe beta\_bar immune\_test\_2 immune\_test\_1 {'0.0Ds': '1.137e+00', '0.0D': '1.333e+00'} 2020-08-14 08:08:12 python morty.py -cn immune\_test\_1,immune\_test\_2 -mo beta -if Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_2\_species\_to\_count.txt -qs [0.0] --master\_output\_dir Examples

BmIWe rho\_bar immune\_test\_1 immune\_test\_2 {'0.0Ds': '7.558e-01', '0.0D': '7.500e-01'} 2020-08-14 08:08:12 python morty.py -cn immune\_test\_1,immune\_test\_2 -mo beta -if Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_2\_species\_to\_count.txt -qs [0.0] --master\_output\_dir Examples

BmIWe rho\_bar immune\_test\_2 immune\_test\_1 {'0.0Ds': '8.796e-01', '0.0D': '7.500e-01'} 2020-08-14 08:08:12 python morty.py -cn immune\_test\_1,immune\_test\_2 -mo beta -if Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_2\_species\_to\_count.txt -qs [0.0] --master\_output\_dir Examples

Every beta run generates 6 entries in the output file, each corresponding to one of the beta diversity parameters, as discussed in §3.2.1. The parameter that corresponds to overlap is R\_bar. In this run, the two communities share a species, and therefore R\_bar with similarity is relatively high. We expect this parameter to be lower if we measure beta diversity when two disjoint communities are compared, as we show in the following run. R\_bar is closer to the minimum value of 0.5 (min(R\_bar) is 1/*n* where *n* is the number of communities; here *n=2*):

Command:  
python3 morty.py -cn 'immune\_test\_1,immune\_test\_3' -mo beta -if "Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_3\_species\_to\_count.txt" -qs '[0.0]' --master\_output\_dir 'Examples'  
  
Screen output:  
2020-08-14 08:31:45

run\_id: BoxSY

Similarity matrix will be generated by:

Function: get\_similarity\_matrix

Imported from: /Users/rohitarora/Documents/GitHub/morty/get\_fast\_similarity.py

Output for run BoxSY written to: Examples/beta\_diversity\_master\_file.txt

2020-08-14 08:31:45

Access the R\_bar entry for this run.  
  
Command:  
grep BoxSY Examples/beta\_diversity\_master\_file.txt | grep R\_bar

Screen output:  
BoxSY R\_bar immune\_test\_1 immune\_test\_3 {'0.0Ds': '5.083e-01', '0.0D': '5.000e-01'} 2020-08-14 08:31:45 python morty.py -cn immune\_test\_1,immune\_test\_3 -mo beta -if Examples/immune\_test\_1\_species\_to\_count.txt,Examples/immune\_test\_3\_species\_to\_count.txt -qs [0.0] --master\_output\_dir Examples

*3.4.2 Run Morty with a custom similarity matrix or function*Since the default similarity function is optimized for immune repertoires, which may not be useful for other systems, Morty allows users to either (*i*) pre-calculate a similarity matrix and supply it to Morty, or (*ii*) point Morty to a python function which can be used to calculate similarity on the fly. We demonstrate use of these options here on alpha diversity calculations in a non-immune repertoire system.  
  
Generate data for a community from the iris dataset.  
  
**import** numpy **as** np  
**import** pandas **as** pd  
**from** sklearn.datasets **import** load\_iris

iris = load\_iris()

iris\_data = pd.DataFrame(data= np.c\_[iris['data'], iris['target']],

columns= iris['feature\_names'] + ['target'])

iris\_input = iris\_data[['sepal length (cm)', 'sepal width (cm)']]

iris\_input.to\_csv('Examples/iris\_input.csv')

# Process input csv to generate community input files, and files with unique species which defines the species order for the similarity matrix.  
**def** process\_input(iris\_csv\_file, species\_to\_count\_file, unique\_species\_file):  
 processed\_input\_list=[] **with** open(iris\_csv\_file) **as** f, open(species\_to\_count\_file, "w") **as** g, open(unique\_species\_file, "w") **as** h: **for** line **in** f: **if** "sepal" **in** line: **continue** id\_, sepal\_length, sepal\_width = str.strip(line).split(",")  
 out\_str = "%s\_%s\_%s" % (id\_, sepal\_length, sepal\_width)  
 processed\_input\_list.append((out\_str))  
 g.write("%s\t1\n" % id\_)  
 h.write("%s\n" % id\_) **return** processed\_input\_list

iris\_input\_list = process\_input('Examples/iris\_input.csv', 'Examples/iris\_input\_species\_to\_count.txt', 'Examples/iris\_input\_uniq\_species.txt')

In the context of this example, we define similarity between two species as the euclidean distance between sepal length and width, and write an example function to that end.

**from** scipy.spatial **import** distance  
  
**def** get\_euclidean\_distance(species\_list):  
 """This function calculates all-against-all euclidean distance   
 between 2-D coordinates of two species"""   
  
 species\_list = [ i.split("\_") **for** i **in** species\_list ]  
  
 similarity\_list=[]  
 **for** species\_1, x1, y1 **in** species\_list:  
 similarity\_for\_this\_species=[]

**for** species\_2, x2, y2 **in** species\_list:

**if** species\_1 == species\_2: sim\_ = 1.

**else**: sim\_ = distance.euclidean((float(x1),float(y1)), (float(x2), float(y2)))

similarity\_for\_this\_species.append(sim\_)

similarity\_list.append(similarity\_for\_this\_species)

similarity\_matrix = np.array(similarity\_list)

**return** similarity\_matrix

We write this function to Examples/euclidean\_similarity.py to access it later.

*3.4.2.1. User-entered similarity matrix*

Now, we calculate the similarity matrix for this iris community outside of Morty and then supply this matrix to Morty.

similarity\_matrix\_input = get\_euclidean\_distance(iris\_input\_list)  
np.save("Examples/similarity\_matrix\_input.npy", similarity\_matrix\_input)

Command:  
python3 morty.py -cn "iris\_input" -mo alpha -**if** "Examples/iris\_input\_species\_to\_count.txt" -qs "[0., 1., 2., inf]" -rf "Examples/iris\_input\_species\_to\_count.txt" -Z "Examples/similarity\_matrix\_input.npy" -uq "Examples/iris\_input\_uniq\_species.txt" --master\_output\_dir "Examples"  
  
Screen output:  
2020-08-14 10:43:54

run\_id: YYphl

Note: Using user-generated similarity matrix.

You have chosen to use a user-generated similarity matrix.

User-generated similarity matrix file: Examples/similarity\_matrix\_input.npy

User-generated unique species order file: Examples/iris\_input\_uniq\_species.txt

Output for run YYphl written to: Examples/alpha\_diversity\_master\_file.txt

2020-08-14 10:43:55

Access the results in the output file.  
  
Command:  
grep YYphl Examples/alpha\_diversity\_master\_file.txt

Screen output:  
YYphl alpha iris\_input ({'0.0Ds': '9.070e-01', '1.0Ds': '8.883e-01', '2.0Ds': '8.677e-01', 'infDs': '4.422e-01'}, {'0.0D': '6.075e+03', '1.0D': '6.075e+03', '2.0D': '6.075e+03', 'infD': '6.075e+03'}) 2020-08-14 10:43:54 python morty.py -cn iris\_input -mo alpha -if Examples/iris\_input\_species\_to\_count.txt -qs [0., 1., 2., inf] -rf Examples/iris\_input\_species\_to\_count.txt -Z Examples/similarity\_matrix\_input.npy -uq Examples/iris\_input\_uniq\_species.txt --master\_output\_dir Examples  
  
*3.4.2.2. Calculating similarity matrix on the fly (user-defined similarity function)*

Now we repeat this calculation, but instead of supplying Morty with the similarity matrix, we point Morty to the function and let it calculate this matrix in real time.

Command:  
python3 morty.py -cn "iris\_input" -mo alpha -**if** "Examples/iris\_input\_species\_to\_count.txt" -qs "[0., 1., 2., inf]" -rf "Examples/iris\_input\_species\_to\_count.txt" -ZF "get\_euclidean\_distance,Examples/euclidean\_similarity.py" --master\_output\_dir "Examples"  
  
screen output:

2020-08-14 11:12:32

run\_id: h3xTD

Similarity matrix will be generated by:

Function: get\_euclidean\_distance

Imported from: Examples/euclidean\_similarity.py

Output for run h3xTD written to: Examples/alpha\_diversity\_master\_file.txt

2020-08-14 11:12:34

Command:  
grep h3xTD Examples/alpha\_diversity\_master\_file.txt  
  
Screen output:  
h3xTD alpha iris\_input ({'0.0Ds': '9.070e-01', '1.0Ds': '8.883e-01', '2.0Ds': '8.677e-01', 'infDs': '4.422e-01'}, {'0.0D': '6.075e+03', '1.0D': '6.075e+03', '2.0D': '6.075e+03', 'infD': '6.075e+03'}) 2020-08-14 11:12:32 python morty.py -cn iris\_input -mo alpha -if Examples/iris\_input\_species\_to\_count.txt -qs [0., 1., 2., inf] -rf Examples/iris\_input\_species\_to\_count.txt -ZF get\_euclidean\_distance,Examples/euclidean\_similarity.py --master\_output\_dir Examples

Note that the alpha diversity results from YYphl and h3xTD are identical. That is what we should expect since the measurment is on the same data, the only difference being that in the former case, we calculated the similarity matrix outside of Morty. This gives the user the flexibility to evaluate the similarity matrix with a function of their choice, even if the function is not compatible with Morty. In the latter case, we pointed Morty to the same function, since it is already compatible with Morty.

**3.5. Unit Testing (-u, --unit\_test)**

*3.5.1 Description*

Performs internal checks to ensure that the script runs without error.

*3.5.2 Usage*

python3 morty.py -u

*3.5.3 Output*

The above command line will test alpha class diversity, beta class diversity, and beta species diversity for q = [0.0, 1.0, 2.0, 3.0, 3.5] and print out the results ("pass" or otherwise warning signs) to standard output. To test species alpha diversity, the unit test of recon\_v3.0.py needs to be run (not run by Morty).

**4. Contact Information**  
  
Questions, comments, and other correspondence should be addressed to Ramy Arnaout at rarnaout@gmail.com.

**5. License**

Morty is made available under the GNU Affero General Public License v3.0 (GNU AGPLv3) licence. Last Updated August 18, 2020.

**6. References**

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