

Project Title: Unit Verification and Validation  
Plan for Kaplan

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# 1 Revision History

Date		Version	Notes
December 3rd, 2018 (Monday)		1.0	First draft

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## 2 Symbols, Abbreviations and Acronyms

symbol	description
T	Test
RNS	Random Number Seed
MG	Module Guide
SRS	Software Requirements Specification
MIS	Module Instance Specification
gac	Genetic Algorithm Control (Module)
CI	Continuous Integration
HPC	High-performance computing
pmem	population member (of ring)
PEP	Python enhancement proposal (from PEP8)

This document provides unit testing cases for each of the modules, except where the module uses an external library (geometry, energy, and rmsd). The purpose of the document is given, as well as the scope of the covered tests. This document is meant to be read alongside the MIS document, since the MIS provides the outputs and inputs of each function and method. The tools needed to run the tests is discussed in Section 4.2.

## 3 General Information

### 3.1 Purpose

This document will identify what testing is going to be done on Kaplan. This document is different from the System VnV Plan in that it considers each module as already written according to the Module Instance Specification (MIS) document. Since each function, method, class, and algorithm has been given, they can be tested using a white box approach, where the inputs, outputs, and transitions between the inputs and outputs are known.

[\[Identify software that is being unit tested \(verified\). —SS\]](#)

### 3.2 Scope

The Hardware-Hiding module will not be covered in this unit testing plan, since the developer does not have any means or the expertise needed to properly test such a module. As mentioned in the System VnV Plan, the energy, geometry, and RMSD modules will be tested by running the tests for the libraries that these modules import.

The most important modules to test are the two input modules: Molecule Input and GA Input. Since this program is likely to be run on a server with multiple iterations of different molecules, checking of the inputs before submission is very important. If the errors in setup are caught early, jobs (that cannot actually run) can be prevented from sitting in queues on the high-performance computing (HPC) clusters.

It will be important to test the Crossover & Mutation (mutations) module, since this is how the solutions will evolve over time. If the new population members are not correctly initialized (or if they are copies of the old population members without any mutation), then the optimization will not work and running the program would have been a waste of resources and time.

The GA Input module (gac) is probably the least important module to test, since it is only running other modules in a sequence. Basic tests, such as: 1. was the Ring initialized, 2. did the Ring change as a result of running the gac module, 3. were the outputs and inputs called, can be done on gac if necessary.

Other modules that will be tested include: fitg, tournament, ring, pmem, and output.

[What modules are outside of the scope. If there are modules that are developed by someone else, then you would say here if you aren't planning on verifying them. There may also be modules that are part of your software, but have a lower priority for verification than others. If this is the case, explain your rationale for the ranking of module importance. —SS]

## 4 Plan

### 4.1 Verification and Validation Team

Mulder, c'est moi.

### 4.2 Automated Testing and Verification Tools

The Ayers' Lab group has a linter called Cardboardlint <https://github.com/theochem/cardboardlint>. If time permits, this linter can be joined with Travis CI (Continuous Integration) to enable static code checking (for PEP8) and code coverage. Prior to enabling this linter, the following libraries can be added to the Travis build:

- coverage
- pylint
- nosetests (also called nose)
- pycodestyle
- pydocstyle (with numpy convention)

The report generated by Travis CI will be uploaded to the VnV Report. The .travis.yml file will be added to the Kaplan repository so the installation

and verification process can be monitored. Eventually the program will be made into a conda package itself, then a conda environment can be used for an easy installation process.

[What tools are you using for automated testing. Likely a unit testing framework and maybe a profiling tool, like ValGrind. Other possible tools include a static analyzer, make, continuous integration tools, test coverage tools, etc. Explain your plans for summarizing code coverage metrics. —SS]

### 4.3 Non-Testing Based Verification

Some jupyter notebooks (<http://jupyter.org/>) will be made by the developer as a way to test the geometry module and the energy module. These notebooks are an easy way to ensure that the imported libraries behave as intended with the Kaplan code and that the developer has correctly interpreted the other libraries' documentation and usage. These notebooks will be helpful later-on as documentation, in case the user wants to manipulate the energy calculations and/or the parts of the geometry that are optimized.

There will be a code review with lab members Kumru Dikmenli and Xiaomin Huang during a weekly meeting. Once the SRS has been updated to address comments from Prof. Paul Ayers (supervisor), there will also be a code walk-through with the supervisor.

## 5 Unit Test Description

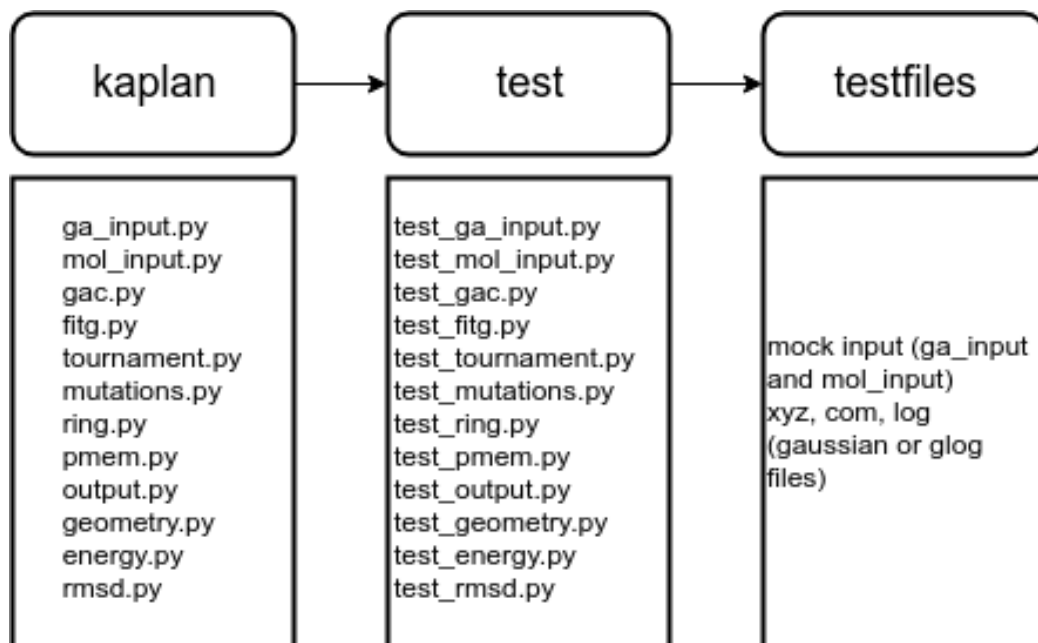


Figure 1: The directory structure for the unit testing. An arrow from A to B implies that B is a subdirectory of A.

The directory structure for testing is as follows (see Figure 1). First we have the *kaplan* directory that contains the code. Within this directory, there is the *test* subdirectory. This *test* directory has a test file (.py) for each module. Within the *test* directory there is a *testfiles* subdirectory, which contains mostly molecule input and output, as well as kaplan-formatted input for the two input modules. Each test file has the naming convention: test\_module\_name.py and each function within each of the test files has the naming convention: test\_function\_name.py. If the test is for a class, then the naming convention for the test becomes: test\_Classname.methodname.py.

[I wasn't sure where to put the above information. It seems relevant to my documentation. Also, I think the naming convention is actually required by nosetests, but I could be wrong. —JG]

[Reference your MIS and explain your overall philosophy for test case selection. —SS]



## 5.1 Tests for Functional Requirements

For many of these tests, the numpy python library testing module will be utilized. Within that testing module, there is an `assert_raises` function. This function is used to ensure that the correct errors are raised for a given function call and function inputs.

[Most of the verification will be through automated unit testing. If appropriate specific modules can be verified by a non-testing based technique. That can also be documented in this section. —SS]

### 5.1.1 GA Input Module

[I couldn't figure out how to make the mref work in this document, even when the MG was added as an external document in the tex file. Any suggestions? —JG]

From Section 6 in the MIS, we have a set of unit tests for the GA Input Module. The purpose of these tests is to ensure that an error is raised if the user does one of the following:

1. Provides a file name that does not exist in the given directory.
2. Forgets to include an input parameter or misspells an input parameter.
3. Puts the same input parameter twice or adds too many input parameters.
4. Provides input values that do not satisfy the program constraints (for example, `num_slots < num_filled`).
5. Provides input values of the wrong type (for example, `num_mevs` is equal to 3.2, which doesn't make physical sense).

The tests should also confirm that correct input can pass without raising errors. A couple of valid and invalid input files will be available in the `testfiles` directory (see Figure 1). The valid input files can also act as example input for instructional purposes.

[I might need to add a test to see what happens when the user tries to open a file that they do not have read permissions for. However, I can't think of a reasonable case where this would happen. I'm also not sure how to create that error without trying to access someone else's files... I'll assume the interpreter error message will be sufficient. —JG]

As per the MIS (Section 6), there are two functions within the `ga.input` module: `read_ga.input`, which checks the number of inputs and ensures the file can be opened (file exists), and `verify_ga.input`, which checks that all of the input parameters have been given and that their values are of the right type and within the necessary bounds.

[Include a blurb here to explain why the subsections below cover the module. References to the MIS would be good. You will want tests from a black box perspective and from a white box perspective. Explain to the reader how the tests were selected. —SS]

# 1. `test_read_ga.input`

Type: automatic

Initial State: None

Input:

file name	error raised	test covered
<code>example_ga.input_file.txt</code>	None	good input does not raise an error
<code>example2_ga.input_file.txt</code>	None	good input can have extra whitespace and is impervious to capitalization
<code>no-such-file</code>	<code>FileNotFoundError</code>	file does not exist and therefore cannot (and should not) be opened
<code>bad1_ga.input_file.txt</code>	<code>ValueError</code>	<code>num_mevs</code> appears twice (too many input parameters)
<code>bad2_ga.input_file.txt</code>	<code>ValueError</code>	<code>num_atoms</code> is not in the input file (missing input parameter)

Output: None

Test Case Derivation: None

How test will be performed: If the `read_ga_input` function can be called with the good input files without raising an error, then the test is assumed to pass. Conversely, if the bad inputs raise the expected error as per the `assert_raises` function, then the test will pass.

## 2. `test_verify_ga_input`

Type: automatic

Initial State: None

Input:

file name or change in ga_input_dict*	error raised	test covered
example_ga_input_file.txt	None	good input does not raise an error
example2_ga_input_file.txt	None	good input can have extra whites- pace and is impervious to capitaliza- tion
bad3_ga_input_file.txt	ValueError	num_geoms is spelt wrong (input file does not contain all of the expected parameters)
num_slots = -1	AssertionError	num_slots must be positive
num_filled = 150	AssertionError	num_filled must be $\leq$ num_slots
num_mevs = -300	AssertionError	num_mevs must be positive
num_swaps = 20	AssertionError	num_swaps must be $\leq$ num_geoms
num_muts = 30	AssertionError	num_muts must be $\leq$ num_atoms-3
num_geoms = -2	AssertionError	num_geoms must be positive
num_atoms = 2	AssertionError	num_atoms must be $\geq$ 4
fit_form = 1	AssertionError	fit_form will only be implemented with one function initially; only fit_form = 0 is accepted
pmem_dist = 57	AssertionError	pmem_dist has to be $\leq$ 1/2*num_slots (rounded down)
coef_energy = -5	AssertionError	coef_energy must be positive
coef_rmsd = -5	AssertionError	coef_rmsd must be positive
t_size = 25	AssertionError	t_size must be $\leq$ num_filled

\* for changes to the ga\_input\_dict, the other parameters are based on the contents of the example\_ga\_input\_file.txt, where we have:

```
ga_input_dict = {'num_mevs': '1000 ', 'num_slots': '100 ',
                  'num_filled': '20 ', 'num_geoms': '3 ',
                  'num_atoms': '10 ', 't_size': '7 ',
                  'num_muts': '3 ', 'num_swaps': '1 ',
                  'pmem_dist': '5 ', 'fit_form': '0 ',
                  'coef_energy': '0.5 ', 'coef_rmsd': '0.5 '}
```

Output: None

Test Case Derivation: None

How test will be performed: as with the tests for `read_ga_input`, these tests will use the `numpy.testing.assert_raises` function to ensure that the correct errors are raised. The `verify_ga_input` function is also responsible for checking the types of the input; if a value (for example, `num_geoms`) is supposed to be an integer and python cannot convert the input to an integer, then an error will be raised. This is not covered by the unit tests, since it is assumed that trying to use incorrect types (a string as an integer) will yield an obvious error.

### 5.1.2 Molecule Input Module

The `mol_input` module will be tested in a similar fashion to the `ga_input_module` (Section 5.1.1), with the added tests as needed to check the input geometry, QCM, and BS. As per the module uses hierarchy in the module guide document, the `mol_input` module uses the geometry and energy modules. Therefore, to test this module properly, both of these other modules must be adequately tested as well.

[Include a blurb here to explain why the subsections below cover the module. References to the MIS would be good. You will want tests from a black box perspective and from a white box perspective. Explain to the reader how the tests were selected. —SS]

#### 1. `test_read_mol_input`

Type: automatic

Initial State: None

Input:

file name	error raised	test covered
example_mol_input_file.txt	None	good input does not raise an error
example2_mol_input_file.txt	None	good input can have extra whitespace and is impervious to capitalization
no-such-file	FileNotFoundError	file does not exist and therefore cannot (and should not) be opened
bad1_mol_input_file.txt	ValueError	qcm appears twice (too many input parameters)
bad2_mol_input_file.txt	ValueError	struct_type is not in the input file (missing input parameter)

Output: None

Test Case Derivation: None

How test will be performed: `numpy.testing.assert_raises`.

## 2. test\_verify\_mol\_input

Type: automatic

Initial State: None

Input:

file name or change in mol_input_dict*	error raised	test covered
example_mol_input_file.txt	None	good input does not raise an error
example2_mol_input_file.txt	None	good input can have extra whites- pace and is impervious to capitaliza- tion
bad3_mol_input_file.txt	ValueError	struct_input is spelt wrong (input file does not contain all of the ex- pected parameters)
qcm = "not-a-method"	ValueError	qcm must be available in the chosen program
basis = "not-a-basis"	ValueError	basis must be available in the chosen program
struct_input = "very-bad- smiles-string"	ValueError	SMILES string must be valid
struct_type = "not-an- option"	AssertionError	struct_type must be one of: "com", "glog", "xyz", "smiles", "name", or "cid"
prog = "unavailable-prog"	AssertionError	prog must equal "psi4"
charge = "0.34"	ValueError	charge must be an integer
multip = -2	AssertionError	multiplicity must be $\geq 0$

\* for changes to the mol\_input\_dict, the other parameters are based on the contents of the example\_mol\_input\_file.txt, where we have:

```
mol_input_dict = {'qcm': 'hf', 'basis': 'sto-3g',
                  'struct_input': 'C=CC=C',
                  'struct_type': 'smiles', 'prog': 'psi4',
                  'charge': '0', 'multip': '1'}
```

Output: None

Test Case Derivation: None

How test will be performed: numpy.testing.assert\_raises.

### 5.1.3 GA Control Module

[Include a blurb here to explain why the subsections below cover the module. References to the MIS would be good. You will want tests from a black box perspective and from a white box perspective. Explain to the reader how the tests were selected. —SS]

#### 1. test\_run\_kaplan

Type: automatic

Initial State: None

Input: the run\_kaplan function will be tested with two sets of inputs, one from example\_ga\_input\_file.txt and example\_mol\_input\_file.txt and the other from example2\_ga\_input\_file.txt and example2\_mol\_input\_file.txt. The contents of these two files can be seen below. Both sets of files are examples of good inputs. Note: the contents below has already passed verification and therefore the floating point and integer numbers are no longer strings.

```
{'num_mevs': 1000, 'num_slots': 100, 'num_filled': 20,
'num_geoms': 3, 'num_atoms': 10, 't_size': 7,
'num_muts': 3, 'num_swaps': 1, 'pmem_dist': 5,
'fit_form': 0, 'coef_energy': 0.5, 'coef_rmsd': 0.5}
{'qcm': 'hf', 'basis': 'sto-3g',
'struct_input': 'C=CC=C', 'struct_type': 'smiles',
'prog': 'psi4', 'charge': 0, 'multip': 1}
```

```
{'num_mevs': 500, 'num_slots': 50, 'num_filled': 10,
'num_geoms': 2, 'num_atoms': 21, 't_size': 5,
'num_muts': 5, 'num_swaps': 0, 'pmem_dist': 24,
'fit_form': 0, 'coef_energy': 0.75, 'coef_rmsd': 0.25}
{'qcm': 'hf', 'basis': 'sto-3g',
'struct_input': 'caffeine', 'struct_type': 'name',
'prog': 'psi4', 'charge': 0, 'multip': 1}
```

Output: None

Test Case Derivation: None



How test will be performed: This test will call `run_kaplan` with the two sets of inputs. For each set of input, assert that an output file was generated, and that the final ring has population members (pmems) in it with non-zero age. Since it is impossible for all of the pmems to be generated in the last tournament, then at least one pmem must have an age greater than zero.

This test may require updating in the future if extinction operators are added to the ring. Since the extinction operators kill off a certain number of pmems, if a refill of the ring is called at the last mating event, then it will be difficult to tell if the ring has undergone any changes as a result of the optimization (since all pmems would then have 0 age). In this case, it might be possible to keep track of when a refill is triggered and assert that there if a pmem with non-zero age, given that a refill was not performed on the last mating event.

#### 5.1.4 *Fit<sub>G</sub>* Module

From the MIS document in Section 9, there are 3 access routines for the *Fit<sub>G</sub>* module: `sum_energies`, `sum_rmsds`, and `calc_fitness`. There is one local function (a generator called `all_pairs_gen`) that is used by the `sum_rmsds` function. Since this is a local function, it cannot be tested. However, the tests for `sum_rmsds` should be thorough to ensure that the local function works as intended.

As per Table 4 in the SRS document, the fitness function should return a positive value. The `coef_energy` and `coef_rmsd` values must be positive (which is checked by the `ga_input` module). The only case where the answer might be negative is if the `fit_form` included a logarithm (since  $\log(n) \leq 0$  for  $n \leq 1$ ). The only `fit_form` in use is a simple linear combination and therefore cannot be negative (unless the functions do not behave as intended).

The `calc_fitness` function is trivial to test, since the `sum_energy` and `sum_rmsd` values can be fixed. All that should be tested is that the number returned is as calculated by hand.

The cases where the `sum_rmsds` returns zero would be easy to test, as the inputs would include a single geometry copied multiple times. It would also be easy to test the returned value of the rmsd calculation with two dissimilar geometries. However, checking that all possible pairs were calculated and summed may require a spreadsheet or jupyter notebook to properly test. A test should also be done to ensure that two geometries rotated and/or

translated in space return an rmsd of zero. Of course, the value actually returned will be non-zero (rounding error and floating point imprecision), but it should be zero within a very small tolerance. This last test is not as important, as it is covered by the rmsd package tests already.

For the energy tests, it would require running psi4 externally and summing the energies for a set of geometries. Once this setup has been done, then the test can be automated by simple assertion that the calculated value is equal to the expected value for fitness.

If the program used to calculate energies or rmsd values is changed or the fit.form is changed, then more tests would be required to ensure that the correct output is calculated by the *Fit<sub>G</sub>* module. However, these outputs should be similar and should be somewhat robust within an arbitrarily small tolerance.

These tests will not have the same requirements as the inputs to Kaplan, as it is still meaningful to calculate energies for molecules of less than 4 atoms. Since energy calculations for smaller molecules run more quickly, then molecular hydrogen can be used for the tests with varying bond lengths.

[Include a blurb here to explain why the subsections below cover the module. References to the MIS would be good. You will want tests from a black box perspective and from a white box perspective. Explain to the reader how the tests were selected. —SS]

#### 1. test\_sum\_energies

Type: automatic (after manual calculations have been performed)

Initial State: None

Input: molecular hydrogen ( $H_2$ ) with 5 bond lengths, with charge = 0, multip = 1, method = “hf”, and basis = “sto-3g”.

test covered	files involved	description
energy summation is correct and positive	H2-1A.xyz, H2-2A.xyz, H2-3A.xyz, H2-4A.xyz, H2-5A.xyz	assert that energy returned is positive and equal to the magnitude calculated using psi4 outside of Kaplan

Output:

From the jupyter notebook using psi4 to calculate energies of 5 geometries of molecular hydrogen, we have (starting with 1Å up to 5Å):

```
energies = [-1.0661355651335753, -0.7839052304170298,  
            -0.6561980302276855, -0.6150178744908754,  
            -0.5991720784780843]
```

```
abs(sum(energies)) = 3.7204287787472503
```

Test Case Derivation: None

How test will be performed:

This work has been summarized in a jupyter notebook. The test will be written in a file that asserts the values from the notebook are equal to the calculated values from the Kaplan code.

## 2. test\_sum\_rmsds

Type: automatic (after manual calculations have been performed)

Initial State: None

Input: molecular hydrogen ( $H_2$ ) with 5 bond lengths, with one geometry that has been translated and rotated in space.

test covered	files involved	description
same geometry twice	H2-1A.xyz (twice)	run sum_rmsds and assert that rmsd is close to zero
same geometry translated and rotated	H2-1A.xyz, H2-1A-transrot.xyz	run sum_rmsds and assert that rmsd is close to zero
all pairs are picked	H2-1A.xyz, H2-2A.xyz, H2-3A.xyz, H2-4A.xyz, H2-5A.xyz	run sum_rmsds and assert that calculated rmsd is as calculated by hand

Output:

The answer for sum\_rmsds for  $H_2$  1Å through to 5Å is: 14.142135623730953. Comparing the rmsd of the rotated and translated  $H_2$  with the regular  $H_2$  of the same bond length should give an rmsd of 0, as should the comparison between two of the same input file.

Test Case Derivation:

From the RMSD formula (see Section 5.2.3 of the SRS), the number of atoms in molecular hydrogen is 2, so we have:

$$RMSD = \sqrt{\frac{1}{2}((x_{11} - x_{12})^2 + (y_{11} - y_{12})^2 + (z_{11} - z_{12})^2 + (x_{21} - x_{22})^2 + (y_{21} - y_{22})^2 + (z_{21} - z_{22})^2)}$$

$$RMSD = \sqrt{\frac{1}{2}((0 - 0)^2 + (0 - 0)^2 + (0 - 0)^2 + (1 - 2)^2 + (0 - 0)^2 + (0 - 0)^2)}$$

$$RMSD = \sqrt{\frac{1}{2}((1 - 2)^2)}$$

which gives the square-root of  $1/2 = 0.707106781$

For increasing bond length, the RMSD changes by  $\sqrt{\frac{1}{2} * (g - h)^2}$ , where g is the bond length of the first set of xyz coordinates and h is the bond length of the second set of xyz coordinates.

How test will be performed:

See the jupyter notebook for more details on how to get the rmsd values using the rmsd package. The output from this notebook will be compared to the output of the code for the same input files.

### 3. test\_calc\_fitness

The tests for this function are already included in the System VnV Plan, in Section 5.1.2.

#### 5.1.5 Tournament Module

As per the MIS Section 10, the tournament module has 3 functions, but only one of these is an access routine: run\_tournament. This access routine is called by the gac module (GA Control) n times, where n = num\_mevs.

[I made a design choice to put the run\_tournament function as a wrapper to the other two local functions. It might be that tournament could be a ring method, but this may reduce the ability of the ring to be a abstract data structure capable of expansion. The other way I could change this would be

to make the other functions part of the `run_tournament` (since the function wouldn't become that much more massive). —JG]

#### 1. `test_run_tournament`

Type: automatic (with some manual work initially)

Initial State:

This test will be run on a ring that has already been initialized for the molecule butane (CCCC). Its attributes (relevant to the tournament) are as follows:

```
num_filled = 5
num_slots = 10
pmem_dist = 2
num_geoms = 3
num_atoms = 14
```

The tournament will be run assuming it is the first mating event, so the age of all pmems is equal to zero. The tournament size will be equal to the `num_filled`, such that all initial pmems participate in the tournament.

Input:

By fixing the random number seed (RNS) for numpy (a python library), the exact dihedral angles that the 5 initial pmems have can be determined reproducibly. Then, the fitness for each of these pmems can be calculated using the *Fit<sub>G</sub>* module. The biggest fitness values of these 5 can be traced back to the pmems.

There are three choices that can be made for the test, as described below:

- (a) Choice of parent-child matching for the update (i.e. does parent1 go with child1 or child2). This choice results in four possible outcomes. The order of updating matters, in case both children are sent to the same slot (then they compete against one another in fitness):

- i. parent1 with child1 then parent2 with child2
  - ii. parent1 with child2 then parent2 with child1
  - iii. parent2 with child2 then parent1 with child1
  - iv. parent2 with child1 then parent1 with child2
- (b) Value chosen for num\_muts.
- (c) Value chosen for num\_swaps.

A test should be performed whereby the num\_muts and num\_swaps are both zero. This test can show what happens when duplicates are added to the ring, and it may be easier to track (and verify) the resulting ring.

Along the same lines as the previous test, a test can be performed whereby num\_muts and num\_swaps are both set to zero, except the tournament is run 1000 times. By the end of the test, the ring should consist almost entirely (if not entirely) of the best pmem in the original population.

Output: Once the code has been written, then the explicit output (fitness values, dihedrals, etc.) can be determined (since we are seeding the random number generator). For now, the test is expected to produce the same offspring given the same RNS is input; the tournament selection, the parents and their ring locations, and the location chosen to place the new children should be constant.

Easy values to test include:

- Check that the num\_filled is at least 5 and no more than 7 (since at most 2 pmems can be added per tournament and none are removed).
- If a child was added, its age should be 1 (assuming 1 tournament starting from the first mating event).
- After one tournament, the median age for the pmems should be 0. In the worst case scenario, two pmems are swapped with children, leaving 3 with age 0 and 2 with age 1.

Test Case Derivation: None

How test will be performed:

```

# set the RNS
numpy.random.seed(0)

# make a ring (and a parser object with vetee)
ring = Ring(3, 14, 10, 2, 0, 0.5, 0.5,
            vetee.structure.Structure('name', 'butane'))

# fill the ring with 5 pmems, at mev=0
ring.fill(5, 0)

# manually (visual inspection) determine
# the 2 best fitness values and their ring locations
# from the population
for i in range(5):
    print(i, ring.pmems[i].fitness)

# using mutations module, generate children
children = generate_children(parent1, parent2,
                             num_muts, num_swaps)

# generate the children pmems and calculate
# their fitness values

# update the ring
ring.update(parent1_index, child2, 0)
ring.update(parent2_index, child1, 0)

# see what the ring looks like after the update
for pmem in ring.pmems:
    print((pmem.ring_loc, pmem.fitness))

# determine if the update made sense based on the
# fitness values of the children vs the original
# population

```

### 5.1.6 Crossover & Mutation Module

The Crossover & Mutation module (mutations module) is called by the tournament module to make new pmems with which to fill and/or update the ring. In the MIS Section 11, there is one access function called `generate_children` and two local functions, `mutate` and `swap`. As with the tournament module (Section 5.1.5), the mutations module relies heavily on the use of random numbers to complete its task. Therefore, there are only some aspects of the output that can be tested.

As with the tournament, the order of `swap` and `mutate` can generate different pmems. It will be assumed for these tests that the `swap` function is called first, followed by the `mutate` function.

#### 1. `test_generate_children`

Type: automatic (with some initial manual work)

Initial State: None

Input:

The values for the dihedrals are negative (since these are not allowed by the `MIN_VALUE` and `MAX_VALUE` constants). Any mutations (where new values are generated) cannot be the same as the original values.

```
parent1 = [[-1,-2,-3,-4,-5], [-1,-2,-3,-4,-5], [-1,-2,-3,-4,-5]]
parent2 = [[-6,-7,-8,-9,-10], [-6,-7,-8,-9,-10], [-6,-7,-8,-9,-10]]
```

```
num_muts, num_swaps = 0, 1    # case 1
num_muts, num_swaps = 0, 2    # case 2
num_muts, num_swaps = 1, 0    # case 3
num_muts, num_swaps = 2, 0    # case 4
num_muts, num_swaps = 1, 1    # case 5
num_muts, num_swaps = 2, 2    # case 6
num_muts, num_swaps = 0, 0    # case 7
```

Output:

Case 1: `parent1` and `parent2` have one location swapped.



- Case 2: parent1 and parent2 have two locations swapped.
- Case 3: parent1 and parent2 have one new value each.
- Case 4: parent1 and parent2 have two new values each.
- Case 5: parent1 and parent2 have one swap and one new value each.\*
- Case 6: parent1 and parent2 have two swaps and two new values each.\*
- Case 7: parent1 and parent2 do not change.

\* With the same RNS, it may be possible to get the same mutations and swaps to occur as with the previous cases.

Test Case Derivation: None

How test will be performed:

The tests will depend on the RNS, which will be set first. The outputs need to then be inspected visually to determine if they make sense. Then the test can be automated to assert that those values are returned as expected. Most of the tests will iterate over the returned lists after swaps and mutations have been performed and check that the values are different by the expected number of values (or are equal as for Case 7).

### 5.1.7 Ring Module

[Include a blurb here to explain why the subsections below cover the module. References to the MIS would be good. You will want tests from a black box perspective and from a white box perspective. Explain to the reader how the tests were selected. —SS]

#### 1. test\_Ring\_init

Type: automatic

Initial State: None

Input:

The parser object here is a vetee structure object (structure inherits from parser). The other inputs (in order of appearance) are: num\_geoms, num\_atoms, num\_slots, pmem\_dist, fit\_form, coef\_energy, and coef\_rmsd.

```
ring = Ring(3, 10, 10, 0, 0, 0.5, 0.5,
            vetee.structure.Structure('name', '1,3-butadiene'))
```

Output: None

Test Case Derivation: None

How test will be performed:

The test will initialize the ring with the values given in the input section. All of the expected attributes will have their values asserted to make sure they are correctly setup.

## 2. test\_Ring\_set\_fitness

Type: automatic

Initial State:

The ring has been initialized as per the init test. Since it starts empty, put a random pmem in slot 0. Note: any pmems generated thus far will not have any fitness value.

Input:

Give one slot that does not have a pmem, and give slot 0 (that currently has no fitness).

Output:

The empty slot should raise a `ValueError` when `set_fitness` is called. The filled slot should result in a non-zero fitness.

Test Case Derivation: None

How test will be performed:

Using `numpy.testing.assert_raises`.

## 3. test\_Ring\_update

Type: automatic Initial State:

The ring has been created with init (as per the init test) and then filled with `ring.fill` (5 pmems). Since the `pmem_dist` is zero, any new child should be competing for the `parent_index` slot.

Future tests should also set the `pmem_dist` to a larger number, however it is difficult to test this case.

[I anticipate index out of range errors for the ring when the `pmem_dist` is high, since if you are looking at a parent slot of index 199 for 200 slots, then  $199 + \text{pmem\_dist}$  of 5 should wrap around to slot 4. This wrapping should be put into the code and tested as well. —JG]

Input:

Pmem with fitness bigger than (1), smaller than (2), and equal to (3) the fitness of the parent.

Output:

- (1) Ring at the parent slot should now have the child instead.
- (2) Ring at the parent slot should still have the parent there.
- (3) Ring at the parent slot should now have the child instead.

Test Case Derivation: None

How test will be performed:

Use `assert` to test slot occupant type (child or parent). The `pmem age` can be used to differentiate between the parent and the child. The fitness value can be set arbitrarily rather than by calling the `set_fitness` method of the ring.

#### 4. `test_Ring_fill`

Type: automatic Initial State:

A few tests should be done here. (1) the ring is completely empty, as with the `init` test. (2) the ring has a filled contiguous segment (10 pmems out of 20). (3) every 2nd slot is filled out of 10 slots. (4) all slots are filled (out of 10).

Input:

`num_pmems = 5` (number of pmems to add) `current_mev = 2` (to set the age of the pmem)

Output:

- (1) expect `num_filled` to become 5.
- (2) expect `num_filled` to become 15.

- (3) expect num\_filled to become 10 and RingOverflowError is not raised.
- (4) expect RingOverflowError to be raised.

Test Case Derivation: None

How test will be performed:

Either assert that num\_filled is the correct value, or use assert\_raises to check that a RingOverflowError is raised.

### 5.1.8 Pmem Module

The pmem module so far only consists of a class with a constructor. In the future versions of Kaplan, it is expected that the class will be expanded. For now, the test will just be to ensure that a pmem object is correctly instantiated.

1. test\_Pmem\_init

Type: automatic

Initial State: None

Input:

(1) ring\_loc = 0  
num\_geoms = 3  
num\_atoms = 14  
current\_mev = 3  
dihedrals = None

(2) ring\_loc = 0  
num\_geoms = 3  
num\_atoms = 5  
current\_mev = 3  
dihedrals = [[1,2], [3,4], [5,6]]

Output:

- (1) pmem object
- (2) pmem object

Test Case Derivation: None

How test will be performed:

Use assert to make sure the values match up with the expected pmem.attribute value. If the dihedrals is None, then some random dihedrals should be generated of the correct size, which should be checked in the test.

### 5.1.9 Output Module

The output module has one function, called `run_output`, which accepts a ring object as input and outputs `num_geoms` output files of xyz format for the pmem with the best conformers (which is found based on the best fitness in the ring). The average fitness is also calculated for the ring. The format for the output file has not yet been decided upon (likely it will be a simple text file as with the inputs). The geometry module is used by the output module to generate the full geometry specification of the conformer (since the pmem within the ring will only contain dihedral angles).

[Note: The energies for each of the conformers in the best pmem should also be returned. This aspect has not been implemented yet or written into the MIS. The pmem object in the future can keep track of which energy and rmsd calculations have been performed. Right now, in order to implement returning the energy, the output module could be given access to the energy module (this would not cause any cycles in the uses hierarchy). —JG]

#### 1. `test_run_output`

Type: automatic (with some initial calculations needed) and manual (for final visual inspection of xyz files)

Initial State: None

Input:

A ring object with 5 pmems of arbitrary fitness and dihedrals will be generated. The ring will have `num_geoms` equal to 3.

Output:

Three output xyz files should be generated. These files should be opened in a visualization program such as VMD (visual molecular dynamics). The average fitness should be correct (as calculated by hand).

Test Case Derivation: None

How test will be performed:

Open each output file in VMD and check that it has the correct number of atoms and the correct atom types. Calculate the average fitness by summing the arbitrary fitness values and dividing by 5.

## **5.2 Traceability Between Test Cases and Modules**

All modules have been covered in this document except for the energy, rmsd, and geometry modules, which will be covered in jupyter notebooks (found in the test directory under jupyter-notebooks).

## 6 Appendix

[This is where you can place additional information, as appropriate —SS]

### 6.1 Symbolic Parameters

[The definition of the test cases may call for SYMBOLIC\_CONSTANTS. Their values are defined in this section for easy maintenance. —SS]