**File used to document any problems encountered during development**

**This document is used as a template for how to properly document problems that I have come across during development so that I can easily refer to them later.**

**The template is as follows:**

1. **Write a description of the feature I am trying to implement**
2. **State what the error description is I receive**
3. **State the number of unit test if applicable**
4. **Describe what raises the error**
5. **Describe the steps taken to solve the issue**
6. **Write a description of the feature I am trying to implement**

Trying to setup the initial package with licensing.

1. **State what the error description is I receive**
2. checking DESCRIPTION meta-information ... WARNING
3. Non-standard license specification:
4. MIT LICENSE
5. **State the number of unit test if applicable**

N/A

1. **Describe what raises the error**

This error is raised when using devtools::check() to check the validity of the files required by the package.

1. **Describe the steps taken to solve the issue**

A solution to the problem was to change the LICENSE line in the DESCRIPTION file to MIT + file LICENCE, where LICENCE is the name of the file required by CRAN. This file contains the information in the format:

YEAR: 2018

COPYRIGHT HOLDER: Ryan Porteous

Then adding this file to the .gitignore file so that GitHub will still correctly recognise the correct license file and adding the GitHub licensing file to .Rbuildignore.

1. **Write a description of the feature I am trying to implement**
2. **State what the error description is I receive**
3. **State the number of unit test if applicable**
4. **Describe what raises the error**
5. **Describe the steps taken to solve the issue**
6. **Write a description of the feature I am trying to implement**

Trying to create the structure of the chromosome and input/output nodes.

1. **State what the error description is I receive**

Warning messages:

1: In `[<-.data.frame`(`\*tmp\*`, i, 1, value = list(c.1. = 1, c.NA. = NA)) :

provided 2 variables to replace 1 variables

2: In `[<-.data.frame`(`\*tmp\*`, i, 1, value = list(c.1. = 1, c.NA. = NA)) :

provided 2 variables to replace 1 variables

1. **State the number of unit test if applicable**

N/A

1. **Describe what raises the error**

Error popped up when trying to execute the script. The reason was due my misunderstanding of R’s data structures.

1. **Describe the steps taken to solve the issue**

I researched my problem and looked at why I was having the issue. I then redesigned the structure I wanted the chromosome to be. I was previously trying to structure it in a 2D manner to make it easier to translate from the visualisation and actual representation of the chromosome. I am moving towards an approach of representing each section as its own data frame and I will just have to enforce constraints to provide the 2D structure I desired.

1. **Write a description of the feature I am trying to implement**

I am trying to write a function which generates the output nodes required

1. **State what the error description is I receive**

==> devtools::test()

Loading caRtesian

Loading required package: testthat

Testing caRtesian

v | OK F W S | Context

x | 31 1 | Population [0.2 s]

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**test-population.R:65: failure: generateOutpus returns a data frame of the correct structure**

outputNodes1$chromoID inherits from `numeric` not `integer`.

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== **Results** ==========================================================================

Duration: 0.4 s

OK: 31

Failed: 1

Warnings: 0

Skipped: 0

Warning message:

package 'testthat' was built under R version 3.4.3

1. **State the number of unit test if applicable**

test-population.R

test\_that(“generateOutputs returns a data … “, {  
 …

expect\_is(outputNodes1$chromoID, “integer”)

}

1. **Describe what raises the error**

I am trying to ensure that the correct structure is used for the output nodes generated and in this particular case I am checking the chromoID column has the type “integer”. When I run the test, it seems the type is actually “numeric”.

1. **Describe the steps taken to solve the issue**

I looked at the area in my code as to why it was producing numerics for this column instead of integers. I changed the appropriate line to use the seq.int function instead of casting the resulting vector from numeric to integer.

1. **Write a description of the feature I am trying to implement**

Unit testing for the creation of the function sets.

1. **State what the error description is I receive**

==> devtools::test()

Loading caRtesian

Loading required package: testthat

Testing caRtesian

v | OK F W S | Context

x | 45 1 | Population [0.2 s]

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**test-population.R:123: failure: makeFunctionNode assigns the correct number of valid inputs**

`arity` not equal to `numInputsChosen`.

Types not compatible: character is not integer

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== **Results** ==============================================================

Duration: 0.4 s

OK: 45

Failed: 1

Warnings: 0

Skipped: 0

Warning message:

package 'testthat' was built under R version 3.4.3

1. **State the number of unit test if applicable**

test-population.R

test\_that(“make FunctionNode returns the correct number … “, {  
 …

expect\_equal(arity, numInputsChosen)

}

1. **Describe what raises the error**

Arity is a character and a character is never equal to an integer which is what numInputsChosen is.

1. **Describe the steps taken to solve the issue**

I didn’t think that the types were the problem and assumed it was the makeFunctionNode function assigning the wrong number of inputs as the unit test suggests. So, I stepped through the function and didn’t find any errors. I then used the class function on the arity column returned from creating a function set and found this to be a character type. This is due to the way I create the data frames, I first convert the function definitions to matrices and matrices are heterogenous, so the integers are converted to strings to match the function names. This error has not appeared until now as the only place that has used the arity so far handles characters as inputs.

To solve this error, I had to do some searching around on StackOverflow for a solution on how to convert a column of a data frame to a different type. This post (<https://stackoverflow.com/questions/2288485/how-to-convert-a-data-frame-column-to-numeric-type>) explained the use of the transform function so this is the approach I took and I used this when creating the function set so that the issue is handled in one location saving potential problems later.

1. **Write a description of the feature I am trying to implement**

Testing that generateFunctionNodes works with different sizes of parameters.

1. **State what the error description is I receive**
2. **State the number of unit test if applicable**
3. **Describe what raises the error**

When the number of columns in the validInputIDs variable was higher than the number of input nodes there would be issues and not all valid nodes would be represented.

For example, if the number of columns was 4 and there were 2 input nodes then 2 valid values would be chopped off.

Another issue was that the validInputIDs was storing duplicates and NA values.

1. **Describe the steps taken to solve the issue**

The method for solving this issue was to set the number of columns accepted by validInputIDs to the largest number out of the number of columns and the number of input nodes. I also had to allow for duplicate values within validInputIDs which will only happen initially when the number of columns is greater than the number of input nodes.

Doing this led to a bias in sampling though so sampleWithoutBiasOrNA had to be implemented to remove this bias.