**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.