

# Singh2015\_solution

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## 1 Solution of Singh *et al.* 2015

### 1.1 Compute the mean RecombinantFraction for each Drosophila Line and InfectionStatus. Print the results like:

Line 45 Average Recombination Rate: W : 0.187 I : 0.191

To read the data, we're going to use the csv module. First, we need to import it:

```
In [1]: import csv
```

Then, we need to go through all the rows in the file, and for each add the RecombinantFraction to the right genetic Line and InfectionStatus. To do so, we need to choose a data structure. Here we use a dictionary, where the keys are given by Line, and each value of the dictionary is another dictionary where the keys W and I index lists of RecombinantFraction.

```
In [2]: my_data = {}
```

```
In [3]: with open('../data/Singh2015_data.csv') as csvfile:
        reader = csv.DictReader(csvfile)
        for row in reader:
            my_line = row['Line']
            my_status = row['InfectionStatus']
            my_recomb = float(row['RecombinantFraction'])
            # Test by printing the values
            print(my_line, my_status, my_recomb)
            # just print the first row
            break
```

```
21 I 0.1826923077
```

Now we need to perform operations for each row. First, we're going to check whether my\_data already contains the Line for that row. If not, we'll create the key-value in the dictionary. Then, we're going to add the value to the list.

```
In [4]: with open('../data/Singh2015_data.csv') as csvfile:
        reader = csv.DictReader(csvfile)
        for row in reader:
```

```

my_line = row['Line']
my_status = row['InfectionStatus']
my_recomb = float(row['RecombinantFraction'])
# if my_line is not present in the dictionary:
if my_line not in my_data:
    # create and initialize with a dictionary containing
    # two empty lists
    my_data[my_line] = {'W': [], 'I': []}
    # Now insert the value in the right list
    my_data[my_line][my_status].append(my_recomb)

```

Now we should have the data organized in a nice structure:

In [5]: my\_data

```

Out[5]: {'21': {'I': [0.1826923077,
0.1850393701,
0.1856540084,
0.1866666667,
0.1904761905,
0.1958762887,
0.2180094787,
0.2534246575],
'W': [0.1288343558,
0.163141994,
0.1674208145,
0.1746478873,
0.175,
0.1779661017,
0.191588785,
0.1961722488,
0.2026578073,
0.2032258065]}},
'40': {'I': [0.1573426573,
0.1614173228,
0.1666666667,
0.1693989071,
0.1740890688,
0.1779141104,
0.1878980892,
0.2110552764,
0.2153846154],
'W': [0.125,
0.156424581,
0.1564885496,
0.1595744681,
0.1602209945,
0.1651376147,

```

```

0.1694915254,
0.1700404858,
0.1710526316,
0.180952381,
0.1828793774,
0.1888888889,
0.1892857143,
0.2123287671,
0.2247706422,
0.2340425532]},
'45': {'I': [0.1666666667,
0.1736111111,
0.1838565022,
0.1862068966,
0.1873015873,
0.1875,
0.188976378,
0.1981707317,
0.1993355482,
0.2068965517,
0.2077922078,
0.2080745342],
'W': [0.1481481481,
0.1625,
0.175862069,
0.1859504132,
0.1906779661,
0.2007722008,
0.2032967033,
0.2033195021,
0.213740458]},
'73': {'I': [0.1666666667,
0.1812297735,
0.1818181818,
0.1850746269,
0.2109090909,
0.2179487179,
0.2183098592,
0.2339449541],
'W': [0.1551724138,
0.1573033708,
0.1653543307,
0.1678321678,
0.1744680851,
0.1802721088,
0.1944444444,
0.1952861953,
0.1956521739,

```

0.2]}}

Time to calculate the means and print the results:

```
In [6]: for line in my_data:
        print('Line', line, 'Average Recombination Rate:')
        # extract the relevant data
        my_subset = my_data[line]
        for status in ['W', 'I']:
            print(status, ': ', end = ' ') # to prevent new line
            my_mean = sum(my_subset[status])
            my_num_elements = len(my_subset[status])
            my_mean = my_mean / my_num_elements
            print(' ', round(my_mean, 3))
        print('') # to separate the lines
```

Line 45 Average Recombination Rate:

W : 0.187

I : 0.191

Line 21 Average Recombination Rate:

W : 0.178

I : 0.2

Line 40 Average Recombination Rate:

W : 0.178

I : 0.18

Line 73 Average Recombination Rate:

W : 0.179

I : 0.199