

# 732A51 Bioinformatics Lab 1

*Raymond Sseguya, Martin Smelik, Duc Duong*

*2018 M11 7*

## Task 1

### Task 1.1

diploid population = Aa,Aa = 2N (parents)

After random mating for first generation: children = AA, Aa, aA, aa

Total new first generation population = 4

Number of AA homozygotes = 1

Number of aa homozygotes = 1

Number of Aa or aA heterozygotes = 2

Proportion of AA homozygotes =  $1/4 = 0.25$

Proportion of aa homozygotes =  $1/4 = 0.25$

Proportion of Aa or aA heterozygotes =  $2/4 = 0.5$

The proportion AA Homozygotes : Aa Heterozygotes : aa homozygotes is

0.25: 0.5 : 0.25

Again after random mating for first generation:

Probability of getting A allele =  $3/6 = 0.5 = p$

Probability of getting a allele =  $3/6 = 0.5 = q$

The proportion AA Homozygotes : Aa Heterozygotes : aa homozygotes is also square of p : 2 times p times q : square of q

$(0.5)^2 : 2 \text{ times } 0.5 \text{ times } 0.5 : (0.5)^2$

0.25: 0.5 : 0.25

This satisfies the Hardy Weinberg equilibrium.

### Task 1.1.b

The probability of getting A allele and a allele will remain the same with continued random mating therefore the Hardy Weinberg equilibrium will always hold.

## Task 3

### 3.1

According to Wikipedia, C. elegans is being extensively used as a model organism. It was the first multicellular organism to have its whole genome sequenced, and as of 2012, is the only organism to have its connectome

(neuronal “wiring diagram”) completed. The *C. elegans* genome contains an estimated 20,470 protein-coding genes.[95] About 35% of *C. elegans* genes have human homologs. Remarkably, human genes have been shown repeatedly to replace their *C. elegans* homologs when introduced into *C. elegans*. Conversely, many *C. elegans* genes can function similarly to mammalian genes.

### 3.2

### 3.3

```
Lab01_Ex4_seq   Reversed:      C.elegans   TTATTGTTTTCCAAGCTTTAATATCAATT-
TATTGTGCCCCGATGTTACCAATTACACTTGA      AAAATCTAAAAAGCTTGGAAC-
TAGCCGAAAATGTGCAGTAAAACAAAATTTCTATAAA  ATCCGAGTTATTTGAAC-
CAAATTCATACTCTTCTCTATTTTATCGTTTTTCCGAGCTCTAA  TCGTATATAATAT-
TACCTATTTTCAGCTAAATGAGCACATCCGTAGCGGAAAACAAAGCA TTGTCAGCTTC-
CGGCGATGTGAATGCGTCCGATGCTTCAGTTCTCTCCAGAGCTTCTCACC  AGACAC-
CCCCTCCAGAATCGCTGGGCTCTCTGGTACTTGAAAGCTGACCGTAACAAGGAA
TGGGAGGATTGTCTGAAGGTAGAAGATTTTTTAAATACGTCCTTTTATCGATTTTTTCCAGA
TGTTTTCACTTTTCGACACTGTGAGGACTTCTGGTCGCTGTACAATCACATTCAGTCTG
CCGGAGGATTGAACTGGGGATCCGATTATTACTTGTTCAAGGAAGGAATCAAGC-
CAATGT      GGGAGGACGTCAACAACGTTCAAGGTGGACGTTGGTTGGTTGTTGTC-
GATAAGCAAGTAC  GTTTTGAGAAATATATTTTATTCAATGAATCATAGAAGCTTCA-
GAGAAGAACGCAATTGC  TCGATCACTACTGGTTGGAGCTGTTGATGGCTATTGTTG-
GAGAGCAATTCGACGAGTACG  GAGACTACATCTGCGGAGCTGTCGTGAATGTTTCGT-
CAAAAGGGTGACAAGGTTTCCTTGT      GGACTCGTGATGCTACTCGCGATGATGT-
CAATCTTCGCATCGGACAGGTTTTGAAGCAGA      AATTGAGCATTCCGGATACTGA-
GATTTTGAGGTAATTTTACAATTTTAGTATTTGCTATC      TAAGTAAAATATTTCCA-
GATACGAAGTTCACAAGGACTCGTCGGCTCGCACCTCATCGAC  TGTCAAGCCACG-
CATATGTCTTCCAGCCAAGGATCCAGCACCAGTGAAGGAAAAGGGACC      AGCCG-
CAACGACTTCTCCATCGAATCCCGGCACGGAGGCTACAGGAACTTCTCCAGCCAC
CCCAACTCCTTAAGCATATTCTAAAGATCTCACCAATTCCTCTCACCGTAAAT-
GAGCTTC  CCCGTA CTCCCAGTCTCAATGTTGTCTTGAAAAATGAACTGTTTTTCG-
GACACGATCATC  GCTTTAACTATTTCGAAAATCAGCTCATTTTTTCAAGTCGTACCC-
CCCACCTAATGTATTGG  TGCTTCCCCCTCCAATTTGTACCTACTGTTTCGCTTCCC-
CCTATTGATTTACCGGTTTTTCG  TATTGCTCTCTTGTTGTTACTAGATTTCGAGACT-
GATCGACGCCTGTAGCCGAATTCGTTT  GTTCTTCAGGTTAATTGATGAATATATATT-
TATTCGGTAAATATAAATAGATATGTTAGT  TATTATTCTTCTTCACACACATGATTTG-
TAGGGCGTTTGATTTTGTACATTTTTTAAAAAT
```

### 3.4

The query sequence is found on the 11th position

### 3.5