BIMM 185 Lab Report Week 8

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Introduction

Last week we went through some example topics in comparative genomics and started with one example project of finding conserved gene paired across genomes to predict protein-protein interactions. We hypothesize that highly interacted proteins are likely to interact physically and close to each other. We again build an inference model to examine our hypothesis. To identify protein-protein interactions, different methods like Genes within the same operon units, gene neighbors, Protein fusions and Phylogenetic Profile are used. For the in-class exercise, we practiced implementing the gene neighbor method to detect conserved genes pairs A. tumefaciens.

Methods and Codes

Our goal is to find all the conserved gene pairs across E.coli and A.tumefaciens that are less than 5 genes away from each other. In order to do that, we first constructed the orthologs table using the blast results that we obtained weeks ago. A SQL view is constructed with 3 attributes, qid(gene_id of genes in E.coli), sid(gene_id of genes in A.tumefaciens), and rid(replicon id of A.tumefaciens replicons) in order to provide convenience for later query by replicon.

The sql command is below:

```
qid) maxtable
    where b.qseqid = maxtable.qseqid and b.bitscore = maxtable.bitscore) b2max
where b1max.qseqid = b2max.sseqid and b1max.sseqid = b2max.qseqid order by b1ma
x.bitscore DESC) o1 inner join genes g1 on o1.qseqid = g1.accession inner join
genes g2 on o1.sseqid = g2.accession;
```

Then for each replicon in A.tumefaciens, directons on that replicon were queried out and stored in a list so that each gene has an index as its position on the replicon.

```
This function gets all the directons of the given replicon

def query_directons(conn, replicon):
    cur = conn.cursor()
    sql_statement = ("select genes.gene_id from genes inner join(select gene_id
, min(left_position) as left_position, max(right_position) as right_position fr
om exons group by gene_id) position on position.gene_id = genes.gene_id where g
enes.replicon_id = {replicon} order by left_position;".format(replicon=replicon
))
    cur.execute(sql_statement)
    result = cur.fetchall()
    #print(result)
    return list(result)
```

To gain the conserved genes(orthologs) between E.coli and the replicon, the previously constructed 'orthologs' view was used.

```
This functions gets all the ortholog gene pairs in E.coli and the given replico

n

def query_orthologs(conn, replicon):
    cur = conn.cursor()
    sql_statement = ("select * from orthologs where rid = {replicon}".format(re

plicon=replicon))
    cur.execute(sql_statement)
    result = cur.fetchall()
    return list(result)
```

After gaining all the data that we need, we iterate through all the genes in E.coli that are also conserved in A.tumefacians replicon, find its location, then iterate through all the genes that are

within 5 genes away from that gene, see if the paired gene is also conserved in A.tumefacians. Then find the position of the 2 conserved orthologs on A.tumefacians and calculate the distance. Output every gene pairs that satisfy our requirement in table with the following columns:

- 1. gene id of gene1 in E.coli
- 2. gene id of gene2 in E.coli
- 3. distance in E.coli
- 4. distance of orthologs in A. tumefaciens

Results

After went through all 4 replicons of A.tumefaciens, a total number of 745 conserved gene pairs were found.

Among the gene pairs, 605 gene pairs were found between E.coli and replicon 2; 126 were found between E.coli and replicon 3; 13 gene pairs were found between E.coli and replicon 4; and 1 gene pair was found between E.coli and replicon 5.

The full list of the conserved gene pairs will be put at the end of this lab report in the appendix section.

Discussion

Last week we learned the whole process from initializing a hypothesis to building a model to examine the hypothesis and use the hypothesis to predict results on unknown testing data. The inference model that we built last week was more complicated compare to the inference model that we built in order to predict operon units due to the collection of the True positive and True negative training sets. The model is more complicated also in the sense of incorperating multiple methods and intergrating scores resulted from different methods into one uniform scale.

Appendix

Resulting conserved gene pairs between E.coli and A.tumefaciens

```
13 14 1 1
24 25 1 1
50 51 1 1
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50
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       3
            3
    53
            2
51
        2
64
    65
       1
            1
64
    66
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       2
65
    66
       1
            1
            5
66
   71
        5
70
   72
        2
            1
76
   77
            1
        1
79
    80
        1
            1
79
    82
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79
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79
    84
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    84
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    85
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            5
82
    83
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82
    84
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    86
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    87
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83
    86
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83
    87
        4
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83
    88
       5
        1
            1
84
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    87
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    88
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    89
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86
    87
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        1
88
    90
        2
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89
    90
        1
            4
89
    91
        2
            5
90
    91
        1
            1
```

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90
       3
90
   94 4
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91
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91
   93 2
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91
   94
       3
92 93 1
           1
92 94
           2
      2
93 94 1
           1
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138 141 3
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164 165 1
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164 166 2
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164 167 3
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164 169 5
165 166 1
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165 169 4
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165 170 5
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166 167 1
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166 170 4
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166 171 5
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167 169 2
167 170 3
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167 171 4
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167 172 5
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169 170 1
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169 171 2
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169 172 3
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169 174 5
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170 171 1
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170 172 2
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170 174 4
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170 175 5
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171 172 1
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171 174 3
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171 175 4
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172 175 3
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172 176 4
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172 177 5
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406 407 1
406 408 2
406 409 3
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463 464 1
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487 488 1
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654 657 3
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654 658 4
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            3
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2264	2268	4	4
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2265	2269	4	4
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2588	2589	1	2
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3145	3149	4	4
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