Integrated simultaneous analysis of different biomedical data types with exact weighted bi-cluster editing

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Abstract

• The explosion of biological data has largely influenced the focus of today’s biology research. Integrating and analysing large quantity of data to provide meaningful insights has become the main challenge to biologists and bioinformaticians. One major problem is the combined data analysis of data from different types, such as phenotypes and genotypes. Here we contribute with an exact algorithm that is based on fixed-parameter tractability.

Bi-Cluster Editing

• Given a graph $G = (V, E)$, can we convert this graph into cliques with at most $k$ edge modifications (or with modification penalty at most $k$)?

Exact Algorithms

Fix Parameter Approach

• NP-hard problems are computable in a time that is polynomial of input size and exponential or worse in a parameter $k$.

Kernelization

• A kernelization is an efficient mapping of the input instances into equivalent instances with a guaranteed upper bound on the size.

$\{x, k\} \mapsto \{x', k'\}$

$O(x') = f(k)$

$O(k') = g(k)$

Branching Strategy

• Branching strategy is the approach of the depth-first searching tree to solve the problem.

We can design faster kernelization and branching strategy.

Results (I)

Artificial Graphs

• We generate random graphs with given vertices and random assigned edge weights.

• Two Gaussian distributions are used to generate the edge weights.

Results (II) : on GWAS data

(a) Proposal

• Vertices: (1) loci/genotypes

• Edges: significant associations

• (2) phenotypes

• To identify groups of variations responsible for groups of diseases.

(b) DATA SOURCES

<table>
<thead>
<tr>
<th>Literature Search</th>
<th>NHGRI Dataset</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Associations</td>
<td>54,776</td>
</tr>
<tr>
<td>Number of SNP loci</td>
<td>52,644</td>
</tr>
<tr>
<td>Number of Phenotypes</td>
<td>87</td>
</tr>
</tbody>
</table>

(c) Putative Associations

• We identified 86 putative associations.

Results (III): on GWAS data

<table>
<thead>
<tr>
<th>Traits/Disease</th>
<th>No. of Newly Found Associations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary tooth development (time to first tooth eruption)</td>
<td>6</td>
</tr>
<tr>
<td>Primary tooth development (number of teeth)</td>
<td>7</td>
</tr>
<tr>
<td>Alcoholism (alcohol dependence factor score)</td>
<td>4</td>
</tr>
<tr>
<td>Plasma coagulation factors</td>
<td>3</td>
</tr>
<tr>
<td>Vitamin D insufficiency</td>
<td>3</td>
</tr>
<tr>
<td>Vitamin D levels</td>
<td>2</td>
</tr>
<tr>
<td>Atrial fibrillation</td>
<td>1</td>
</tr>
<tr>
<td>Nonsyndromic cleft lip with or without cleft palate</td>
<td>1</td>
</tr>
<tr>
<td>Plasma levels of Protein C</td>
<td>1</td>
</tr>
<tr>
<td>Total</td>
<td>58</td>
</tr>
</tbody>
</table>

References:


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