CORRIGENDUM

Combining diverse evidence for gene recognition in completely sequenced bacterial genomes

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The authors of the above paper wish to note errors in gene start prediction accuracy given in Table 2. The correct version of the table is as follows.

Table 2. Comparison of the gene prediction results with the sets of sequences from the PIR-International and the genome sequencing projects

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Percentage of correctly identified genes</th>
<th>Percentage of correct starts for correctly identified genes</th>
<th>Percentage of correctly predicted genes with correct starts using &quot;leftmost ATG&quot; procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Length&gt;100</td>
<td>Length &gt; 35</td>
<td>Length&gt;100</td>
</tr>
<tr>
<td>SUBPIR</td>
<td>93.3%</td>
<td>-</td>
<td>80.2%</td>
</tr>
<tr>
<td>ECOPIR</td>
<td>96.3%</td>
<td>-</td>
<td>65.8%</td>
</tr>
<tr>
<td>SUBGEN</td>
<td>98.9%</td>
<td>88.9%</td>
<td>79.1%</td>
</tr>
<tr>
<td>ECOGEN</td>
<td>99.1%</td>
<td>87.1%</td>
<td>70.0%</td>
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