XBenchMatch uses as input the result of a schema matching algorithm (set of mappings and/or an integrated schema) and generates statistics about the quality of this input and the performance of the matching tool. A demo version of the prototype is available at http://www.lirmm.fr/duchatea/XBenchMatch.

**GOALS:** extensibility, portability, simplicity (ease of use), scalability, genericity, completeness

### MAPPING QUALITY MEASURES

- **Precision** = \(|T_{map} \cap T_{ex}| / |T_{map}|\)
- **Recall** = \(|T_{map} \cap T_{ex}| / |T_{ex}|\)
- **F-measure** = \((2 \cdot \text{precision} \cdot \text{recall}) / (\text{precision} + \text{recall})\)

### INTEGRATED SCHEMA QUALITY MEASURES

1. **Backbone measure, BM,** corresponds to the size of the largest common subtree of \(S_g\) and \(S_i\) (measured in nodes), seen against the background of the integrated schema \(S_i\). 
   \[BM = |\text{LCSub}(S_i, S_g)| / |S_i|\]
2. **Structural overlap** corresponds to the number of nodes shared by \(S_i\) and \(S_g\) and included in a common subtree. \(\text{Sub}\) is the set of all disjoint subtrees (each containing a minimum of two nodes) common to \(S_i\) and \(S_g\). \(k_{Sub}\) is the total number of elements of all subtrees in \(\text{Sub}\).
   
   \[\text{StructuralOverlap} = k_{Sub} / |S_i|\]
3. **Structural proximity** considers the number of subtrees common to \(S_i\) and \(S_g\). \(o\) is the number of elements in \(S_i\) that are not included in any common subtree.
   
   \[\text{StructuralProximity} = k_{Sub} / \sqrt{|S_i| \cdot |\text{Sub}| + o}\]
SCHEMAS

1. Person schemas are small and strongly heterogeneous.
2. Purchase orders, XCBL collection 3, demonstrate matching of a large schema to a smaller one.
3. University course schemas are from Thalia [4].
4. Biological schemas correspond to Uniprot protein DB, and GeneCards integrate data from over 100 databases.

TESTED MATCHERS

Porsche, COMA++ and Similarity Flooding.

Experiments

![Figure 1. Architecture of XBenchMatch](image1)

![Figure 2. Matching precision on the three scenarios for three schema matchers.](image2)

![Figure 3. Matching quality of the four scenarios for three schema matchers.](image3)

<table>
<thead>
<tr>
<th></th>
<th>Person</th>
<th>University</th>
<th>Order</th>
<th>Biology</th>
</tr>
</thead>
<tbody>
<tr>
<td>NB nodes (S₁ / S₂)</td>
<td>11 / 10</td>
<td>18 / 15</td>
<td>20 / 144</td>
<td>719 / 80</td>
</tr>
<tr>
<td>Avg NB of nodes</td>
<td>11</td>
<td>15</td>
<td>452</td>
<td>800</td>
</tr>
<tr>
<td>Max depth (S₁ / S₂)</td>
<td>4 / 4</td>
<td>5 / 3</td>
<td>3 / 3</td>
<td>7 / 3</td>
</tr>
<tr>
<td>NB of Mappings</td>
<td>5</td>
<td>15</td>
<td>10</td>
<td>57</td>
</tr>
</tbody>
</table>

Table 1: Summary of four evaluation scenarios.