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Application of sequential pattern mining to the analysis of visitor trajectories

Nyoman Juniarta, Amedeo Napoli
nyoman.juniarta@loria.fr, amedeo.napoli@loria.fr

Introduction
In this work, we demonstrate the proof of concept of clustering 254 visitors based on their trajectories in a museum. We used a real dataset from Haifa Museum (Figure 1), where each trajectory is treated as a sequence of itemsets. We applied \( \text{sim}_{ACS} \) as a similarity measure between any two sequences.

<table>
<thead>
<tr>
<th>START</th>
<th>END</th>
<th>ARTIFACT</th>
</tr>
</thead>
<tbody>
<tr>
<td>...</td>
<td>...</td>
<td>GlassOvenVessels</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td></td>
</tr>
</tbody>
</table>

Figure 1. An example of raw dataset from one visitor.

Behavior of visitors
According to [1], a visitor can be grouped as one of four defined behavior: ant, grasshopper, butterfly, and fish, as illustrated in Figure 2. These behaviors are described by the movement of a visitor around the artifacts in a museum.

![Behavior of visitors](Image)

Sequence
Sequence is an ordered list of itemsets. A sequence \( s = (s_1, s_2, \ldots, s_m) \) is a subsequence of \( s' = (s_1, s_2, \ldots, s_n) \) if there exist indices \( 1 \leq i_1 < i_2 < \cdots < i_m \leq n \) such that \( s_j \subseteq s'_{i_j} \) for all \( j = 1, \ldots, m \) and \( m \leq n \).

\[
S = \{(a, b), (c, d), (a, c, d)\}
\]

Subsequences Not subsequences
\( \langle a, b \rangle \) \( \langle b, c \rangle \)
\( \langle c, a, c \rangle \) \( \langle d, a, b \rangle \)
\( \ldots \) \( \ldots \)

Sequence clustering
In order to cluster a set of sequences, a similarity measure must be defined. Distance between any two sequences can be measured by \( \text{sim}_{ACS} \) [2], that counts all their common subsequences.

\[
\text{sim}_{ACS} = \frac{\phi_d(s_1, s_2)}{\max\{\phi_d(s_1), \phi_d(s_2)\}}
\]

\( \phi_d(s) \) is the number of all distinct subsequences of \( s \), and \( \phi_d(s_1, s_2) \) is the number of all common subsequences between \( s_1 \) and \( s_2 \).

Clustering of visitors
In order to group visitors according to their trajectories, each trajectory was converted into a sequence of itemsets. An itemset corresponds to an artifact, and it possesses the information about duration and distance between previous artifact. These two elements were discretized such that duration has values short and long, while distance has near and far. Example:

\[
v_1 = (\ldots, \{\text{short}, \text{near}\}, \{\text{short}, \text{far}\}, \{\text{short}, \text{near}\}, \ldots)
\]

\[
v_2 = (\ldots, \{\text{long}, \text{far}\}, \{\text{long}, \text{far}\}, \{\text{short}, \text{near}\}, \ldots)
\]

Having the sequences of itemsets and non-Euclidean similarity measure, we applied hierarchical clustering over 254 sequences, using \textit{hclust} from R software.

Result
Using 15 clusters as \textit{hclust}'s dendrogram cut, we obtained 4 big clusters and 11 small clusters, as shown in Figure 3.

![Result](Image)

We calculated the presence of four possible itemsets in each cluster to map them into four visiting patterns. An \textit{ant} corresponds to \{long, near\} itemset, while \textit{fish} contains \{short, near\}. The \{long, far\} itemset can be correlated with both \textit{butterfly} and \textit{grasshopper}, but the latter has relatively short sequence. Furthermore, within the 11 small clusters, the four possible itemsets have relatively the same support. This suggests that they correspond to visitors who frequently change their behavior while visiting the museum.

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References