An expert study on hierarchy comparison methods applied to biological taxonomies curation

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Comparison of hierarchies aims at identifying differences and similarities between two or more hierarchical structures. In the biological taxonomy domain, comparison is indispensable for the reconciliation of alternative versions of a taxonomic classification. Biological taxonomies are knowledge structures that may include large amounts of nodes (taxa), which are typically maintained manually. We present the results of a user study with taxonomy experts that evaluates four well-known methods for the comparison of two hierarchies, namely, edge drawing, matrix representation, animation, and agglomeration. Each of these methods is evaluated with respect to seven typical biological taxonomy curation tasks. To this end, we designed an interactive software environment through which expert taxonomists performed exercises representative of the considered tasks. We evaluated participants' effectiveness and level of satisfaction from both quantitative and qualitative perspectives. Overall quantitative results evidence that participants were less effective with agglomeration whereas they were more satisfied with edge drawing. Qualitative findings reveal a greater preference among participants for the edge drawing method. Also, from the qualitative analysis, we obtained insights that contribute to explain the differences between the methods and provide directions for future research.

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Abstract

18   Comparison of hierarchies aims at identifying differences and similarities between two or more
19   hierarchical structures. In the biological taxonomy domain, comparison is indispensable for the
20   reconciliation of alternative versions of a taxonomic classification. Biological taxonomies are
21   knowledge structures that may include large amounts of nodes (taxa), which are typically
22   maintained manually. We present the results of a user study with taxonomy experts that
23   evaluates four well-known methods for the comparison of two hierarchies, namely, *edge
24   drawing*, *matrix representation*, *animation*, and *agglomeration*. Each of these methods is
25   evaluated with respect to seven typical biological taxonomy curation tasks. To this end, we
26   designed an interactive software environment through which expert taxonomists performed
27   exercises representative of the considered tasks. We evaluated participants' effectiveness and
28   level of satisfaction from both quantitative and qualitative perspectives. Overall quantitative
29   results evidence that participants were less effective with *agglomeration* whereas they were more
30   satisfied with *edge drawing*. Qualitative findings reveal a greater preference among participants
31   for the *edge drawing* method. In addition, from the qualitative analysis, we obtained insights that
32   contribute to explain the differences between the methods and provide directions for future
33   research.

34

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Introduction

37   Visual comparison of hierarchies has been prevalent in information visualization research
38   because it is relevant for a wide range of domains such as tracking changes in software projects,
39   comparing budgets, and describing dynamics of organizational structures, among others. In this
40   work, we study the comparison of hierarchies in the domain of biological taxonomies.

41

Taxonomies are hierarchies created by experts to classify living organisms. Through classification, mutually resembling organisms are placed together in categories known as *taxonomic ranks,* which, in turn, make up the levels of the hierarchy. The main taxonomic ranks include *domain*, *kingdom*, *phylum*, *class*, *order*, *family*, *genus*, and *species*. Each node within the hierarchy is referred to as a taxon, that is, a name given to a group of organisms; for instance *Vertebrates* and *Mammals* are two taxa, the former is placed at the *phylum* taxonomic rank and latter at the *class* taxonomic rank. Species and sub-species are placed at the lower level of the hierarchy and their scientific names are expressed with a *binomial system of nomenclature* that uses a Latin grammatical form. The first part is the genus and the second part is the *specific epithet*. For instance, the domestic cat's scientific name is *Feliz catus* (formerly known, for many years, as *Felix domesticus*), where the epithet name is *catus* and the genus is *Feliz*. Upper levels of the cat's taxonomy are: family *Felidae*, order *Carnivora*, class *Mammalia*, phylum *Chordata*, and kingdom *Animalia*. For a taxon to be recorded in a taxonomy, it must have been described in a publication, either as a new group or as a review of an existing group of organisms. Therefore, besides the taxon name, taxa should include the author's name and the year of publication, which allows readers to determine under which judgment the classification was devised. After almost three centuries since modern taxonomy was first established by Carl Linnaeus (Linné & Gmelin, 1767) one might think that most organisms on Earth have been identified and classified, and that taxonomies are rather static. However, on one hand, it is estimated that only about 1.5 million from approximately 11 million species of macro organisms haven been identified and described (Larsen et al., 2017). On the other hand, the dynamics of taxonomic work has lead experts worldwide to end up with different versions of the classifications. Taxa names represent concepts whose definition depends on the authors' criteria, which eventually gives rise to conflicting versions of a taxonomy. These multiple versions will require corrections and re-classifications in order to come to an integrated version that can more accurately document biodiversity. That is how taxonomists often face the problem of reconciling different versions of a taxonomy. For such reconciliation efforts, biological taxonomists require to perform a series of curation tasks. Sancho-Chavarría et al. have characterized ten main curation tasks (Sancho-Chavarria et al., 2016, 2018) that involve taxonomic changes when comparing two versions T_1 and T_2 of a taxonomy. Table 1 provides a description of those ten tasks organized into three categories, namely, *pattern identification*, *query*, and *edition*.

Pattern identification tasks include the identification of *congruent*, *merged*, *split*, *renamed*, *moved*, and *added/excluded* taxa, as well as the *overview* of changes and the visualization of a *summary* of the resulting comparison. Congruence refers to same taxonomic concepts present in both versions of a taxonomy. A split occurs when taxonomists determine that a group that was so far considered a unit in a version of a taxonomy (e.g., a particular group of species of butterflies) actually consists of several groups of species that should be described separately. Conversely, a merge happens when taxonomists decide that several independent taxa should be classified and combined into the same group. A change of name (i.e., rename) is usually due to a typo that needs to be corrected. A taxon appears moved when it has been re-classified and placed in a different location, within the other version of the taxonomy. An addition occurs when a new taxon is added to the taxonomy, either because it is a new discovery or because it had not been previously recorded in the database. Exclusions refer to taxa that are contained in version T_1 but that are missing in the alternative version T_2. It is important to note that, from a taxonomic point of view, once a species is discovered it is kept in the taxonomy even if the species becomes

88   extinct; however, in this work we consider exclusions because it is important that taxonomists
89   know when records are missing in the database. The *overview changes* task refers to the
90   possibility of globally overviewing all differences between two versions of a taxonomy. The
91   *summarize* task consists of obtaining statistical information on changes. Curation tasks in the
92   *Query* category enable users to obtain detailed information on taxa. The *retrieve details* task lets
93   users obtain attributes of a taxon, for instance, the year of publication and the authors' names.
94   The *focus* task refers to the action that users perform when focusing on a group of organisms.
95   Through *filter*, users may find taxa that satisfy some given conditions and through *find*
96   *inconsistencies*, users may recognize differences due to errors or missing information (e.g., typos
97   or undefined names). The *Edition* category comprises just one task that is rather ample, namely,
98   the process through which experts make changes to T_1 and/or T_2 after analyzing the results of a
99   comparison.
100
101   For this research, we selected the tasks that interviewed taxonomists considered were the most
102   representative for the identification of differences and similarities: 1. Identify congruence, 2.
103   Identify corrections (splits, merges, moves and renames), 3. Identify additions/exclusions, and 4
104   Overview changes. Additionally, the splits and merges are considered only at species level.
105   Previous research has contributed with visual models and tools to support the comparison of
106   alternative versions of a taxonomy (Lin et al.; Graham, Craig & Kennedy, 2008; Dang et al.,
107   2015). However, in practice, most taxonomists still rely on simple indented lists to carry out the
108   curation process with little computational assistance. We believe this endeavor can be eased with
109   the support of a hierarchy comparison visualization system. Graham and Kennedy (Graham &
110   Kennedy, 2010) surveyed the comparison of hierarchies and organized the visualization methods
111   into five categories, namely, *edge drawing*, *coloring*, *animation*, *matrix representation*, and
112   *agglomeration*. The *edge drawing* method presents the two hierarchies as separate structures
113   where differences and similarities are represented by edges from nodes in T_1 to the associated
114   nodes in T_2. The *coloring* method represents similar nodes with the same color. *Animation* shows
115   changes as smooth transitions from one hierarchy to the other. In a *matrix* representation one
116   hierarchy is placed along the vertical axis and the other one along the horizontal axis; matrix
117   cells indicate relationships between nodes of the compared hierarchies. The *agglomeration*
118   method visually merges both hierarchies into an integrated list.
119
120   The open question that we address in this work is how well these methods support the above
121   curation tasks between two versions T_1 and T_2 of a taxonomy. From the five methods, we leave
122   out coloring as an independent condition since color can be used across all methods. We
123   designed and conducted a user study where twelve expert taxonomists evaluate those four
124   methods. We wanted participants to interact with each of the four methods in a close-to-reality
125   scenario. We developed an interactive software environment that integrates the four methods and
126   allows users to easily navigate from one method to another while doing the assessment exercises.
127   We wanted to capture the essence of each method and avoided the introduction of features that
128   could potentially favor any particular method. We also carefully selected the data. Datasets
129   contain sufficient types of changes to carry out exercises for all tasks and were also selected to
130   avoid the introduction of any bias due to the potential prior knowledge of the data by the experts.
131   Participants performed the same exercises with each method; however, the target taxa were not
132   the same, also to avoid bias from a learning effect. Immediately after performing the exercises
133   related to a task, participants were asked to answer a user satisfaction questionnaire in order to

134 evaluate each method in relation to the completion of that task. We registered the participants'
135 answers along with their interactions and thinking out-loud comments. We performed a
136 quantitative analysis on the participants' responses to the exercises (i.e., whether they answered
137 correctly or not) an also on their user satisfaction assessment. Additionally, we obtained
138 qualitative findings based on the participants' feedback throughout the session. The software, the
139 data, the questionnaire, and the analysis materials are publicly posted in Github at
140 https://github.com/lsanchoc/MethodsTasksUserStudy.
141
142 Our contribution with this work is twofold. On one hand, we assessed the effectiveness and level
143 of participants' satisfaction with each visualization method. On the other hand, we obtained a set
144 of themes that contribute to explain the differences between the methods and provide valuable
145 insights for future work on the design of software tools for the comparison of biological
146 taxonomies.
147
148 The rest of this paper is organized as follows. Section 2 presents related work. Section 3 details
149 the study design. It includes a description of the interactive software environment, the
150 participants' profile, the characteristics of the datasets, the user study protocol, and the
151 questionnaire. Section 4 describes the results of the study. In Section 5, we discuss the results
152 and present limitations and implications of the study. Finally, in Section 6 we present
153 conclusions and future work.
154
155

156 Related Work

157 Comparison—understood as the examination of two or more items to determine similarities and
158 differences—is a means that facilitates the process of interpreting information. Gleicher et al.
159 (Gleicher et al., 2011) provide a comprehensive survey of visual comparison approaches
160 focusing on comparing complex objects. They analyze a number of publications, systems and
161 designs, looking for common themes for comparison, and propose a *general categorization of*
162 *visual designs for comparison* that consists of three general categories, namely, juxtaposition,
163 superposition, and explicit encoding. The juxtaposed designs place the objects to be compared
164 separately, in time or space. The superposed designs place the objects to be compared one over
165 the other in an overlay fashion. The explicit encoded designs show the relationships between
166 objects explicitly and is generally used when the relationships between objects are the subject of
167 comparison. Hybrid designs are also possible and usually combine two categories. More
168 recently, a set of considerations to understand comparison tasks and their challenges has been
169 discussed (Gleicher, 2018), as well as comparison in the context of exploratory analysis (von
170 Landesberger, 2018).
171
172 As mentioned above, for the comparison of biological taxonomies we are considering the
173 methods surveyed by Graham and Kennedy (Graham & Kennedy, 2010) for the comparison of
174 two hierarchies, namely, *edge drawing*, *matrix*, *animation* and *agglomeration*. Each of these
175 methods can be mapped to the mentioned *general categorization of visual designs for*
176 *comparison*. So, the *edge drawing* method comprises characteristics from both juxtaposition
177 (hierarchies are placed separately side by side) and explicit encoding (edges encode the relations
178 between nodes); the *matrix* layout corresponds to an explicit encoding design since the matrix

179 cells can explicitly indicate the relations among taxa; and *agglomeration* corresponds to a
180 superposed design.
181
182 Previous works on hierarchy comparison match these categories. For instance, TreeJuxtaposer
183 (Munzner et al., 2003) compares phylogenetic trees by using a juxtaposed layout. It presents a
184 novel focus+context technique for guaranteed visibility and comparison is approached by
185 coloring. Holten and van Wijk (Holten & van Wijk, 2008) present a visualization method where
186 hierarchies are structured as icicle plots placed in juxtaposition. Relations are explicitly
187 represented by edges arranged through hierarchical edge bundles to reduce cluttering. The
188 Taxonomic Tree Tool (Lin et al.) uses a juxtaposed layout to compare biological taxonomies. It
189 combines glyphs to explain the relations between taxa. ProvenanceMatrix (Dang et al., 2015)
190 compares two taxonomies using a matrix representation. Relations are explicitly displayed
191 through two mechanisms: glyphs and edges. Beck and Diehl (Beck & Diehl, 2010) compare two
192 software architectures that use a matrix. Hierarchies here are represented as icicle plots.
193
194 Examples that use animation for comparison are scarcer. Ghoniem and Fekete (Ghoniem &
195 Fekete, 2001) use animation to visualize the transition between two alternative representations of
196 the same tree laid out as treemaps. Considering agglomeration-based designs, Beck et al. (Beck
197 et al., 2014) present a nested icicle plot approach for comparing two hierarchies and Guerra-
198 Gomez et al. (Guerra-Gómez et al., 2012) contrast two trees for the visualization of both node
199 value changes as well as topological differences for the comparison of budgets. Unlike the above
200 mentioned work, which did not focus on biological taxonomies, Graham and Kennedy (Graham
201 & Kennedy, 2007) propose an agglomerated visualization based on directed acyclic graphs for
202 the comparison of multiple biological taxonomies. Lutz et al. (Lutz et al., 2014) compared
203 directory structures and conducted a qualitative user study to identify usage strategies. Also,
204 Graham et al. (Graham, Kennedy & Hand, 2000) analyzed set-based hierarchies and
205 agglomerated graph-based visualizations for the comparison of botanical taxonomies.
206
207 Our work differs from previous studies in that, for the first time, four visualization methods
208 described in (Graham & Kennedy, 2010), are assessed for the comparison of pairs of biological
209 hierarchies with respect to typical curation tasks.
210

211

Study Design

213 The research question addressed is: "How well does each method support carrying out biological
214 taxonomy curation tasks?" This is assessed both quantitatively and qualitatively. On one hand,
215 we aim at obtaining a quantitative understanding of the participants' effectiveness and level of
216 satisfaction. On the other hand, we also aim at obtaining qualitative insights on the capacity of
217 each method to carry out tasks for the comparison of biological taxonomies. We therefore
218 explore how users interact with the visualizations and what their judgment of each method is. We
219 opted for a within-subject design study that involves four experimental conditions, one for each
220 method (*edge drawing*, *matrix*, *animation*, and *agglomeration*). In this way, each participant
221 could test and contrast all methods. The study fits into the category "Evaluating Visual Data
222 Analysis and Reasoning (VDAR)" (Lam et al., 2012). In this approach, the goal is to assess how
223 a visualization tool supports the analytic process for a particular domain. Accordingly, in our
224 study we want to evaluate how each implemented method supports the identification of

225 similarities and differences for the curation of biological taxonomies. The development of a
226 stable and reliable software environment, such as the one that we use, responds to such type of
227 evaluation.
228
229 **The Software Environment**
230 We developed an interactive web-based software environment that integrates in the same
231 environment the four methods for visual comparison of biological taxonomies described in the
232 Introduction section. The software environment was designed to investigate how these four
233 methods support the taxonomy curation tasks described in Table 1. We decided to develop a
234 functional system in which participants get a realistic impression. Also, we provided remote
235 web-based access to the software because many of the participants were located in different parts
236 of the world. Figure 1 illustrates the user interface of the software environment. The two
237 taxonomies to be compared, T_1 and T_2, are displayed as indented lists. Each method
238 implementation is accessible by easily clicking on a tab. Users can inspect the data through the
239 provided basic zooming features and by vertically scrolling for all methods. Additionally,
240 horizontal scrolling is provided for *matrix*. The visualization layout is of course method-
241 dependent. For *edge drawing* and *animation*, taxonomies are placed juxtaposed. T_1 is placed on
242 the left side of the screen and T_2 on the right side. For *matrix*, taxonomy T_1 is also placed on the
243 left side but T_2 is at the top of the matrix. Finally, for *agglomeration*, T_1 and T_2 are interleaved
244 and centered horizontally.
245
246 The main menu is common to all methods. It is located at the top of the window and contains
247 eight toggle buttons that display the changes induced by each type of curation task that we are
248 considering, namely, *congruence*, *splits*, *merges*, *moves*, *renames*, *new*, *exclusions*, and an
249 additional *all* button. For example, when the *splits* switch is on, the visualization shows how
250 each taxon with a split in T_1 is divided into taxa contained in T_2. The system is flexible enough to
251 allow users to turn several buttons on at the same time, in case they want to have several types of
252 changes displayed simultaneously. For *animation* (see Fig. 1 c)) additional controls to play and
253 stop animations were added.
254
255 The color-coding scheme of the toggle buttons is also the same across all methods and defines
256 the types of changes to be visualized. Blue indicates congruent taxa, pink stands for splits,
257 orange for merges, light green for moves, light brownish purple for renames, red for exclusions,
258 and green for added taxa. The representation of relations depends on the comparison method. For
259 agglomeration, relations have to be inferred since data is interleaved and no explicit additional
260 marks or lines can be included easily. Hence, for this method we decided to use an augmented
261 color code in order to have a cue that would make it easier for participants to recognize to which
262 taxonomy a node belongs and to highlight the types of changes between T_1 and T_2 (i.e., the
263 relations between nodes). For this, we use the same hues but with different intensity, so the light
264 nuanced nodes in the agglomerated structure indicate that they belong to the taxonomy of origin
265 T_1 while the darker nuanced nodes indicate that they belong to the taxonomy of destination T_2. A
266 legend was added to explain this color-coding. In the *agglomeration* method relations are
267 permanent but not explicit.
268
269 In the *edge drawing* and *matrix* methods, relations are explicit and permanent. For instance, with
270 the *edge drawing* method, a split of a taxon x in T_1 into taxa p, q, and r in T_2 is shown as three

271   pink edges going horizontally from taxon x to p, q, and r in taxonomy T_2. In the *matrix* method,
272   the same split case is shown as marked colored cells $(x; p)$, $(x;q)$, and $(x; r)$ respectively.
273
274   For *animation*, we considered two design choices: "animation by movement" and "animation by
275   emergence". In the former, an animation consists of moving the target taxon from T_1 to its new
276   position in T_2. In the latter, the target taxon would fade out from T_1 and would gradually appear
277   in T_2. In either case, relations are explicit although temporary because they disappear when the
278   animation is finished. We chose the first option because the paths followed by each moving
279   taxon provides better traceability cues than the second one. Considering the split case described
280   above, the animation would show x moving towards taxonomy T_2. On its way, x splits and
281   disappears to let p, q and r appear and keep moving until each of them reaches its definitive
282   position in T_2. The *animation* method per se does not necessarily involve leaving an explicit trace
283   (as *edge drawing* does).
284
285   Two curation tasks do not involve relations between nodes in the alternative taxonomies,
286   namely, *identify new taxa added* and *identify excluded taxa*. Given that inclusions and exclusions
287   take place only in one of the taxonomies, the system visualizes these situations only in the
288   taxonomy in which they occurred. Thus, excluded taxa are visualized in red color in taxonomy
289   T_1 and included taxa in green color in taxonomy T_2. Without the use of color, asking users to
290   visually infer which taxa were excluded from T_1 and which ones were included into T_2 would
291   require too much mental effort, specially when taxonomies are large.
292
293   The software was developed for the purpose of evaluating the methods, it was not intended to be
294   a final product, therefore, some interaction functions were only implemented at a basic level, e.g.
295   navigation and zoom, and other functions were not included at all, e.g. the search function and
296   statistics. We developed the software incrementally through several iterations until we reached
297   balanced implementations of the four methods. At the end of each iteration, computer science
298   students tested the software. Tests were also conducted involving an experienced taxonomist and
299   a PhD student in computer science.
300

301   **Participants**
302   Twelve experts from our professional network participated in the assessment. Table 2
303   summarizes the participants' profiles. Each participant was given an identification number,
304   ranging from E1 to E12. Eight of them are botanists (three of which are also Forestry engineers),
305   two biologists (one entomologist and one ichthyologist), one ecologist, and one computing
306   engineer (with 21 years of experience in biodiversity informatics). In addition, three of them
307   reported Biodiversity Informatics as a second area of expertise. One participant holds an
308   Engineering degree, five have a Master's degree, and six have a PhD degree. Their average
309   professional experience was 28 years and their average experience in the taxonomy field was 23
310   years; this includes taxonomic classification, taxonomy nomenclature, and curation of biological
311   taxonomies. Ten participants are male and two female. Three participants worked as full time
312   university professors and the rest worked full time at herbaria, museums, or biodiversity
313   conservation initiatives. Participants came from three different countries and their expertise was
314   with different taxonomic groups of organisms.
315

316   **Datasets**

317   We carefully selected and designed the datasets, taking into account the level of familiarity
318   participants might have with the data. Although taxonomists, in general, have extensive
319   knowledge on certain groups of species, in practice, a taxonomist is only expert on a limited
320   group of organisms. In addition, because of the large number and complexity of groups of
321   species, their expertise is also geographically focused. Thus, despite of having ten botanists in
322   our group of experts, all of them specialize in different groups of plants. In order not to favor any
323   participant and avoid the eventual bias, we did not choose groups of species that were known by
324   any of the experts. Therefore, we chose an unfamiliar taxonomy. It should not be very large since
325   we did not want to burden participants by spending too much time performing the user study.
326   However, at the same time, the dataset should be large enough to contain representative cases of
327   all types of changes. We therefore used a small-size real taxonomy and derived artificial variants
328   from it.
329
330   We downloaded a set of 66 species of amphibians from the Catalogue of Life website
331   (http://www.catalogueoflife.org/) with a total of 96 nodes. We called this the *seed taxonomy*
332   from which we derived variations on the datasets (derived taxonomies) to be used for each
333   method. We programmed an *artificial taxonomy generator* to which we input as parameters the
334   percentage of splits, merges, movements, renames, additions, and exclusions that we wanted to
335   add to the seed taxonomy T_1. The generator randomly selected the taxa to introduce the changes
336   and verified that only one change was introduced to each taxa to be modified. In this way, we
337   prevented data conflicts, since more than one change to a taxon could generate inconsistent data.
338   We also verified that, although questions were identical, the datasets would produce different
339   answers for each method. The amount of nodes in the derived datasets varied between 78 to 116
340   nodes. Table 3 describes the main characteristics of the four derived datasets, that is, the amount
341   of nodes, of species, of splits cases, merges, moves, renames, new, and excluded taxa. The goal
342   of this setup was to ask experts to visualize changes in four pairs of datasets: (T_1, T_2), (T_1, T_3),
343   (T_1, T_4), and (T_1, T_5), with respect to *edge drawing*, *matrix*, *animation*, and *agglomeration*,
344   respectively. The derived datasets T_2, T_3, T_4 and T_5 are similar because they are all obtained from
345   the seed taxonomy and have roughly the same number of changes. We avoided the use of the
346   same pair of datasets across all visualization methods in order to neutralize a potential bias
347   introduced by a learning effect.
348

349   **User Study Protocol**
350   We planned the user study for a 2-hour session with each participant. During the session,
351   participants would work with the interactive software environment to perform some exercises
352   and to answer questions from a questionnaire. Seven out of the twelve experts lived overseas;
353   therefore, the session was conducted remotely via a video call for them. For the rest of
354   participants, sessions were face-to-face. For participants in remote sessions, at the beginning of
355   the session, we shared a link were the software and data were hosted. In case of the face-to-face
356   interviews, we supplied a laptop computer. In both settings, access to the software environment
357   was via web browser. We followed the same interview protocol for all participants.
358
359   A written guide and a 15-minute descriptive video of the software environment were available to
360   the participants at least two days before the session, so that they could get familiar with it.
361   Access to the software environment, datasets, and questionnaire was not provided before the
362   interview session.

363

364 A moderator was in charge of leading the session and assisted participants, while an observer
365 was taking notes. Participants did not have to write down the answers; both the moderator and
366 the observer would write the participants' answers on an answer sheet that they had previously
367 prepared. Audios of the interviews were recorded for later confirmation of answers and analysis.
368 At the beginning of the session, we checked to see if the participants had studied the guide and
369 video beforehand and if they had any questions. In case they had not done so or if they needed to
370 clarify any aspect, the moderator offered a demonstration of the software and resolved the
371 doubts. Exercises were not started until both the participant and moderator felt they were ready;
372 only then did the moderator provide the link for participants to access the interactive
373 environment. Working speed was not to be measured and participants were made aware of the
374 fact that they had no time limit to answer the questions and were able to express any inquiry,
375 doubt or suggestion at any time. Participants were also asked and reminded to think aloud while
376 solving the questions. Our goal was to get insights on how they carry out the data exploration
377 and the tasks.

378

379 We designed an instrument that consists of twelve task performing exercises, nine method
380 assessment questions and one open-ended comments section. The task performing exercises have
381 clearly correct answers and were intended to measure the participants' effectiveness. The method
382 assessment questions were intended to obtain participants' perception. The purpose of the open-
383 ended question was to obtain additional feedback on user satisfaction and suggestions for a
384 future design of an interactive visualization system. The study started with an exercise where
385 participants had to identify the most common type of change (overview task). Next, exercises
386 were targeted to identify splits, merges, renames, moves, added or excluded taxa, and ended with
387 an overview question again. Each task-performing exercise had to be answered with each
388 method. For instance, instructions such as "Use the Matrix method: Explore the visualization and
389 find into what taxa *Babina caldwelli* was split?" were followed by the same question for all
390 methods. However, the taxon to be used in each exercise (*Babina caldwelli*) was different for
391 each method.

392

393 We randomized the order in which participants used each method on each question. Participants
394 performed the exercises related to one task (for instance, identification of splits) and then were
395 asked to assess each method to perform such task. The nine method-assessment questions
396 consisted of five-level Likert scale items that assessed how good each method was to carry out
397 the task. In the course of the session, participants had access to a copy of the questions and
398 instructions, especially because taxa names were in Latin, and we wanted to avoid any
399 confusion.

400

401 **Analysis**
402 For the analysis of the results, we organized the participants' responses into a spreadsheet. We
403 gathered three types of data: a) the effectiveness data, i.e., whether the participants answered
404 each question correctly or incorrectly, b) the user satisfaction data, i.e., the Likert-scale ratings
405 that participants gave to each method after accomplishing each task, and c) the qualitative data,
406 i.e., the thinking-aloud comments and the suggestions that participants provided during the
407 session. Quantitative analysis was performed on data of types a) and b) by using a statistical
408 package. We used non-parametric statistics with alpha=0.05, and compared medians to

409 determine that differences are not due to chance. For the analysis of effectiveness, we used the
410 Cochran's Q test, which can be used when you have a group of people performing a series of
411 tasks where the outcome is dichotomic (e.g. success or failure). For the analysis of participants'
412 satisfaction, we used the Friedman test, which is appropriate for within-subjects designs that
413 have three or more conditions, and particularly it can be used for the analysis of ordinal data,
414 such as the Likert-scale responses (MacKenzie, 2013). When necessary, both tests were followed
415 by pairwise comparison using Dunn's test with Bonferroni correction.
416
417 For the qualitative analysis, we applied the following procedure. The responses were first placed
418 in the same order in which the questions were presented to the participants, and, then, they were
419 sorted by method. Two columns were designated for each participant, one to record their
420 comments and suggestions (e.g., E1) and another one to afterwards register the codes generated
421 during the qualitative analysis (e.g., E1-codes). Secondly, we listened to the audio recordings
422 checking for additional feedback from the participants, which we added to the spreadsheet.
423 Thirdly, we conducted a qualitative analysis: the first author made several coding passes using
424 *open coding* (Charmaz, 2006) to obtain a first coding version that was then shared with the other
425 authors. We coded participants' interactions and feedback. Repeated or related topics were
426 grouped together, revised and re-grouped through several refinement cycles until we reached an
427 agreement with twelve categories to finally conclude with four meaningful themes. During the
428 process, we also organized the positive and negative comments, as well as the participants'
429 suggestions for improving the methods.
430

431 ## Results
432
433 The study took 2:15 hours on average per participant. We first present quantitative results on
434 participants' effectiveness and satisfaction, and then findings from the qualitative analysis.
435
436 **Effectiveness**
437 The results of the participants' effectiveness on the task-performing exercises are summarized in
438 Table 4. Overall results indicate that participants obtained more correct answers with *matrix*
439 (94%), then with *edge drawing* (88%), followed by *animation* (87%) and then with
440 *agglomeration* (73%). We tested for statistical significance by using Cochran's Q test for N=12
441 and DF=3. We did not find significant differences on participants' responses between pairs of
442 methods (*matrix*, *edge*), (*matrix*, *animation*), and (*edge*, *animation*). However, we did find
443 differences (χ^2=40.480, p-value = 0.05) between agglomeration (73%) and the other methods,
444 meaning that participants were less effective with the agglomeration method.
445
446 We also did a quantitative analysis on responses to each exercise. We did not find significant
447 differences among participants' responses when identifying: a) into which taxa a taxon was split
448 (exercise 2), b) whether species were merged and how (exercises 4 and 5), c) whether species
449 were renamed (exercises 6 and 7), d) whether any species were added to a version of the
450 taxonomy (exercise 9), and e) whether any species were excluded (exercise 10). We found
451 significant differences in participants' responses in identifying: a) an overview of changes
452 (exercises 1 and 12), b) which species were most divided (exercise 3), c) moved taxa (exercise
453 8), and d) all changes on a taxon (exercise 11). For these cases, a post hoc pairwise comparison
454 was performed in order to determine where the differences occurred:

- Exercise 1. Overview of changes. We found differences (χ^2=25.500, p-value < 0.05) between the following pairs of methods: (*animation, edge drawing*), (*matrix, edge drawing*) and (*agglomeration, edge drawing*). This indicates that the effectiveness with *edge drawing* (8%) was lower with respect to *agglomeration* (75%), *animation* (92%) and *matrix* (92%).
- Exercise 3. Identification of splits. We found differences (χ^2=17.571, p-value <0.05) between pairs of methods (*edge drawing, agglomeration*) and (*matrix, agglomeration*). These results indicate that the effectiveness with *agglomeration* was different with respect to the other methods. Participants were less effective with *agglomeration* (33%) and more effective with *edge drawing* (100%) and *matrix* (92%).
- Exercise 8. Identification of moved taxa. We found differences (χ^2=21.000, p-value < 0.05) between pairs of methods (*animation, agglomeration*), (*edge drawing, agglomeration*), and (*matrix, agglomeration*). This indicates that participants were less effective with *agglomeration* (42%) whereas they were more effective with the other methods (100%).
- Exercise 11. Focus on a taxon. We found differences (χ^2=9.692, p-value < 0.05) between the pair of methods (*agglomeration, matrix*). This indicates that participants were less effective with *agglomeration* (50%) and more effective with *matrix* (100%).
- Exercise 12. Overview of changes. We found differences (χ^2=10.714, p-value < 0.05) between pairs of methods (*animation, agglomeration*), (*edge drawing, agglomeration*), and (*matrix, agglomeration*). This indicates that participants were less effective with *agglomeration* (17%) than with *animation* (58%), *edge drawing* (58%), and *matrix* (58%).

Satisfaction Level

Right after carrying out the task-performing exercises for each task, participants answered a Likert-scale questionnaire to assess the methods. The questions had the following structure: "How good do you think each method is in order to perform task t? For each method provide a rating between 1 and 5, where 1 stands for 'poor', 2 for 'fair', 3 for 'good', 4 for 'very good', and 5 for 'excellent'". We performed a statistical analysis on the participants' ratings using the Friedman test. Table 5 summarizes the results for N=12 and DF=3. We did not find any difference in participants' responses to accomplish the task for the identification of excluded species (question 10e). Neither we found differences regarding the identification of added species (question 9e) after running the post pairwise comparison. On the contrary, we found differences in participants' responses to carry out tasks for the identification of the most common type of change (1e), splits (3e), merges (5e), renaming (7e), moves (8e), changes to a taxon (12e) and the general methods assessment question (13). The post hoc pairwise comparison gave the following results:

- Question 1e-overview (χ^2=12.588, p-value =0.05). We found differences between pairs of methods (*animation, edge drawing*). Participants gave a better rating to the *edge drawing* method (median = 3.29) than *animation* (median = 1.79).
- Question 3e-splits (χ^2=33.055, p-value = 0.05). We found differences between pairs of methods (*agglomeration, matrix*) (*agglomeration, edge drawing*) (*animation, matrix*), and (*animation, edge drawing*). There was no difference between *agglomeration* and *animation*, and neither *matrix* and *edge drawing*. Participants ratings for *agglomeration* (median = 1.50) and *animation* (median = 1.50) were the lowest while for *matrix* (median = 3.21) and e*dge drawing* (median = 3.79) were the highest ones.

- Question 5e-merges (χ^2=20.050, p-value = 0.05). We found differences between pairs of methods (*animation*, *edge drawing*) and (*agglomeration*, *edge drawing*). Participants assessed the *edge drawing* method with the highest rating (median = 3.71) compared to *agglomeration* (median = 2.0) and *animation* (median = 1.71).
- Question 7e-renames (χ^2=21.559, p-value < 0.05). We found differences between pairs of methods (*animation*, *edge drawing*) and (*agglomeration*, *edge drawing*). Participants assessed the *edge drawing* method with the highest rating (median = 3.67) than *agglomeration* (median = 2.13) and *animation* (median = 1.50).
- Question 8e-moves (χ^2=24.295, p-value = 0.05). We found differences between pairs of methods (*agglomeration*, *edge drawing*) and (*animation*, *edge drawing*). Participants assessed the *edge drawing* method with the highest rating (median = 3.83) than *agglomeration* (median = 1.54) and *animation* (median = 1.88).
- Question 12e-focus (χ^2=16.057, p-value = 0.05). We found differences between pairs of methods (*animation*, *edge drawing*) and (*agglomeration*, *edge drawing*). Participants assessed the *edge drawing* method with the highest rating (median = 3.46) than *agglomeration* (median = 1.88) and *animation* (median = 1.79).
- Question 13-general assessment of all methods. (χ^2=16.057, p-value = 0.05). We found differences between pairs of methods (*animation*, *edge drawing*) and (*agglomeration*, *edge drawing*). Participants assessed the *edge drawing* method with the highest rating (median = 4.97) than *agglomeration* (median = 2.97) and *animation* (median = 2.84).

It is important to notice that response for question 13 summarizes the participants' level of satisfaction.

Findings from Qualitative Analysis

Regarding *edge drawing*, all participants referred to this method throughout all exercises with expressions such as: "easy", "very direct", "I can easily relate taxa", "it is very fast", "I do not have to think too much", and "you can see ... at a glance". One participant (E6) said that it was the best because "you can clearly see the origin and the destination". Another participant (E7) considered that *edge drawing* "is familiar, it is similar to an 'associate' type of exercise".

Participants' feedback on *matrix* highlighted this method as good for the visualization of general overviews and the identification of patterns, eight participants mentioned it (E2, E3, E7, E8, E9, E10, E11, and E12). Five participants (E6, E7, E10, E11 and E12) mentioned that *matrix* was the fastest one. Another participant (E2) recognized that "it is easy to see in a row the changes to a taxon". Three participants (E10, E11 E12) considered that the required vertical and horizontal scrolling add complexity and two other participants (E2 and E10) mentioned that scaling could be a problem. One participant (E1) complained that he had to use his fingers on the screen to follow the relations in the two dimensions. Eleven participants complained about the vertical name implementation in the top hierarchy (all except E2), and two participants (E1 and E10) found navigation difficult because parts of the hierarchies were off the screen.

Regarding *animation*, two participants (E1 and E8) rated it positively indicating that it was "dynamic", and therefore "fun". However, eight out of the twelve participants described this method in negative terms such as "difficult", "ineffective", "hard to follow", "complicated", "not intuitive", and "waiting until the end of the animation is a waste of time". Five participants

546 considered that the *animation* was not necessary. Participants emphasized that changes between
547 the two taxonomies were very difficult to follow because they could very soon forget what
548 happened, especially if taxonomies were large. Five participants indicated that, while taxa were
549 moving, it was easy to lose track of the relation between origin and destination because the taxa
550 were moving. Most participants speeded up the animation, giving the impression that they
551 wanted it to get to an end quickly, but some had to execute it several times before being able to
552 solve the exercise.
553
554 Participants indicated that it was very difficult to carry out the tasks with the *agglomeration*
555 method, except for the identification of excluded taxa. Eight participants (E2, E5, E7, E8, E9;
556 E10, E11, E12) referred to *agglomeration* as very good when looking for specific taxa or to
557 focusing on a small part of the taxonomy. However, all participants also described it in negative
558 terms, such as "difficult", "very complicated", "requires too much effort", "not evident",
559 "confusing", and "very difficult to know origin and destination". Participants complained that
560 this method involved many variables that were difficult to remember (that is, many color hues)
561 and that it required considerable effort to recognize differences. However, two participants
562 thought that the *agglomeration* view could be complementary to *edge drawing*, and that it could
563 work well for small taxonomic groups.
564
565 We coded and organized the participants' feedback until we reached themes that we considered
566 meaningful. Our observations show four specific issues that are relevant when performing tasks
567 for the curation of biological taxonomies:
568
569 • **Explicit representation of changes**. Changes are visualized through relations among taxa. Nine
570 out of twelve participants clearly indicated that being able to identify the origin and
571 destination of relations was very important to recognize changes when comparing biological
572 taxonomies. Participants' suggestions such as; "add edges to animation", "add edges to
573 matrix", or "add numbers to each change in the agglomeration method" are indications that
574 they would prefer to see relations explicitly and, therefore, prefer methods that explicitly
575 represent the changes.
576 • **Efficiency**. Participants often commented about speed and time needed to solve the exercises.
577 Across exercises, they referred to the importance of understanding what is going on at a
578 glance. They expressed feeling frustrated when having to wait for the animation to end. They
579 speeded up the animation when they felt that solving the exercise was taking too much time.
580 Participants considered that having to scroll horizontally and relate rows and columns of the
581 matrix or having to interpret different colors as in agglomeration were steps that consumed
582 time.
583 • **Multiple views**. Several participants commented that the methods could be complementary;
584 for instance, that the *edge drawing* and the *matrix* methods could be used to visualize all
585 cases at once whereas the *animation* and the *agglomeration* methods could be useful when
586 analyzing smaller groups of species. They explained that, by combining several methods, the
587 advantages of one method could overcome the disadvantages of another one. On the other
588 hand, the experts also emphasized the convenience of having both overview and detailed
589 views; the first one to obtain a general understanding of changes and the second one to obtain
590 detailed information on a focused part of the taxonomies.

591 • **Visual and numerical summaries**. When asked for amount of taxa that match a certain
592 condition, participants expressed their frustration because they had to count manually and
593 suggested to add statistics to the software environment. Although obtaining statistical
594 information is one of the tasks for the curation of biological taxonomies, we decided to leave
595 it out of this study on purpose in order to force participants focus on the visualizations. The
596 intention of quantity-related questions was to see if participants were able to visually identify
597 magnitude of changes (for instance, matrix resulted good). We obtained confirmation on the
598 importance of providing numerical understanding of changes.
599
600 **Suggested Improvements**
601 The methods that received most suggestions for improvement were the ones that had the lowest
602 participants' effectiveness and preference. Suggestions for agglomeration focused on
603 mechanisms that would make the relations explicit somehow and allow them to be recognized
604 quickly. For instance: a) add numbers instead of different color hues to indicate taxa of the
605 origin and taxa of the destination, b) use a different color hue for each change (not only for each
606 type of change), c) instead of using several color hues, consider glyphs or some other visual
607 cues, d) color the background of the text instead of the text, e) visually separate the taxonomies
608 on user's demand, f) separate the legend so that hues associated to origin are placed on the left
609 side and the hues associated to the destination are placed on the right side of the screen. For
610 animation participants provided suggestions such as: a) add a time slider and a rewind button, b)
611 identify each change with a number, c) add traces as in edge drawing, d) identify each specific
612 change with a different color, e) maybe consider the use of animation for comparing a small part
613 of the taxonomies. For matrix, participants also made suggestions to improve the visualization of
614 relations; for instance, a) add a feature to freeze rows or columns in place and ease the
615 visualization of relations when vertical or horizontal scrolling is needed, b) add horizontal and
616 vertical guiding lines to ease following the relations, c) add a colored rectangle around the
617 excluded or added taxa in order to highlight these changes, d) add edges in order to make the
618 relations more explicit, e) consider the matrix method as a way to feed a database with the
619 relations between the two taxonomies. Suggestions for edge drawing included: a) use more
620 intense color hues and b) provide features that ease the comparison between taxa of higher
621 taxonomic ranks (for instance, at the family level). Three participants (E3, E5, E6) mentioned on
622 several occasions that the identification of relations was easier when the involved taxa were
623 closer together, within the same view. They expressed this thought as they were solving matrix
624 and agglomeration exercises. On the other hand, four participants (E3, E6, E10, E12) mentioned
625 that vertical scrolling was fine in edge drawing, since "it is very familiar". Feedback obtained
626 from the open-ended comments section of the questionnaire also included suggestions for
627 enhancements to the implementation of the methods. Regarding the representation of hierarchies,
628 participants' suggestions included the elimination of lines that indicate hierarchical structure and
629 to use only indentation as a visual cue to recognize hierarchy (some participants believed that the
630 visualization could look cleaner). They also mentioned that the visual clutter caused by long
631 names might be overcome by using abbreviations when possible (for instance, for the genus part
632 of the species names).
633

Discussion

635

636   The research question we investigated was how well each of the four methods of hierarchy
637   comparison supports the tasks of curing two versions of a taxonomy. The quantitative and
638   qualitative results revealed differences among the methods. The difference in effectiveness
639   occurred only with respect to agglomeration, as the participants were the least effective with this
640   method. One likely explanation is that in all methods, the changes between the two taxonomies
641   were consistently represented throughout predetermined colors for each type of change, but in
642   agglomeration each change was represented by two tonalities of the predetermined color, one to
643   indicate the taxon of origin and the other to indicate the taxon of destination. This might have
644   added complexity that affected the participants' effectiveness with this method. Overall,
645   participants were very effective with the other three methods, which might be because the
646   participants could take as much time as they considered necessary to solve the exercises. The
647   number of correct answers with animation and with edge drawing was quite similar (125 and 126
648   respectively). In spite of this similarity in the participants' accuracy, and that both methods used
649   juxtaposed layouts, the user satisfaction results indicate greater participants' preference for edge
650   drawing. Comparing the amount of correct answers, participants showed similar performance in
651   many exercises with edge drawing and matrix. The difference between these two methods comes
652   mainly from the responses to the overview exercise where they had to identify "1. Which is the
653   most common type of change?" where only one participant answered correctly with edge
654   drawing and 11 participants with matrix. This might indicate that matrix works well to get a
655   general overview of changes. This is reflected also in the participants' feedback when they
656   highlighted that this method was good for pattern recognition.
657   The effectiveness on recognizing new taxa or excluded taxa was similar with all methods. This is
658   explained by the fact that both new and excluded species are visualized only in one of the
659   taxonomies, and require no relations between the involved taxonomies.
660   In another respect, we noticed that participants were more effective at identifying changes at the
661   lowest level of the taxonomy (i.e, species level) than when trying to recognize changes at upper
662   levels (such as at the genus level, exercise 12). This might suggest the convenience of having
663   summary overviews on changes at higher-level taxa.
664   Both the quantitative and the qualitative analysis coincide that the agglomeration method ranked
665   last. In spite that the results on effectiveness did not show clear differences among animation,
666   edge drawing and matrix, both the participants' feedback on satisfaction and the qualitative
667   findings suggest edge drawing in the first place.
668
669   **Threats to Validity**
670   Various factors can limit the validity of the results of these kind of studies, including the amount
671   of participants, the choice of the datasets, the design of the study, and the data analysis. After
672   completing a first set of nine interviews, we recorded the data on a spreadsheet and did a
673   preliminary processing. Afterwards, when we finished all twelve interviews, we noticed that the
674   qualitative results repeated (that is, with 33% more participants than in the preliminary
675   processing). Such consistency is an indication of dependability regarding the qualitative results.
676   A restriction of the study is the small size of the datasets, which contained between 78 and 116
677   nodes. As the data were unknown to all participants, the datasets had to be restricted to a small
678   size in order to carry out the study in reasonable time. Still, the datasets contained all types of
679   required changes to perform the tasks. In the case of the dataset for matrix, it turned out a little
680   smaller than the other ones, but large enough to allow users to experience both horizontal and

681 vertical scrolling, so we considered it was fine for the study; however, the difference in size
682 compared to the other datasets might have added some bias to the study.
683 Although the transferability of results is limited by a) the specific domain application, b) the
684 tasks studied, and c) the data sets, the comparison of hierarchical structures is independent of the
685 application domain; thus, some features of the study might contribute to other contexts where
686 users need to identify divided, joined, moved or renamed nodes between two hierarchies.
687 The within-subject design is employed in studies with a small number of participants. All
688 participants interacted with every method. In this way, we expected to reduce biases associated
689 with individual differences. However, the within-subject design may bias participants because of
690 the carry over effect; that is, once participants perform a task with one method they may expect
691 certain conditions to happen in the next method to evaluate. We tried to counterbalance bias from
692 the learning and tiring effects by asking participants to interact with the methods in a randomly
693 established order. In addition, although the questions were identical, the data sets would produce
694 different answers for each method in order to prevent the learning effect.
695 A bias may be introduced by the design of the study or the design of the interactive software
696 environment. We tried to implement the essence of the methods as well as to keep a standard
697 user interface for all visualizations (same main menu and color codes throughout all methods),
698 but some limitations may come from implementation decisions. For instance, zooming and
699 scrolling features were limited and not designed for large amounts of data; also, participants
700 were unsatisfied with regard to the vertical text orientation of the matrix implementation.
701 We aimed to objectively examine the collected data. For the quantitative part of the study, we
702 used statistical tests to analyze if the differences between the medians were significant. For the
703 qualitative part of the study we carefully organized the data and coded the participants' feedback
704 and interactions through several refinement cycles. By counting and grouping similar feedback
705 from participants, we were able to define the codes and themes. Nonetheless, the interpretation
706 of the data may be subject to the perspective of the researchers.
707
708 **Implications**
709 The participants performed well with edge drawing and consider it, in general, the best method;
710 despite they did not have the best performance with it. For overview tasks, participants showed
711 similar effectiveness with matrix and animation, however they preferred matrix.
712 Results indicate that identifying explicitly the origin and destination of taxa is very relevant for a
713 more efficient identification of changes; edge drawing and matrix methods seem to have
714 facilitated it. The participants' need to determine origin and destination may explain that edge
715 drawing outperformed animation in both effectiveness and user satisfaction. Both methods
716 present the taxonomies in a juxtaposed layout, however, relations are not explicit in animation.
717 Some participants considered that animation could be useful to focus on changes in small
718 taxonomic groups, which reaffirms the scope of animations, as indicated by Graham and
719 Kennedy [11].
720 During the sessions, we noticed that sometimes taxonomists wanted to see the big picture and
721 then focus on a smaller group of organisms of their interest. Also, sometimes they wanted to go
722 directly to the group they want to inspect. Thus, future research should consider easily toggling
723 between overview and detailed views as well as search and filtering functions. Text (that is, taxa
724 names) is crucial when comparing taxonomies. Visual cues such as color, size, shapes or glyphs
725 are not enough to recognize the differences and similarities. Text must be legibly. The users
726 would have to read names, which would need to be accommodated efficiently avoiding

727 cluttering. Unlike other studies, we were not assessing how participants use the tool [18], neither
728 we were measuring the prototype efficiency for comparing hierarchies [12]. Instead, our
729 contribution lays in the assessment of the four visualization methods for the comparison of pairs
730 of biological hierarchies with respect to curation tasks.
731
732

733 ## Conclusions and Future Work

734

735 This study contributes insights on the capacity of four visualization methods for hierarchy
736 comparison in typical biological taxonomy curation tasks. Twelve expert taxonomists took part
737 in a study and provided feedback. We performed quantitative as well as qualitative analysis. The
738 results clearly show differences among the methods, on both users' effectiveness and
739 satisfaction: the edge drawing method was preferred over other methods.
740 In this study, the data sets were selected to avoid bias, all participants used the same datasets, and
741 participants were able answer the questions in reasonable time. However, it will be interesting to
742 design a similar study with larger datasets. Another approach would be to design a study in
743 which the data would be specific and familiar to each participant.
744 Enhancements such as providing multiple views, adding visual cues at inner taxonomic rank
745 levels, and avoiding overloading caused by long names and hierarchical structure lines, are
746 insights for future research. Functions for searching, statistics and queries to retrieve the
747 information of a taxon will be considered in a future design of a visualization environment. We
748 also plan to further research on visual summary views to facilitate the comparison at different
749 taxonomic rank levels.
750
751

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758
759

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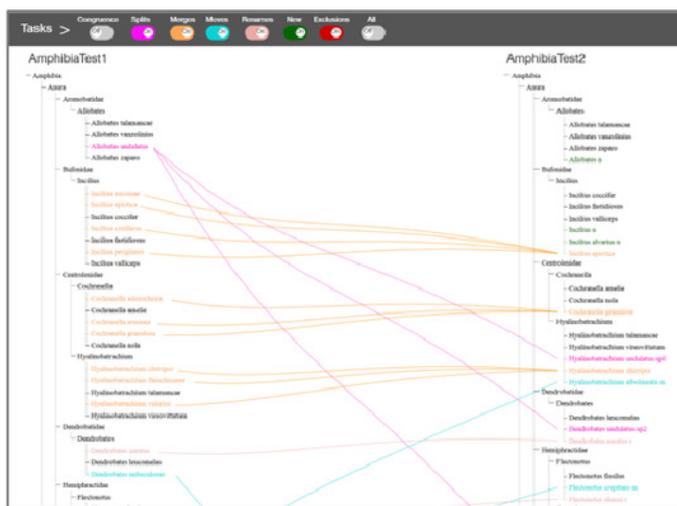
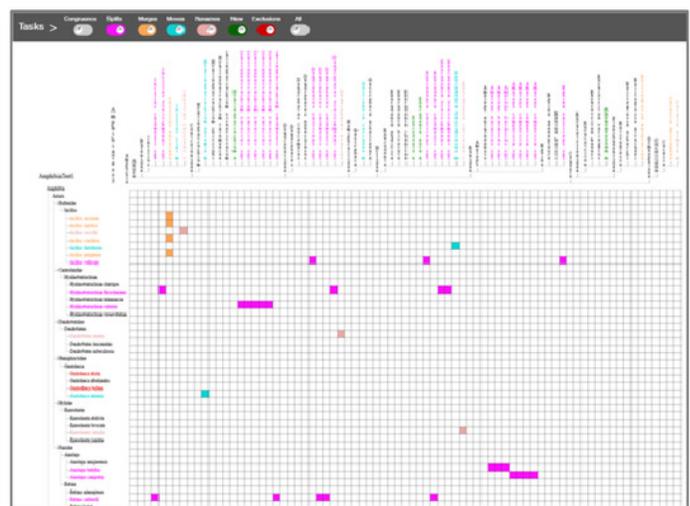
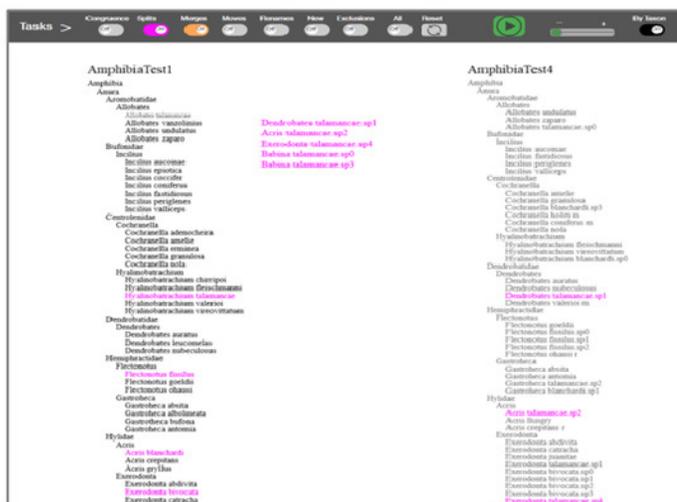
Figure 1

Visualization methods in the interactive software environment for the assessment of hierarchy comparison methods.

Each of the four implemented hierarchy comparison methods for biological taxonomies comparison.

Biological taxonomy curation tasks.

Category	Task
Pattern Identification	*1. Identify congruence*: Identify same taxonomic concepts.
	2. Identify corrections: Identify splits, merges, moves, renames.
	3. Identify additions/exclusions: Identify new or missing taxa.
	4. Overview changes: Obtain a global view of changes.
	5. Summarize: Obtain numerical understanding of change.
Query	*6. Find inconsistencies*: Recognize violation of rules (e.g. repeated names)
	7. Filter: Find cases that satisfy certain conditions.
	8. Retrieve details: Retrieve the attributes of a particular concept.
	9. Focus: Navigate and see the information in detail.
Edit	*10. Edit*: Make changes to the taxonomies.

Participants' profile.

Id	Area	Degree	Professional Experience (years)
E1	Botany, Bioinformatics	PhD	32
E2	Botany, Forestry	MSc	10
E3	Informatics, Bioinformatics	Engineer	21
E4	Botany, Forestry	PhD	28
E5	Botany	MSc	15
E6	Botany, Bioinformatics	PhD	31
E7	Botany, Forestry	Master	21
E8	Botany	MSc	21
E9	Botany	PhD	23
E10	Biology	MSc	30
E11	Ecology	PhD	12
E12	Ichthyology	PhD	32

Derived datasets.

	T_2	T_3	T_4	T_5
Nodes	116	78	105	114
Species	86	55	75	84
Splits	6	6	7	9
Merges	7	3	5	3
Moves	6	4	4	6
Renames	7	4	6	6
New	6	4	3	6
Excluded	4	3	4	8

Comparison of participants' effectiveness using Cochran's Q test.

Exercise	Frequency (%)				χ^2	p-value
	Agg	**Ani**	**Edg**	**Mat**		
1. Which is the most common type of change?	9 (75)	11 (92)	1 (8)	11 (92)	25.500	0.000
2. Into what taxa was taxon "t" split?	11 (92)	10 (83)	11 (92)	11 (92)	3.000	0.392
3. Which species was split most?	4 (33)	7 (58)	12 (100)	11 (92)	17.571	0.001
4. Was species "s" merged with any other species?	11 (92)	11 (92)	12 (100)	12 (100)	3.000	0.392
5. With which other species was taxon "t" merged?	12 (100)	11 (92)	12 (100)	12 (100)	3.000	0.392
6. Which is the new name of taxon "t"?	12 (100)	12 (100)	12 (100)	12 (100)	–	–
7. Which was the previous name of "t"?	11 (92)	12 (100)	12 (100)	12 (100)	3.000	0.392
8. Which species were moved to genus "g"?	5 (42)	12 (100)	12 (100)	12 (100)	21.000	0.000
9. Which family has the most species added?	11 (92)	11 (92)	12 (100)	12 (100)	2.000	0.572
10. Genus to which more than one species were excluded?	11 (92)	12 (100)	12 (100)	12 (100)	3.000	0.392
11. What types of changes occurred to taxon "t"?	6 (50)	9 (75)	11 (92)	12 (100)	9.692	0.021
12. Identify which genus shows most changes.	2 (17)	7 (58)	7 (58)	7 (58)	10.714	0.013
Effectiveness (overall)	**105 (73)**	**125 (87)**	**126 (88)**	**136 (94)**	**40.480**	**0.000**

Comparison of participants' satisfaction using Friedman test.

Question How good do you think is each method in order to …	Median				$\chi 2$	p-value
	Agg	**Ani**	**Edg**	**Mat**		
1e- … identify the most common type of change?	2.08	1.79	3.29	2.83	12.588	0.006
3e- ... identify splits?	1.50	1.50	3.79	3.21	33.055	0.000
5e- ... identify merges?	2.00	1.71	3.71	2.58	20.050	0.000
7e- … identify renaming of taxa?	2.13	1.50	3.67	2.71	21.559	0.000
8e- … identify moves?	1.54	1.88	3.83	2.75	24.295	0.000
9e- … identify new species added?	2.75	2.63	2.96	1.67	9.539	0.023
10e- ... identify excluded taxa?	2.67	1.88	2.79	2.67	7.062	0.070
12-e- … identify changes to a taxon?	1.88	1.79	3.46	2.88	16.057	0.001
13- ... visualize differences and similarities between two taxonomies? (Overall)	2.97	2.84	4.97	4.09	25.064	0.000