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4 **Oral Fairy Tale or Literary Fake? Investigating the Origins**
5 **of Little Red Riding Hood Using Phylogenetic Network**
6 **Analysis**

7

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21

22 *Abstract*

23

24 The evolution of fairy tales often involves complex interactions between oral and
25 literary traditions, which can be difficult to tease apart when investigating their
26 origins. Here, we show how computer-assisted stemmatology can be productively
27 applied to this problem, focusing on a long-standing controversy in fairy tale
28 scholarship: did Little Red Riding Hood originate as an oral tale that was adapted by
29 Perrault and the Brothers Grimm, or is the oral tradition in fact derived from literary
30 texts? We address this question by analysing a sample of 24 literal and oral versions
31 of the fairy tale Little Red Riding Hood using several methods of phylogenetic
32 analysis, including maximum parsimony and two network-based approaches
33 (NeighbourNet and TRex). While the results of these analyses are more compatible
34 with the oral origins hypothesis than the alternative literary origins hypothesis, their
35 interpretation is problematised by the fact that none of them explicitly model lineal
36 (i.e. ancestor-descendent) relationships among taxa. We therefore present a new
37 likelihood-based method, PhyloDAG, which was specifically developed to model
38 lineal as well as collateral and reticulate relationships. A comparison of different
39 structures derived from PhyloDAG provided a much clearer result than the
40 maximum parsimony, NeighbourNet or TRex analyses, and strongly favoured the
41 hypothesis that literary versions of Little Red Riding Hood were originally based on
42 oral folktales, rather than vice versa.

43

44 **1. Introduction**

45

46 Recent years have witnessed a boom in computational approaches to the reconstruction of
47 literary traditions, fuelled by the adoption of phylogenetic techniques from evolutionary

48 biology and the development of custom-made software for textual analysis (Howe et al.,
49 2001; Roos & Heikkilä, 2009). So far, research in this field has focused on the transmission
50 histories of hand-copied manuscripts, where the accumulation of errors and occasional
51 innovations can be modelled as a branching process analogous to the diversification of
52 biological lineages by descent with modification. Recently, it has been argued that a similar
53 approach can shed light on the evolution of oral traditions, such as folktales (Tehrani, 2013),
54 legends (Stubbersfield & Tehrani, 2013) and myths (d'Huy, 2013). Although these stories are
55 not literally copied in the way that manuscripts or DNA sequences are, their basic plot
56 elements, motifs, characters and symbols exhibit clear evidence of both fidelity of
57 transmission as well as cumulative change through time. Recent case studies (Tehrani, 2013)
58 demonstrate that careful analyses of these features make it possible to reconstruct deep and
59 robust stemmata, which can in turn yield potentially crucial insights into the origin and
60 development of oral tales.

61

62 One of the key issues in this area concerns the complex interactions between oral and
63 literary traditions, which are often difficult to disentangle. For example, it is well known that,
64 historically, many so-called fairy tales (i.e. traditional short stories containing fantastical or
65 magical elements) have been adapted by writers inspired by oral story-tellers and vice versa.
66 In such cases, it can be extremely problematic to establish in which medium a given tale
67 originated. While most folklorists have tended to assume that fairy tales are rooted in oral
68 tradition, some scholars have argued that they may in fact be derived from written texts. Most
69 notably, Ruth Bottigheimer (Bottigheimer, 2002, 2010) proposed that fairy tales are a
70 primarily literary genre that was invented by the sixteenth century writer Giovanni Francesco
71 Straparola and subsequently popularised by other authors such as Basile, Perrault and the
72 Brothers Grimm. While these authors presented their stories as though they were borrowed
73 from the tales told by common folk, Bottigheimer suggests this was simply a stylistic ruse,
74 and that the direction of transmission was much more likely to be the other way around. In

75 support of this point, she highlights that the earliest literary versions of fairy tales were
76 written centuries earlier than the supposedly more authentic oral versions collected by
77 folklorists. Bottigheimer's controversial thesis has been rejected by most experts (Ben-Amos,
78 Ziolkowski, Silva, & Bottigheimer, 2010), who point out that absence of evidence hardly
79 constitutes evidence for absence, especially given that oral traditions, by definition, lack a
80 written record. However, by the same token, nor can it be proved that oral fairy tales predate
81 the earliest written versions. In this paper, we show how techniques developed in computer-
82 assisted stemmatology can help break this impasse, and shed new light on the missing links
83 between oral and literary traditions in fairy tales.

84

85 Our case study focuses on a tale whose origin has long been the subject of intense
86 controversy: Little Red Riding Hood. The tale, which is classified as ATU 333 in the Aarne-
87 Thompson-Uther (ATU) Index of International Tale Types, famously tells the story of a
88 young girl who is attacked by a wolf disguised as her grandmother. There are numerous
89 theories about the source of the tale, from pre-Christian sun myths (Saintyves, 1989) or
90 medieval coming-of-age rites (Verdier, 1978) to Chinese folk tradition (Haar, 2006). While
91 these ideas remain difficult to substantiate, the modern tradition of Little Red Riding
92 Hood/ATU 333 can be traced back to 1697, when the first classic version of the story, *Le*
93 *Petit Chaperon Rouge*, was published by the French author Charles Perrault in his collection
94 of purportedly traditional stories, *Histoires ou Contes du Temps Passé* (Tales of Past Times)
95 (1697). A second classic version of Little Red Riding Hood (*Rotkäppchen*) was published in
96 1813 in the first volume of Jacob and Wilhelm Grimm's *Kinder und Hausmärchen*
97 (Children's and Household Tales) (1812). In this version, unlike Perrault's, Little Red and her
98 grandmother are rescued by a passing huntsman, who slices open the villain's stomach and
99 sews it up again with stones. Although, like the other tales in that volume, *Rotkäppchen* was
100 ostensibly collected from ordinary German peasant folk, Grimm scholars have established
101 that the brothers' source for the tale was actually an educated woman of French-Huguenot

102 descent named Marie Hassenpflug, who was almost certainly familiar with Perrault's
103 enormously popular *Contes* (Zipes, 1993).

104

105 While the Perrault and Grimm tales provided the model from which all subsequent
106 literary Little Red Riding Hoods are derived, the origins of the oral tradition of ATU 333, and
107 its relationship to these two "classic" versions, are much less well understood. Most
108 folklorists believe that Perrault based his tale on a traditional French werewolf tale, probably
109 from his mother's native region of Touraine, which was the site of a series of werewolf trials
110 in the sixteenth and seventeenth centuries (Zipes, 1993, p. 20). It is claimed that variants of
111 the tale survived into the nineteenth and twentieth centuries in the oral literatures of south-
112 east France, the Alps and northern Italy (Delarue, 1951; Rumpf, 1989). These tales,
113 commonly referred to as simply 'The Story of Grandmother' (following Delarue 1951) are
114 typically more gory than Perrault's censored version – for example, the girl is tricked into
115 eating some of her grandmother's remains. More importantly, rather than being a helpless
116 victim, the girl typically outwits the wolf/werewolf by tricking him into letting her go outside
117 to urinate. Although the provenance and antiquity of the tradition remains unknown, it has
118 been suggested that it may go back to medieval times. This is supported by an eleventh
119 century Latin poem by Egbert of Liège, which relates a local Walloon folktale in which a
120 young girl encounters a wolf in the woods, and is saved by the supernatural protection
121 afforded by her red tunic, a baptism gift from her godfather, (Ziolkowski, 1992). Although it
122 is debateable as to whether or not this tale represents a direct ancestor to Little Red Riding
123 Hood (Berlioz, 1991), the echo of common motifs like the young girl in the woods, the
124 villainous wolf, the red outfit given to her by a relative, etc. certainly point to some kind of
125 historical connection between them.

126

127 Nevertheless, other researchers are extremely sceptical that the oral variants held up
128 by folklorists can be regarded as "independent" descendents of the pre-Perraudian oral

129 tradition. Instead, they suggest that, like the Brothers Grimm version, these tales are more
130 likely to be vernacular interpretations of published texts. For example, in an essay that
131 strongly resonates with Bottigheimer's ideas, Hüsing (1989) writes that Little Red Riding
132 Hood “represents one of the loveliest French literary tales, perhaps being the most successful
133 fake that we have in the entire genre”, which nonetheless lacks the characteristic stylistic
134 features of authentic oral fairy tales (such as incompleteness). Similarly, Berlioz (1991) and,
135 indeed, Bottigheimer herself (2010, p. 64), argue that there is no evidence to suggest that
136 Little Red Riding Hood existed in oral tradition prior to the publication of Perrault's *Contes* at
137 the end of the seventeenth century.

138

139 In this paper, we aim to shed more light on these issues by taking a quantitative
140 stemmatological approach to investigate the relationships between oral and literary traditions
141 of Little Red Riding Hood. Our study builds on Tehrani's (2013) recent phylogenetic analyses
142 of the ATU 333 type tales, which investigated the relationships between oral European
143 variants (plus Perrault and Grimm) to similar stories from other parts of the world, especially
144 Africa and East Asia. Tehrani's study did not, however, address the question of whether Little
145 Red Riding Hood originated in an oral or literary medium, nor did it examine interactions
146 between the two traditions of ATU 333. Below, we outline how these issues were tackled in
147 this study.

148 **2. Materials**

149

150 A total of 23 texts of Little Red Riding Hood were selected for analysis (see ‘Sources’ in
151 Appendix A). To be clear, the aim of the analyses was not to produce a comprehensive
152 stemma of the Little Red Riding Hood tradition – which would involve hundreds, if not
153 thousands of texts – but to investigate a specific problem concerning the relationship of oral
154 versions of the tale to literary versions. Specifically, we sought to test whether Perrault based

155 his tale on a pre-existing oral tradition, or if both the oral and literary traditions derive from
156 the classic versions of Perrault and the Grimms published in the seventeenth and nineteenth
157 centuries respectively.

158

159 Our dataset included 12 Franco-Italian oral tales collected in the nineteenth and
160 twentieth centuries that cover most of the major variations in the plot and character found in
161 the folk traditions of these regions. For example, in some cases Little Red Riding Hood lacks
162 her characteristic red hood and is simply described as a young girl. In many variants the
163 protagonist outwits the villain to escape, but in others she is eaten. The character of villain,
164 meanwhile, can take several forms, such as a wolf, witch or werewolf. In one group of Italian
165 tales (three of which are included here) known as ‘Catterinetta’ – formerly categorized as a
166 distinct subtype of ATU 333 (Aarne & Thompson, 1961) – the villain is actually the relative
167 that the girl went to visit (usually an aunt or uncle). She/he takes revenge on the girl for eating
168 the food that was in her basket and replacing them with cakes made from donkey dung. The
169 dataset also included Egbert’s 11th century poem, the classic versions of Little Red Riding
170 Hood published by Perrault and the Brothers Grimm in the seventeenth and nineteenth
171 centuries respectively, five examples of literary versions of Little Red Riding Hood from the
172 late nineteenth and early twentieth centuries sampled from the deGrummond’s Children’s
173 Literature Research Collection curated by the University of Southern Mississippi
174 (<http://www.usm.edu/media/english/fairytales/lrrh/lrrhhome.htm>), and three oral variants
175 from beyond the hypothesised ATU 333 cradle (two from Portugal and one from Lusatia in
176 modern day Poland) that are thought to be based on literary texts, and which provide another
177 useful point of comparison with the Franco-Italian oral versions.

178

179 Next, we constructed a matrix that coded the presence or absence of 58 traits (or, in
180 phylogenetic parlance, “characters”) identified in the 23 texts. The traits included features
181 such as the red hood worn by the girl, the character of the wolf, the girl being eaten and so on

182 (the full list of characters and the matrix are provided in Appendix A). The matrix only
183 included traits that occurred in at least two tales, which might give clues about common
184 ancestry. Traits that occurred in just a single text were excluded, since these would not be
185 informative about relationships.

186

187 The matrix was analysed using several methods of phylogenetic/stemmatic
188 reconstruction, each of which are described in the sections below. We predicted that, if the
189 oral origins hypothesis is correct, then the literary tradition instigated by Perrault and also
190 comprising the Grimms' *Rotkäppchen*, later published versions and oral copies from Portugal
191 and Lusatia, should constitute a distinct lineage nested within a larger family of Franco-Italian
192 folktales. Conversely, if the latter are derived from textual sources, they would be expected to
193 comprise a lineage (or lineages) that split off from the literary tradition instigated by Perrault
194 and continued by the Brothers Grimm. In the last analysis we introduce a method,
195 PhyloDAG, that directly tests for ancestor-descendent relationships, while also allowing us to
196 incorporate contamination between texts and/or oral traditions.

197

198 **3. Phylogenetic Tree Analysis**

199

200 Our first analysis employed the most-widely used method for reconstructing relationships
201 among texts in stemmatology, maximum-parsimony (Howe et al. 2001). Maximum
202 parsimony involves finding the tree(s) that minimises the number of evolutionary changes
203 required to explain shared traits among a group of taxa (in this case, versions of Little Red
204 Riding Hood) under a branching model of descent with modification. We carried out the
205 maximum parsimony analysis in the software program PAUP 4.0* (Swofford, 1998). The
206 results are shown in Figure 1.

207

208 **Fig. 1 "Parsimony tree" about here.**

209

210 The tree is rooted using the oldest text, Egbert's 11th century poem ("Latin"), as an outgroup.
211 Under the oral origins hypothesis, Egbert's text represents the earliest known witness of the
212 oral tradition of ATU 333 prior to Perrault, so it can be assumed that all the other texts (both
213 oral and literary) are descended from a common ancestor of more recent origin. Under the
214 literary origins hypothesis, Egbert's text would be excluded from the Little Red Riding Hood
215 tradition, which is assumed to have originated six centuries later. Thus, both hypotheses
216 would position Egbert's text as an outgroup with respect to the other texts.

217

218 The tree indicates that the literary versions of Little Red Riding Hood form a clade, or branch,
219 that also includes the three oral "copies" from Portugal and Lusatia, as well as an Italian tale
220 called *Three Girls*. Although the latter is technically a folktale, it is much closer to literary
221 versions of ATU 333 than traditional versions of 'The Story of Grandmother' (for example,
222 the girl is eaten and then subsequently cut out of the wolf's stomach), and is probably derived
223 from published texts. The literary clade forms part of a larger grouping that comprises
224 variants of the Franco-Italian tale 'The Story of Grandmother', but excludes variants of the
225 Italian 'Catterinetta' tale (represented by *Catterinetta*, *Serravalle* and *UncleWolf*), which form
226 a separate lineage splitting off at the root of the tree. Thus, as predicted by the oral origins
227 hypothesis, the results of the maximum parsimony analysis suggest that the literary texts
228 share a last common ancestor (LCA) of more recent origin than the LCA of the oral variants.

229

230 It is worth noting, however, that there are some inconsistencies between the tree and existing
231 knowledge and theories about the Little Red Riding Hood tradition. For example, one of the
232 literary variants (*Goldenhood*) and a Portuguese oral "copy" (*Consigliere*) form a clade that
233 appears to be descended from a common ancestor of more ancient origin than Perrault. Since
234 the literary tradition is known to have originated with Perrault, this anomaly can probably be

235 attributed to an error of the maximum parsimony estimation, possibly as a consequence of
236 contamination (or “reticulation” in phylogenetic jargon) between the literary and oral
237 traditions. Contamination is likely to be common in fairy tale traditions as multiple oral and
238 literary versions of a tale may circulate at the same time within and between geographical
239 areas, and sometimes get mixed together (e.g. Tehrani 2013). Since the underlying model
240 used in maximum parsimony analysis does not explicitly allow for horizontal transmission
241 across lineages, it can sometimes erroneously interpret similarities that result from this
242 process as primitive traits (i.e. the traits exhibited by the hybrid taxon are assumed to be
243 inherited from an ancestral taxon that existed before the lineages leading to the two donor
244 taxa split), thereby “dragging” highly contaminated variants deeper into the structure of the
245 tree. This effect might similarly explain the position of one of the oral variants, *Joisten*, which
246 is claimed to have borrowed traits from literary texts (Zipes, 1993, pp. 5-6), but appears in
247 this tree to have split off from the LCA of the oral and literary tradition prior to the
248 emergence of the latter. Another issue with maximum parsimony analysis is that it focuses
249 solely on reconstructing collateral phylogenetic relationships (i.e. relationships based on
250 common descent), rather than ancestor-descendent relationships. Consequently, it is not clear
251 from the tree whether the position of Perrault should be interpreted as ancestral or collateral
252 with respect to the other literary variants, while the position of the Grimm text is similarly
253 ambiguous. These examples highlight the need to be cautious in drawing strong conclusions
254 from the topology of the parsimony tree, or indeed other methods that assume a pure
255 branching model of evolution.

256

257 **4. Network Analysis**

258

259 Phylogenetic networks provide an alternative approach to reconstructing cultural and
260 biological evolution where relationships are not strictly tree-like. A number of methods for

261 detecting different kinds of reticulation events have been proposed (Morrison, 2011). Many of
262 the methods are specific to certain mechanisms, for instance, recombination and therefore not
263 necessarily appropriate for modeling fairy tale traditions where the blending process is rather
264 poorly understood and probably varies significantly from case to case.

265

266 Below, we present results from two popular network methods, NeighborNet and T-
267 Rex. In addition, we present a new method, PhyloDAG, which is based on maximum
268 likelihood analysis and allows generic directed networks or DAGs (directed acyclic graph).
269 We also apply a parametric bootstrap test to compare a number of network hypotheses
270 obtained by the PhyloDAG method.

271 *4.1 NeighborNet Analysis*

272

273 A popular method for studying data that may involve reticulation is NeighborNet (Bryant &
274 Moulton, 2003), (Huson & Bryant, 2006). In the terminology of Morrison (2011),
275 NeighborNet is a data-display method. In other words, it does not attempt to construct a
276 genealogical hypothesis that accurately represents the actual evolutionary history. Rather it
277 attempts to represent the possibly conflicting phylogenetic signals in the data, so that non-
278 tree-like structures may result either by actual reticulation or by other mechanisms such as
279 evolutionary reversal or convergent evolution. Neither does the NeighborNet attempt to
280 suppress statistically insignificant signals in the data which tends to result in very complex
281 networks with a large number of non-tree-like structures.

282

283 Figure 2 shows the NeighborNet obtained for the data in our study by using the
284 SplitsTree4 software¹. The network shows similar clusters to the maximum parsimony
285 analysis, distinguishing the literary variants (including the Portuguese and Lusatian oral
286 copies) from Franco-Italian oral versions of ‘The Story of Grandmother’ and versions of the
287 Italian ‘Catterinetta’ tale, which form a separate group. The "boxiness" of the network

288 suggests probable lines of contamination within and between these sub-groups. However, the
289 network has the typical problem associated with this method, which is that the middle part of
290 the network is a very complex dense mesh of interconnected points that correspond to various
291 weak conflicting signals in the data. Furthermore, all the most of the extant versions (the
292 labelled points) are at the end of a long edge, suggesting that none of them (except perhaps
293 one root node) are ancestors of the others. This makes is very hard to interpret the result in a
294 way that would be informative for the questions we are presently considering. In particular,
295 we can tell almost nothing from the network about the influence of Perrault and the Brothers
296 Grimm on the oral tradition, or vice versa.

297

298 **Fig. 2 "NeighborNet" about here.**

299 *4.2 T-Rex Analysis*

300

301 Another technique from phylogenetics that can be used to model reticulation is T-Rex (Boc,
302 Diallo, & Makarenkov, 2012). It starts from a tree structure and by comparing the pairwise
303 distances computed from the data to the distances expected based on the tree, it identifies
304 parts of the tree that fail to accurately match the distances in the data. In case certain groups
305 of taxa are more similar to each other than the tree would lead us to expect, a reticulation
306 edge may be introduced. The underlying tree structure is obtained by Neighbor-Joining
307 (Saitou & Nei, 1987). The number of reticulation edges can be chosen by the user. We chose
308 to include five of them in an attempt to discover the most significant contamination events.

309

310 The result of the T-Rex analysis is shown in Figure 3. The backbone phylogeny is
311 largely similar to the parsimony tree, and indicates that the literary versions of Little Red
312 Riding Hood form a branch that split from the lineage leading to modern oral variants of the
313 traditional Franco-Italian tale ‘The Story of Grandmother’. Versions of the Italian tale
314 ‘Catterinetta’ form a sister group to these tales. One notable difference between the T-Rex

315 phylogeny and the parsimony tree is the position of *ThreeGirls*. As mentioned above,
316 *ThreeGirls* is an Italian oral tale that shares notable features in common with the
317 Grimms' *Rotkäppchen*. Whereas the parsimony analysis indicated that *ThreeGirls* was likely
318 to be derived from literary texts (as per the Portuguese and Lusatian oral versions of ATU
319 333), T-Rex suggests that *ThreeGirls* is descended from an oral ancestor that preceded the
320 literary tradition, but has been contaminated by the latter (N.B. although the reticulation edges
321 in T-Rex are undirected, the well-documented influence of literary fairy tales – particularly
322 the Grimms' *Kinder und Hausmärchen* – on European oral traditions (Zipes, 2013) support
323 this interpretation). This is consistent with the NeighbourNet graph, which grouped
324 *ThreeGirls* with oral variants, but indicated substantial conflict in the data surrounding its
325 relationships to other tales. The T-Rex analysis proposed several other reticulation edges that
326 suggest substantial mixing within regions between literary and oral traditions of ATU 333,
327 notably between Perrault's classic text and French oral tales, and between the Italian variants
328 of 'The Story of Grandmother' and 'Catterinetta'. More puzzlingly, the structure also
329 suggests contamination from the Egbert's medieval poem and a modern literary version of
330 Little Red Riding Hood (*CupplesLeon*). Since a careful reading of both texts revealed no
331 obvious link between them (e.g. characteristic features of the medieval version that occur in
332 *CupplesLeon* but not in the Perrault or Grimm tales from which it is certainly derived)) we
333 assume this to be an estimation error (the precise cause of which would require a more
334 detailed deconstruction of the search algorithm that is beyond the scope of the current paper).
335 A more general problem with the interpretation of the results of the T-Rex analysis is that,
336 like the parsimony and NeighbourNet structures, all the variants are represented as leaf nodes.
337 Consequently, it is not easy to evaluate direct lines of descent between historical and modern
338 variants, most particularly the relationships of Perrault and the Brothers Grimm to literary and
339 oral tales that were published/recorded more recently.

340

341

Fig. 3 "T-Rex" about here.

342 *4.3 PhyloDAG*

343

344 We will now propose an alternative approach to network analysis. Our approach is likelihood
345 based and, as we will show below, it solves many of the issues in existing network and tree-
346 based methods.

347

348 Likelihood based phylogenetic inference involves a probabilistic sequence evolution
349 model characterizing the evolutionary process. A popular example of such a model is the
350 Jukes-Cantor model (Jukes & Cantor, 1969) that gives the probability of the four DNA
351 symbols, A,T,G, and C, changing into other symbols or remaining unchanged in a certain
352 period of time, and also depending on the mutation rate. Given such a model, the likelihood
353 of a phylogenetic tree is obtained as the probability that the observed data sequences are
354 produced when the tree structure is fixed and the lineages evolve independently according to
355 the sequence evolution model and branching occurs according to the tree structure. The
356 maximum likelihood method for phylogenetic inference attempts to find the tree structure,
357 including the edge lengths that determine the expected amount of change along each edge, for
358 which the likelihood is the highest possible.

359

360 Strimmer and Moulton (2000) describe a simple extension of the likelihood defined
361 for phylogenetic trees that is also applicable to networks, hence allowing reticulation edges to
362 be added into a tree. We improve and extend the method by Moulton and Strimmer in two
363 ways. First, we introduce a more efficient technique for approximating the likelihood of
364 phylogenetic network. Second, we propose a simple search procedure that considers
365 additional reticulation edges in a given tree structure and also estimates the edge lengths by a
366 simple sampling technique. As a result, our method which we call PhyloDAG operates in a
367 similar fashion as T-Rex: it takes as input a matrix of character data such as DNA sequences
368 or a set of features, and an initial tree structure, and produces a network where a given
369 number of reticulation edges have been added to the tree, together with its likelihood value. In

370 contrast to T-Rex, however, PhyloDAG can be used to evaluate tree and network structures
371 where some of the extant taxa are placed at internal nodes so that they represent ancestors of
372 some of the other taxa. For a more detailed description of the PhyloDAG method, see
373 Appendix B. Different network or tree structures can be compared using a statistical test
374 known as the parametric bootstrap, which we will also outline below, see Appendix C.

375

376 We start the PhyloDAG method with a parsimony tree, Fig. 1, obtained from data
377 matrix in Table II. We then use PhyloDAG to evaluate its likelihood (setting the number of
378 reticulation edges to zero). The parsimony tree yields log-likelihood the value -863.4 .²

379

380 Next, we manipulated the topology of the tree to explore different scenarios
381 concerning the origins of the literary and oral traditions of ATU 333. This involved moving
382 the Perrault and Grimm texts into different internal positions in the tree where they would be
383 either ancestral to both the oral and literary variants, or ancestral to the literary variants and
384 collateral to the oral variants (i.e. descended from a common oral ancestor). We did not
385 attempt manipulations which are incompatible with existing knowledge about the tales, such
386 as the chronology of the literary variants (for example, we did not experiment with making
387 Grimm's 1812 tale ancestral to Perrault's 1697 version). It is important to note that these
388 manipulations alone will not, as a rule, yield a higher likelihood score than a normal tree. This
389 is because any such manipulated tree is equivalent to a special case of a tree where the taxon
390 in the internal position is in fact a leaf node but the edge pointing it has length zero. Hence,
391 the likelihood value of the tree where the taxon is a leaf node will never be lower than the
392 likelihood of the tree where it is an internal node when the edge lengths in both models are
393 optimized so as to maximize the likelihood. The interesting question is whether a
394 hypothesis involving observed ancestral taxa is better when we allow possible contamination,
395 i.e., reticulation edges in addition to the tree. The PhyloDAG method provides a tool for
396 answering this question.

397

398 We used PhyloDAG to search for reticulation edges that improve the likelihood
399 score. As a starting point for the search, we use different variations of the parsimony tree
400 (Fig. 1) where either Perrault or Grimms is moved into an ancestral position, considering a
401 number of different nearby positions just above or next to the position of the said taxa in the
402 parsimony tree. The search produced 11 alternative structures, which we label by *a, b, c, d, e,*
403 *f, g, h, i, j,* and *k*. Figures 5 and 6 show respectively networks *c* and *d*, which are of particular
404 importance for our discussion below. The other networks are given for completeness in
405 Appendix D.³

406

407 As an indication of how well the models "fit" the data, we report the log-likelihood
408 value of each of the models. For example, the log-likelihood of network *c* is -862.4 , and the
409 log-likelihood of network *d* is -865.5 . Networks *b, c* and *g* achieve a higher log-likelihood
410 value than the parsimony tree (-863.4). However, the likelihood values should not be taken to
411 be the final evaluation of the models because of two reasons. First, the likelihood evaluation
412 is approximate due to the random sampling procedure included in the method (see Appendix
413 B). Second, perhaps more importantly, the log-likelihood score tends to favor complex
414 models because they have more adjustable parameters that make it easier to achieve high log-
415 likelihood values for most data sets. To provide a statistically sound goodness-of-fit measure,
416 below we propose to use a parametric bootstrap technique.

417 *4.4 Parametric Bootstrap*

418

419 It is important to note that a network hypothesis is typically more complex than a tree
420 hypothesis (it has more parameters), which may lead to so called over-fitting: choosing a too
421 complex hypothesis considering its statistical support. To avoid over-fitting, we applied a
422 parametric bootstrap test to compare the tree hypotheses and the different network
423 hypotheses; for more details, see Appendix C.

424

425 Table I summarizes the results of the bootstrap test. The results are not unanimous
 426 but there is a relatively strong (considering the small sample size) signal indicating that
 427 models *b*, *c*, and *g* have the best statistical support. Among them, model *c* (fourth row in
 428 Table I, and Fig. 4) fares especially well, and is only rejected with low statistical confidence
 429 when compared to models *b* and *g*, while the latter two are both rejected in more
 430 comparisons. All three models place *Perrault* in an internal position that makes it ancestral to
 431 all the literary variants. However, there is some disagreement regarding the position of the
 432 Grimms' tale: Model *b* (see Appendix D) has *Grimm* as a terminal node, whereas both *c* and *g*
 433 place *Grimm* as an ancestral source for subsequent literary versions. Although the bootstrap
 434 test was unable to discriminate between these possibilities, previous research into the history
 435 of Little Red Riding Hood strongly support the latter scenario (Zipes, 1993).

436

437 TABLE I. STATISTICAL HYPOTHESIS TEST RESULTS (PARAMETRIC BOOTSTRAP). ROWS: NULL HYPOTHESIS.
 438 COLUMNS: ALTERNATIVE HYPOTHESIS. 'tree': PARSIMONY TREE. '.': NOT REJECTED. '+': REJECTED AT
 439 SIGNIFICANCE LEVEL 0.05. '*': REJECTED AT SIGNIFICANCE LEVEL 0.01.

440

NULL HYPOTHESIS	ALTERNATIVE HYPOTHESIS											
	tree	<i>a</i>	<i>b</i>	<i>c</i>	<i>d</i>	<i>e</i>	<i>f</i>	<i>g</i>	<i>h</i>	<i>i</i>	<i>j</i>	<i>k</i>
tree		*	*	*	*	+	*	*	*	.	*	.
<i>a</i>	.		*	*	*	*	*	*	*	.	*	*
<i>b</i>	.	.		+	+	+	+	+	+	.	*	+
<i>c</i>	.	.	+		.	.	.	+
<i>d</i>	.	+	*	*		+	.	*	.	.	*	+
<i>e</i>	+	*	*	+	*		*	*	+	.	*	*
<i>f</i>	+	*	*	*	.	*		*	+	.	+	.
<i>g</i>	+	.	+	.	*	*	*		.	.	+	.
<i>h</i>	*	*	*	*	*	*	*	*		*	*	*
<i>i</i>	*	*	*	*	*	*	*	*	*		*	*
<i>j</i>	*	*	*	*	*	*	*	*	*	.	.	*
<i>k</i>	*	*	*	*	*	*	*	*	*	.	.	*

441

442

443

Fig. 4 "PhyloDAG network c" about here.

444

445 More significantly, all three models *b*, *c*, and *g* are consistent with the oral origins
446 hypothesis. The literary tradition instigated by Perrault (placed as an internal node in all three
447 models) is represented as an offshoot of a lineage that also gave rise to the French and Italian
448 tale 'The Story of Grandmother'. The models further suggest that the variants of the Italian
449 tale of *Catterinetta* comprise a separate group that split from the other oral and literary
450 variants prior to *Perrault*. However, the models show that these various subgroups of ATU
451 333 did not develop in isolation of one another. All three indicate contamination both within
452 and between the literary and oral traditions of the tale. For example, like the T-Rex structure,
453 models *b*, *c*, and *g*, all suggest reticulation played an important role in the tale *ThreeGirls*.
454 However, whereas the T-Rex analysis suggested that *ThreeGirls* was descended from an oral
455 ancestor that preceded the first written versions of Little Red Riding Hood, the PhyloDAG
456 models are more consistent with the parsimony results, which situated the tale within the
457 literary group. Specifically, models *b*, *c*, and *g*, indicate that *ThreeGirls* is descended from the
458 Grimm's text, which was mixed with elements from oral tradition (notably the Italian
459 *Catterinetta* tale, as shown in models *c* and *g*, with which it shares distinctive motifs like
460 angering the villain by replacing the contents of the basket). Contamination also appears to be
461 evident in the Portuguese tale *Consigliere* and French literary tale *Goldenhood*, which might
462 explain their anomalous positions in the parsimony tree, which made them a sister clade to the
463 Perrauldian literary tradition. As explained earlier, reticulation can be a major source of error
464 in inferring phylogenetic trees, for example by dragging affected taxa deeper into the
465 structure of the tree. By incorporating reticulation edges in PhyloDAG, we found that models
466 in which Perrault was ancestral to *Consigliere* and *Goldenhood* fitted the data much better
467 than models in which these tales formed a sister clade, i.e. *a* and *e*, which were rejected in all
468 the bootstrap comparisons with every other model except one (*i*, discussed below).

469

470 We analysed six structures that supported the alternative literary origins hypothesis.
471 Among them, the one that is best supported by the data – albeit not as well as the oral origins

472 models, *b*, *c*, and *g* – is model *d*, see Fig. 5. The other network structures are given in
473 Appendix D. Models *f*, *i* and *k* represent Perrault as the ancestor of all modern versions of
474 ATU 333, including the literary variants and the oral tales 'The Story of Grandmother' and
475 'Catterinetta'. Model *f* represents the Grimm tale as a leaf node, while in *i* and *k* the Grimm
476 tale is shifted into different internal positions within the PhyloDAG. In the bootstrap
477 comparisons, all three models are rejected against the tree and the oral origin scenarios
478 represented in *b*, *c* and *g*. Models *d*, *h* and *j* represent Perrault as the ancestor of the literary
479 variants of Little Red Riding Hood and the oral tale 'The Story of Grandmother', but not of
480 versions of 'Catterinetta', which consistently come out as a sister group to the other tales in the
481 analyses. The Grimm tale is positioned as a leaf node in model *d* and as an internal node in *h*
482 and *j*. Model *d* is supported against the parsimony tree, but rejected with high statistical
483 support against the oral origins models *b*, *c*, and *g*. Models *h* and *j* are rejected in all the
484 comparisons.

485

486 **Fig. 5 "PhyloDAG network d" about here.**

487

488 In sum, the inclusion of lineal and reticulate relationships using PhyloDAG produced
489 a number of structures that fit the data better than the parsimony tree. Structures consistent
490 with the oral origins hypothesis were less frequently rejected in the bootstrap comparisons
491 than those that are consistent with the literary origins hypothesis, with all three of the top
492 performing models (*b*, *c* and *g*) falling into the former category. However, it should be noted
493 that the evidence from the bootstrap test comparisons is not all in one direction, since models
494 *b* and *g* (oral) are rejected against *d* and *f* (literary). On the other hand, model *c* (oral) is
495 supported with high statistical confidence against both literary origins models. Thus, overall,
496 the results of the PhyloDAG analyses indicate that the literary tradition of Little Red Riding
497 Hood has its roots in oral folktales, rather than the other way around.

498

499 **5. Conclusions**

500

501 Our aim in this paper has been to shed light on a complex question in the historiography of
502 fairy tales: is it possible to identify whether particular stories originated as traditional
503 folktales or authored texts? We have proposed that a useful strategy for addressing this
504 question is to adopt the kind of quantitative, computational approach that has been so
505 successfully used to reconstruct manuscript stemmata. Our case study focused on testing two
506 long-standing competing hypotheses about the origins of Little Red Riding Hood. The first
507 suggests the tale originally evolved in French and Italian oral tradition, adapted by Charles
508 Perrault in the late seventeenth century, and subsequently copied by The Brothers Grimm to
509 establish the classic form of the tale found in present day popular culture. The second
510 hypothesis proposes that the tale was a literary invention in the first place, and that
511 “traditional” variants collected by folklorists are actually adaptations of Perrault’s and
512 Grimm’s texts.

513

514 We initially tested these hypotheses by analysing 23 oral and literary variants of
515 Little Red Riding Hood/ATU 333 using one of the most popular methods in computer-assisted
516 stemmatology – maximum parsimony analysis. While the general structure of the tree
517 returned by this analysis seemed to be more compatible with the oral origins hypothesis than
518 the literary origins hypothesis, this conclusion is mitigated by two problems with interpreting
519 the results: firstly, maximum parsimony does not incorporate reticulation (contamination),
520 which can lead to errors in estimating phylogenetic relationships; secondly, the method does
521 not model lineal (ancestor-descendent) relationships among observed taxa, making it difficult
522 to draw firm conclusions about the role of classic historic texts (i.e. Perrault and Grimm) on
523 contemporary literary and oral variants. Alternative methods for modelling reticulate
524 evolution, such as NeighbourNet and T-Rex, provide a means for addressing the first of these
525 problems but not the second. As such, their usefulness for addressing the question in hand

526 turned out to be limited. We therefore introduced a new approach – PhyloDAG – which
527 handles both lineal and reticulate relationships in a statistically sound way. This enabled us to
528 compare different models for the evolution of Little Red Riding Hood and directly test the
529 oral hypothesis against the literary hypothesis. Our results pointed strongly toward the former,
530 with the best models indicating that Perrault adapted his tale from oral folktales, rather than
531 vice versa.

532

533 Of course, we cannot extrapolate any general conclusions about the origins of fairy
534 tales from a single case study. It is entirely possible – likely, even – that other tales originated
535 in a literary medium before passing into oral tradition, as suggested by Bottigheimer. What
536 we have shown here is that the problem of establishing these facts is far from intractable, and
537 can be solved using principled and powerful computational methods. We anticipate that the
538 application of these methods will generate new insights into the origins and development of
539 different types of fairy tale, as well as other kinds of cultural traditions (Lipo, O’Brien,
540 Collard, & Shennan, 2006; Mace, Holden, & Shennan, 2005).

541

542

543

544 **Endnotes**

1 The SplitsTree4 software is available at www.splitstree.org.

2 We follow the convention to give likelihood values in logarithmic scale, so that probabilities, which are always less than one, become negative numbers.

3 We chose to include all 11 networks in order to give an indication of the range of possible network hypotheses we considered and to quantify the statistical uncertainty by means of the bootstrap test.

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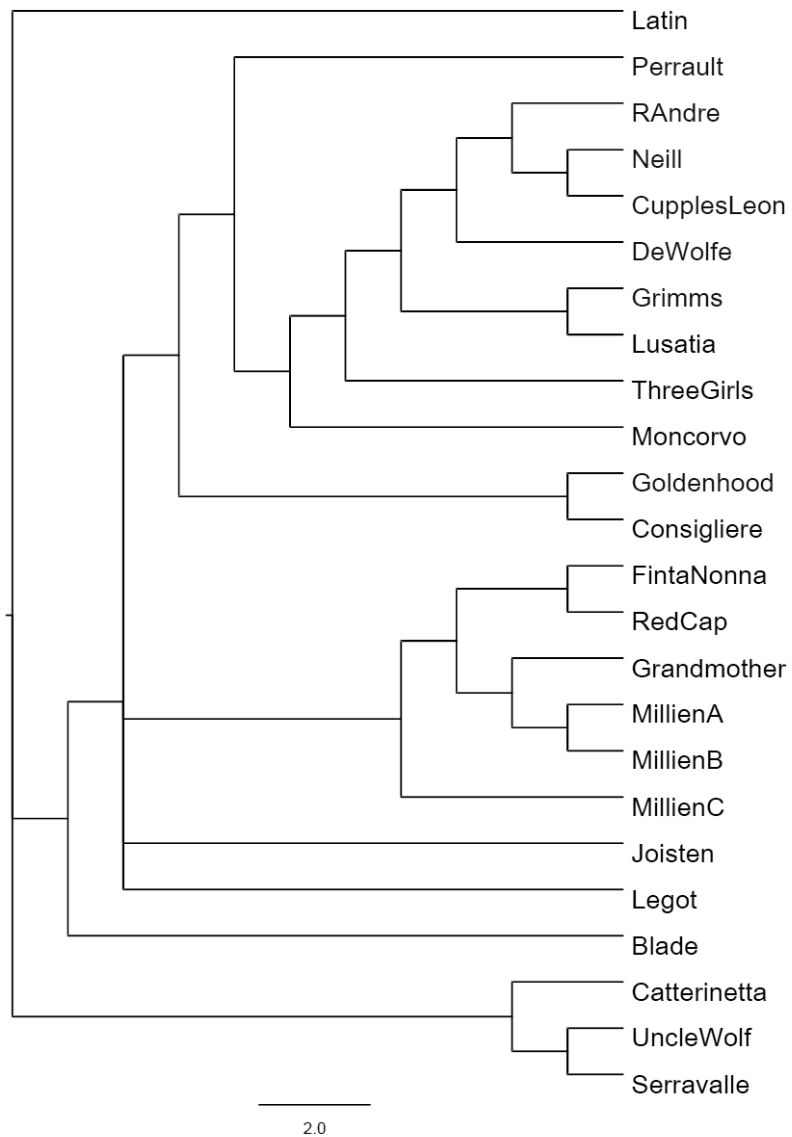
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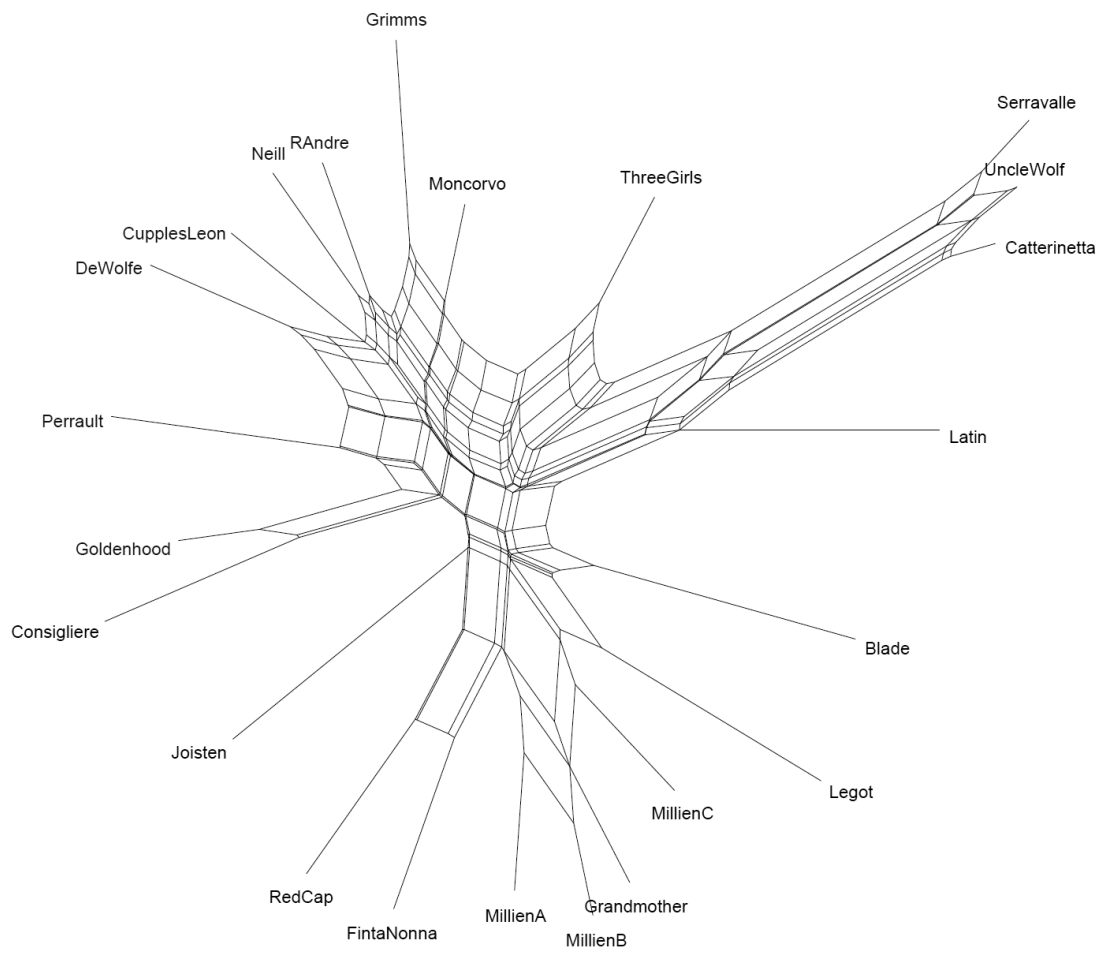
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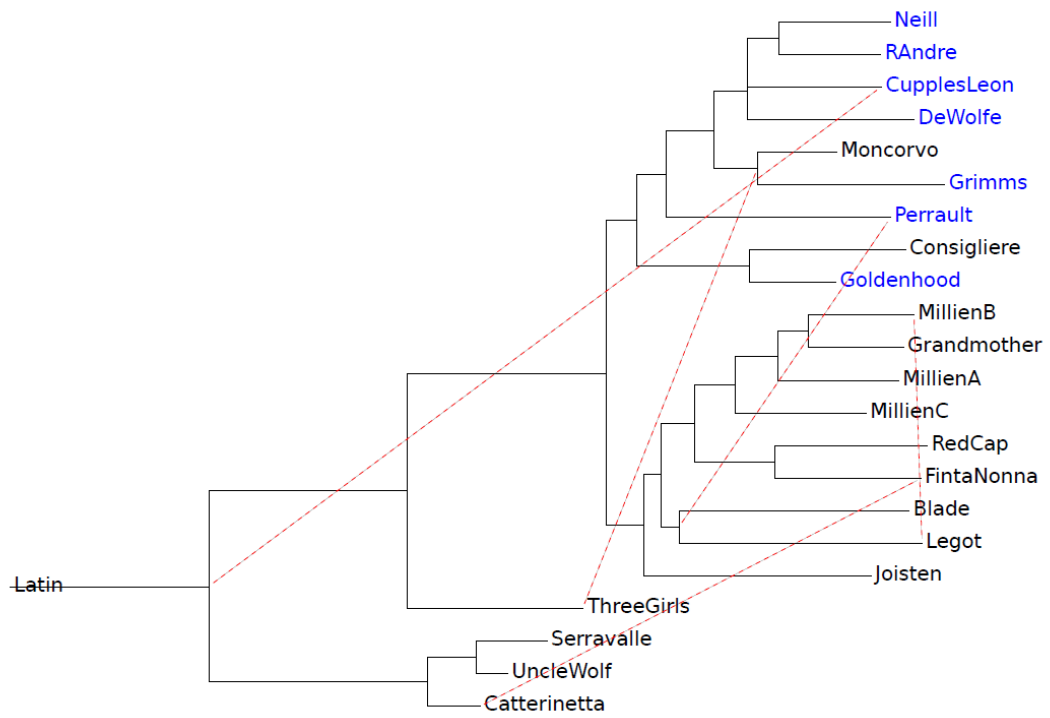
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Fig. 1 Parsimony tree. Log-likelihood -863.4.



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Fig. 2 NeighborNet. The network is obtained by Splitstree4 (Huson and Bryant, 2006) with default settings.



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Fig. 3 T-Rex. The underlying Neighbor-Joining tree is shown with solid black lines and five additional reticulation edges are shown with dotted red lines.



Fig. 4 PhyloDAG network *c.* Log-likelihood -862.4.

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Fig. 5 PhyloDAG network *d*. Log-likelihood -865.5.

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Appendix A. Data

Sources

Taxon name	Reference
Perrault	Perrault, C. (1697). "Le Petit Chaperon Rouge" <i>Histoire ou contes du temps passe</i> .
Grimm	Grimm J. & Grimm W. (1812). "Rotkäppchen". <i>Kinder- und Hausmärchen</i> . Gottingen, no. 26
Lusatia	A. H. Wratislaw (1889) "Little Red Hood". <i>Sixty Folk-Tales from Exclusively Slavonic Sources</i> London: Elliot Stock, pp. 97-100
Neill	Neill, J. (1908). <i>Little Red Riding Hood</i> . Chicago: Reilly & Lee Co. Downloaded from The University of Southern Mississippi Little Red Riding Hood Project: http://www.usm.edu/media/english/fairytales/lrrh/lrrhhome.htm
Randre	Andre, R. (1888). <i>Red Riding Hood</i> . New York: McLoughlin Bros. Downloaded from The University of Southern Mississippi Little Red Riding Hood Project: http://www.usm.edu/media/english/fairytales/lrrh/lrrhhome.htm
CupplesLeon	Gruelle J. B. (1916). <i>All About Little Red Riding Hood</i> . New York: Cupples & Leon. Downloaded from The University of Southern Mississippi Little Red Riding Hood Project: http://www.usm.edu/media/english/fairytales/lrrh/lrrhhome.htm
DeWolf	DeWolfe (1890). <i>Red Riding Hood and Cinderella</i> . DeWolfe, Fiske, and Co. Downloaded from The University of Southern Mississippi Little Red Riding Hood Project: http://www.usm.edu/media/english/fairytales/lrrh/lrrhhome.htm
Goldenhood	Marelles, C. 1895. "The True Story of Little Goldenhood". <i>Andrew Lang, The Red Fairy Book, 5th edition</i> . London and New York: Longmans, Green, & Co. pp. 215-19
Consigliere	Vaz da Silva, F. (1995). Capuchinho vermelho em Portugal. <i>Estudos de Literatura Oral 1</i> , p. 38-58
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ThreeGirls	Calvino, I. (1956, trans. 1980 by G. Martin) "The Wolf and the Three Girls". <i>Italian Folktales</i> . Harmondsworth: Penguin, pp.26-27
MillenA	Millen, A. (1887). 'Little Red Riding Hood: Version 1'. Zipes, J. 2013. <i>The Golden Age of the Folk and Fairy Tales</i> . Indianapolis: Hackett. P 170-1

MillenB	Millen, A. (1887). 'Little Red Riding Hood: Version 2' zipes, J. 2013. <i>The Golden Age of the Folk and Fairy Tales</i> . Indianapolis: Hackett. P 172
MillenC	Millen, A. (1887). 'The Little Girl and the Wolf' zipes, J. 2013. <i>The Golden Age of the Folk and Fairy Tales</i> . Indianapolis: Hackett. P 173
Grandmother	Delarue, P. (1956). "The Story of Grandmother". <i>The Borzoi Book of French Folktales</i> . New York: Alfred Knopf, pp. 230-233.
FintaNonna	Calvino, I. (1956, trans. 1980 by G. Martin) "The False Grandmother". <i>Italian Folktales</i> . Harmondsworth: Penguin, pp.116-117
RedCap	Schneller, C. (1867, trans. 2007 by D. Ashliman). "Cappelin Rosso". <i>Märchen und Sagen aus Wälschtirol: Ein Beitrag zur deutschen Sagenkunde</i> . Innsbruck: Verlag der Wagner'schen Universitäts-Buchhandlung, pp. 9-10
Blade	Blade, Jean-Francois. (1886). 'The Wolf and the Child' zipes, J. 2013. <i>The Golden Age of the Folk and Fairy Tales</i> . Indianapolis: Hackett. P 169
Legot	Legot M. (1885). 'Little Red Riding Hood: The Version of Tourangelle'. Zipes, J. 2013. <i>The Golden Age of the Folk and Fairy Tales</i> . Indianapolis: Hackett. p167
Joisten	Joisten, C. Untitled. Recounted in Zipes, J. (1993) <i>The Trials and Tribulations of Little Red Riding Hood</i> . New York: Routledge, pp. 5-6.
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UncleWolf	Calvino, I. (1956, trans. 1980 by G. Martin) "Uncle Wolf". <i>Italian Folktales</i> . Harmondsworth: Penguin, pp.49-50.
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List of characters

- 1 Protagonist [0] girl [1] boy
- 2 Girl wears red hood: [0] absent [1] present
- 3 Who made red hood: [0] absent [1] mother [2] grandmother [3] godfather
- 4 Girl goes to visit relative: [0] absent [1] granny [2] aunt [3] mother
- 5 Relative is a witch: [0] absent [1] present [2] fairy
- 6 Granny sick [0] absent [1] present
- 7 Girl told to fetch pan from relative: [0] absent [1] present

- 8 Girl told not to stay from path: [0] absent [1] present
- 9 Carries basket: [0] absent [1] present
- 10 Cargo: bread: [0] absent [1] present
- 11 Cargo: soup: [0] absent [1] present
- 12 Cargo: custard: [0] absent [1] present
- 13 Cargo: butter: [0] absent [1] present
- 14 Cargo: cakes: [0] absent [1] present
- 15 Cargo: eggs: [0] absent [1] present
- 16 Cargo: wine: [0] absent [1] present
- 17 Girl plays in forest: [0] absent [1] present
- 18 Girl eats the cargo: [0] absent [1] present
- 19 Villain is [0] ogre [1] wolf [2] werewolf [3] devil
- 20 Reconnaissance - villain finds out where the girl is going: [0] absent [1] present
- 21 Villain and girl take separate paths: [0] absent [1] pins vs needles [2] short vs long
- 22 Woodcutters are in the forest: [0] absent [1] present
- 23 Wolf impersonates girl: [0] absent [1] present
- 24 Grandmother gives instructions on opening door: [0] absent [1] present
- 25 Girl replaces cargo [0] absent [1] dung [2] nails
- 26 Monster eats granny: [0] absent [1] present
- 27 Monster dresses up in grannys clothes: [0] absent [1] present
- 28 Monster disguises voice: [0] absent [1] present
- 29 Girl eats remains of granny: [0] absent [1] present
- 30 Girl eats body parts: [0] absent [1] present [2] refuses
- 31 Girl eats granny teeth: [0] absent [1] present
- 32 Girl drinks blood: [0] absent [1] present [2] refuses
- 33 The girl is warned about the danger: [0] absent [1] by monster [2] by animals
- 34 Girl flees home boards up house: [0] absent [1] present
- 35 Monster stalks girl "I'm coming!": [0] absent [1] present
- 36 Wolf tells girl to take off clothes: [0] absent [1] present
- 37 Throws clothes into fire: [0] absent [1] present
- 38 Wolf tells girl to get into bed: [0] absent [1] present
- 39 Dialogue: [0] absent [1] present
- 40 My what! Head [0] absent [1] present
- 41 My what! Arms [0] absent [1] present
- 42 My what! Feet [0] absent [1] present
- 43 My what! Legs [0] absent [1] present
- 44 My what! Ears [0] absent [1] present
- 45 My what! Teeth [0] absent [1] present
- 46 My what! Eyes [0] absent [1] present
- 47 My what! Nose [0] absent [1] present
- 48 My what! Hands [0] absent [1] present
- 49 My what! Mouth [0] absent [1] present
- 50 My what! Hairy [0] absent [1] present
- 51 Girl eaten: [0] absent [1] present
- 52 Girl cut out of stomach: [0] absent [1] present
- 53 Girl saved [0] absent] by [1] hunstman [2] woodcutters [3] father [4] mother [5] townsfolk [6] granny

- 54 Girl saved by magic cloak: [0] absent [1] present [2] magic wand
- 55 Girl tricks wolf: [0] absent [1] present
- 56 Wolf chases girl [0] no [1] to her house
- 57 Wolf killed: [0] absent [1] present
- 58 Wolf's stomach sewn up with stones inside

643

644 **Matrix**

645

646	[Character no.	1	10	20	30	40	50]
647	Latin	0	1	3	0	0	0	0
648	Perrault	0	1	2	1	0	1	1
649	RAndre	0	1	1	1	0	0	0
650	DeWolfe	0	1	2	1	0	0	0
651	Neill	0	1	2	0	1	0	0
652	CupplesLeon	0	1	1	0	1	0	0
653	Grimms	0	1	2	1	0	1	1
654	Lusatia	0	1	2	1	0	0	0
655	Goldenhood	0	1	2	0	1	0	0
656	FintaNonna	0	0	9	1	0	0	0
657	Grandmother	0	0	9	1	0	0	0
658	Joisten	0	1	0	1	0	0	0
659	RedCap	0	1	0	1	0	0	0
660	Catterinetta	0	0	9	2	1	0	0
661	UncleWolf	0	0	9	2	1	0	0
662	Serravalle	0	0	9	2	1	0	0
663	ThreeGirls	0	0	9	3	0	1	0
664	Legot	0	0	9	1	0	0	0
665	Blade	1	0	9	2	0	0	0
666	MillienA	0	0	9	1	0	0	0
667	MillienB	0	0	9	1	0	0	0
668	MillienC	0	0	9	1	0	0	0
669	Consigliere	0	1	2	0	1	0	0
670	Moncorvo	0	1	2	0	1	0	0

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672 N.B. the value 9 represents a "gap" state for characters that were redundant or not relevant for a
 673 particular tale. For example, if the girl did not carry a basket (character 9) then characters relating to the
 674 contents of the basket (10-16) – which logically could not be present – were coded as gap characters

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676

677 **Appendix B. Description of the PhyloDAG method**

678
679 Strimmer and Moulton (2000) proposed a likelihood-based method for comparing different
680 phylogenetic hypotheses that correspond to directed acyclic graphs (DAGs). Each node in the
681 graph corresponds to a taxon, either extant or hypothetical (unobserved). The edges in the
682 DAG correspond to direct inheritance where the origin of the edge, the "parent", is the
683 immediate ancestor and the end of the edge, the "child", is the offspring. Cases where a taxon
684 has only one parent are modelled by using familiar sequence evolution models such as the
685 Jukes-Cantor model. However, when a taxon has more than one parent, a different
686 evolutionary model is assumed: each of the parent taxa is given a relative weight, and each
687 character is inherited from a parent that is randomly chosen based on these weights.
688 Inheritance from a parent follows the same model as in the case where there is only one edge
689 pointing to the node in question.

690
691 Computing the likelihood of a DAG model, i.e., the probability that a given set of
692 sequences is obtained as the outcome of the given DAG, is hard. Moulton and Strimmer
693 proposed a random sampling technique to approximate the likelihood. Their technique
694 eventually converges to the exact likelihood value but in practice it may take a large number
695 of samples, and hence, a long time, before obtaining accuracy that is sufficient for comparing
696 different DAGs.

697
698 We have developed an alternative approximation which is not based on random
699 sampling but instead uses a technique called loopy belief propagation, see (Murphy, Weiss, &
700 Jordan, 1999). It is not guaranteed to converge to the exact value but on the other hand, it is
701 often significantly faster than random sampling. In our experiments (not shown here, see
702 (Nguyen & Roos, in preparation)), it produces better accuracy than a number of different
703 random sampling techniques with less computation time. We also extend the earlier method
704 by Strimmer and Moulton by including a parameter learning step where the edge lengths that
705 characterize the amount of evolutionary change along each edge in the network are learned
706 from the data so that they need not be given as input to the PhyloDAG method.

707
708 In practice, the PhyloDAG method takes as input a set of sequences and a tree
709 structure. It then considers all possible additional edges between any two nodes in the tree –
710 including edges between two extant nodes, edges between an extant and an hypothetical node,
711 and edges between two hypothetical nodes – in turn and evaluates the likelihood of the
712 network where the edge in question is included in addition to the edges in the initial tree
713 structure. The edge or the edges that improve the likelihood score the most are included in the
714 output network. Often it is useful to also set an upper bound on the number of edges that are
715 added so as to obtain a more easily interpreted network where only the most significant
716 reticulation events are included. In the present work, we limited the number of additional
717 edges to four to facilitate the interpretation of the models.

718
719 We used the Jukes-Cantor model, which can be directly extended to handle any other
720 number of character states than four, for modeling the evolution of individual features and
721 following Moulton and Strimmer, set the weights on the parents to be uniform so that each
722 parent taxon has the same influence on the dependent taxon.

723

724 **Appendix C. Parametric bootstrap**

725

726 Parametric bootstrapping for testing phylogenetic topologies, i.e., tree structures, was first
727 suggested by (Huelsenbeck & Crandall, 1997). Our implementation is primary based on the
728 later description by (Posada, 2003). The testing procedure of topology M_0 (null hypothesis)
729 against topology M_1 (alternative hypothesis) can be briefly described as follows.

730

- 731 1. Estimate the parameters (edge lengths) in models M_1 and M_0 by maximum likelihood.
732 Denote the maximum likelihood estimates (MLEs) by θ_1 and θ_0 , respectively.
- 733 2. Calculate the log-likelihood ratio (LLR) $l(D|M_1, \theta_1) - l(D|M_0, \theta_0)$, where
734 $l(D|M_1, \theta_1)$ and $l(D|M_0, \theta_0)$ are the log-likelihood of the data given structure M_1
735 and M_0 with MLE parameters respectively.
- 736 3. From structure M_0 with estimated parameters θ_0 , draw $K=1000$ simulated data sets
737 which all have the same size and missing data as the original data set.
- 738 4. For each simulated data set D_i , estimate parameters $\tilde{\theta}_1$ and $\tilde{\theta}_0$ for both structures, and
739 calculate the LLR $l(D_i|M_1, \tilde{\theta}_1) - l(D_i|M_0, \tilde{\theta}_0)$. Use these to obtain an approximate
740 distribution of the LLR between M_0 and M_1 under the null hypothesis M_0 .
- 741 5. Let F be the number of time that the LLR on simulated datasets is bigger than the
742 LLR on the original data in Step 2. If the quotient F/K (in this case $K=1000$) is
743 smaller than a predefined threshold (0.05 or 0.01), the null hypothesis is rejected.

744

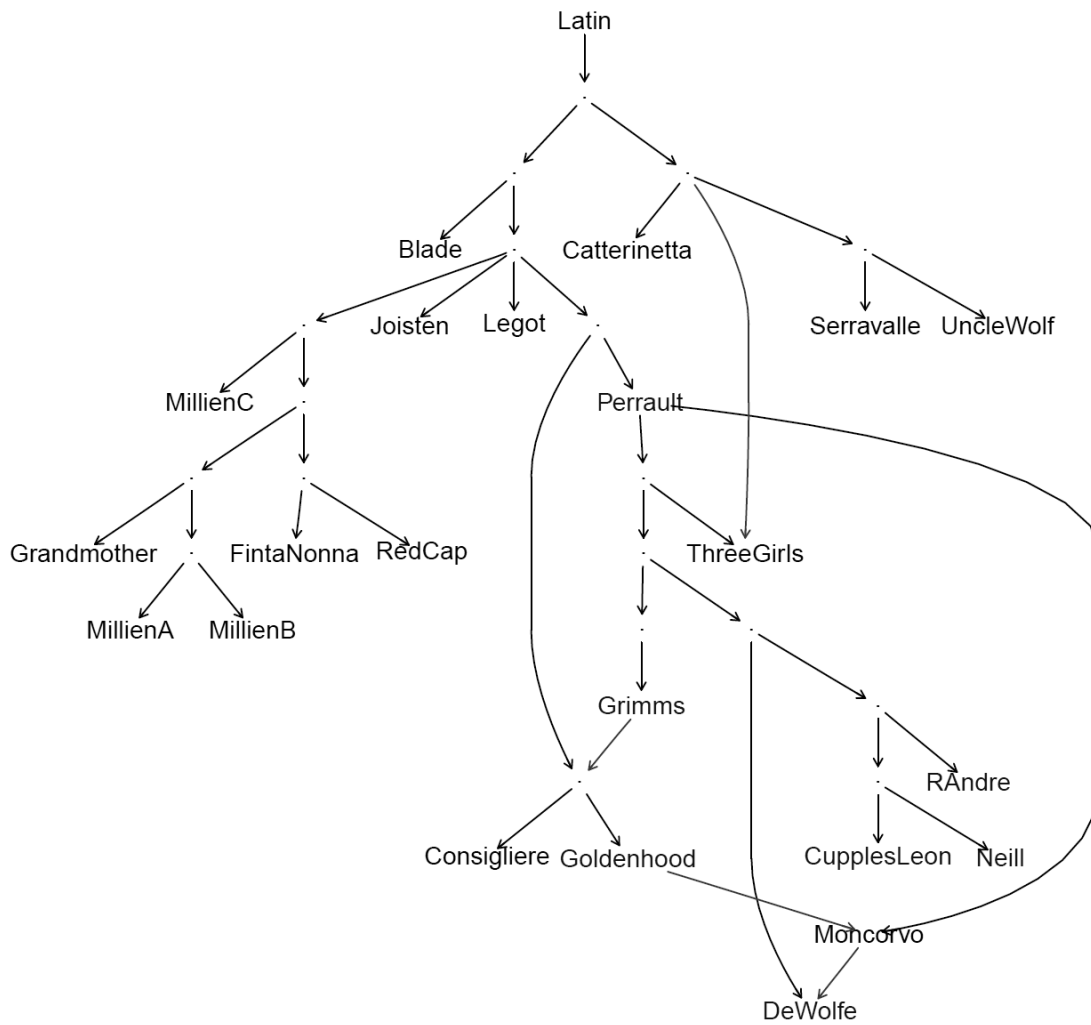
745 The intuition is that if the null hypothesis is true, then the simulated data sets in Step 4 are
746 drawn from the same distribution as the observed data. This implies that the LLR based on
747 the observed data, computed in Step 2, follows the same distribution as the LLR values for
748 the simulated data in Step 4. Suppose now that the LLR for the observed data, which
749 measures how much better model M_1 fits the observed data than M_0 , is higher than almost all of
750 the simulated LLR values. By the above reasoning, this must be unlikely since the observed
751 LLR value is supposed to be drawn from the same distribution as the simulated ones, and we
752 are lead to reject the null hypothesis. It is obvious that such a test is valid in the sense that if
753 the null hypothesis is true, it is unlikely to be rejected.

754

755 **Appendix D. Additional results.**

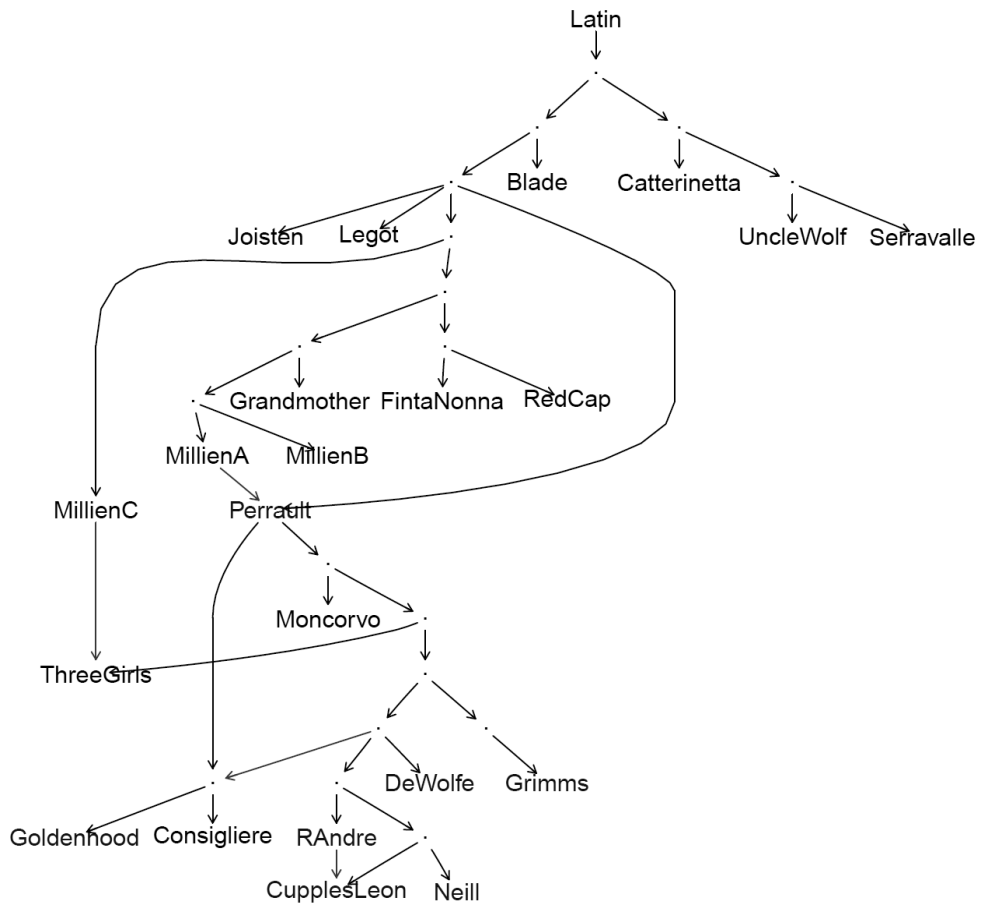
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757 Networks *c* (Fig. 4) and *d* (Fig. 5) are representative examples among the two main
758 hypotheses: the oral origins hypothesis (network *c*) and the literary origins hypothesis
759 (network *d*). Figures 6–14 show the rest of the networks for completeness.



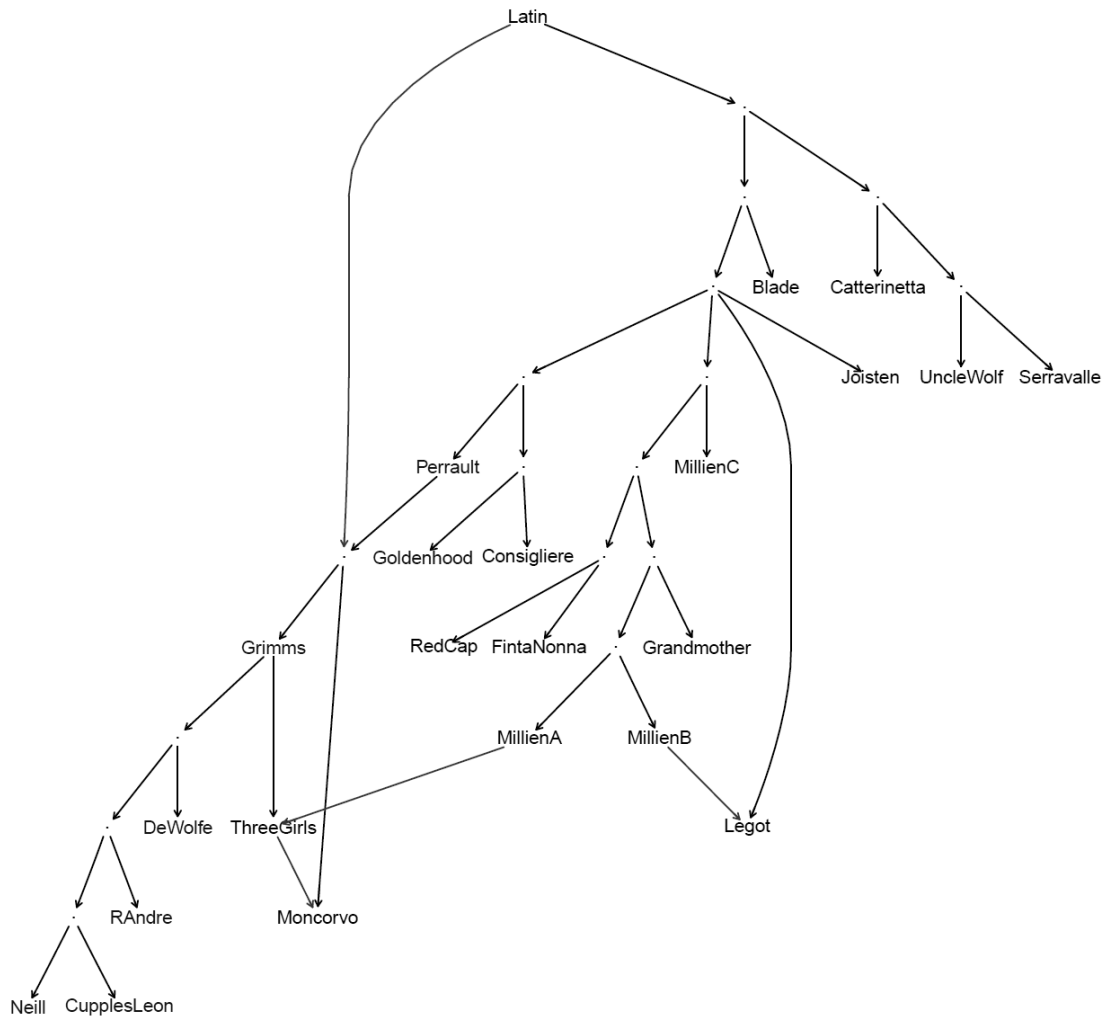
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Fig. 6 PhyloDAG network *a*. Log-likelihood -875.6.



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Fig. 7 PhyloDAG network *b*. Log-likelihood -862.3.



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Fig. 8 PhyloDAG network *e*. Log-likelihood -867.0.

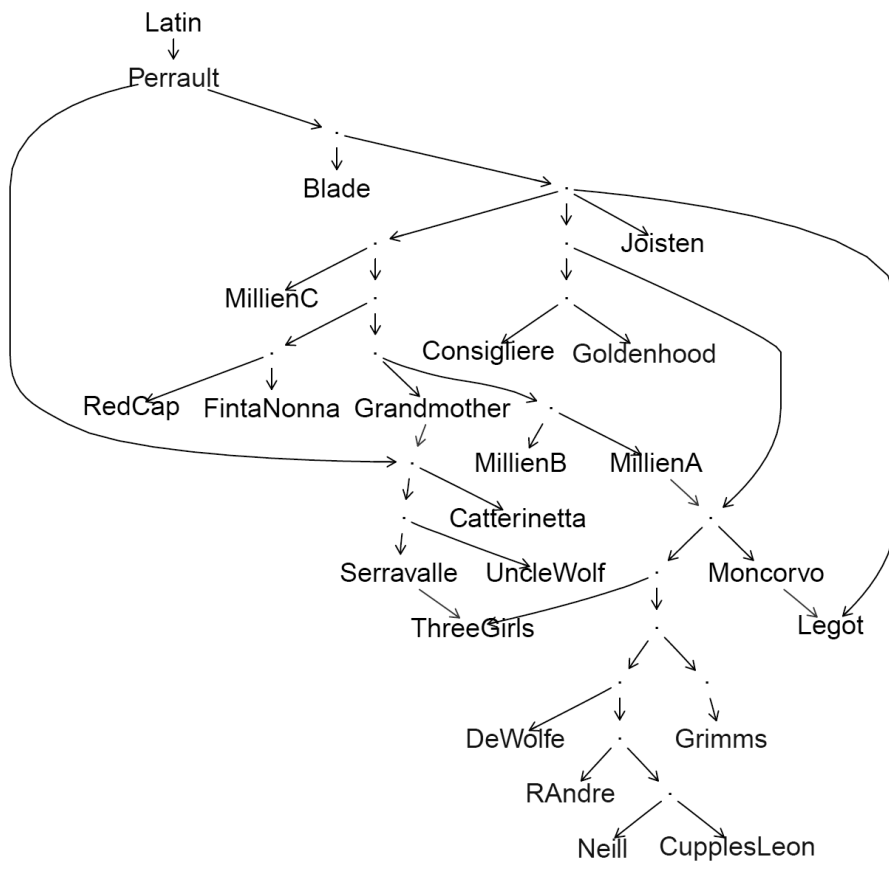
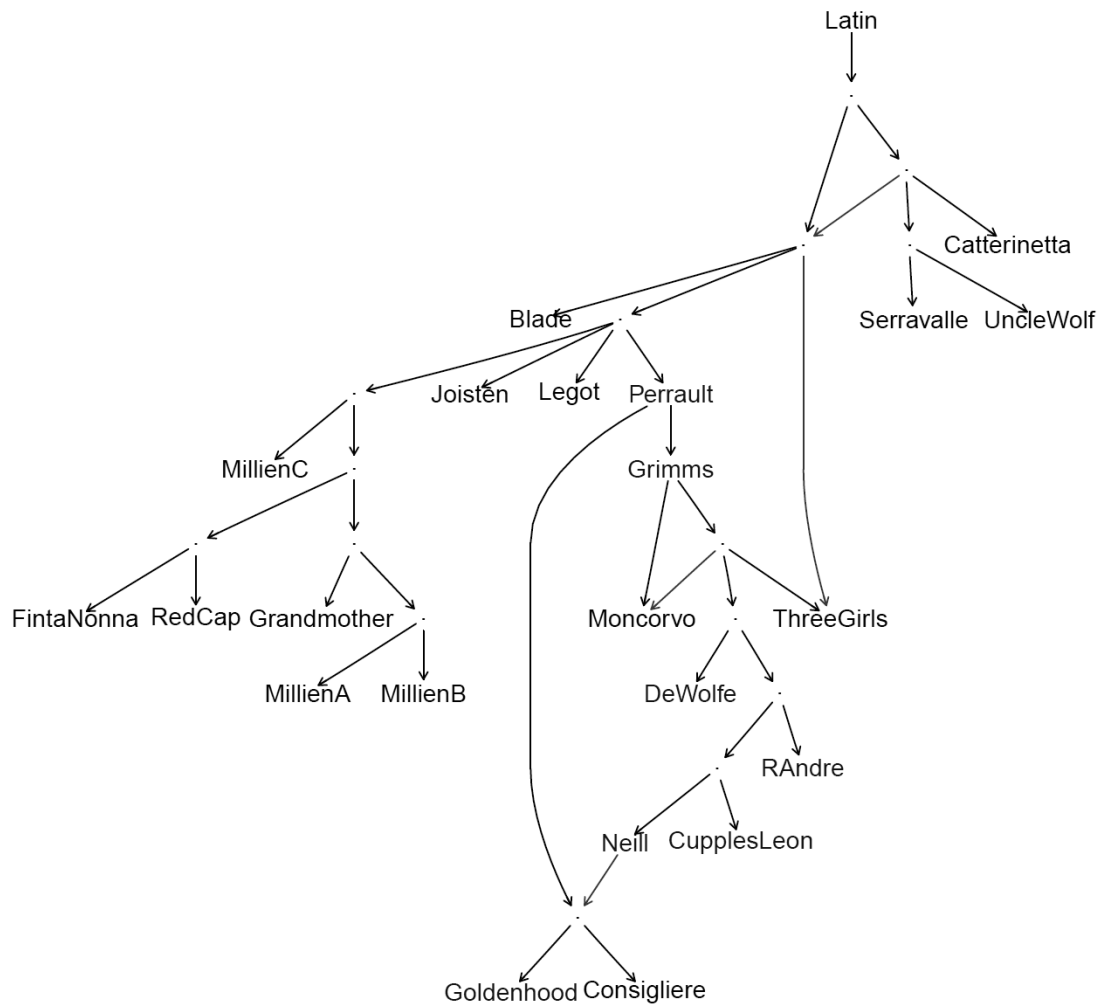


Fig. 9 PhyloDAG network *f*. Log-likelihood -884.6.

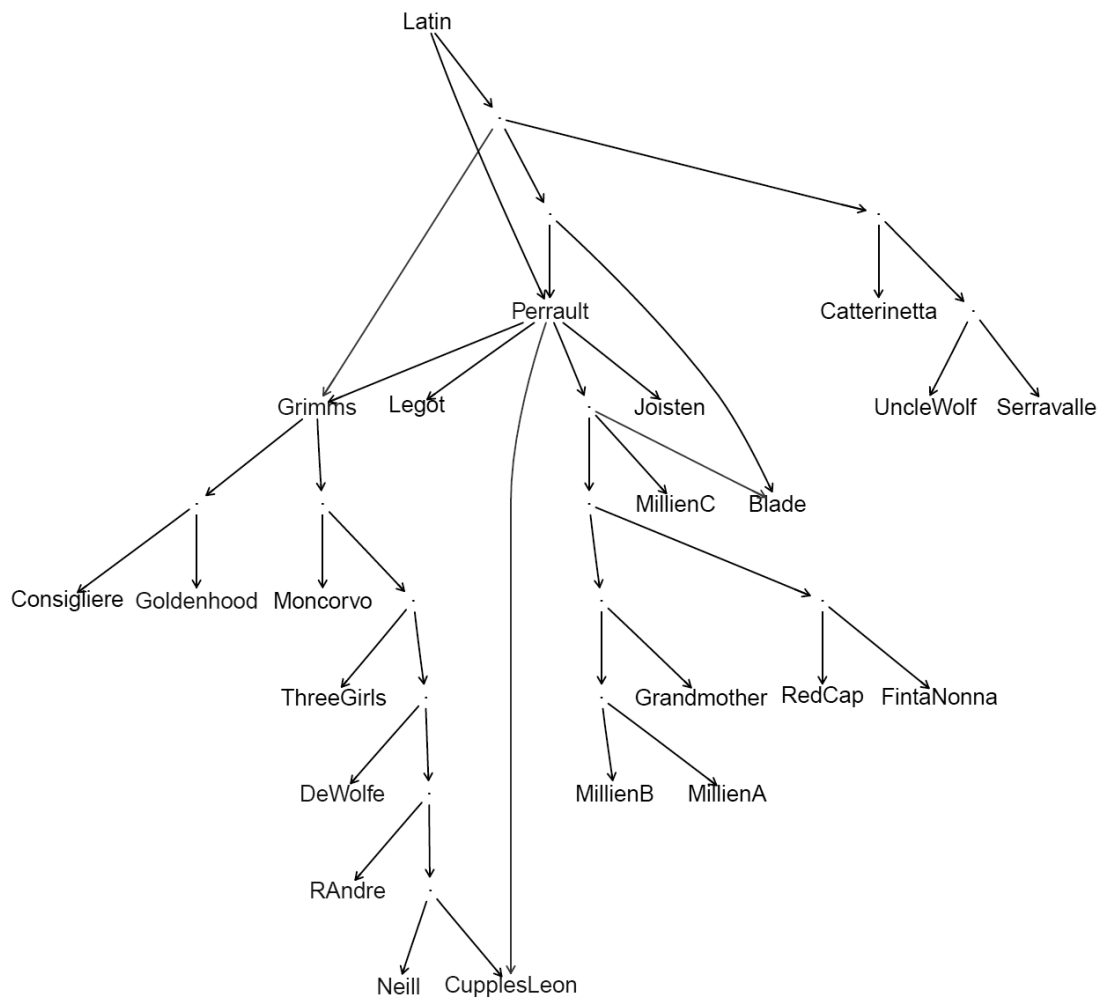
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Fig. 10 PhyloDAG network *g*. Log-likelihood -847.6.

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Fig. 11 PhyloDAG network *h*. Log-likelihood -896.76.

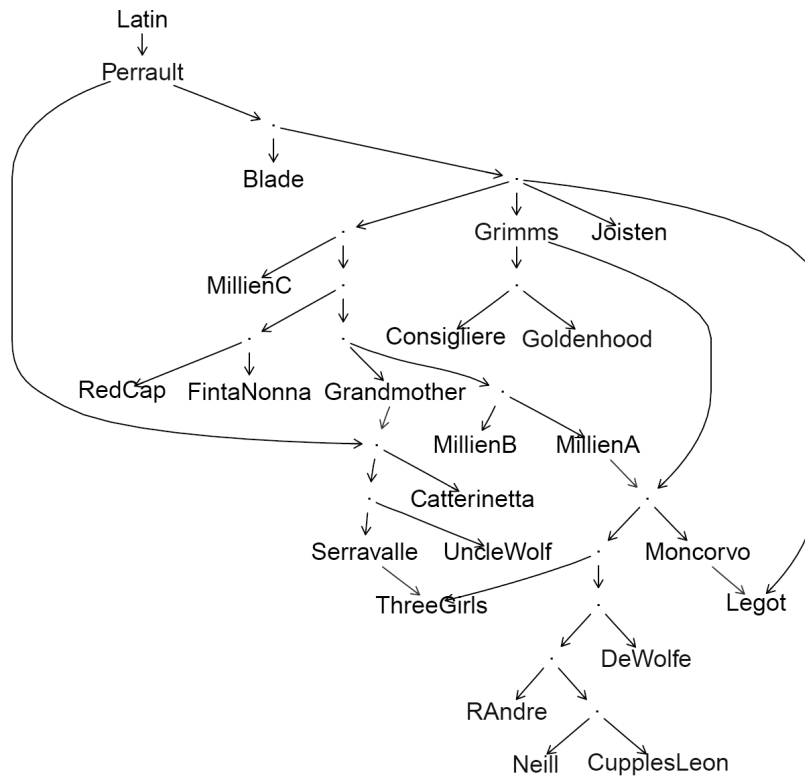
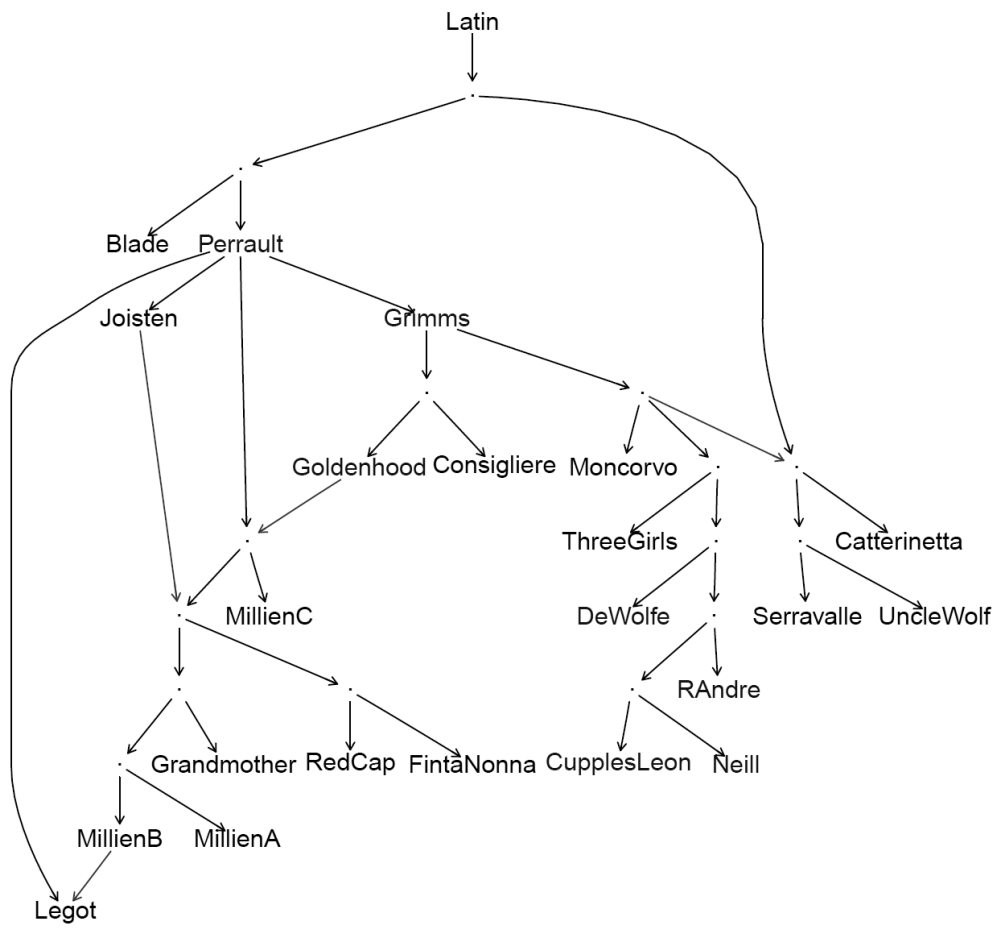


Fig. 12 PhyloDAG network *i*. Log-likelihood -897.32.

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Fig. 13 PhyloDAG network *j*. Log-likelihood -870.13.



Fig. 14 PhyloDAG network k . Log-likelihood -870.87.

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