

Well-Behaved Variants Seldom Make the Apparatus: Stemmata and Apparatus in Digital Research

by Barbara Bordalejo, University of Saskatchewan

To David Greetham, *in memoriam*.

...the editor of a traditional critical text is, in the very layout of the edition, enshrining a hierarchy of variants: those which make it onto the textual page are somehow in a different class from those which are printed in apparatus and collation.

(D. C. Greetham, *Textual Scholarship*)

Introduction

This article focuses on the analysis of variants using digital resources, with a particular emphasis on the Canterbury Tales Project research and with some examples of other projects I have observed. It shows how by using a system integrating different analytical resources, specialized research tools become more accessible to scholars without the need for a background in computing.

In the article on collation, co-authored with Adam Vázquez, we discuss what it means to collate, describe the full-text collations produced by the Canterbury Tales Project, and explain how collating in this manner presents multiple advantages over other approaches to the comparison of texts (Bordalejo and Vázquez 2020). We do not go into detail about what to do after the collation leads to variant identification. Here I describe the methods we use for researching the data obtained from our collation process and their uses within the framework of our project with the goal of producing the type of stemmatological research in which we focus. I describe in detail how we generate NEXUS files for use with phylogenetic analysis, the methods of phylogenetic inference, and the settings we regularly use for our research. I discuss how the combination of phylogenetic analysis and our specialized database, VBase, are core tools for our understanding of textual transmission. Finally, I conclude the article with examples of our apparatus and how they link to the stemmata, demonstrating that our research implies thousands of minute decisions, each of which carries its own weight on the final product.

The Means of Textual Criticism

There is a temptation when studying primary sources to discern and explain the most minute details of the documents at hand. It is easy to get lost within a single manuscript, allowing every mark on the page to take on a new meaning and making its representation the subject of endless revision and debate. Transcription, however, is a means of textual criticism, not its end. The preparation and process of semi-automatic computer-assisted collation are so time-consuming,

particularly when we are working with more than fifty witnesses of significant length, that by the time a researcher emerges on the other side, she discovers herself surrounded by a sea of variants. Collation, however, is also a means of textual criticism, not its end. The analysis of variants, with all its intricacies, appears, initially, like the area in which a textual critic might focus her efforts to unveil the mysteries of the transmission of the text. The analysis of variants is one of the many requirements in the production of editions and, occasionally, it might be the sole focus and end of textual-critical research. For many scholars, however, the analysis of variants is a means of textual criticism, not its ends.

Some might think that a research focus on philology and textual criticism is akin to falling into a rabbit hole. In fact, textual scholarship is more a lair than a hole, with interconnected tunnels leading in different directions and labyrinthian passages revealing only a few final destinations. However, if we have the right tools, we might be able to trace these paths, map their layout, and reach a better understanding of the lair.

Textual Communities

The current phase of the Canterbury Tales Project is supported by Textual Communities, a web-based system optimized for all aspects of the production of editions or, as stated in its launch-document, “an environment for the collaborative online creation of scholarly editions” (Robinson 2019b). Textual Communities can be used to create editions of all sorts of text, but it is particularly adept at the production of editions of texts preserved in large traditions. The integration of CollateX and the Collation Editor (Smith 2019), developed by Catherine Smith (University of Birmingham), indicates that collation is a fundamental interest of the developers of this system.

Within Textual Communities, one can transcribe TEI-XML documents and validate them against a default DTD. The system creates two separate trees for each file, one representing the structure of the document and the other understanding the text as a communicative act (Robinson 2018; 2019a). This double tree structure allows us to retrieve the first line of the first folio in the Hengwrt manuscript or the first line of Chaucer’s *Canterbury Tales*.

As explained in the article on collation (Bordalejo and Vázquez 2020), the Collation Editor (Smith 2019) allows textual scholars to fine-tune the processes of regularization and alignment to produce precise collations that become the bases of all our other analyses and of the apparatus for our editions.

Extracting Data from Textual Communities

Using Universal Resource Identifiers (URIs), scholars are able to retrieve the XML apparatus from the Textual Communities databases. Some instructions on how to do this can be found as

part of the Textual Communities wiki, where there are a few examples of the naming structure for the URIs (Robinson 2020).

Peter Robinson completed a new regularization of the Wife of Bath's Prologue in 2019, and this is currently stored in the Textual Communities database. By using a positive collation URI, scholars can extract an XML apparatus, with an optimized alignment intended for use with phylogenetic software, as seen in figure 1.

```
<app from="10" n="CTP2:entity=WBP;line=2" to="12" type="main">
  <lem wit="Base">is right</lem>
  <rdg n="a" varSeq="1" wit="Ad1 Ad3 Base Bo1 Bo2 Bw Ch Cp Cx1 Cx2 Dd Dl Ds1 En1 En3
  Fi Gl Ha2 He Hg Ht La Lc Ld1 Ld2 Ln Mc Mg Mm Ne Nl Ph2 Pn Ps Ra1 Ra3 Ry2 Se Si Sl1 Sl2 Tc1
  To1 Wy">is
  right<wit><idno>Ad1</idno><idno>Ad3</idno><idno>Base</idno><idno>Bo1</idno><idno>Bo2</idno>
  <idno>Bw</idno><idno>Ch</idno><idno>Cp</idno><idno>Cx1</idno><idno>Cx2</idno><idno>Dd</
  idno><idno>Dl</idno><idno>Ds1</idno><idno>En1</idno><idno>En3</idno><idno>Fi</idno><idno>
  Gl</idno><idno>Ha2</idno><idno>He</idno><idno>Hg</idno><idno>Ht</idno><idno>La</idno><idno>Lc
  <idno>Ld1</idno><idno>Ld2</idno><idno>Ln</idno><idno>Mc</idno><idno>Mg</idno><idno>Mm</idno><idno>Ne</idno><idno>Nl</idno><idno>Ph2</idno><idno>Pn</idno><idno>Ps</idno>
  <idno>Ra1</idno><idno>Ra3</idno><idno>Ry2</idno><idno>Se</idno><idno>Si</idno><idno>Sl1</
  idno><idno>Sl2</idno><idno>Tc1</idno><idno>To1</idno><idno>Wy</idno></wit></rdg>
  <rdg n="b" varSeq="2" wit="Ha4">it were<wit><idno>Ha4</idno></wit></rdg>
  <rdg n="c" varSeq="3" wit="Ra2">it is right<wit><idno>Ra2</idno></wit></rdg>
  <rdg n="d" varSeq="4" wit="El Py">were
  right<wit><idno>El</idno><idno>Py</idno></wit></rdg>
  <rdg n="e" varSeq="5" wit="Hk Ph3 Pw Ry1
  Tc2">right<wit><idno>Hk</idno><idno>Ph3</idno><idno>Pw</idno><idno>Ry1</idno><idno>Tc2</
  idno></wit></rdg>
  <rdg n="f" type="om" varSeq="6" wit="Ii
  Ma">om<wit><idno>Ii</idno><idno>Ma</idno></wit></rdg>
</app>
<app from="14" n="CTP2:entity=WBP;line=2" to="14" type="main">
  <lem wit="Base">ynogh</lem>
  <rdg n="a" varSeq="1" wit="Ad1 Ad3 Base Bo1 Bo2 Bw Ch Cp Cx1 Cx2 Dd Dl Ds1 El En1
  En3 Fi Gl Ha2 Ha4 He Hg Hk Ht Ii La Lc Ld1 Ld2 Ln Mc Mg Mm Ne Nl Ph2 Ph3 Pn Ps Pw Py Ra1
  Ra2 Ra3 Ry1 Ry2 Se Si Sl1 Sl2 Tc1 Tc2 To1
  Wy">ynogh<wit><idno>Ad1</idno><idno>Ad3</idno><idno>Base</idno><idno>Bo1</idno><idno>Bo2</
  idno><idno>Bw</idno><idno>Ch</idno><idno>Cp</idno><idno>Cx1</idno><idno>Cx2</idno><idno>Dd
  </idno><idno>Dl</idno><idno>Ds1</idno><idno>El</idno><idno>En1</idno><idno>En3</idno><idno>
  >Fi</idno><idno>Gl</idno><idno>Ha2</idno><idno>Ha4</idno><idno>He</idno><idno>Hg</idno><
  idno>Hk</idno><idno>Ht</idno><idno>Ii</idno><idno>La</idno><idno>Lc</idno><idno>Ld1</idno>
  <idno>Ld2</idno><idno>Ln</idno><idno>Mc</idno><idno>Mg</idno><idno>Mm</idno><idno>Ne</idno>
  <idno>Nl</idno><idno>Ph2</idno><idno>Ph3</idno><idno>Pn</idno><idno>Ps</idno><idno>Pw</
  idno><idno>Py</idno><idno>Ra1</idno><idno>Ra2</idno><idno>Ra3</idno><idno>Ry1</idno><idno>
  Ry2</idno><idno>Se</idno><idno>Si</idno><idno>Sl1</idno><idno>Sl2</idno><idno>Tc1</idno><
  idno>Tc2</idno><idno>To1</idno><idno>Wy</idno></wit></rdg>
  <rdg n="b" type="om" varSeq="2" wit="Ma">om<wit><idno>Ma</idno></wit></rdg>
</app>
```

Fig. 1. Wife of Bath Prologue XML apparatus, extracted from Textual Communities. Regularized and aligned by Peter Robinson.

XML Apparatus Structure

Each word (a token in CollateX language) is assigned an even number; thus, 2, 4, 6, etc., leaving the uneven numbers free in case of additions. The encoding of each place of variation is given as `<app from="10" n="CTP2:entity=WBP:line=2" to="12" type="main">`. In this particular case, “10” refers to what would be position five within the line. It could have said “from=”10” and “to=”10”, which would have referred to a single word in the base text. Instead, we have “from=”10” and “to=”12,” corresponding to positions 5 and 6 in the line. By contrast, the following word, “ynough” appears on its own. `<app from="14" n="CTP2:entity=WBP:line=2" to="14" type="main">`.

In between the element attributes that determine the position in the line, we have another one, `n="CTP2:entity=WBP:line=2,"` pointing out at the exact place in which this is occurring in the Wife of Bath’s Prologue. The attribute states that we are referring to line 2 of the entity “Wife of Bath’s Prologue,” which is part of the Canterbury Tales Project phase 2. In this file, we observe the effects of Robinson’s double structure system in which we can decide to call the text of the work (a section of the *Canterbury Tales* known as The Wife of Bath’s Prologue). We could have, similarly, called upon a particular line within a specific document by using a different URI. The final attribute within the app entity is `type="main."` This indicates that the section in question is present as opposed to text not present (`type="om"`) or to a physical gap (`type="lac"`). On the next line of code in figure 1, we find the `<lem>` element with an attribute “Base,” the lemma against which all witnesses are compared and which has been tuned during the collation process to present the words in positions 10 and 12 together as a phrase. Thus, the lemma becomes “is right,” rather than being split into two lemmata, “is” and “right.” This alignment is an improvement both for the phylogenetic analysis and for the readability of the apparatus once it is generated.

The following element is the reading proper, `<rdg>`, which has the attributes `n` (which has values a, b, c, etc.) and `varSeq` (with values 1, 2, 3, etc.). Both attributes are generated by Smith’s Collation Editor, the tool we use for both regularization and alignment. Immediately, this is followed by the attribute “wit” and with the sigils of the different witnesses as value. The content of the element `<rdg>` is, in this case, two words, the reference reading from the base text, “is right,” and the sigils of the individual witnesses marked up with the element “idno.” This is followed by the other readings in this place of variation.

Stemmatology

Once we have a reliable XML apparatus, which has undergone both regularization and alignment for stemmatological analysis and for optimal human reading upon conversion, this can be processed within Textual Communities to obtain a NEXUS file. This operation is carried out, within Textual Communities, by choosing the options `Manage => Collation => Convert Collation output to NEXUS file`.

NEXUS File and Variant Matrix

NEXUS files are commonly used in bioinformatics and are a standard format for phylogenetic software (Maddison, Swofford, and Maddison 1997). Each file has several sections, formally known as blocks. Every NEXUS file has, at least, a taxa block (a taxon is an organism recognized by researchers as a unit) and a data block. Our groupings refer to texts, not organisms, so each taxon is represented by a sigil corresponding to one of our witnesses. A typical NEXUS file (Bordalejo and Robinson 2020b) used by Canterbury Project researchers will have a block called statelabels, which records all the variants at every place of variation within that section of the text. Thus, for example:

```
3277 CTP2_entity_WBP_line_484_2_2 i and for_i  
3278 CTP2_entity_WBP_line_484_4_12 made_hym_of_the_same  
3279 CTP2_entity_WBP_line_484_14_14 wode hode clothe wede  
3280 CTP2_entity_WBP_line_484_16_18 a_troce a_croce a_cote a_groce an_hode
```

Although the syntax is not designed for human reading, it is not difficult to understand. Each entry has an individual identifier in consecutive order, followed by the line indicators and the position within the line. The example above can be read as follows: these are characters 3277, 3278, 3279 and 3280 of the Wife of Bath's Prologue's line 484 locations 2 to 18 within phase 2 of the Canterbury Tales Project. The positions within line WBP484 are given in even numbers. This is part of the processing by Catherine Smith's Collation Editor (Smith 2019). Because of the limitations of CollateX, which does not have regularization or alignment facilities, Textual Communities has also embedded a version of Smith's Collation Editor. Catherine Smith, working for the Institute for Textual Scholarship and Electronic Editing at the University of Birmingham, developed the Collation Editor to regularize and align the Greek New Testament. For anyone familiar with the *Editio Critica Maior*, the use of only even numbers is understandable.

2,14 τί τὸ ὄφελος, ἀδελφοί μου,
2 4 6 8 10

2-10 b τι το οφελος αδελφε μου
c τι οφελος αδελφοι μου
d ἦ τι οφελος αδελφοι μου
e τι το οφελος αδελφοι
f τι το οφελος αγαπητοι μου
g αδελφοι τι το οφελος (Λ)
h αγαπητοι τι το οφελος (Λ)
i αδελφοι μου αγαπητοι τι το οφελος (Λ)
j τι (το) οφελος αδελφοι (μου) αγαπητοι (μου)

Fig. 2. The text and condensed apparatus of the *Editio Critica Maior*

The concept is that variants are given in reference to the text present in the base text using the even number system, but when text not present in the base text comes to light, this is labelled with odd numbers. Smith has followed the same architecture in her program, not only because her software is in use at the Institute for New Testament Research in Muenster for the continued work on the *Editio Critica Maior* and the Nestle-Aland edition, but also because the idea is both sound and successful in practice.

Returning to the specifics of the previous example (Figure 1), the places of variation are separated by a space in the nexus file, while phases are presented as a unit by using the underscore. This means that place of variation 2, the first in this line, has three variants:

I
And
For I

While place of variation 14, the third in the line, has four variants:

wode
hode
clothe
wede

The second place of variation in the line is a phrase, “made hym of the same,” formed of places of variation 4 to 12. This means that the words are in the second to the sixth positions in the line.

For the Wife of Bath’s Prologue, there are 5463 places of variation after regularization and alignment.

The following block of the NEXUS file is the taxlabels block, where a number is assigned to each witness, starting with 0 for the Base text and going to 88, which corresponds to Wynkyn de Worde’s edition.

The final section of a Canterbury Tales Project NEXUS is the variant matrix, just called Matrix in our file.

```
[3276] CTP2_entity_WBP_line_484_whole 00101100000010000101100100001010000011111001000011000100001111001101000000100000011001010  
[3277] CTP2_entity_WBP_line_484_2_2 007077000000700007077007020070700000777700700007710070000777007707000000700000077007070  
[3278] CTP2_entity_WBP_line_484_4_12 007077000000700007077007000070700000777700700007700070000777007707000000700000077007070  
[3279] CTP2_entity_WBP_line_484_14_14 007077000000700007077007000070700003777700700007700270000777007707000230700000077007170  
[3280] CTP2_entity_WBP_line_484_16_18 007077111011710117177117111171711100777711711117711471111777711770711142371111177117170
```

Fig. 3. Detail of the matrix in the Wife of Bath’s Prologue NEXUS file.

The matrix is very difficult to read for humans, though not impossible. Each variant has been assigned a number. For example, in places of variation 16 and 18, which have been aligned together, there are four phrase variants:

a troce
a croce
a cote
a groce
an hode

Each of these variants gets assigned a number 0 (a troce), 1 (a croce), 2 (a cote), 3 (a groce), 4 (an hode). Text not present is marked with a question mark. Consider the following:

```
[3280] CTP2_entity_WBP_line_484_16_18
00?0??111011?1011?1??11?1111?1?11100????11?1111??114?1111?
??11??0?111423?111111??11?1?0
```

Witnesses that agree with the base text are represented as 0. By counting the position and reconciling that with the position of each witness sigil in the taxlabel block, one could figure out which witnesses agree with the base text, which with reading 1, 2, 3 or 4. Although not impossible to interpret, the task is time-consuming and not advisable. For human reading, it is much easier to present a regular apparatus. The NEXUS file is only needed if we intend to process it with Phylogenetic Analysis Using Parsimony and Other Methods (Swofford 2003), henceforth PAUP, or other bioinformatics software. The NEXUS file for the Wife of Bath Prologue used in these examples was generated from the apparatus produced after Robinson's regularization (Bordalejo and Robinson 2020a).

Phylogenetic Analysis Methods

For textual scholars handling relatively large amounts of data, the use of computers might be quite obvious. And yet, only a small number of textual scholars make regular use of any kind of computer-assisted stemmatological method. Howe et al. outline the reasons to employ these as part of one's research:

These methodologies collectively offer several advantages to textual scholars. The use of computers means that the dataset can be sensitively yet comprehensively handled, which is particularly important if it comprises copies of a long text, for which a manual analysis may prove unwieldy. Multiple approaches can be applied to the same dataset for the purposes of comparison and testing. Perhaps most importantly for scholars of vernacular traditions, not all phylogenetic analyses are tied to

the assumption that a single ancestor is responsible for each extant copy and some copies are capable in principle of showing multiple affiliations. (Howe, Connolly, and Windram 2012, 56)

The ability to comprehensively handle data is one of the most significant aspects of the use of this software, because of the computer's capacity to accurately record the enormous amounts of data derived from a single textual tradition (for a comparison between manual and computer-assisted methods, see Bordalejo and Vázquez 2020). And yet, the open possibility of continued testing of different approaches (including different models of phylogenetic inference) cannot be underestimated. Through the years, we have done precisely this by employing multiple methods with the same dataset. Peter Robinson experimented with other software, such as SplitsTree (Huson and Bryant 2006), which I also tested for my work on the order of the *Tales* (Bordalejo 2003). PAUP (Swofford 2003) produced clearer results than SplitsTree and has become the standard tool for Canterbury Tales Project research. Although serious effort has gone into the development of software specializing in literary and historical textual transmission, neither RHM (Roos and Heikkilä 2009) nor SemStem (Roos and Zou 2011) has yet been made widely available. We have already incorporated some tools to facilitate computer-assisted stemmatological analysis, and we continue conversations for the integration of stemmatological software into Textual Communities. Our aim is to present a seamless interface to the users with the file conversion happening in the background in a similar way to which we currently convert the apparatus output into a NEXUS file. We plan to integrate the software within Textual Communities to facilitate its use through a single interface and to produce results ready for display as part of digital editions produced using the Textual Communities API.

To detail the debate over the validity of stemmatological methods in textual criticism would be beyond the purview of this paper, however, a brief account of the ongoing discussion around such methods demonstrates the impact/importance of our work. Although stemmatological methods have been used successfully to explore diverse textual traditions (Barbrook et al. 1998; Spencer, Bordalejo, Robinson, et al. 2003; P. Robinson 2003; Chaucer 2004; 2006; Eagleton and Spencer 2006; H. F. Windram et al. 2008; Phillips-Rodriguez 2010; P. M. W. Robinson 2012), the singular idea that the relationship between phylogenetic analysis and manuscript transmission was of analogy, rather of identity, prompted targeted essays focussing on the relationship between the two (Mooney et al. 2004). Independently of its justification, the use of tools originally developed for a specialized field and later implemented in another has not been without criticism (Robins 2007, Hanna 2000, Cartlidge 2001). For this reason, various experiments were carried out with artificial textual traditions (Spencer et al. 2004; Roos and Heikkilä 2009) and, when these were still not considered enough, a response to the criticisms was published (Howe, Connolly, and Windram 2012) followed by further theoretical explanations (Bordalejo 2016). Those interested in the use of phylogenetic analysis or other stemmatological tools would acquire reasonable knowledge from the texts mentioned above.

The success of phylogenetic methods with various textual traditions has been paralleled in other fields, most notably anthropology (Tehrani and Collard 2002; Tehrani and Collard 2009), folklore (Tehrani 2013; Tehrani, Nguyen, and Roos 2016), and archeology (Mendoza Straffon 2016). These applications, beyond molecular evolution, with its expansion to non-biological fields, gave rise to the concept of “phylomemetics” (Howe and Windram 2011).

I have written about the theory and practice of using phylogenetic analysis in the research context of medieval manuscript traditions (Bordalejo 2003, 90-112). However, since the work remains unpublished, it seems pertinent to summarize some important matters in this piece. Phylogenetic software looks into the nucleotide sequences to discover the three-letter words that encode individual amino acids and how the copying process sometimes results in the loss of a nucleotide that gets replaced by a different one giving rise to a mutation. A mutation, if successful, will be inherited and become a feature (Bordalejo 2003, 91-92). The software can express its results as networks or trees. Stenmatologists might tend to favour tree-building software because its output appears closer to that of conventionally constructed stemmata. The type of data used and the tree-building method sort phylogenetic software into categories.

Data Handling: Discrete vs. Distance

The data for use with phylogenetic software can be approached directly by structuring the data as a NEXUS file, as described above (this is what the Canterbury Tales Project does with textual data); or data can be converted into a distance matrix, as was done with the *Canterbury Tales* tale-order data (see below). When the only step for processing is the restructuring of data, we talk about a discrete method. When the data is processed and converted into a distance matrix, we talk about distance methods.

Page and Holmes explain that “[d]istance methods are based on the idea that if we knew the actual evolutionary distance between all members of a set of sequences, then we could easily reconstruct the evolutionary history of those sequences (Page and Holmes 1998, 179). Unweighted pair-group method using arithmetic averages (UPGMA), Least Squares (LS), Minimum Evolution (ME), and Neighbor Joining (NJ) are all distance methods (Nei and Kumar 2000, 87-113). For each pair of taxa (or witnesses), the evolutionary distance, which is a measure of genetic diversity, is calculated. The constructed tree considers the relationships between the distance values (Nei and Kumar 2000, 87).

Although it might seem obvious that by removing the conversion into a distance matrix, one might also remove the possibility for errors or the introduction of intermediate models that will impact the data in one way or another, not all data is liable to simple restructuring. Such was the case of the tale-order data I was analyzing as part of my NYU doctoral thesis (Bordalejo 2003). The tale-order work was based on my recoding of the charts by John Manly and Edith Rickert

(Manly and Rickert 1940), but these data required conversion prior to analysis. Matthew Spencer, who was also part of the STEMMA Project, suggested that we should use distance methods and was the first to convert my tables so we could test phylogenetic software with non-textual data. This serves as an example of the use of distance methods when direct data restructuring is not possible.

Spencer's breakpoint distance method worked when witnesses shared a significant number of missing items and also when there were fewer common items missing between any given pair. Spencer's algorithm generated upper and lower bound data which differ from each other in that "[t]he lower limit occurs when no common items were lost, and the upper limit is approached if there are many lost common items" (Spencer et al., unpublished). However, breakpoint distance "is only reliable when the number of transpositions is small" (Spencer, Bordalejo, Wang, et al. 2003, 102). At the time, Wang and Warnow had just devised Inverse of Expected BreakPoint Distance (INBP), which seemed better suited for the tale-order research (Wang 2001). Both methods are described in our article, "Analyzing the Order of Items in Manuscripts of *The Canterbury Tales*" (Spencer, Bordalejo, Wang, et al. 2003), where we also present ME trees based on this data. Fuller results of the tale-order analysis are presented in my NYU doctoral thesis which concludes that there is an undeniable coherence between tale-order and textual transmission in the tradition which suggests that the order was more often than not copied from an exemplar while, in few occasions, it was purposely altered by scribes or their supervisors (Bordalejo 2003. 190 and ff.). Because of the nature of the data, we built trees using minimum evolution and neighbor joining, both phylogenetic inference methods that accept distance values as data input.

Discrete methods, in contrast, use structured data without further processing. In that way, they are one step closer to the data than distance methods. Some data, like the tale-order data, because of their nature, must be encoded before processing. The NEXUS file based on the Wife of Bath's apparatus is a restructuring of the data to be processed by phylogenetic software, but the data is not changed by such restructuring. Discrete methods "endeavour to avoid the loss of information that occurs when sequences are converted into distances" (Page and Holmes 1998, 187), which means that another degree of separation between the data and the resulting tree is avoided. Maximum Parsimony (MP) and Maximum Likelihood (ML) are discrete methods of phylogenetic inference. These methods differ on how they choose the trees they present:

The two major discrete methods are maximum parsimony and maximum likelihood. Maximum parsimony chooses the tree (or trees) that require the fewest evolutionary changes. Maximum likelihood chooses the tree (or trees) that of all trees is the one that is most likely to have produced the observed data (Page and Holmes 1998, 187).

In my previous study, I explain that although these methods are particularly well-suited for dealing with textual variation, the fact that maximum parsimony searches for the trees with the least number of changes is liable to present a simplified version of what might be a more complex tradition (Bordalejo 2003, 93). However, there is a more significant problem with MP. Nei and Kumar synthesize it as follows:

If there are no backwards and no parallel substitutions (no homoplasy) at each nucleotide site and the number of nucleotides examined (n) is very large, MP methods are expected to produce the correct (realized) tree (Nei and Kumar 2000).

Homoplasy refers to both parallel and convergent evolution, both of which are cases of independent development of the same features. Textual scholars are familiar with this phenomenon during which different scribes in completely separate occasions introduce the same change to the text. Manly and Rickert call it agreement by coincidence. We know from experience that this type of inference does not work well with highly contaminated traditions. We are fortunate that, in working with 15th-century witnesses of the *Canterbury Tales*, contamination is not as much of an issue as it is with larger traditions with a life-span of several centuries like that of the Mahabharata or the Greek New Testament. It is clear that models of phylogenetic inference that could cope with contamination and coincidental agreement would be advantageous for large classical and medieval textual traditions.

The Canterbury Tales Project

When I started at the Canterbury Tales Project in 1999, Robinson was experimenting with SplitTrees. *The General Prologue on CD-ROM* (Solopova 2000) presented trees that were produced using SplitTrees and that were informative about an early split in the textual tradition from which Robinson hypothesized the alpha hyparchetype (a lost manuscript from which roughly half of the tradition descended).

Despite this breakthrough, the control offered by PAUP was unparalleled, and its results were consistent with aspects of the textual tradition confirmed independently. Take, for example, the fundamental groups proposed by Manly and Rickert:

Group *a*: Cn Dd En1 Ds Ma

Group *b*: He Ne Cx1 Tc2

Group *c*: Cp La Sl2

Group *d*: En2 Ll1 Lc Mg Pw Mm Ph3 Ry2 Ld2 Dl Ha2 Sl1

Independent pairs: Ad3 and Ha5, Bo1 and Ph2, En3 and Ad1, Mc and Ra1, Ps and Ha1, and Ra2 and Ht

These groupings and most of the pairs are confirmed by analysis carried out by members of the Canterbury Tales Project (Chaucer 1996; P. M. W. Robinson 1997; P. Robinson 2003; Bordalejo 2003; Chaucer 2004). By using phylogenetic software, we have been able to confirm part of Manly and Rickert's manual analysis of the *Tales*. The phylogenetic trees offer enough new avenues of enquiry to open paths for further research. There are two main conclusions from our analyses that improve or correct Manly and Rickert:

- 1) The tales and sections did not circulate independently; witnesses share both for text and non-textual elements the same overall relationships.
- 2) Hg, El, Ch, (Ad3, Ha5), (Bo1, Ph2), (En3 Ad1), Mc and Ra1, Ps and Ha1, and Bo2 and Ht represent independent lines of descent from the archetype. We call them the o witnesses (Robinson 1997, 80).

Neither of these two corrections to Manly and Rickert signal incompetency nor carelessness. They were both excellent editors and researchers. The hypothesis of the independent circulation of the *Tales* appears to have support from the fact that the work was left unfinished and some units shifted positions, but both the textual and non-textual data indicate that the *Canterbury Tales* circulated as a book rather than in booklets (Chaucer 1996; Bordalejo 2002; 2003; Chaucer 2004; 2006).

Our editions always present what we call Variant Maps, representations of the relations among the witnesses produced using phylogenetic software and displayed as unrooted tree-like graphs. Some scholars will consider this controversial, but I want to state it here as clearly as possible: the unrooted graphs which we call Variant Maps in our editions are stemmata. They are based on data informed by editorial judgement at every point and show genetic relations among textual witnesses. Although we could root our stemmata, a root is not necessary because that would not change the relationships between the nodes. We deliberately choose not to create a visualization reminiscent of manual stemmata. It is not necessary.

Why Maximum Parsimony

Because maximum parsimony does not require further data processing, it seems preferable to other approaches for use with textual variation. The underlying model of phylogenetic inference, seeking the most parsimonious tree, "...creates a tree that represents the smallest overall number of independent mutations..." (Howe, Connolly, and Windram 2012, 63). Elsewhere, I explain that these trees should not be expected to conform to the historical reality of a manuscript tradition, as they can only take into account the input data, which is generally textual rather than extra-textual (Bordalejo 2016, 568).

As we tested methods, parsimony became our choice because maximum likelihood required both more time and computer resources while not offering significantly better results. For a tradition with fewer witnesses, one can use maximum parsimony, and PAUP will do an exhaustive search

for all the possible trees before settling into the most parsimonious one. However, above a certain number of witnesses, it is better to start with a heuristic search:

A provisional MP tree is first constructed by using a procedure called step-wise addition algorithm, and this provisional MP tree is then subjected to some kind of branch swapping to find a more parsimonious tree (Nei and Kumar 2000).

The Canterbury Tales Project routinely uses heuristic searches for the production of stemmata. We complement these searches by comparing them with consensus trees when more than one equally parsimonious tree is found. When a section of a tree surprises researchers, and we need to know how reliable a tree is, we use bootstrapping, a sampling technique that is repeated one hundred times to offer a percentage result in which higher numbers point towards higher reliability (for more details about bootstrapping see Higgs and Attwood 2005, 169 and ff.).

The caveat for the use of maximum parsimony is the problem of agreement by coincidence that, in large enough numbers, would produce an incorrect topology for the tree. Since, at the moment, no solution is offered within maximum parsimony, one has to look elsewhere for a possible solution. T-REX is a webserver for the inference, validation, and visualization of phylogenetic trees developed by members of the Department of Computer Sciences at the Université du Québec à Montréal and which deals with the issue of lateral gene transfer (Boc, Philippe, and Makarenkov 2010; Boc, Diallo, and Makarenkov 2012). Testing T-REX with textual traditions opens the possibility of solving a significant problem within computer-assisted stemmatology. This would have at least as much impact as the application of Chi-Square for the detection of a change of exemplar (Windram, Howe, and Spencer 2005; Phillips-Rodriguez, Howe, and Windram 2009).

Using phylogenetics to explore the tradition

After the apparatus data is formatted into a NEXUS file, it can be uploaded to PAUP (or another phylogenetic application accepting the same type of format). We follow the principles outlined above, setting the software to seek maximum parsimony trees using heuristic searches.

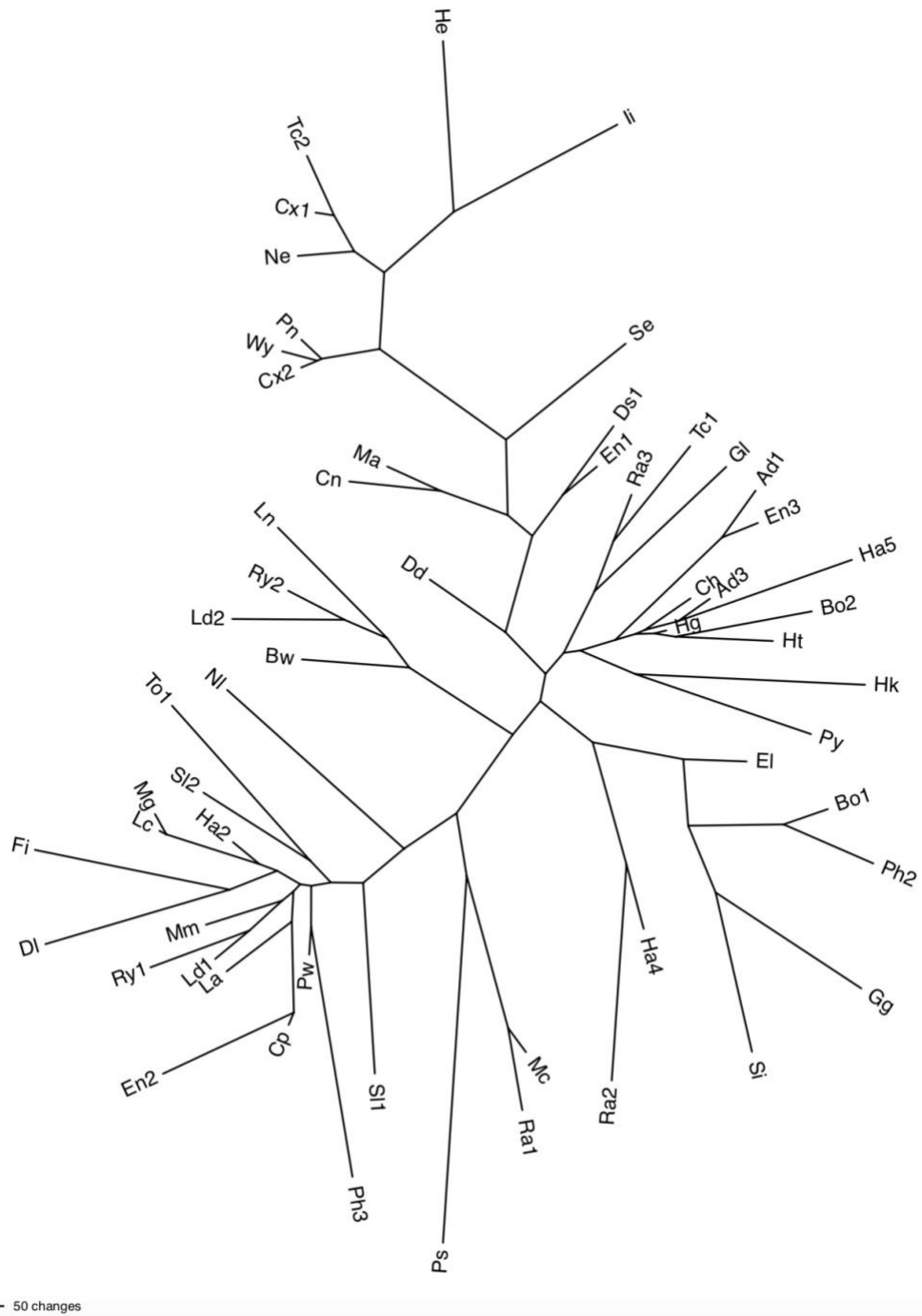


Fig. 4. Stemma of lines 1 to 400 of the Wife of Bath's Prologue.

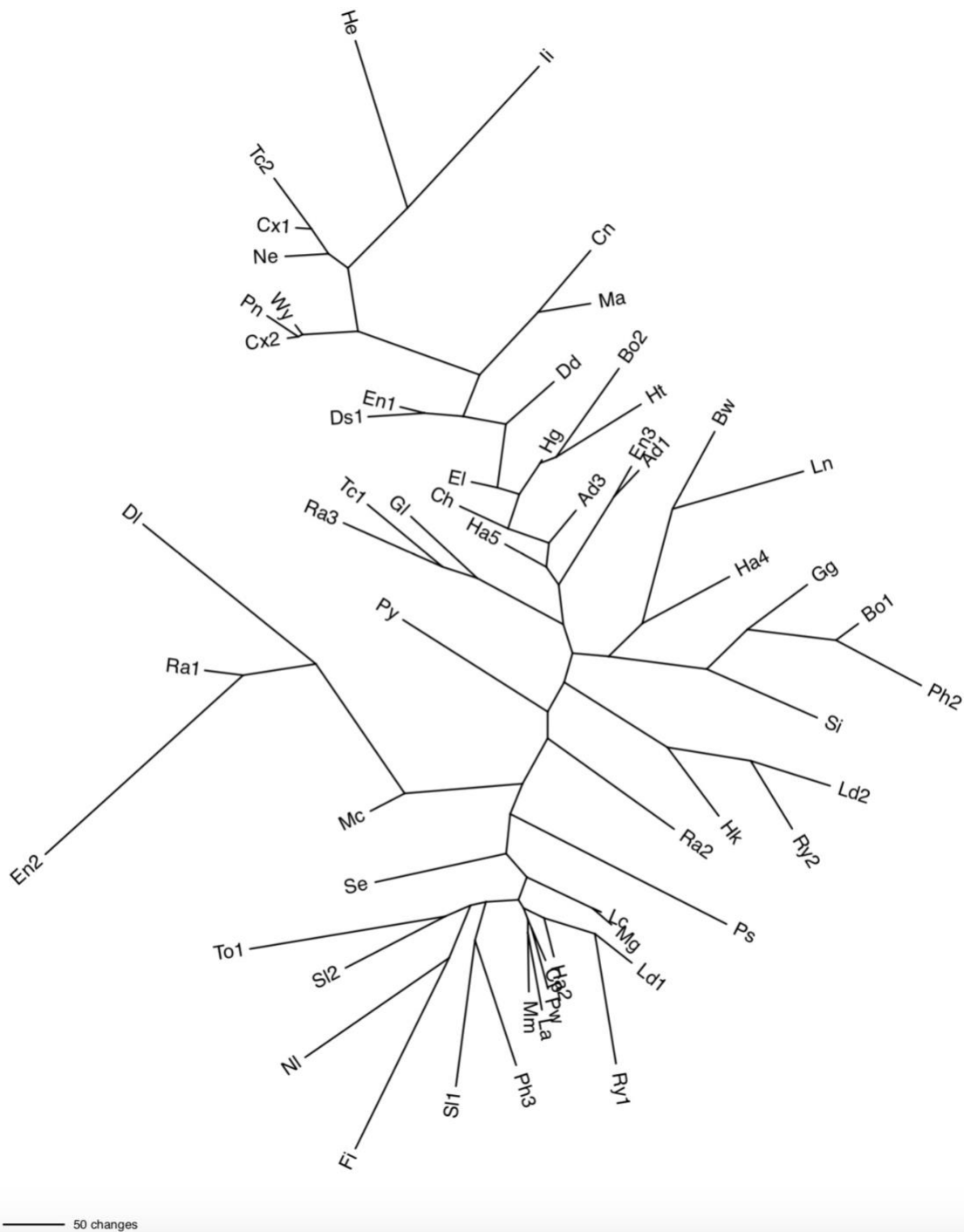


Fig. 5. Stemma of lines 401 to the end of the Wife of Bath's Prologue.

For the Wife of Bath's Prologue, we built two separate stemmata because we know that the Ellesmere manuscript (E1) changed exemplars around line 400. This became very clear during the research that led to the publication of *The Wife of Bath's Prologue* on CD-ROM (Chaucer 1996; Robinson 1997, 79), and was independently confirmed by the chi-square analysis carried

out by Windram, Howe, and Spencer, who point out the exact place of maximum chi-square value is character 3384, “which corresponds to line 404 in the text and is the location most likely to be the site of manuscript recombination” (Windram, Howe, and Spencer 2005, 194–95). This example shows very clearly the change of Ellesmere’s habitual position within the stemmata (clustering close to Hengwrt [Hg] and Christ Church [Ch]) as it does in figure 5, to branching with Bo1, Ph2, Gg and Si (figure 4). For most scholars, just the shift from one place to another is remarkable. However, Ellesmere grouping with those manuscripts is the same pattern of variation found in the Squire’s Tale (Bordalejo 2002, 200–203). Gg has the tendency to shift positions in the stemmata, suggesting either a contaminated exemplar or multiple sources for the manuscript resulting in conflation.

Manly and Rickert, for all their laboriously accurate work on the *Canterbury Tales* (Manly and Rickert 1940) were unable to understand major sections of the tradition, particularly archetypal variation and the internal relationships within the *d* group. There is simply too much data for humans to comprehend it easily without the aid of computational methods, as explained above in relation to the manuscripts carrying archetypal variation. Moreover, despite their correct identification of four manuscript groups (*a*, *b*, *c*, *d*), Manly and Rickert were not able to make sense of archetypal variation retained in separate lines of descent, a series of witnesses which we have termed O, and which do not represent a genetic group.

VBase

No matter how clear our understanding of how phylogenetic software works or what inference model underlies our results, it would be foolish to accept the resulting trees with blind confidence. For this reason, our editions include VBase, a variant database that allows us to perform complex queries in relation to variant distribution. Analyzing these queries helps us further analyze our trees and explain why the phylogenetic software rendered a given tree in a particular way.

The Variant Map for line 65 of the Miller’s Tale shows an odd distribution in which Ellesmere agrees with the *b* group (Cx1, Ne, He, and Tc2) against both Hengwrt and Christ Church. Our experience is that these three manuscripts (El, Hg, and Ch) form a compact trio that often appears with other O witnesses and, since silk/grene are not readings that arise simply by mistake, we might want to explore them further (see figure 6). VBase can retrieve answers to highly sophisticated questions, which might help us understand whether there is more to this place of variation.

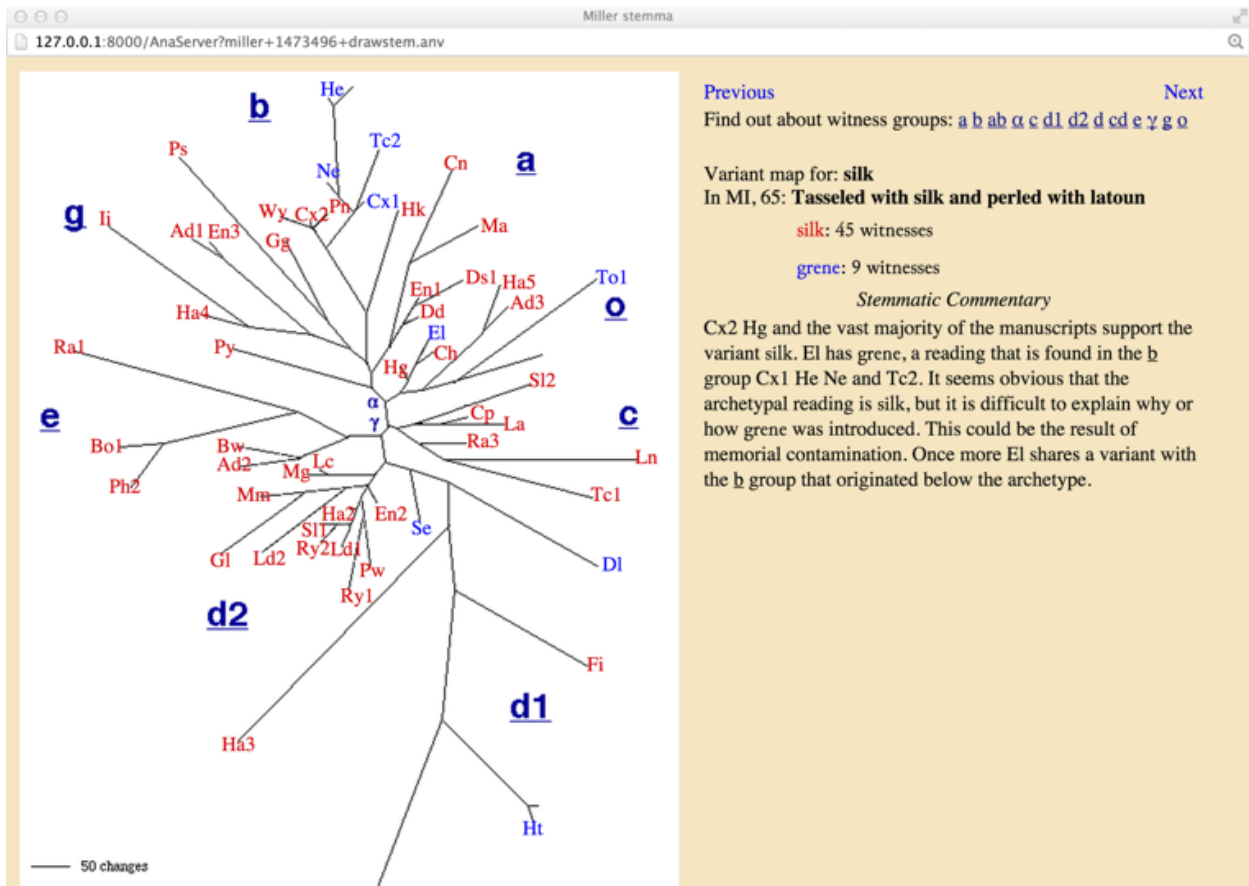


Fig. 6. Miller's Tale Variant Map (Chaucer 2003).

One might want to start with a relatively simple query that retrieves all the variants that support *b* as a genetic group. In order to establish which variants determine the *b* group, one must carry out a search, as illustrated in figure 7. In our edition, we have preset some searches (and offer additional information on them) to facilitate the use of VBase for anyone without an in-depth knowledge of the textual tradition of the *Canterbury Tales*.

There are three main steps for the retrieval of the *b* variants:

1. Eliminate archetypal readings, expressed in <14 of all and in two or more of Hengwrt, Ellesmere and Christ Church. That is, they should appear in fewer than two of the three or <2 of Hg El Ch (these witnesses share archetypal variation, and the *b* variants arose below the archetype).
2. Distinguish from the *a* group by excluding variants present in more than two of one of the *a* subgroups, expressed as <2 of En1 Ds1 Dd; and any variants in more than one of the other *a* subgroup (<2 of Ma Cn Dd). Notice that one witness, Cambridge CUL Dd 4.24, appears twice because it shares variants with both subgroups of *a* (*b* must have variants exclusive to itself to be considered a genetic group and these cannot be shared with another genetic group).

- The separation of *b* is established by those variants that follow the above conditions while appearing in three *b* witnesses or in >2 of Cx1 He Tc2 Ne Ox1.

Miller's Tale 1 Cp Text/Image Go! Contents Find! SCHOLARLY DIGITAL EDITIONS

Results of search for variants in *b* witnesses

From: Line To: FR

Not in	< or >	<2	of	Hg El Ch
Not in	< or >	<2	of	En1 Ds1 Dd
Not in	< or >	<2	of	Ma Cn Dd
Not in	< or >	>2	of	Cx1 He Tc2 Ne Ox1
Not in	< or >	<14	of	\all
Not in	< or >		of	
Not in	< or >		of	
Not in	< or >		of	

Count the hits in every manuscript (don't use last input row) Check to clear all Press submit to search

Make Variant Group Profile for [Make Outline Variant Group Profiles](#) [Make Full Variant Group Profiles](#)

Get variants for: a b ab g α c d d1 d2 γ e cd Hg not El El not Hg o
Find out about: a b ab g α c d d1 d2 γ e cd Hg not El El not Hg o

Search for variants in *b* witnesses: in <2 of Hg El Ch in <2 of En1 Ds1 Dd in <2 of Ma Cn Dd in >2 of Cx1 He Tc2 Ne Ox1 in <14 of \all

50 of total 222 hits

L1-7: This gooth aright vnbokeled is the male; [Variant map](#)

		3 mss	Cx1 Ne Tc2
gooth	51		Ad1 Ad2 Ad3 Bo1 Bo2 Ch Cn Cp Cx2 Dd D1 Ds1 El En1 En3 Fi Gg Gl Ha2 Ha3 Ha4 Ha5 He Hg Hk Ht li La Lc Ld2 Ln Ma Mg Mm Nl Ph2 Pn Ps Pw Py Ra1 Ra2 Ra3 Ry1 Ry2 Se S11 S12 Tc1 To1 Wy

L1-7: This gooth aright vnbokeled is the male; [Variant map](#)

		3 mss	Cx1 Ne Tc2
right	4		Ad1 En3 Ha4 li
aright	46		Ad2 Ad3 Bo1 Bo2 Ch Cn Cp Cx2 Dd D1 Ds1 El En1 Fi Gg Gl Ha2 Ha3 Ha5 He Hg Hk Ht La Lc Ld2 Ma Mg Mm Nl Ph2 Pn Ps Pw Py Ra1 Ra2 Ra3 Ry1 Ry2 Se S11 S12 Tc1 To1 Wy

Fig. 7. VBase preset search for *b* group variants (Chaucer 2003).

The evidence indicates that *b* is a genetic group: there are 222 variants shared by the *b* witnesses, that are not present in a significant number of the rest of the witnesses. VBase makes it possible to conduct all sorts of specialized queries. If one were curious as to the number of variants that Ellesmere shares with *b* against Hengwrt and the rest of the textual tradition, one could simply adjust the query, as seen in figure 8. VBase returns 32 places of variation showing that Ellesmere, one of the most important manuscripts of the *Tales* and a manuscript that is generally in agreement with Hengwrt and Christ Church, preserves 32 instances of variation likely to have originated below the archetype and linking it to one of the most textually removed from the origin of the tradition. I will not argue here about the reasons for this, discussed elsewhere (Chaucer 2004, *Stemmatic Commentary*, MI65). This is merely an example of how VBase can be used to explore questions related to witness relationships.

Miller's Tale 1 Cp Text/Image Go! Contents Find! SCHOLARLY DIGITAL EDITIONS

Enter query:

From: Line To: FR

Not in	< or >	<1	of	Hg Ch
Not in	< or >	<2	of	En1 Ds1 Dd
Not in	< or >	<2	of	Ma Cn Dd
Not in	< or >	>2	of	Cx1 He Tc2 Ne Ox1
Not in	< or >	<14	of	\all
Not in	< or >	>0	of	Ei
Not in	< or >		of	
Not in	< or >		of	

Count the hits in every manuscript (don't use last input row) Check to clear all Press submit to search

Make Variant Group Profile for [Make Outline Variant Group Profiles](#) [Make Full Variant Group Profiles](#)

Get variants for: a b ab g α c d d1 d2 γ e cd Hg not Ei El not Hg o
 Find out about: a b ab g α c d d1 d2 γ e cd Hg not Ei El not Hg o

Search for variants: in <1 of Hg Ch in <2 of En1 Ds1 Dd in <2 of Ma Cn Dd in >2 of Cx1 He Tc2 Ne Ox1 in <14 of \all in >0 of Ei

32 of total 32 hits

MI-19: Ful fetisly dight with herbes swoote; Stemmatic Commentary * + Variant map

y dight	13 mss	Ad2 Cx1 Cx2 Ei Ha4 He Ht li Ne Ox1 Pn To1 Wy
dight	42	Ad1 Ad3 Bo1 Bw Ch Cn Cp Dd D1 Ds1 En1 En2 En3 Fi Gg Gl Ha3 Ha5 Hg Hk La Lc Ld1 Ld2 Ln Ma Mg Mm Ni Ph2 Ps Pw Py Ra1 Ra3 Ry1 Ry2 Se Sll Sl2 Tc1 Tc2

MI-49: A ceynt she werde barred al of sylk; Stemmatic Commentary * + Variant map

ybarred	13 mss	Ad3 Bo1 Bw Cx1 D1 El Ha5 He Ht Ne Ph2 Tc2 To1
barred	38	Ad1 Ad2 Ch Cn Cp Cx2 Dd Ds1 En1 En2 En3 Fi Gl Ha3 Ha4 Hg li La Lc Ld1 Ld2 Ln Ma Mg Mm Pn Ps Pw Py Ra1 Ra3 Ry1 Ry2 Se Sll Sl2 Tc1 Wy
b ^c ceynt	1	Gg

Fig. 8. VBase modified search to isolate variants shared by Ellesmere and the *b* group (Chaucer 2003).

VBase is instrumental in helping us understand the variation on which PAUP has based every section of the tree. Manly and Rickert's correct assessment of the fundamental witness groups shows that it is possible to observe and analyze data and make the correct deductions without the help of a computer. But further investigation, such as in my query trying to isolate the variants in which Ellesmere agrees with *b*, requires more precise tools.

Using a combination of PAUP and VBase, we have been able to understand the witnesses we call O. This is not a genetic group, but witnesses that represent independent lines of descent from the archetype. The O witnesses often preserve archetypal readings which are lost elsewhere in the tradition. These variants puzzled Manly and Rickert who were not able to correctly classify them. This is not a criticism of their work, but rather it is evidence of the difficulties editors face when dealing with very large datasets.

Miller's Tale 1 Cp Text/Image Go! Contents Find! SCHOLARLY DIGITAL EDITIONS

Results of search for variants in **o** witnesses

From: Line To: FR

Not in	(< or > >1 of)	Hg El Ch
Not in	(< or > <15 of)	\all
Not in	(< or > of)	
Not in	(< or > of)	
Not in	(< or > of)	
Not in	(< or > of)	
Not in	(< or > of)	
Not in	(< or > of)	

Count the hits in every manuscript (don't use last input row) Check to clear all Press submit to search

Make Variant Group Profile for [Make Outline Variant Group Profiles](#) [Make Full Variant Group Profiles](#)

Get variants for: a b ab g α c d d1 d2 γ e cd Hg.not.El El.not.Hg o
 Find out about: a b ab g α c d d1 d2 γ e cd Hg.not.El El.not.Hg o

Search for variants in **o witnesses: in >1 of Hg El Ch in <15 of \all**

37 of total 37 hits

L1-4: **And worthy for to drawn to memorie**; Stemmatic Commentary * + [Variant map](#)

to	9 mss	Ch Dd El En1 Gg Hg Ps Pw To1
in	41	Ad1 Ad2 Bo1 Bo2 Bw Cp Cx1 Cx2 Ds1 En2 En3 Fi G1 Ha2 Ha3 Ha4 Ha5 He Hk Ht Ii La Lc Ld2 Mg Mm Ne Nl Ph2 Pn Py Ra1 Ra2 Ra3 Ry2 Se S11 S12 Tc1 Tc2 Wy
into	4	Ad3 Cn Dl Ma
\in/	1	Ln
vnto	1	Ry1

L1-31: **And therefore if that I mysspeke or seye**; Stemmatic Commentary * + [Variant map](#)

that I	12 mss	Ad2 Bo2 Ch Dd El En1 Ha4 Ha5 Hg Ht Ln Ph2
I	41	Ad1 Ad3 Bo1 Bw Cn Cp Cx1 Cx2 Dl Ds1 En3 Fi Gg Gl Ha2 Ha3 He Hk Ii La Lc Ld1 Ld2 Ma Mg Mm Ne Nl Pn Pw Py Ra1 Ra3 Ry1 Ry2 Se S11 S12 Tc1 Tc2 Wy

Fig. 9. VBase preset search for O variants (Chaucer 2003).

To search for O variants, one sets up a query in which the target is present in at least two of Hengwrt, Ellesmere and Christ Church and in fewer than 15 of all other witnesses. Technically, all archetypal variants preserved by any witness in the tradition should be O variants but, for our purposes, O variants are those that have been preserved (often on account of their difficulty) by a few scribes in a few witnesses derived in a more or less direct way from the archetype of the tradition (Chaucer 2004). These variants, because of their distribution within many lines of descent, and their nature, are likely to be Chaucerian. There are 37 such variants in the Miller's Tale, as shown in figure 9.

VBase allows researchers to carry out complex searches asking precise questions. Some of those questions might come from hypotheses put forward by other scholars or by one's own observations of particular witnesses in the tradition. However, when PAUP presents unexpected groupings or places witnesses in surprising positions in the tree topology, VBase can help us understand what part of the data supports the visual representation and why.

The Edition Apparatus

In most cases, readers do not seek to get profoundly involved with research on textual variation, or they require a synthetic view of a particular place of variation. Our apparatus, built from our curated collations, offers various ways to approach the *Canterbury Tales* variants. We strive to present apparatus that are readable, but we also want them to be useful beyond the purposes of our own research.

[Previous](#) [MI 2](#) [Variant map](#) [Next](#)

A riche gnof that gestes heeld to bord
 choffe and gestes hadde at
 Chorle heeld gestes
 g^{n/}uffe
 \gnouf/ choffe

[Show original spellings](#)

gnof 43 wits. [Ad1](#) [Ad2](#) [Ad3](#) [Bo1](#) [Bw](#) [Ch](#) [Cn](#) [Cp](#) [Cx2](#) [Dd](#) [Dl](#) [Ds1](#) [El](#) [En1](#) [En3](#) [Fi](#) [Gg](#) [Gl](#) [Ha3](#) [Ha4](#) [Ha5](#) [Hg](#) [Hk](#) [Hr](#) [La](#)
 [Lc](#) [Ld1](#) [Ma](#) [Mg](#) [Mm](#) [Ph2](#) [Pn](#) [Pw](#) [Py](#) [Ra1](#) [Ra3](#) [Ry1](#) [Ry2](#) [Sl1](#) [Sl2](#) [Tc1](#) [To1](#) [Wy](#)

choffe 6 wits. [Cx1](#) [Ii](#) [Ld2](#) [Ne](#) [Se](#) [Tc2](#)

Chorle 3 wits. [He](#) [Ni](#) [Ox1](#)

g^{n/}uffe 1 wit. [Ln](#)

\gnouf/ choffe 1 wit. [Ps](#)

[Verse By Verse](#) [Show Witnesses](#)

A riche gnof that gestes heeld to bord 33 wits.
 A riche choffe that gestes hadde to bord 3 wits.
 A riche gnof that gestes hadde to bord 6 wits.
 A riche gnof and gestes heeld to bord 2 wits.
 A riche gnof that heeld gestes to bord 1 wit.
 A riche Chorle that gestes hadde to bord 3 wits.
 A riche choffe that gestes heeld at bord 1 wit.
 A riche choffe that gestes heeld to bord 2 wits.
 A riche g^{n/}uffe that gestes heeld to bord 1 wit.
 A riche \gnouf/ choffe that gestes hadde at bord 1 wit.

Fig. 10. The synoptic apparatus, the regularized apparatus, and the lineated apparatus. (Chaucer 2003).

Our previous editions have presented a synthetic view of the line, which we call the synoptic apparatus (top section of figure 10). The variants appear in the middle section, which corresponds to the regularized apparatus. The last section presents an aligned lineated apparatus in which the colours suggest how it should be read vertically.

The synoptic apparatus shows all the possible variants in each place of variation but gives no indication as to which of the horizontal reading combinations is an actual line present in one of the witnesses (the lineated apparatus offers that). Instead, it offers the complete line variation at a glance.

The middle section of the apparatus shows the regularized forms of each word, although the original spellings can be shown by clicking on the link that turns them on. By having the information in three different formats, we seek to facilitate its comprehension and to make the data easily digestible.

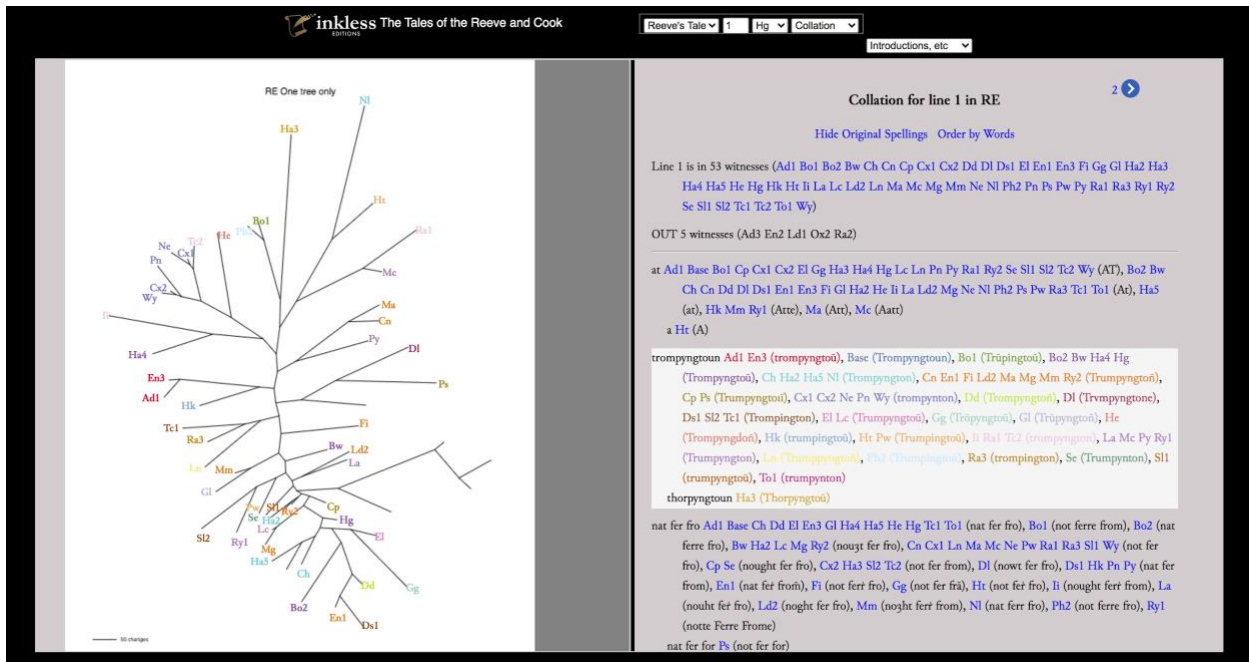


Fig. 11. The Variant Map, the regularized apparatus, and the original spellings. (Chaucer 2020).

In our newest editions, produced via the Textual Communities API, we can show each variant linked to the colour coded stemma. Figure 11 presents the unregularized spellings of *Trompyngtoun*, highlighting the enormous variation of spellings in toponyms, which the regularized collation shows to be quite consistent.

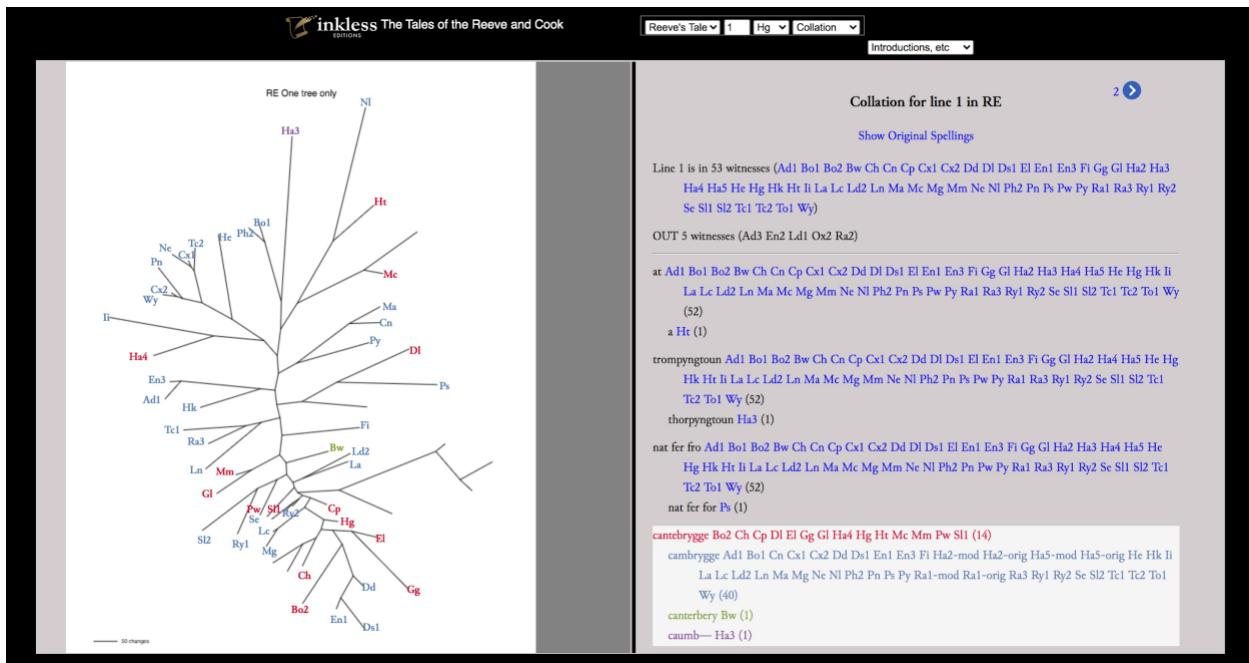


Fig. 12. The Variant Map and the regularized apparatus (Chaucer 2020).

The regularized collation of Cantebrygge/ Cambrygge, however, shows a typical example of an O variant, in which the distribution of the *lectio difficilior*, Cantebrygge appears in independent lines of descent in different sectors of the stemma.

The Ends of Textual Criticism: Integrating Tools to Edit the *Canterbury Tales*

The Canterbury Tales Project, throughout its almost thirty years of history, has pioneered approaches to digital editing, produced cutting edge research, and tested various publication platforms. Today, the full development of Textual Communities, implementing CollateX and the Collation Editor as well as file conversion facilities, presents the integration of well-developed systems while still seeking to innovate.

A significant proportion of our research could be carried out by hand, but then we would be left with little time to attempt new approaches. A future avenue of exploration would be on the application of software that solves some of the problems with maximum parsimony, namely agreement by coincidence; T-REX reputedly does this, but it remains to be tested with textual data. Although I have no reason to believe that it would not work, given our experience with other bioinformatics software; but the quality of the results needs to be evaluated, particularly whether said results are good enough to warrant the effort of presenting the data in a different format, learning the new software, and fully understanding its underlying model.

All of this work, from the decisions as to what to transcribe and how to encode the text, passing through the processes of regularization and alignment, to every minute setting on how we express our data, are critical acts and require editorial judgement. The time we are able to save for ourselves now can be used to prioritize investigating new ways to explore textual traditions. Moreover, we also save time for those who would use our work in their own research. The methods we employ work, but they take time to learn and effort to understand. I have tried to give a detailed account not only of why we do it but how, so scholars interested in testing these approaches might be encouraged to try them.

We have not yet, as part of our editions, offered a critical text (although these are included in the Canterbury Tales Project's publication plans). Perhaps, for this reason, we have not presented a hierarchy of variants in our apparatus, and yet, by privileging a regularization towards the spellings in Hengwrt, we have normalized them and pushed the text towards a vision that is not real. In the wild, the *Canterbury Tales* variants come in all sorts of colours and flavours, not in the tame forms we present in our regularized apparatus, but in the fauvist diversity of their original spellings and dadaist rearrangements.

Bibliography

Barbrook, Adrian C., Christopher J. Howe, Norman Blake, and Peter Robinson. 1998. "The

- Phylogeny of The Canterbury Tales.” *Nature* 394 (6696): 839–839.
<https://doi.org/10.1038/29667>.
- Boc, Alix, Alpha B. Diallo, and Vladimir Makarenkov. 2012. “T-REX: A Web Server for Inferring, Validating and Visualizing Phylogenetic Trees and Networks” *Nucleic Acids Research (W1)*: W573–W579.
- Boc, Alix, Hervé Philippe, and Vladimir Makarenkov. 2010. “Inferring and Validating Horizontal Gene Transfer Events Using Bipartition Dissimilarity.” *Systematic Biology* 59 (2): 195–211. <https://doi.org/10.1093/sysbio/syp103>.
- Bordalejo, Barbara. 2002. “The Manuscript Source of Caxton’s Second Edition of The Canterbury Tales and Its Place in the Textual Tradition of the Tales.” De Montfort University.
https://www.academia.edu/2987324/THE_MANUSCRIPT_SOURCE_OF_CAXTONS_SECOND_EDITION_OF_THE_CANTERBURY_TALES_AND_ITS_PLACE_IN_THE_TEXTUAL_TRADITION_OF_THE_TALES.
- Bordalejo, Barbara. 2003. “The Phylogeny of the Order in the ‘Canterbury Tales.’” PhD Thesis, New York, N.Y.: New York University, Graduate School of Arts and Science.
<http://search.proquest.com/mlaib/docview/54046613/36CD5C07D51F43FAPQ/2>.
- Bordalejo, Barbara. 2016. “The Genealogy of Texts: Manuscript Traditions and Textual Traditions.” *Digital Scholarship in the Humanities* 31 (3): 563–577.
<https://doi.org/10.1093/llc/fqv038>.
- Bordalejo, Barbara, and Peter M. W. Robinson. 2020a. “Wife of Bath’s Prologue Regularized Apparatus.” Zenodo. <https://doi.org/10.5281/zenodo.3928655>.
- Bordalejo, Barbara, and Peter M. W. Robinson. 2020b. “Wife of Bath’s Prologue NEXUS File.” Zenodo. <https://doi.org/10.5281/zenodo.3929763>.
- Bordalejo, Barbara, and Adam Vázquez. 2020. “You’re Collating Just Fine and Other Lies You’ve Been Telling Yourself.” *Unpublished*, July.
<https://doi.org/10.5281/zenodo.3930286>.
- Chaucer, Geoffrey. 1996. *Chaucer: The Wife of Bath’s Prologue on CD-ROM*. Edited by Peter Robinson. Cambridge: Cambridge University Press.
- Chaucer, Geoffrey. 2004. *The Miller’s Tale on CD-ROM*. Edited by Peter Robinson. Canterbury Tales Project. Leicester: Scholarly Digital Editions. <http://www.sd-editions.com/AnaAdditional/miller/images/millerhome.html>.
- Chaucer, Geoffrey. 2006. *The Nun’s Priest’s Tale on CD-ROM*. Edited by Paul Thomas. Leicester: Scholarly Digital Editions. <http://www.sd-editions.com/NP/index.html>.
- Eagleton, Catherine, and Matthew Spencer. 2006. “Copying and Conflation in Geoffrey Chaucer’s Treatise on the Astrolabe: A Stemmatic Analysis Using Phylogenetic Software.” *Studies in History and Philosophy of Science Part A* 37 (2): 237–68.
<https://doi.org/10.1016/j.shpsa.2005.08.020>.
- Higgs, Paul G., and Teresa K. Attwood. 2005. *Bioinformatics and Molecular Evolution*. Hoboken, UNITED KINGDOM: John Wiley & Sons, Incorporated.
<http://ebookcentral.proquest.com/lib/usask/detail.action?docID=428071>.
- Howe, Christopher J., Ruth Connolly, and Heather F. Windram. 2012. “Responding to Criticisms of Phylogenetic Methods in Stemmataology.” *SEL Studies in English Literature 1500-1900* 52 (1): 51–67. <https://doi.org/10.1353/sel.2012.0008>.
- Huson, D. H., and D. Bryant. 2006. “Application of Phylogenetic Networks in Evolutionary Studies.” *Mol. Biol. Evol* 23 (2): 254–67.

- Maddison, David R, David L Swofford, and Wayne P Maddison. 1997. "NEXUS: An Extensible File Format Forr Systematic Information." *SYSTEMATIC BIOLOGY* 46: 32.
- Manly, John M., and Edith Rickert. 1940. *The Text of the Canterbury Tales Studied on the Basis of All Known Manuscripts, Manly, John M.; Rickert, Edith ; with the Aid of Mabel Dean e. a.; with a Chapter on Illuminations by Margaret Rickert*. Chicago (Ill.): University of Chicago press.
- Mendoza Straffon, Larissa, ed. 2016. *Cultural Phylogenetics*. Vol. 4. Interdisciplinary Evolution Research. Cham: Springer International Publishing. <https://doi.org/10.1007/978-3-319-25928-4>.
- Mooney, Linne R., Christopher J Howe, Adrian C Barbrook, and Peter M. W. Robinson. 2004. "Parallels between Stemmatology and Phylogenetics." In *Studies in Stemmatology II*, edited by Pieter van Reenen, August den Hollander, and Margot van Mulken. Philadelphia, NETHERLANDS, THE: John Benjamins Publishing Company. <http://ebookcentral.proquest.com/lib/usask/detail.action?docID=623163>.
- Nei, Masatoshi, and Sudhir Kumar. 2000. *Molecular Evolution and Phylogenetics*. Oxford ; New York: Oxford University Press.
- Page, Roderic D. M., and Edward C. Holmes. 1998. *Molecular Evolution: A Phylogenetic Approach*. Oxford ; Malden, MA: Blackwell Science.
- Phillips-Rodriguez, Wendy J. 2010. "Some Considerations About Reading Stemmata." *Ecdotica* 9: 16–23.
- Phillips-Rodriguez, Wendy J., Christopher J. Howe, and Heather F. Windram. 2009. "Chi-Squares and the Phenomenon of 'Change of Exemplar' in the Dyūtaparvan." In *Sanskrit Computational Linguistics*, edited by Gérard Huet, Amba Kulkarni, and Peter Scharf, 5402:380–90. Berlin, Heidelberg: Springer Berlin Heidelberg. https://doi.org/10.1007/978-3-642-00155-0_20.
- Robins, William. 2007. "Editing and Evolution." *Literature Compass* 4 (1). <https://doi.org/10.1111/j.1741-4113.2006.00391.x>.
- Robinson, Peter. 2003. "The History, Discoveries, and Aims of the Canterbury Tales Project." *The Chaucer Review* 38 (2): 126–39.
- Robinson, Peter M. W. 1997. "A Stemmatic Analysis of the Fifteenth-Century Witnesses to The Wife of Bath's Prologue." In *The Canterbury Tales Projects Occasional Papers*, edited by Peter M. W. Robinson and Norman Blake, 69–132. II.
- Robinson, Peter M. W. 2012. "The Textual Tradition of Dante's Commedia and the Barbi's Loci." *Ecdotica* 9: 1–32.
- Robinson, Peter M. W. 2018. "Textual Communities XML File Format - Textual Communities - Wiki." June 27, 2018. <https://wiki.usask.ca/display/TC/Textual+Communities+XML+file+format>.
- Robinson, Peter M. W. 2019a. "Creating and Implementing an Ontology of Documents and Texts (ADHO 2018) - Textual Communities - Wiki." January 31, 2019. <https://wiki.usask.ca/pages/viewpage.action?pageId=1324745355>.
- Robinson, Peter M. W. 2019b. "Launch Document, 28 June 2018 - Textual Communities - Wiki." March 23, 2019. <https://wiki.usask.ca/display/TC/Launch+document%2C+28+June+2018>.
- Robinson, Peter M. W. 2020. "Getting Materials from TC via URI/Linked Open Data - Textual Communities - Wiki." April 8, 2020. <https://wiki.usask.ca/pages/viewpage.action?pageId=1306492976>.

- Roos, T., and T. Heikkilä. 2009. "Evaluating Methods for Computer-Assisted Stemmatology Using Artificial Benchmark Data Sets." *Literary and Linguistic Computing* 24 (4): 417–33. <https://doi.org/10.1093/lc/fqp002>.
- Roos, Teemu, and Yuan Zou. 2011. "Analysis of Textual Variation by Latent Tree Structures." In *2011 IEEE 11th International Conference on Data Mining*, 567–76. Vancouver, BC, Canada: IEEE. <https://doi.org/10.1109/ICDM.2011.24>.
- Smith, Catherine. 2019. *Itsee-Birmingham/Collation_editor_core 1.0.4*. Zenodo. <https://doi.org/10.5281/zenodo.3539578>.
- Spencer, Matthew, Barbara Bordalejo, Peter Robinson, and Christopher J. Howe. 2003. "How Reliable Is a Stemma? An Analysis of Chaucer's Miller's Tale." *Literary and Linguistic Computing: Journal of the Association for Literary and Linguistic Computing* 18 (4): 407–22.
- Spencer, Matthew, Barbara Bordalejo, Li-San Wang, Adrian C. Barbrook, Linne R. Mooney, Peter Robinson, Tandy Warnow, and Christopher J. Howe. 2003. "Analyzing the Order of Items in Manuscripts of The Canterbury Tales." *Computers and the Humanities* 37 (1): 97–109.
- Spencer, Matthew, Elizabeth A Davidson, Adrian C Barbrook, and Christopher J Howe. 2004. "Phylogenetics of Artificial Manuscripts." *Journal of Theoretical Biology* 227 (4): 503–11. <https://doi.org/10.1016/j.jtbi.2003.11.022>.
- Swofford, D. L. 2003. *PAUP* Phylogenetic Analysis Using Parsimony (*and Other Methods)* (version 4.0a (build 167)). Sunderland, Massachusetts: Sinauer Associates.
- Wang, Li-San. 2001. "Exact-IEBP: A New Technique for Estimating Evolutionary Distances between Whole Genomes." In *Algorithms in Bioinformatics*, edited by Olivier Gascuel and Bernard M. E. Moret, 2149:175–88. Berlin, Heidelberg: Springer Berlin Heidelberg. https://doi.org/10.1007/3-540-44696-6_14.
- Windram, H. F., P. Shaw, P. Robinson, and C. J. Howe. 2008. "Dante's Monarchia as a Test Case for the Use of Phylogenetic Methods in Stemmatic Analysis." *Literary and Linguistic Computing* 23 (4): 443–63. <https://doi.org/10.1093/lc/fqn023>.
- Windram, Heather F., Christopher J. Howe, and Matthew Spencer. 2005. "The Identification of Exemplar Change in the Wife of Bath's Prologue Using the Maximum Chi-Squared Method." *Literary and Linguistic Computing* 20 (2): 189–204. <https://doi.org/10.1093/lc/fqi001>.