Learning the CBGM by Design

Greek Paul Project Webinar 28 April 2022

Joey McCollum

Australian Catholic University Institute for Religion and Critical Inquiry

🔽 james.mccollum@myacu.edu.au

@jamesjmccollum

jjmccollum

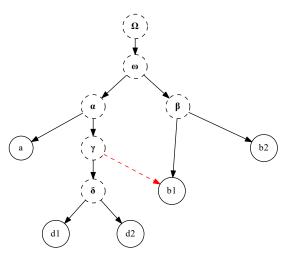




- Developed over thirty years by Gerd Mink, culminating in the latest updates to the Editio Critica Maior (ECM)
- Important reading:
 - Gerd Mink, "Problems of a Highly Contaminated Tradition: The New Testament. Stemmata of Variants as a Source of a Genealogy for Witnesses," in *Studies in Stemmatology II*, ed. Pieter van Reenen, August den Hollander, and Margot van Mulken (Amsterdam: John Benjamins Publishing, 2004), 13–85
 - Peter J. Gurry, A Critical Examination of the Coherence-Based Genealogical Method in New Testament Textual Criticism, NTTSD 55 (Leiden: Brill, 2017)
 - Tommy Wasserman and Peter J. Gurry, A New Approach to Textual Criticism: An Introduction to the Coherence-Based Genealogical Method, RBS 80 (Atlanta, GA: SBL Press, 2017)
 - Andrew Charles Edmondson, "An Analysis of the Coherence-Based Genealogical Method Using Phylogenetics," (PhD diss., University of Birmingham, 2019), https://etheses.bham.ac.uk/id/eprint/9150/



• Intended to solve *contamination*, or mixture across branches of the textual tradition





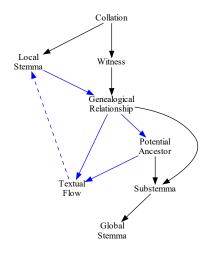
- Methodological assumptions:
 - 1. Scribes typically copied their exemplars with fidelity.
 - 2. If a scribe introduced a variant, then it came from some other reading.
 - 3. Scribes typically used fewer sources rather than many.
 - 4. Scribes typically used closely related sources rather than distant ones.



- Not a new methodology for evaluating variant readings, but a "meta-approach" to be used on top of existing methods
- Not a way to make computers do textual criticism, but a way for them to help us refine human judgments

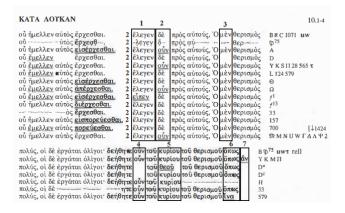


• "Iterative workflow" highlighted in blue





- To compare manuscripts' texts, we must first align them at independent variation units
- Variant readings occur at variation units



(Source: Swanson, New Testament Greek Manuscripts, Luke, 183)



- Variation units serve as our points of comparison between witnesses in the CBGM
- Think of them as the columns of a table and the witnesses as rows

	3Jo 1:1/2	3Jo 1:1/6	3Jo 1:1/8	 3Jo 1:15/23
GA 69	a	afl	a	 a
GA 1739	a	a	b	 a
GA 2243	b	a	a	 a



This is readily encoded in TEI XML format

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                Swanson, Reuben J., ed. <emph>New Testament Greek Manuscripts: Variant
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                            <rde n="2" wit="f1"><w>ειπεν</w></rde>
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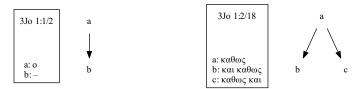


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έλεγεν
        B & C 1071 uw
        D75
-λεγεν
ἔλεγεν
έλεγεν
ἔλεγεν
       YKSII 28 565 τ
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       I. 124 579
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        33
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       157
έλεγεν 700
                  [↓1424
έλεγεν ΜΜΝ UW ΓΔΛΨ2
```

The Local Stemma



- The basic unit of comparison
- One for each variation unit
- A graphical representation of our judgments of readings
- Kurt Aland's "local genealogical" principle



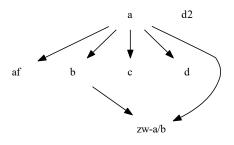
The Local Stemma



- Some are more complicated
 - defective readings (e.g., misspellings, reconstructions)
 - orthographic readings (e.g., regional differences)
 - split attestations of the same reading (coincidental agreement)
 - ambiguous readings (can be reconstructed as more than one reading)
- Some of these may be collapsed with other substantive readings



• Computationally, just a directed graph.

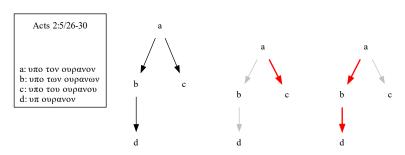


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  <node n="af" />
  <node n="b" />
  <node n="c" />
  <node n="d" />
  <node n="d2" />
  <node n="zw-a/b" />
  <arc from="a" to="af" />
  <arc from="a" to="b" />
  <arc from="a" to="c" />
  <arc from="a" to="d" />
  <arc from="a" to="zw-a/b" /:</pre>
  <arc from="b" to="zw-a/b" /:</pre>
```

The Local Stemma



- Relationships between readings are determined by checking for a path between them
- a = b: path of length 0
- a > b: path of length > 0 from a to b
- NOREL: no path from a to b, but both have a common ancestor
- UNCL: same as NOREL, but no common ancestor (reserved for when we don't know where a reading fits in the stemma)



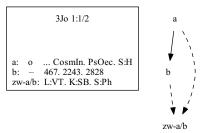


- For the CBGM's purposes, a witness is a sequence of readings
- Typically, the *text* of a known manuscript, minus the material baggage (date, provenance, etc.)
 - "How texts relate" \(\neq \) "How manuscripts relate"

	3Jo 1:1/2	3Jo 1:1/6	3Jo 1:1/8	 3Jo 1:15/23
GA 69	a	afl	a	 a
GA 1739	a	a	b	 a
GA 2243	b	a	a	 a



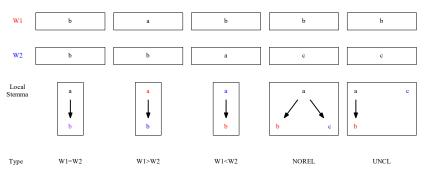
- Versions and fathers can also be treated as witnesses
- But back-translation may be ambiguous, and patristic citations may be "lacunose"



Genealogical Relationships



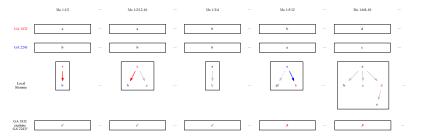
• The relationship of two witnesses is the overall pattern *of the relationships of their readings* at all variation units where both are extant



Genealogical Relationships



- We say that one reading *explains* another if
 - it is the same reading (explanation by agreement), or
 - there is an edge in the local stemma from it to the other reading



- Lacunae do not have to be explained, and they cannot explain readings
- The *cost* of a genealogical relationship is the number of explained readings that are not agreements (so the cost in the example above is 2)

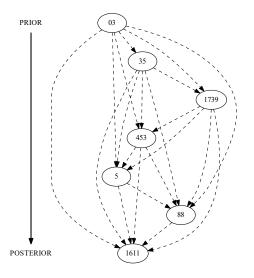
Genealogical Relationships



It is convenient to encode genealogical relationships with *bit-arrays*



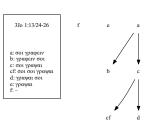
• Potential ancestor = "more prior than posterior readings"

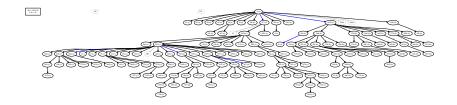


Textual Flow at a Variation Unit



- Textual flow is a tool for helping us revise our judgments in a local stemma
- Not a global stemma (our ultimate goal), but still important







- How do we find a given witness's *textual flow ancestor*?
- We specify a connectivity limit κ (i.e., a radius of "close-enough" neighbors)
- Then, for each witness:
 - 1. List its potential ancestors, sorted from most agreement to least
 - 2. If one of the first κ has the same reading at this unit, then select it
 - 3. If not, then choose the first (non-lacunose) potential ancestor
- Core idea: use *general relationships* (between witnesses) to find *specific relationships* (between readings in a local stemma)



 Often, we just want to know the textual flow for witnesses with a specific reading

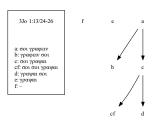


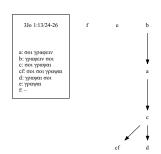
• (Numbers on edges represent the rank of the closest potential ancestor with the same reading, if it's not 1)

Textual Flow for a Variant Reading

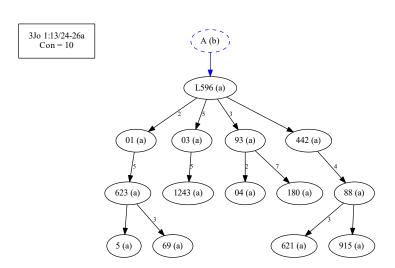


• We can use it to evaluate alternate hypotheses about the initial text (A)





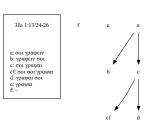




Textual Flow for a Variant Reading

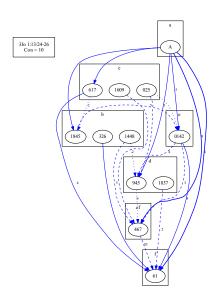


 Or, we can look only at the parts of textual flow where a reading gets changed to find the most likely sources of unexplained readings (e and f)



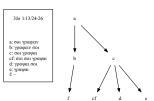
Textual Flow for a Variant Reading







- Between coherence (a form of external evidence) and internal evidence, we can attempt to explain previous unexplained readings
- A necessary step for our ultimate goal of constructing a global stemma

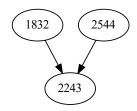


The Substemma(ta) of a Witness



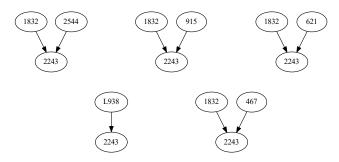
- The *substemma* of a witness is the portion of the global stemma consisting of the witness and its ancestors in the stemma
- Requirement: *every* extant reading in the witness must be explained by a reading in at least one of its ancestors

Explained by GA 1832	•••	X	>	>	✓	
Explained by GA 2544	•••	✓	X	X	✓	
Explained by Either	•••	√	✓	✓	✓	





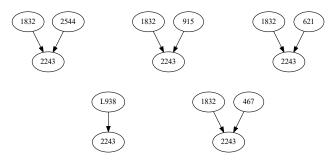
- A witness may have multiple valid substemma (i.e., ones that explain all
 of its readings), but some are better than others
- Two of the CBGM's methodological assumptions are important here:
 - 3. Scribes typically used fewer sources rather than many.
 - 4. Scribes typically used closely related sources rather than distant ones.



The Substemma(ta) of a Witness



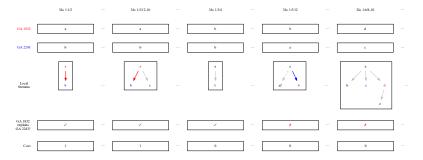
- Based on assumption 3, we should prefer substemmata with fewer ancestors ("parsimony")
- Based on assumption 4, we should prefer substemmata with ancestors that agree as often as possible with the witness
- A balancing act: the substemma {L938} is more parsimonious, but may not explain as many readings by agreement



The Substemma(ta) of a Witness



 A simple cost function for each ancestor is "the number of variation units where the ancestor explains the witness by descent and not agreement"



Finding a (Good) Substemma

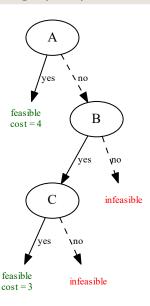


- ullet Also called $substemma\ optimization$
- For n potential ancestors, a *weighted set cover* problem with n sets (and 2^n-1 combinations to check!)

Substemma	Variation	Cost			
{A}	1	1	1	1	4
{B}	✓	1	Х	Х	1
{C}	Х	1	1	1	2
{A, B}	✓	1	1	1	4+1=5
{A, C}	✓	1	1	1	4+2=6
{B, C}	1	1	1	1	1+2=3
{A, B, C}	√	✓	1	1	1+2+4=7

Finding a (Good) Substemma

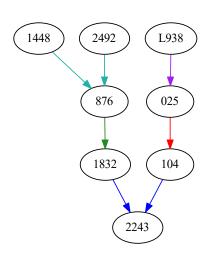




- If a witness has many potential ancestors, then checking all $2^n 1$ possible substemmata by brute force is prohibitive
- The branch-and-bound heuristic (pictured left) finds all minimum-cost substemmata quickly in practice
- Easily adapted to find all substemmata within a given cost



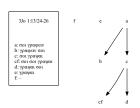
- Just as the local stemma relates readings, the global stemma relates witnesses
- Combination of all substemmata into a single graph

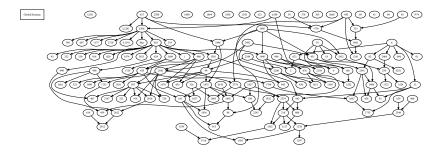


The Global Stemma



- But every reading in every local stemma except the initial one must be explained by another reading
- Otherwise...

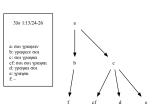


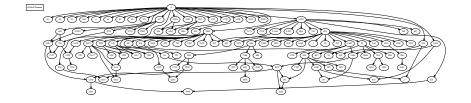


The Global Stemma



• If we "complete" every local stemma (and ignore or manually account for super fragmentary witnesses) ...







- How is this different than a textual flow diagram?
 - · A witness can have more than one ancestor
 - All readings in a witness must be explained by readings in its ancestor(s)
 - More computationally intensive, so takes a bit longer to produce

Field trip



- The open-cbgm library (my implementation of the CBGM, based on these principles) is freely available at https://github.com/jjmccollum/open-cbgm, and the standalone command-line utility is available at https://github.com/jjmccollum/open-cbgm-standalone
 - Supported on Windows, Mac, and Linux
- The INTF's official implementation (using a Docker container) is now also available (download and instructions at http://ntvmr.uni-muenster .de/intfblog/-/blogs/download-the-cbgm-docker-container)



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