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

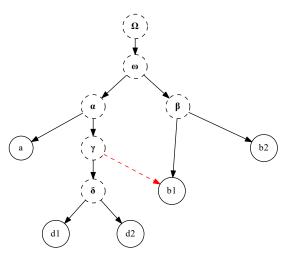




- Developed over thirty years by Gerd Mink, culminating in the latest updates to the *Editio Critica Maior (ECM)*
- Recommended reading:
 - Gerd Mink, "Problems of a Highly Contaminated Tradition: The New Testament. Stemmata of Variants as a Source of a Genealogy for Witnesses," in *Studies in Stemmatology 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





- Key assumption: *no hypothetical ancestors* (except the *Ausgangstext* A)
- Other important assumptions:
 - ${\bf 1.} \ \ {\bf Scribes\ typically\ copied\ their\ exemplars\ with\ fidelity.}$
 - 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.



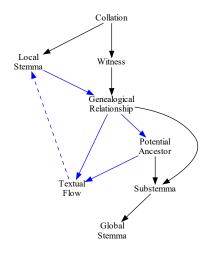
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- Other important assumptions:
 - 1. Scribes typically copied their exemplars with fidelity.
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 - 3. Scribes typically used fewer sources rather than many.
 - 4. Scribes typically used closely related 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

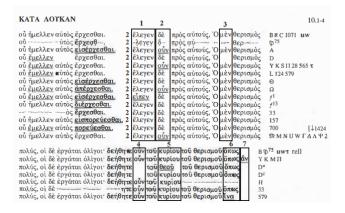


• "Iterative workflow" highlighted in blue





- 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 | ь | a | a | a |



This is readily encoded in TEI XML format

```
<?xml version='1.0' encoding='UTF-8'?>
<TEI xmlns="http://www.tei-c.org/ns/1.0">
               <title>A collation of Luke 10:2 in Swanson</title>
                Swanson, Reuben J., ed. <emph>New Testament Greek Manuscripts: Variant
    <text xml:lang="GRC">
            <div type="book" n="B03">
                <div type="chapter" n="B03K10">
                            <rdg n="1" wit="f13"><w>ελεγεν</w></rdg>
                            <rdg n="1-f1" type="defective" wit="P75">
                            <rde n="2" wit="f1"><w>ειπεν</w></rde>
```



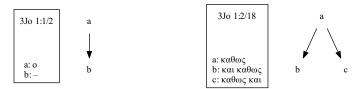
```
B ⋈ C 1071 uw
έλεγεν
        D75
-λεγεν
ἔλεγεν
ἔλεγεν
ἔλεγεν
       Y K S II 28 565 τ
ἕλεγεν L 124 579
ἔλεγεν
ἔλεγεν Ω
είπεν
έλεγεν f13
ἔλεγεν
        33
έλεγεν
       157
έλεγεν 700
                  [J1424
έλεγεν ΜΜΝΟΨΓΔΛΨ2
```

```
reading_support = {
    "f13": "1",
    "P75": "1-f1",
    "f1": "2"
}
```

The Local Stemma



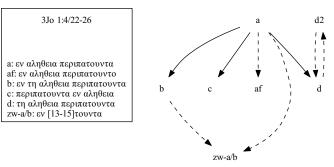
- The basic unit of comparison
- One for each variation unit
- A graphical representation of our judgments of readings
- Kurt Aland's "local genealogical" principle



The Local Stemma

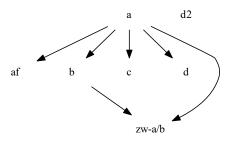


- Some are more complicated
 - defective readings (e.g., misspellings, reconstructions)
 - orthographic readings (e.g., regional differences)
 - *split* attestations of the same reading (coincidental emergence)
 - ambiguous readings (can be reconstructed as more than one reading)
- Some of these may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





• Computationally, just a directed graph.

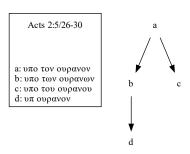


```
graph type="directed">
  <node n="a" />
  <node n="af" />
  <node n="b" />
  <node n="c" />
  <node n="d" />
  <node n="d2" />
  <node n="zw-a/b" />
  <arc from="a" to="af" />
  <arc from="a" to="b" />
  <arc from="a" to="c" />
  <arc from="a" to="d" />
  <arc from="a" to="zw-a/b" /:</pre>
  <arc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

The Local Stemma



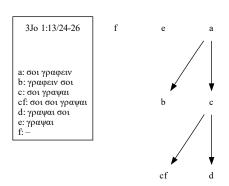
- Relationships between readings are determined by checking for a path between them
- a = b (agreement): path of length 0
- a > b (prior): path of length > 0 from a to b
- a < b (posterior): path of length > 0 from b to a
- NOREL (no relationship): no path from a to b, but both have a common ancestor



The Local Stemma



- UNCL (unclear): same as NOREL, but no common ancestor (reserved for when we don't know where a reading fits in the stemma)
- We say that one reading *explains* another if
 - it is the same reading (explanation by agreement), or
 - there is a path of length 1 from it to the other reading
- Lacunae do not have to be explained, and they cannot explain readings



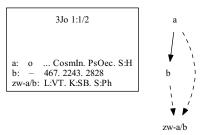


- For the CBGM's purposes, a witness is a sequence of readings
- Typically, the *text* of a known manuscript, minus the material baggage (date, provenance, etc.)
 - "How texts relate" ≠ "How manuscripts relate"

| | 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 |



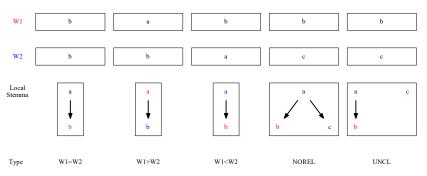
- Versions and fathers can also be treated as witnesses
- But back-translation may be ambiguous, and patristic citations may be "lacunose"



Genealogical Relationships



- The relationship of two witnesses is the overall pattern *of the relationships of their readings* where both are extant
- The *cost* of a genealogical relationship is the number of explained readings that are not agreements (so the cost in the example below is 1)



Genealogical Relationships



• It is convenient to encode genealogical relationships with *bitmaps*

Genealogical Relationships

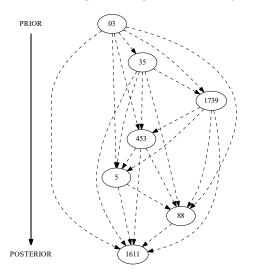


- For d units and n witnesses, $\sim n^2 d$ comparisons as one-time work
- \bullet The compare_witnesses module (below) presents this computed data

| Genea: | logical | compa | risons fo | or W1 = | 5 (116 exta | nt passa | ges): | | | | |
|--------|---------|-------|-----------|---------|-------------|----------|---|-------|------|------|--------|
| W2 | DIR | NR | PASS | EQ | | W1>W2 | W1 <w2< th=""><th>NOREL</th><th>UNCL</th><th>EXPL</th><th>COST</th></w2<> | NOREL | UNCL | EXPL | COST |
| 623 | | | 116 | 112 | (96.552%) | | | | | 115 | 3.000 |
| A | | | 116 | 104 | (89.655%) | | | | | 116 | 12.000 |
| 025 | | | 116 | | (88.793%) | | | | | 111 | 8.000 |
| 319 | | | 116 | | (88.793%) | | | | | 111 | 8.000 |
| 398 | | | 116 | | (88.793%) | | | | | 111 | 8.000 |
| 507 | | | 116 | | (88.793%) | | | | | 111 | 8.000 |
| 617 | | | 116 | | (88.793%) | | | | | 112 | 9.000 |
| 1175 | | | 116 | | (88.793%) | | | | | 111 | 8.000 |
| 1890 | | | 116 | | (88.793%) | | | | | 110 | |
| Byz | | | 114 | | (89.474%) | | | | | 110 | 8.000 |
| 049 | | | 116 | | (87.931%) | | | | | 109 | 7.000 |
| 0142 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 1 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 35 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 326 | | | 116 | | (87.931%) | | | | | 109 | 7.000 |
| 424 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 468 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 1448 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 1609 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 2186 | | | 116 | | (87.931%) | | | | | 109 | |
| 2423 | | | 116 | | (87.931%) | | | | | 110 | 8.000 |
| 2805 | | | 115 | | (88.696%) | | | | | 108 | |
| L938 | | | 116 | | (87.931%) | | | | | 111 | 9.000 |
| | | | 116 | | (87.069%) | | | | | | |
| 18 | | | 116 | | (87.069%) | | | | | 109 | 8.000 |
| 43 | | | 116 | | (87.069%) | | | | | | |



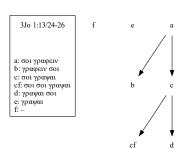
• Potential ancestor = "more prior than posterior readings"

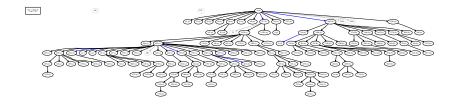


Textual Flow at a Variation Unit



- 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



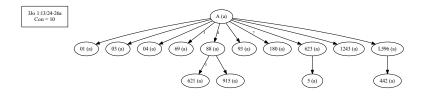




- How do we find a given witness's *textual flow ancestor*?
- We specify a connectivity limit κ (i.e., a radius of "close-enough" neighbors)
- Then, for each witness:
 - 1. List its potential ancestors, sorted from most agreement to least
 - 2. If one of the first κ has the same reading at this unit, 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)



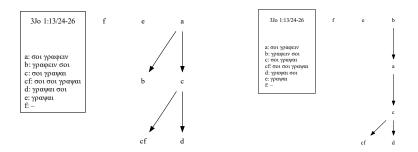
 Often, we just want to know the textual flow for witnesses with a specific reading



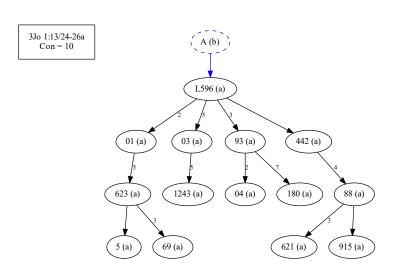
• (Numbers on edges represent the rank of the closest potential ancestor with the same reading, if it's not 1)



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



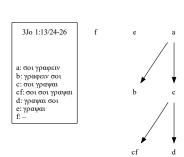




Textual Flow for a Variant Reading

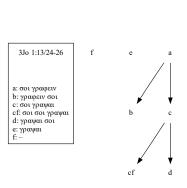


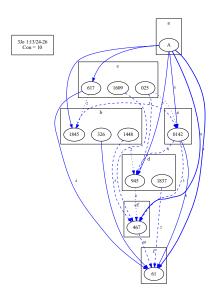
 Or, we can look only at the parts of textual flow where a reading gets changed to find the most likely sources of unexplained readings (e and f)



Textual Flow for a Variant Reading

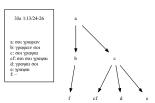








- Between coherence (a form of external evidence) and internal evidence, we can attempt to explain previous unexplained readings
- A necessary step for our ultimate goal of constructing a global stemma

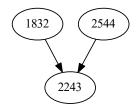


The Substemma(ta) of a Witness



- 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

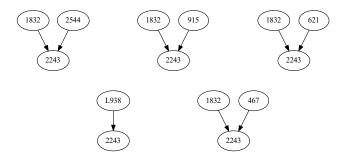
| Explained by GA 1832 | ••• | X | ✓ | > | ✓ | |
|----------------------|-----|-------------|-------------|-------------|----------|--|
| Explained by GA 2544 | ••• | ✓ | X | X | ✓ | |
| Explained by Either | ••• | > | > | > | √ | |



The Substemma(ta) of a Witness



- 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.
- A balancing act: the substemma {L938} is more parsimonious, but may not explain as many readings by agreement



Finding a (Good) Substemma

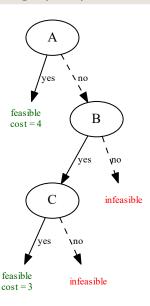


- Also called substemma optimization
- For n potential ancestors, a *weighted set cover* problem with n sets (and 2^n-1 combinations to check!)

| Substemma | Variation | Cost | | | |
|-----------|-----------|----------|---|---|---------|
| {A} | √ | 4 | | | |
| {B} | ✓ | √ | X | X | 1 |
| {C} | X | ✓ | ✓ | ✓ | 2 |
| {A, B} | √ | 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+2+4=7 |

Finding a (Good) Substemma

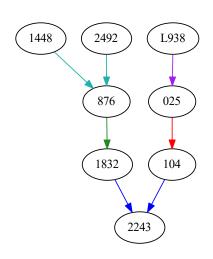




- If a witness has many potential ancestors, then checking all $2^n 1$ possible substemmata by brute force is prohibitive
- The *branch-and-bound* heuristic (pictured left) finds all minimum-cost substemmata quickly in practice
- Easily adapted to find all substemmata within a given cost



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



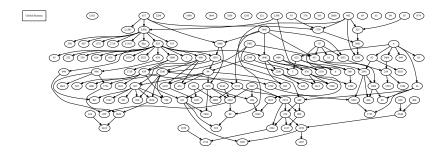
The Global Stemma



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

3Jo 1:13/24-26 f c a

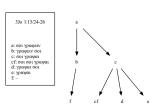
a: σοι γραφειν
b: γραφειν σοι c: σοι γραψι
cf: σοι σοι γραψι
cf: σοι σοι γραψι
ci-γραψι σοι c: γραψια σι
f: -

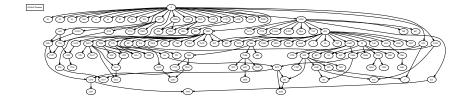


The Global Stemma



• 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)



- Edmondson, Andrew Charles. "An Analysis of the Coherence-Based Genealogical Method Using Phylogenetics." PhD diss., University of Birmingham, 2019. https://etheses.bham.ac.uk/id/eprint/9150/.
- Gurry, Peter J. A Critical Examination of the Coherence-Based Genealogical Method in New Testament Textual Criticism. NTTSD 55. Leiden: Brill, 2017.
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- Swanson, Reuben J., ed. New Testament Greek Manuscripts: Variant Readings Arranged in Horizontal Lines against Codex Vaticanus. Luke. Sheffield: Sheffield Academic Press, 1995.
- Wasserman, Tommy, 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.