# Learning the CBGM by Design

Greek Paul Project Webinar 28 April 2022

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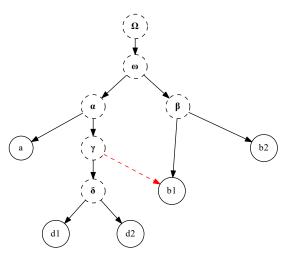




- Developed over thirty years by Gerd Mink, culminating in the latest updates to the *Editio Critica Maior (ECM)*
- Recommended reading:
  - Gerd Mink, "Problems of a Highly Contaminated Tradition: The New Testament. Stemmata of Variants as a Source of a Genealogy for Witnesses," in *Studies in Stemmatology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



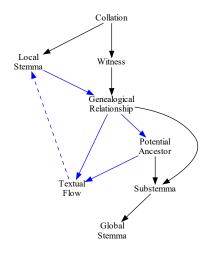
- Key assumption: no hypothetical ancestors (except the Ausgangstext A)
- Other important assumptions:
  - 1. Scribes typically copied their exemplars with fidelity.
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  - 3. Scribes typically used fewer sources rather than many.
  - 4. Scribes typically 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

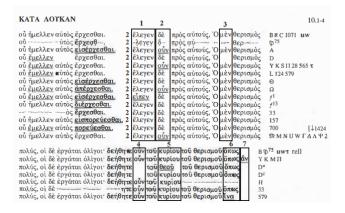


• "Iterative workflow" highlighted in blue





- 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>
```



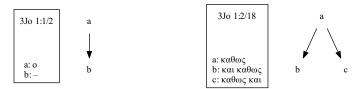
```
B ⋈ C 1071 uw
έλεγεν
        D75
-λεγεν
ἔλεγεν
ἔλεγεν
ἔλεγεν
       Y K S II 28 565 τ
ἕλεγεν L 124 579
ἔλεγεν
ἔλεγεν Ω
είπεν
έλεγεν f13
ἔλεγεν
        33
έλεγεν
       157
έλεγεν 700
                  [J1424
έλεγεν ΜΜΝΟΨΓΔΛΨ2
```

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

## **The Local Stemma**



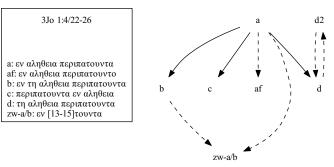
- The basic unit of comparison
- One for each variation unit
- A graphical representation of our judgments of readings
- Kurt Aland's "local genealogical" principle



#### **The Local Stemma**

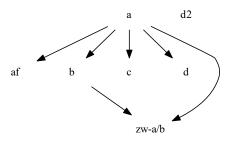


- Some are more complicated
  - defective readings (e.g., misspellings, reconstructions)
  - orthographic readings (e.g., regional differences)
  - *split* attestations of the same reading (coincidental emergence)
  - ambiguous readings (can be reconstructed as more than one reading)
- Some of these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





• Computationally, just a directed graph.

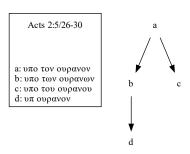


```
graph type="directed">
  <node n="a" />
  <node n="af" />
  <node n="b" />
  <node n="c" />
  <node n="d" />
  <node n="d2" />
  <node n="zw-a/b" />
  <arc from="a" to="af" />
  <arc from="a" to="b" />
  <arc from="a" to="c" />
  <arc from="a" to="d" />
  <arc from="a" to="zw-a/b" /:</pre>
  <arc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

## The Local Stemma



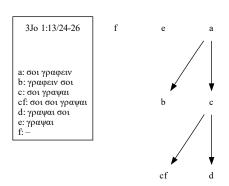
- Relationships between readings are determined by checking for a path between them
- a = b (agreement): path of length 0
- a > b (prior): path of length > 0 from a to b
- a < b (posterior): path of length > 0 from b to a
- NOREL (no relationship): no path from a to b, but both have a common ancestor



#### 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



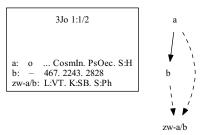


- For the CBGM's purposes, a witness is a sequence of readings
- Typically, the *text* of a known manuscript, minus the material baggage (date, provenance, etc.)
  - "How texts relate" ≠ "How manuscripts relate"

	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



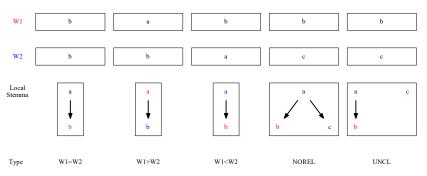
- Versions and fathers can also be treated as witnesses
- But back-translation may be ambiguous, and patristic citations may be "lacunose"



# **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**

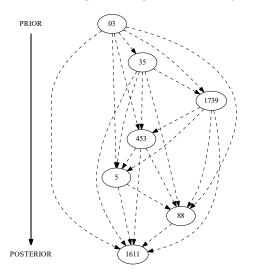


- For d units and n witnesses,  $\sim n^2 d$  comparisons as one-time work
- $\bullet$  The compare\_witnesses module (below) presents this computed data

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%)						



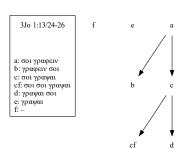
• Potential ancestor = "more prior than posterior readings"

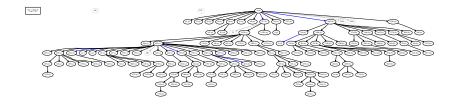


#### **Textual Flow at a Variation Unit**



- 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



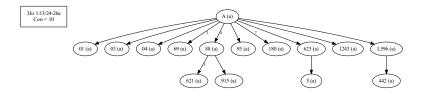




- How do we find a given witness's *textual flow ancestor*?
- We specify a connectivity limit κ (i.e., a radius of "close-enough" neighbors)
- Then, for each witness:
  - 1. List its potential ancestors, sorted from most agreement to least
  - 2. If one of the first  $\kappa$  has the same reading at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



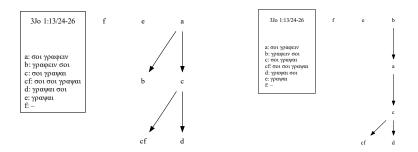
 Often, we just want to know the textual flow for witnesses with a specific reading



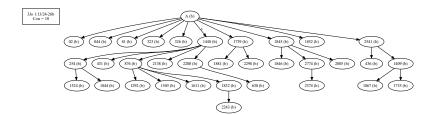
• (Numbers on edges represent the rank of the closest potential ancestor with the same reading, if it's not 1)



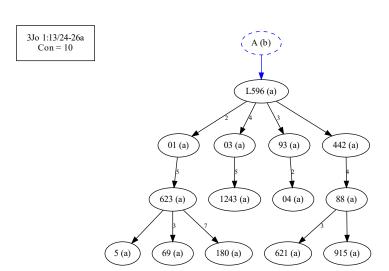
• We can use it to evaluate alternate hypotheses about the initial text (A)







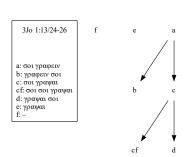




# **Textual Flow for a Variant Reading**

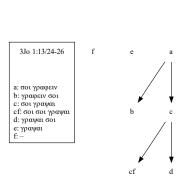


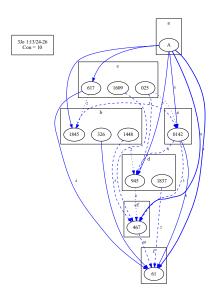
 Or, we can look only at the parts of textual flow where a reading gets changed to find the most likely sources of unexplained readings (e and f)



# **Textual Flow for a Variant Reading**

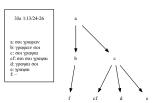








- Between coherence (a form of external evidence) and internal evidence, we can attempt to explain previous unexplained readings
- A necessary step for our ultimate goal of constructing a global stemma

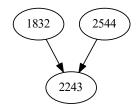


## The Substemma(ta) of a Witness



- 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

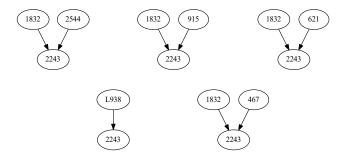
Explained by GA 1832	 X	>	>	<b>✓</b>	
Explained by GA 2544	 <	X	X	✓	
Explained by Either	 <b>✓</b>	✓	✓	✓	



## 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

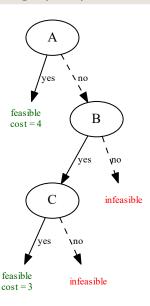


- ullet Also called  $substemma\ optimization$
- For n potential ancestors, a *weighted set cover* problem with n sets (and  $2^n-1$  combinations to check!)

Substemma	Variation	Cost			
{A}	1	4			
{B}	<b>✓</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}	<b>√</b>	✓	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

## Finding a (Good) Substemma

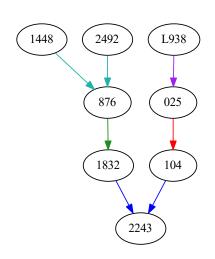


 In practice, the optimize\_substemmata module finds all desired substemmata in seconds.

```
Substemmata for witness W1 = 5 (116 extant passages):
ANCESTORS
                                                               AGREE
623, 2344
623, 69
623, 33
623, 326
623, 2541
623, 1890
623, 049
623, 2186
623, 307
623, 400
623, 429
623, 453
623, 918
623, 180
```



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

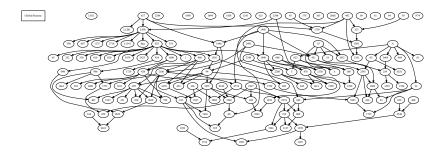




- But every reading in every local stemma except the initial one must be explained by another reading
- Otherwise...

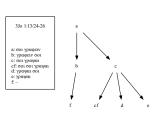
3Jo 1:13/24-26 f e a

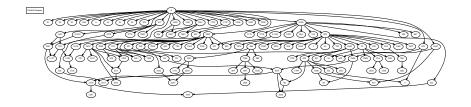
a: σοι γραφειν
b: γραφειν σοι c: σοι γραψαι
cf: σοι σοι γραψαι
cf: σοι σοι γραψαι
c: γραψαι σοι c: γραψαι
f: -





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



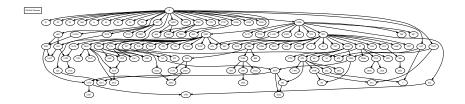




• If we "complete" every local stemma (and ignore or manually account for super fragmentary witnesses) ...



(Source gallica.bnf.fr / Bibliothèque nationale de France)

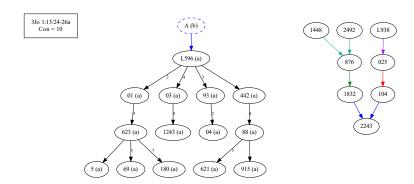




\*Field trip\*



- 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





- 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.
- Mink, Gerd. "Problems of a Highly Contaminated Tradition: The New Testament. Stemmata of Variants as a Source of a Genealogy for Witnesses." Pages 13–85 in *Studies in Stemmatology II*. Edited by Pieter van Reenen, August den Hollander, and Margot van Mulken. Amsterdam: John Benjamins Publishing, 2004.
- 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.