

Names Are Not Good Enough: Reasoning over Taxonomic Change in the *Andropogon* Complex¹

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Abstract. The performance of taxonomic names and concepts to act as identifiers of changing taxonomic content is analyzed and visualized using a novel Answer Set Programming reasoning approach. The Euler/ASP toolkit is applied to a use case of eight succeeding classifications, ranging from 1889 to 2006, of a 'complex' of grasses in the genus *Andropogon* in the Carolinas and surrounding areas. Based on an input of 64 constituent concepts and 131 Region Connection Calculus articulations provided by an expert taxonomist, nine pairwise and logically consistent alignments are inferred and visualized as merge taxonomies that reflect the hierarchical relationships of congruent and non-congruent taxonomic concepts. The respectively valid names are integrated with these results, thus permitting quantitative assessments of name/concept resolution. Accordingly, 65.2% of 46 possible instances of congruence were realized in the alignments. Incongruent concepts were twice as common as their counterparts. Usages of different names failed to continuously identify congruent concepts in 66.7% of 30 cases, and the same names incorrectly identified incongruent concepts in 33.9% of 59 cases. Concept-level articulations can take into account both member- and property-based information when identifying similarities and differences between succeeding taxonomic perspectives. Names and nomenclatural relationships, in turn, are limited to establishing 'identity' based on subsets of ostensibly designated (type) members. Using names-based identifiers to represent and reason over changing taxonomic content in the Semantic Web domain will be similarly limited.

Keywords: answer set programming, biological nomenclature, data integration, knowledge representation and reasoning, provenance, region connection calculus, taxonomic concepts, visualization

1. Introduction

Taxonomic names are necessary but not sufficient for representing and integrating biodiversity data for the Semantic Web [3,24,39]. The reasons for this insufficiency are systemic and well known to most contributors and many users of biological taxonomies [2,7,44]. Ultimately they are rooted in the way in which 'identity' is established according to the rules of nomenclature which guide the creation and perpet-

uation of valid and invalid names for perceived taxonomic groups [37,42]. The *Codes* of nomenclature stipulate (*inter alia*) that name identity is grounded in the Principle of Typification [18,56]. This means, generally, that taxonomic groups receive the same valid name or different names based on the established identity of individual type specimens (e.g., for taxa of the species rank), or individual type taxa (e.g., for taxa of the genus rank), that are designated at their respective moments of baptism.

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Typically both a type and a diagnosis (feature-based circumscription) are provided when anchoring the meaning or referential extension of a taxonomic name [19,23,25]. However, the former arbiter – i.e., the type identity – has special weight when dealing with alternative name/taxon assignments. Resolution of such conflicts can proceed almost irrespective of the wider referential extensions and circumscriptions associated with the type-anchored names. Another relevant, *Code*-mandated naming rule is the Principle of Priority [45] which states that in case of (again, type-centric) synonymy, the oldest available name remains the valid one.

As inferences of the configuration of taxonomic groups change over time and in light of new evidence, the application of the rules of nomenclature tends to create semantically complex networks of many-to-many relationships among valid and invalid names and feature- or member-based circumscriptions [24,29,63]. Thus in spite of the great and lasting relevance of *Code*-compliant taxonomic names in labeling and interconnecting biodiversity data [47,48,53], these names have inherent and measurable shortcomings as identifiers of unique *taxonomic* perspectives promoted by succeeding expert and user communities. Sound knowledge representation and reasoning in the taxonomic domain requires due recognition of, and semantic compensation for, the insufficiencies inherent in using names and name relationships as identifiers and connectors of unique taxonomic *concepts* [22,23,39].

Current solutions to overcome the taxonomic name/concept discordance usually take one of two major pathways. One common 'solution' is to assemble single, comprehensive taxonomies of particular groups, with periodically updated and citable versions [7,44,54]. This approach offers an immediate and valuable service to users. However in the longer term it will lead to multiple distinct perspectives represented by earlier and later versions of the unitary taxonomy [4,25,61]. Overlapping sets of names are reused from version to version, with varying circumscriptions, and no explicit tracking of taxonomic provenance [12]. Such unitary systems essentially *propagate* ambiguous name/concept alignments.

Several alternatives to unitary classifications are being developed under the term *taxonomic concept approach*.² They share a convention, established in [3], to annotate and hence further resolve taxonomic names *according to* (sec.) particular authors and cir-

umscriptions, as in: *Andropogon virginicus* Linnaeus (name, name author) *sec.* Weakley (2006) [63] (concept author, year). The added of resource resolution allows for coherent and independent representations of alternative name/concept hierarchies [24]. In a subsequent step such hierarchies can be compared and aligned using a variety of similarity indicators; including nomenclatural relationships (synonymy, etc.), member composition, or diagnostic features [11,15,23,30,60].

Here we use the novel Euler/ASP toolkit [11] to perform concept-level reasoning for the *Andropogon* use case [24]. Euler/ASP is a successor of CleanTax [57,58,59] which pioneered the use of multi-taxonomy representation, combined with Region Connection Calculus *articulations* (RCC-5; [50]) and First-Order Logic (FOL) reasoners [41], to align and merge alternative taxonomies. RCC-5 includes five basic relationships that compare the extensions of taxonomic concepts; viz. congruence (\equiv), proper inclusion (\supset), inverse proper inclusion (\subset), overlap ($\supset\subset$), and exclusion (\cap) [23]. Ambiguity can be asserted using the disjunction 'or'.

Under the present workflow approach an expert provides an initial, typically partial set of articulations among concepts entailed in multiple taxonomies. The toolkit ingests the taxonomies (T_1, T_2), articulations (A), and takes into account three additional (and optionally relaxable) constraints (C): (1) *non-emptiness* – a given concept has minimally one representing instance; (2) *sibling disjointness* – two given child concepts of a parent concept are exclusive of each other; and (3) *coverage* – a given parent concept is completely circumscribed by the union of its child concepts. The toolkit is able to deploy both FOL and Answer Set Programming (ASP) reasoners [27,28] which are grounded in Stable Model Semantics [40]. It includes an interactive workflow to assess and repair logical inconsistencies in the input alignment, identify the set of maximally informative relations (MIR), reduce ambiguities in the output, and visualize one or more possible world *merge taxonomies* [11].

The feasibility and utility of the RCC-5/ASP reasoning approach is demonstrated based on a real-life use case. In particular, we review the history of name/concept relationships in the *Andropogon* Linnaeus 'complex' – a lineage of grasses (Poaceae) – in the Carolinas and surrounding areas. Using an expert-made alignment among eight pertinent classifications of the complex authored from 1889 to 2006, we show how the Euler/ASP toolkit can ingest these data, reason over taxonomic concept similarities and differ-

² The present contribution is not intended as a comprehensive review of solutions to the name/concept alignment problem.

ences, and infer and visualize pairwise merge taxonomies that furthermore display nomenclatural information for performance comparison. We provide quantitative assessments of name/concept resolution across all alignments. The final discussion concentrates on the significance of the outcomes and prospects for a wider adaptation of concept-centric knowledge representation and reasoning over changing taxonomic content in the Semantic Web.

2. Analyzing the *Andropogon* Use Case

2.1. Taxonomic antecedents

The concept history of the *Andropogon* complex relevant to our analysis is reviewed in [63]. The corresponding alignment, made by expert taxonomist A.S. Weakley, was published in [24] and forms the basis for the use case data input and reasoning. Strictly speaking this use case concerns the *A. virginicus-A. glomeratus* complex *sec. Weakley* (2006) [63] in the Carolinas and surrounding areas. It is therefore much narrower in scope than the entire genus *Andropogon* *sec. Clayton et al.* (2013) [13] which includes more than 100 species worldwide. For the present purpose we refer to the '*Andropogon* use case' or '*Andropogon* complex' as comprising only the concepts and articulations that constitute Weakley's (2006) specific example (Figure 1, Table 1).

Fig. 1. Tabular representation of names, concepts, and articulations for eight succeeding classification of the *Andropogon* complex. Vertical columns represent classifications whereas horizontal rows contain information on name identity and taxonomic overlap. Cell shadings indicate congruent concepts. The numbers correspond to concepts listed in Table 1. See text for further details.

The respective authors and treatments³ of the use case include, in chronological sequence: Hackel (1889) [35], Small (1933) [55], Blomquist (1948) [5], Hitchcock & Chase (1950) [36], Radford *et al.* (1968; herein abbreviated as RAB) [49], Godfrey & Wooten (1979) [32], Campbell (1983) [8], and Weakley (2006) [63]. The alignment shown in Figure 1 requires some interpretation as it encodes taxonomic congruence as a function of occupying the same row position and width [23]. For instance, *A. virginicus* var. *glaucus* subvar. *glaucus* *sec. Hackel* (1889) (concept 4) == *A. capillipus* var. *capillipes* *sec. Weakley* (2006) (concept 55). Accordingly, the particular articulation between two concepts pertaining

³ To ease the reader's recognition of each classification we spell out author names for the eight classifications throughout the paper.

to different classifications may be 'read off' by tracing their cell positions and extensions – encoded with unique shadings – across the respective columns.

The consistent column depth between the eight taxonomies, i.e. the fact that Figure 1 displays an overall rectangular shape, also indicates that the upper taxonomic limits of the complex are assessed as congruent throughout (==). Concepts 1, 13, 17, 24, 31, 33, 39, and 53 all have the same referential extension. In other words, while the taxonomic subdivisions within this complex have varied greatly among succeeding classifications, each treatment concurs on the top-level circumscription of the *Andropogon* complex (*sec. auctorum*) for the purpose of this use case (Figure 1, Table 1).

Another aspect in need of interpretation is the representation of higher-ranked entities. These entities are not explicitly named and delimited in Figure 1 because concepts are broken down to their narrowest subcomponents which are then aligned. However the entities are implied by the nomenclatural conventions that guide each of the source taxonomies, and are usually explicit therein. For instance, the existence of two variety-level concepts *A. glomeratus* var. *glomeratus* *sec. Weakley* (2006) (concept 63) and *A. glomeratus* var. *hirsutior* *sec. Weakley* (2006) (concept 62) also indicates the presence of the species-level concept *A. glomeratus* *sec. Weakley* (2006) (concept 61).

Here we opt to 'fill in' this implied upper taxonomy to yield a more comprehensive and widely relevant use case for reasoning over taxonomies containing up to four ranked levels (Figure 2). In some instances we have added nominal (type-representing) taxon names and concepts to obtain comparable entities at each rank (e.g., *Andropogon virginicus* var. *viridis* *sec. Hackel* [1889] was added as concept 6, comparable to concept 3 of the same rank). The complete list of 64 input concepts is provided in Table 1, and the corresponding classification hierarchies are displayed in Figure 2.

Fig. 2. Fully hierarchical representations of the eight input classifications, including 64 implied and nominal taxon names/concepts based on the column/row representation displayed in Figure 1. See also Table 1.

2.2. Nomenclatural complexity

The *Andropogon* use case, while not exceptional in its complexity [22,24,61], clearly illustrates the limitations of taxonomic names to serve as reliable identifiers of perceived taxonomic entities. In Figure 1, the

name *Andropogon virginicus* occurs in each classification but ultimately represents six non-congruent taxonomic entities. Only the 1889/1983 and 1933/2006 perspectives are reciprocally congruent in their extensions. Indeed, "*Andropogon virginicus*" may variably refer to the entire complex (sec. RAB 1986) or to mutually overlapping subsets of the complex (e.g., sec. Blomquist 1948 and sec. Godfrey & Wooten 1979). Conversely, concepts 12, 22, 52, and 64 have congruent taxonomic extensions, yet each carries a non-identical species epithet.

We recognize that the respective sets of valid names and synonyms can convey *some* significant aspects of the entities and articulations derived from Figure 1. For instance, Campbell (1983: p. 225) [8] lists seven synonyms for *Andropogon virginicus* var. *virginicus* (concept 44) of which one is the "subvar. *genuinus* Hackel" (concept 7; where $7 > 44$). Similarly, Campbell (1983: 232) [8] lists *Andropogon macrourus* as a synonym of *Andropogon glomeratus*. This relationship aligns well with Hackel's (1889) concept ($8 = 48$), but less so with the non-congruent concepts of *Andropogon glomeratus* by (e.g.) Blomquist (1948; concept 23; where $23 < 48$) or Hitchcock & Chase (1950; concept 30; where $30 < 48$ and $23 >> 30$). Hence the published sets of valid names and synonyms in each treatments can recover *parts* of Figure 1; though typically in an incomplete and unidirectional sense. Synonymous names may also assume disparate semantic roles across taxonomies depending on the selection of valid names and their extensions. Reconstructing the *entire* set of articulations requires concept-level representation and reasoning.

2.3. Input configuration and workflow execution

The Euler/ASP toolkit is Open Source and available for download at [10]. The software can be cloned on-line and then deployed on a desktop using the command-line interface. An overview of the available reasoning and output generation options is available through the toolkit ("euler --help"). Additional software dependencies include Python 2.X (toolkit coding language), the Answer Set Programming reasoners DLV [16] and Potassco (*Gringo* and *claspD*) [27], and GraphViz [26] for visualizing the merge taxonomies. A fuller description of the workflow for creating, ingesting, processing, and visualizing taxonomies and alignments with the Euler/ASP toolkit is provided in [11].

The methods for encoding concepts, parent/child relationships, and articulations are in accordance with [22] and [23]. The relevant 131 input articulations are provided in Table 2; they are logically deducible from the nomenclatural and taxonomic information displayed in Figures 1 and 2. Figure 3 shows an example – in this case of the expert-made alignment of concepts in Small (1933) and Blomquist (1948) – of the basic text file format that the toolkit utilizes to start of the reasoning process.

Fig. 3. Screenshot of the Euler/ASP toolkit input file for the Small (1933) versus Blomquist (1948) alignment; encoded as "taxonomy 1" and "taxonomy 2", respectively (see also Figures 4 and 5, and Table 2). In the taxonomy section, "(13 14 15 16)" means: concept 13 *is the parent of* concepts 14, 15, and 16 (jointly). In the articulations section, "1.13" means: taxonomy 1, concept 13. The "[l/r]#sum" signature is used to express congruence with an additive group of concepts.

Once the toolkit is set up, the command "euler -i [input file name] --iv" can be used to visualize the input taxonomies (T_1, T_2) and articulations (A) *prior* to launching the reasoning process (Figure 4). In the present analysis the constraints (C) of non-emptiness, sibling-disjointness, and coverage were applied in all cases [57]. The Hackel (1889) and RAB (1968) classifications each contain concept pairs (concepts 6/7 and 31/32, respectively) with different names and Linnaean ranks but congruent taxonomic extensions. These relationships were accommodated with a non-coverage annotation (e.g., "6 7 nc") which allows a parent concept to either entail or equal the circumscription of its child. For taxonomic reasoning purposes each member of the pair is treated identically.

Fig. 4. Visualization of input concepts and articulations used to align the Small (1933) and Blomquist (1948) taxonomies, represented by green rectangles and yellow octagons, respectively. Solid arrows indicate *is_a* relationships among parent and child concepts of the same taxonomy. Dashed grey arrows show individually valid input articulations; and the three dashed orange arrows represent the additive articulation $16 = 21 + 22 + 23$. See also Table 2.

Nine pairwise taxonomy alignments were inferred and visualized (Figures 5–13). Seven of these follow a linear, chronological path from 1889 to 1933, 1933 to 1948, etc., to 1983 to 2006. They jointly represent the shortest time intervals over which classificatory changes have taken place. One additional alignment concerns the Hitchcock & Chase (1950) and Godfrey & Wooten (1979) classifications; this was done to potentially bridge the loss of resolution along the chain of reference caused by the single-concept RAB (1968) taxonomy. Lastly, Hackel (1889) and Weakley (2006) were aligned to assess nomenclatural and

taxonomic stability over the longest time period covered in this use case. The choice of alignments is further examined in the Discussion.

All pairwise alignments were obtained using the command "euler -i [input file name] -e mnpw --rcgo". The "-e mnpw" stands for *polynomial encoding* (mn) of the input conditions for ASP reasoning, with an output that includes *all* stable possible world models (pw). The appended "--rcgo" produces *reduced containment graphs* (rcg), showing also overlapping articulations (o). Therefore the command generates: (1) the set or MIR that constitute the alignment (output as a .csv file); (2) *all* logically consistent possible world alignments (also in .csv format); and (3) visualizations of the latter in GraphViz (output as .dot and .png files). At present the toolkit labels concepts as shown in Figure 3 ("1.15", etc.). To render the output more legible, these labels were replaced with the concept identifiers and abbreviations in Table 1 ("1933:AV [15]") using vector graphics editing software.

2.4. Assessments of name/concept resolution

In line with the name/concept resolution theme motivated in the Introduction, we annotated the nine merge taxonomies to expose similarities and differences in these complementary approaches to identify taxonomic content (Figure 5). In the case of congruent concepts (grey squares with octagonal inner margins), the symbols "=" and "≠" are used to express whether the corresponding names are identical or not. Conversely, concepts that are taxonomically incongruent and hence unique to one of the two classifications aligned (green rectangles or yellow octagons), received either a "+" if they also had a unique name, or a "-" if their name is shared (non-unique) with the other taxonomy (albeit under an incongruent circumscription). The number of occurrences of each symbol was recorded to yield cumulative totals and percentages of nomenclatural and taxonomic consistency across all alignments [22,24,29]. The top-level concept – i.e., the *Andropogon (virginicus)* 'complex' sec. *auctorum* – was excluded from the totals because of its underspecified nomenclatural identity across different treatments.

3. Results

Due to the high precision of the input articulations, all pairwise comparisons yielded a single, logically consistent and unambiguously resolved possible

world merge taxonomy. In what follows we analyze aspects of each alignment according to the sequence of Figures 5–13. We then review the quantitative assessments of name/concept resolution as summarized in Table 3.

3.1. Sequential analysis of merge taxonomies

Fig. 5. Merge taxonomy visualization for the Hackel (1889; T₁) and Small (1933; T₂) alignment. Concept abbreviations are provided in Table 1. TC # = taxonomic concept identifier (see Table 1). The legend applies to this and all subsequent Figures (Figures 6–13), as does the convention to display non-congruent concepts in the earlier taxonomy (T₁) as green rectangles and those of the later taxonomy (T₂) as yellow octagons.

The Hackel (1889) and Small (1933) taxonomies are rather different in their degrees of taxonomic resolution (12 versus 4 concepts) but otherwise remarkably congruent (Figure 5). Each of Small's (1933) four concepts has a congruent counterpart in Hackel's (1889) earlier treatment; however, each also has a different name. Six of Hackel's (1889) non-congruent concepts – i.e., concept 4–5 and 9–12 – represent more finely resolved taxonomic entities that nevertheless integrate up to Small's (1933) concepts 3 and 8, respectively. Most problematic is the name *Andropogon virginicus*, used in a more inclusive sense by Hackel (1889) (concept 2) than by Small (1933) (concept 15).

Fig. 6. Merge taxonomy visualization for the Small (1933; T₁) and Blomquist (1933; T₂) alignment. See legend of Figure 5 for annotation conventions. The overlapping articulation of concepts 16 and 19 is logically grounded in (1) the two proper inclusion arrows originating from concepts 21 and 22 and (2) the additional single arrows (concepts 23 and 15 == 20, respectively) that are subsumed differentially under the concepts 16 and 19.

Although Small (1933) and Blomquist (1948) make use of the same set of species-level epithets – i.e., *A. capillipes*, *A. glomeratus*, and *A. virginicus* – the latter two names are used incongruently, resulting in a complex merge taxonomy (Figure 6). Of particular interest is the overlapping articulation of *A. glomeratus* sec. Small (1933) (concept 16) and *A. virginicus* sec. Blomquist (1948) (concept 19). These concepts *share* the inclusion of exactly two taxonomic subentities, namely the *glaucopsis* (concept 21) and *tenuispathus* (concept 22) varieties of *A. virginicus* sec. Blomquist (1948). These subentities are not recognized in name by Small (1933) who instead subsumes them under a wider concept of *A. glomeratus* which also includes the narrower *A. glomeratus* sec. Blomquist (concept 23). Conversely, Blomquist's (1948) concept of *A. virginicus* (concept

19) is so wide as to entail the identically named concept 15 of Small's (1933) taxonomy *and* the aforementioned two varieties (concepts 21 and 22). Taxonomically, then, the species-level concept *A. virginicus* sec. Small (1933) and the variety-level concept *A. virginicus* var. *virginicus* sec. Blomquist (1948) are congruent. The name/concept relationships inherent in this alignment are arguably more complex than those of the preceding one (Figure 5), in spite of the higher degree of reuse of species-level taxonomic names.

Fig. 7. Merge taxonomy visualization for the Blomquist (1948; T₁) and Hitchcock & Chase (1950; T₂) alignment. See legend of Figure 5 for annotation conventions.

The lack of name/concept correspondence is even more marked in the alignment of the Blomquist (1948) and Hitchcock & Chase (1950) taxonomies (Figure 7). Each classification recognizes seven concepts of which three are taxonomically congruent and also consistently named (i.e., 18 == 25 [=], 20 == 29 [=], and 21 == 28 [=]). Again, the same three species epithets are used across treatments; and those for *A. glomeratus* (concepts 23 and 30) and *A. virginicus* (concepts 19 and 26) have overlapping articulations. However, whereas in the preceding alignment (Figure 6) the two concepts of *A. glomeratus* (concepts 16 and 23) have a relation of proper inclusion (16 > 23), the identically named entities in the subsequent alignment (Figure 7) are overlapping (23 >> 30). Thus the four reciprocally non-congruent species-level concepts (19, 23, 26, and 30) each have three subentities that integrate up differentially to constitute the parent concepts, resulting in four overlapping articulations.

Of particular interest is the overlap of the two *A. glomeratus* concepts 23 and 30. This articulation is counter-intuitive at first because neither concept shares congruent children (or at least taxonomically overlapping children) that would somehow account for the overlap. Reexamination of the nature of the overlap in Figure 1 is informative; accordingly, the overlap concerns a *subentity* within each treatment's concept of *A. glomeratus* for which neither provides a uniquely associated name. The overlap constitutes, literally, "that taxonomic entity which is entailed in each treatment's concept of *A. glomeratus* yet is neither overlapping with *A. virginicus* var. *tenuispathus* sec. Blomquist (1948) (concept 22) nor with *A. virginicus* sec. *hirsutior* sec. Hitchcock & Chase (1950) (concept 29)". Other authors such as Hackel (1889; *A. macrourus* var. *abbreviatus* – concept 11)

or Weakley (2006; *A. glomeratus* var. *glomeratus* – concept 63) have used uniquely referring names for their respective congruent subentities. However in the narrow context of the alignment in Figure 7 this entity remains unnamed, and consequently the blue dashed line between concepts 23 and 30 is the only visual representation of the overlap (the toolkit command "-e mncb" visually adds the unnamed entity; not shown here).

We can refer to concepts whose circumscriptions are grounded in newly inferred taxonomic overlap as *merge concepts*. They are not explicit components of the input concept 'vocabulary' in the 1948 and 1950 classifications (Table 1), and no unique names are immediately available to refer to them as distinct subentities of the merge. Such names would have to be coined anew in the merge (see Discussion). The presence of unnamed merge concepts contributes to the complexity of the alignment. Not only are there taxonomically unique concepts (concepts 19, 23, 26, and 30) with non-unique names, but certain congruent concept subentities (23 >> 30) have no suitable name at all.

Fig. 8. Merge taxonomy visualization for the Hitchcock & Chase (1950; T₁) and RAB (1968; T₂) alignment. See legend of Figure 5 for annotation conventions.

Fig. 9. Merge taxonomy visualization for the RAB (1968; T₁) and Godfrey & Wooten (1979; T₂) alignment. See legend of Figure 5 for annotation conventions.

The two alignments involving the RAB (1968) classification are examined in conjunction (Figures 8 and 9). Both are influenced by the comparatively coarse or inclusive RAB (1968) perspective which contains only a single concept *A. virginicus* within the complex (i.e., concepts 31 *and* 32 under the toolkit's non-coverage convention). In contrast, Hitchcock & Chase (1950) and Godfrey and Wooten (1979) recognize 6 and 5 narrower concepts, respectively. This means that there are no congruent merge concepts at the species- or variety-levels as circumscribed by the latter authors, and no shared and valid names *within* the complex (Table 3). The more resolved 1950 and 1979 taxonomies are merely reproduced in the merge in their original configuration.

The wide notion of *A. virginicus* sec. RAB (1968) causes non-continuity along the entire 1889–2006 chain of reference. Congruent taxonomic lineages such as concepts 3 == 14 == 18 == 25 == 34 == 41 == 54 or concepts 7 == 15 == 20 == 27 == 36 == 44 + 47 == 57 are interrupted by this taxonomy. An alignment of the two taxonomies pre- and postdating

the RAB (1968) classification can ameliorate the loss of referential continuity, and is depicted in Figure 12.

Fig. 10. Merge taxonomy visualization for the Godfrey & Wooten (1979; T₁) and Campbell (1983; T₂) alignment. See legend of Figure 5 for annotation conventions.

The alignment of the Godfrey & Wooten (1979) and Campbell (1983) taxonomies is indicative of both higher-level concept overlap and differential degrees of lower-level concept resolution. Together these differences produce a highly incongruent merge (Figure 10). Only 2 of maximally 5 congruent concept articulations are realized, i.e. concepts 34 == 41 and 38 == 49. Neither concept pair has the same taxonomic name or rank, however. Campbell's (1983) perspective is the most narrowly resolved of all taxonomies, with 13 concepts established within the complex. Of these, 11 concepts have no congruent counterpart in Godfrey & Wooten (1979) which in turn has 3 concepts that have no immediate congruence with Campbell (1983); viz. *A. virginicus* sec. Godfrey & Wooten (1979) (concept 35) and its included varieties (concepts 36 and 37).

On the other hand, 10 out of the 14 non-congruent concepts in the alignment also carry unique names (+). Nine of Campbell's (1983) lower-level concepts (concepts 42–47, 50–52) are readily integrated with 4 lower-level concepts (concepts 34, 36–38) in Godfrey & Wooten (1979). A critical overlapping articulation is manifested in the intersection of concepts 35 and 40 (each named *A. virginicus*) and 48 (named *A. glomeratus*). The two Campbell (1983) -endorsed concepts each contain subentities unique to them (i.e., 40 > [34 == 41] and 48 > [38 == 49]) while also including other subentities (concepts 36 and 37, respectively) that are shared with *A. virginicus* sec. Godfrey & Wooten (1979) (concept 35). The concept of Godfrey & Wooten (1979), however, is poorly aligned with *any* concept in Campbell (1983) since its immediate child concepts are also unique to Godfrey & Wooten (1979) (35 == 36 + 37).

Fig. 11. Merge taxonomy visualization for the Campbell (1983; T₁) and Weakley (2006; T₂) alignment. See legend of Figure 5 for annotation conventions.

In contrast with several of the preceding merges, the alignment of the Campbell (1983) and Weakley (2006) perspectives is largely congruent (Figure 11). The degree of taxonomic resolution is similar, with 14 and 12 concepts recognized. Nine of maximally 11 congruent articulations are realized in the merge, although only 4 of these share the same name. The

additional resolution of *A. virginicus* var. *virginicus* sec. Weakley (concept 58) into 2 more narrowly circumscribed subentities in Campbell (1983) (concepts 45 and 46) is not very problematic. Of greater concern are the non-congruent usages of the names *A. glomeratus* (concepts 48 and 61) and *A. virginicus* (concepts 40 and 57). In each case the identically named concept of Campbell (1983) properly includes that of Weakley (2006). Moreover, each of Campbell's (1983) species-level concepts includes 1–2 additional species-level concepts of Weakley (2006) (40 > 54 and 48 > 60 + 64). However, because these articulations do not entail overlap, concept-level resolution is less complex than in preceding alignment.

Fig. 12. Merge taxonomy visualization for the Hitchcock & Chase (1950; T₁) and Godfrey & Wooten (1979; T₂) alignment. See legend of Figure 5 for annotation conventions.

The taxonomies of Hitchcock & Chase (1950) and Godfrey & Wooten (1979) are aligned (Figure 12) to transcend the reference gap caused by the RAB (1968) classification (Figures 8 and 9; see above). The 1950 and 1979 perspectives are more similar in their respective numbers of concepts. In spite of this, their alignment is not straightforward. Two congruent concept pairs (25 == 34, 27 == 36) carry the same name, and one additional pair (28 == 38) has different names. Beyond this the two overlapping articulations involving *A. virginicus* sec. Hitchcock & Wooten (1950) (concept 26) are noteworthy. This is the only instance among all nine alignments where overlap concerns concepts of unequal taxonomic rank; viz. the species level and the variety level. The concept *A. virginicus* var. *abbreviatus* sec. Godfrey & Wooten (1950) (concept 37) properly includes *A. virginicus* var. *hirsutior* sec. Hitchcock & Chase (1950) (concept 29); this shared subsumption constitutes the overlap 26 >> 37. Making matters worse, the *variety*-level concept 37 also entails the *species*-level concept *A. glomeratus* sec. Hitchcock & Chase (1950) (concept 30).

As a corollary of the above, the overlap of the identically named *A. virginicus* concepts 26 and 35 requires careful interpretation. Each concept properly includes the congruent *A. virginicus* var. *virginicus* concepts 27 and 36. The concept pair 28 == 38 is unique to concept 26; however concept 37 is properly included in concept 35 and only overlapping with concept 26. The merge effectively transforms *parts* of *A. virginicus* and *A. virginicus* var. *abbreviatus* sec. Godfrey & Wooten (concepts 35 and 37) into merge concepts (see also Figure 7 and analysis). Yet in the

1950/1979 alignment the concepts *A. virginicus* var. *hirsutior* (concept 29) and *A. glomeratus* (concept 30) sec. Hitchcock & Chase (1950) are available to represent these merge-contingent subentities visually.

Fig. 13. Merge taxonomy visualization for the Hackel (1889; T₁) and Weakley (2006; T₂) alignment. See legend of Figure 5 for annotation conventions.

The final alignment spans the 117-year time interval between Hackel (1889) and Weakley (2006) (Figure 13). Curiously it contains 8 of out maximally 11 congruent concept pairs; though all 8 have different names. Indeed, *A. virginicus* is the only valid name (out of 20 names total) that has persisted throughout the entire time period. Parallels with the Campbell (1983) and Weakley (2006) merge are apparent (compare concepts 8, 48, and 60 + 61 +64), suggesting that the 1889/1983 merge (not shown here) is similarly resolved.

The main instances of name/concept incongruence are inherent in Hackel's (1889) wider species-level concepts *A. virginicus* (concept 2) and *A. macrourus* (concept 8); each properly includes at least two species-level concepts recognized by Weakley (2006).

3.2. Assessments of name/concept resolution

The information displayed in Figures 5–13 is suited to derive quantitative name/concept resolution patterns from the *Andropogon* use case (Table 3). Accordingly, a total of 46 instances of congruent concepts (below the upper boundary) was theoretically possible given the nine alignments and 64 constituent concepts. Of these, 30 instances (65.2%) were realized. The 1889/1933, 1983/2006, and 1889/2006 merges contain the highest numbers and percentages of congruent concepts (jointly accounting for 20/30 instances). Taxonomic congruence is more limited throughout the 1933–1983 interval (Figures 6–10). Overall, the number of incongruent concepts (59) outweighs that of congruent concepts (30) by a ratio of nearly 2:1.

No more than 10 of the congruent merge concept pairs have identical taxonomic names. This means, cumulatively, that the same name serves as a semantically accurate identifier of congruent taxonomic entities in 21.7% of 46 cases where such a role could have obtained. The loss of continuity in naming is most marked in the 1889/1933, 1979/1983, 1983/2006, and 1889/2006 merges; they jointly account for 18/20 instances where the same name was

available to identify a congruent concept yet was not actually used.

An inverse relationship of semantic disparity between names and concepts exists when the same name denotes a taxonomically incongruent set of concepts. This occurred in 20 (33.9%) out of 59 possible cases.

In summary, (1) only 65.2% of the theoretically possible 46 instances of congruence were realized in the nine alignments; (2) incongruent concepts were twice as common as their counterparts; (3) usages of different names failed to continuously identify congruent concepts in 66.7% of 30 actual cases; and (4) the same names incorrectly identified incongruent concepts in 33.9% of 59 actual cases. While issues (1) and (2) are commensurate with the advancement of systematic inferences [25], issues (3) and (4) arise mainly because of the differential ability of name relationships versus concept articulations to track taxonomic provenance.

4. Discussion

In light of the detailed analysis and interpretation of the alignment results in the preceding sections we limit our discussion to more overarching themes; viz. the significance of the novel visualizations, implications for name/concept resolution, and future research directions.

4.1. Significance of merge taxonomy visualizations

Representations of taxonomic concept information and concept relationship visualizations have advanced significantly over the past 20 years [2,3,11,33,34,64]. Within this context the Euler/ASP toolkit is the first platform to leverage RCC-5 relationships and stable model reasoning to yield merge taxonomies that *combine* all pertinent data (T₁,T₂,A,C) into coherent tree-like visualizations.

The utility of these merge taxonomies is apparent – compare (e.g.) Figures 1–4 and 6, all of which contain information on the alignment of the Small (1933) and Blomquist (1948) classifications. Figure 1, while highly adequate for the present use case, is less well suited to represent relationships among concepts nested into many taxonomic ranks or phylogenetic levels. It is best for showing 'flat' hierarchies. Figure 2 provides (at most) nomenclatural relationships (which are effectively misleading), whereas Figures 3 and 4 reflect the input data but contain no inferences of concept identity.

In contrast, the novel toolkit merge visualizations (Figures 5–13) fully account for the taxonomic and nomenclatural input information *as well as* the inferred and logically consistent reasoning outcomes. The relative proportion and position of grey squares versus green rectangles or yellow octagons⁴ provides an immediate sense of the extent and localization of taxonomic congruence and incongruence (compare, e.g., Figures 10 and 11). Further surveying of occurrences "≠" and "–" symbols can convey information on the degree to which validly recognized names mirror the inferred taxonomic congruence patterns.

Of particular value is the ability to understand the underlying causes of overlapping articulations (e.g., Figures 6 and 7). Overlap tends to be the most complex relationship between concepts, yet it is readily accounted for in the visualizations if at least one of the input taxonomies entails a subsumed concept that embodies the overlap. If this is not the case than an unnamed merge concept is created which can optionally be visualized as well. Thus the Euler/ASP toolkit merge visualizations have clear advantages over conventional multi-tree graphs, reviewed in [34], in conveying provenance information across taxonomic classifications.

4.2. Implications for name/concept resolution

The semantic complexity of the *Andropogon* use case as depicted in Figure 1 is neither trivial nor highly exceptional. Research into the long-term provenance of names and concepts as applied to particular organismal lineages is bound to reveal exemplar cases that are considerably less, or more, difficult to reconstruct [1,14,22,24,29,46,52,61]. Some of the name/concept complexity may be managed pragmatically through human social processes; for instance, through an adherence to conservative re-naming practices or 'standardized' taxonomies [4,31,38,54,62]. The ability of human expert speakers to *contextualize* names and thus reliably delimit their meanings further improves the performance of names in taxonomy [20,22,47]. However, none of these mitigating practices fundamentally alter the insight that the valid taxonomic names and nomenclatural relationships are not designed to fully track the identity and provenance of taxonomic concepts. Computational logic struggles with modeling what "*Andropogon virginicus*" means 'under usual conditions'. Something beyond names is needed if taxonomic perspec-

tives are to be translated into entities fit for representation and reasoning in the logic- and machine processing-driven Semantic Web.

In an analogy to delimiting phenotypic features [21,51], fixing the referential extension of taxonomic names is *not* merely a matter of ostension; i.e. of identifying in-group exemplars (such as types). Such practices invariably under-specify the actual name extension, rendering the corresponding name identifiers semantically vague and inept for precise reasoning. Instead it is more appropriate to represent the name-to-perceived-taxon linkage as a matter of theory construction, subject to all kinds of considerations and actions that theories experience in science in general. In this context, the RCC-5 articulations [23] and other means of comparison [15] outperform the traditional *Code*-compliant methods for representing concept identities and relationships.

The insufficiencies of names and name relationships to act as identifiers of taxonomic content are nowhere more apparent than in cases of concept overlap (Figures 6–7, 10, and 12). Whenever succeeding taxonomies include overlapping concepts, the differences among these perspectives are rooted in something *other* than the desired degree of resolution [17,43,46,52]. For instance, both Blomquist (1948) and Hitchcock & Chase (1950) concur that there are three (identically named) species-level concepts entailed in the *Andropogon* complex. They also concur that *A. virginicus* has three variety-level child concepts. In short, they agree on the degree to which concepts should be resolved at broad and finer levels of this use case (Figure 2). However, they disagree on the *relative extent* to which different available and type-anchored names *reach out* to their perceived and necessarily more inclusive taxonomic entities that are presumed to be causally sustained in nature [6]. As a result of this differential weighting of name/concept interconnections, the referential extensions of the three species-level concepts overlap in complex ways (Figure 7). One can expect such overlap to become more frequent at higher taxonomic levels [24] where the performance of names as identifiers of congruence becomes exceedingly poor.

Concept-level articulations can take into account *both* member- and property-based information when identifying similarities and differences between succeeding taxonomic perspectives [23]. Names and nomenclatural relationships, in turn, are limited to establishing identity based on subsets of the ostensibly designated (type) members. Representation and reasoning over changing taxonomic content in the Semantic Web domain will be similarly lim-

⁴ We note that the shape and color selections (see legend in Figure 5) are merely conventional.

ited.⁵ Identifiers whose meanings change inadvertently or even unascertainably from one taxonomy to the next are suboptimal vehicles for integrating biodiversity data.

4.3. Future research directions

Reasoning over taxonomic change remains in its infancy [11,30,57]. New informatics research, more powerful and versatile software applications, and large-scale demonstrations of the practical utility of aligning concepts and visualizing merge taxonomies are needed to further promote this approach. The present analysis of the *Andropogon* use case brings out some of the reasoning potential while leaving room for further work. In particular, the eight classifications of the complex lend themselves to 28 possible pairwise comparisons, of which only 9 are presented here. This omission is deliberate; future versions of the Euler/ASP toolkit will have the ability to infer and visualize more than two input taxonomies simultaneously. In doing so the ASP reasoners will make use of transitive relationships such as "if concepts 7 == 15 and 15 == 20 then 7 == 20". We can then ask to what extent the 7 sequential (Figures 5–11) and 2 additional alignments (Figures 12–13) are sufficient for recovering the full set of 28 pairwise alignments based solely on the transitive powers of logic reasoning. Answers to such questions will have relevance for the scalability of this approach, and should inform the experts' practice of providing input articulations.

Additional use case-based demonstrations should focus (*inter alia*) on aligning larger and more phylogeny-centric taxonomies. The *Andropogon* use case (Figure 1) is somewhat peculiar in that all classifications range over a congruent upper boundary and all cover the internal taxonomic domain completely. Furthermore the expert's input alignment for this use case has a high degree of precision and certainty leading to unambiguous inference outcomes. Other use cases will involve new challenges such as the integration of both traditional ranked classifications and more finely bifurcating phylogenies, partial ingroup representations due to specific taxonomic or geographic foci, and ambiguous input alignments and output merges [22,24]. These conditions present additional reasoning, workflow, and visualization challenges that remain underexplored.

Lastly, the merge taxonomies may include entities that result from the proper (inverse) inclusion or

overlap of two or more input concepts. They will thus generate merge concepts – corresponding to unique Euler sets – for which there are no adequate taxonomic names. The case of the overlap between *A. glomeratus* sec. Blomquist (1948) versus sec. Hitchcock & Chase (1950) demonstrates this phenomenon (see Figure 7 and corresponding analysis). Merge concepts may play a critical role in understanding taxonomic provenance at different analytical scales; however at present there is no set of formal rules to label these entities. Therefore advances in reasoning over taxonomic change should also stimulate the development of new ways to refer to the products of merge taxonomies.

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⁵ Discussing the implications of these limitations for the reliability of comparative analyses [46] is beyond the present scope.

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Table 1

List of 64 concepts that constitute the ranked entities in the eight input classifications of the *Andropogon* use case. The identifier numbers (ID) are used consistently throughout this paper. Latin name authors are omitted but may be found (e.g.) in [8] and [63]. Abbreviations are used to label concepts succinctly in the merge taxonomies. See also Figures 1 and 2.

ID	Name	According To (sec.)	Abbreviation	Rank
1	<i>Andropogon</i>	Hackel (1889)	1889:A	Genus (upper limit)
2	<i>Andropogon virginicus</i>	Hackel (1889)	1889:AV	Species
3	<i>Andropogon virginicus</i> var. <i>glaucus</i>	Hackel (1889)	1889:AVG	Variety
4	<i>Andropogon virginicus</i> var. <i>glaucus</i> subvar. <i>glaucus</i>	Hackel (1889)	1889:AVGG	Subvariety
5	<i>Andropogon virginicus</i> var. <i>glaucus</i> subvar. <i>dealbatus</i>	Hackel (1889)	1889:AVGD	Subvariety
6	<i>Andropogon virginicus</i> var. <i>viridis</i>	Hackel (1889)	1889:AVV	Variety (nominal)
7	<i>Andropogon virginicus</i> var. <i>viridis</i> subvar. <i>genuinus</i>	Hackel (1889)	1889:AVVG	Subvariety
8	<i>Andropogon macrourus</i>	Hackel (1889)	1889:AM	Species
9	<i>Andropogon macrourus</i> var. <i>glaucopsis</i>	Hackel (1889)	1889:AMGL	Variety
10	<i>Andropogon macrourus</i> var. <i>hirsutior</i>	Hackel (1889)	1889:AMH	Variety
11	<i>Andropogon macrourus</i> var. <i>abbreviatus</i>	Hackel (1889)	1889:AMA	Variety
12	<i>Andropogon macrourus</i> var. <i>genuinus</i>	Hackel (1889)	1889:AMGE	Variety
13	<i>Andropogon</i>	Small (1933)	1933:A	Genus (upper limit)
14	<i>Andropogon capillipes</i>	Small (1933)	1933:AC	Species
15	<i>Andropogon virginicus</i>	Small (1933)	1933:AV	Species
16	<i>Andropogon glomeratus</i>	Small (1933)	1933:AG	Species
17	<i>Andropogon</i>	Blomquist (1948)	1948:A	Genus (upper limit)
18	<i>Andropogon capillipes</i>	Blomquist (1948)	1948:AC	Species
19	<i>Andropogon virginicus</i>	Blomquist (1948)	1948:AV	Species
20	<i>Andropogon virginicus</i> var. <i>virginicus</i>	Blomquist (1948)	1948:AVV	Variety
21	<i>Andropogon virginicus</i> var. <i>glaucopsis</i>	Blomquist (1948)	1948:AVG	Variety
22	<i>Andropogon virginicus</i> var. <i>tenuispathus</i>	Blomquist (1948)	1948:AVT	Variety
23	<i>Andropogon glomeratus</i>	Blomquist (1948)	1948:AG	Species
24	<i>Andropogon</i>	Hitchcock & Chase (1950)	1950:A	Genus (upper limit)
25	<i>Andropogon capillipes</i>	Hitchcock & Chase (1950)	1950:AC	Species
26	<i>Andropogon virginicus</i>	Hitchcock & Chase (1950)	1950:AV	Species
27	<i>Andropogon virginicus</i> var. <i>virginicus</i>	Hitchcock & Chase (1950)	1950:AVV	Variety
28	<i>Andropogon virginicus</i> var. <i>glaucopsis</i>	Hitchcock & Chase (1950)	1950:AVG	Variety
29	<i>Andropogon virginicus</i> var. <i>hirsutior</i>	Hitchcock & Chase (1950)	1950:AVH	Variety
30	<i>Andropogon glomeratus</i>	Hitchcock & Chase (1950)	1950:AG	Species
31	<i>Andropogon</i>	RAB (1968)	1968:A	Genus (upper limit)
32	<i>Andropogon virginicus</i>	RAB (1968)	1968:AV	Species
33	<i>Andropogon</i>	Godfrey & Wooten (1979)	1979:A	Genus (upper limit)
34	<i>Andropogon capillipes</i>	Godfrey & Wooten (1979)	1979:AC	Species
35	<i>Andropogon virginicus</i>	Godfrey & Wooten (1979)	1979:AV	Species
36	<i>Andropogon virginicus</i> var. <i>virginicus</i>	Godfrey & Wooten (1979)	1979:AVV	Variety
37	<i>Andropogon virginicus</i> var. <i>abbreviatus</i>	Godfrey & Wooten (1979)	1979:AVA	Variety
38	<i>Andropogon glaucopsis</i>	Godfrey & Wooten (1979)	1979:AG	Species
39	<i>Andropogon</i>	Campbell (1983)	1983:A	Genus (upper limit)
40	<i>Andropogon virginicus</i>	Campbell (1983)	1983:AV	Species
41	<i>Andropogon virginicus</i> var. <i>glaucus</i>	Campbell (1983)	1983:AVG	Variety
42	<i>Andropogon virginicus</i> var. <i>glaucus</i> "drylands variant"	Campbell (1983)	1983:AVGD	Subvariety (variant)
43	<i>Andropogon virginicus</i> var. <i>glaucus</i> "wetlands variant"	Campbell (1983)	1983:AVGW	Subvariety (variant)
44	<i>Andropogon virginicus</i> var. <i>virginicus</i>	Campbell (1983)	1983:AVV	Variety
45	<i>Andropogon virginicus</i> var. <i>virginicus</i> "old-field variant"	Campbell (1983)	1983:AVVO	Subvariety (variant)
46	<i>Andropogon virginicus</i> var. <i>virginicus</i> "smooth variant"	Campbell (1983)	1983:AVVS	Subvariety (variant)
47	<i>Andropogon virginicus</i> var. <i>decipiens</i>	Campbell (1983)	1983:AVD	Variety
48	<i>Andropogon glomeratus</i>	Campbell (1983)	1983:AG	Species
49	<i>Andropogon glomeratus</i> var. <i>glaucopsis</i>	Campbell (1983)	1983:AGGLA	Variety
50	<i>Andropogon glomeratus</i> var. <i>hirsutior</i>	Campbell (1983)	1983:AGH	Variety
51	<i>Andropogon glomeratus</i> var. <i>glomeratus</i>	Campbell (1983)	1983:AGGLO	Variety
52	<i>Andropogon glomeratus</i> var. <i>pumilus</i>	Campbell (1983)	1983:AGP	Variety
53	<i>Andropogon</i>	Weakley (2006)	2006:A	Genus (upper limit)
54	<i>Andropogon capillipes</i>	Weakley (2006)	2006:AC	Species
55	<i>Andropogon capillipes</i> var. <i>capillipes</i>	Weakley (2006)	2006:ACC	Variety
56	<i>Andropogon capillipes</i> var. <i>dealbatus</i>	Weakley (2006)	2006:ACD	Variety

57	<i>Andropogon virginicus</i>	Weakley (2006)	2006:AV	Species
58	<i>Andropogon virginicus</i> var. <i>virginicus</i>	Weakley (2006)	2006:AVV	Variety
59	<i>Andropogon virginicus</i> var. <i>decepiens</i>	Weakley (2006)	2006:AVD	Variety
60	<i>Andropogon glaucopsis</i>	Weakley (2006)	2006:AGLA	Species
61	<i>Andropogon glomeratus</i>	Weakley (2006)	2006:AGLO	Species
62	<i>Andropogon glomeratus</i> var. <i>hirsutior</i>	Weakley (2006)	2006:AGLOH	Variety
63	<i>Andropogon glomeratus</i> var. <i>glomeratus</i>	Weakley (2006)	2006:AGLOG	Variety
64	<i>Andropogon tenuispatheus</i>	Weakley (2006)	2006:AT	Species

Table 2

List of 131 input articulations – asserted by Weakley [24,63] and further derived from Figure 1 – among concepts pertaining to eight classifications of the *Andropogon* complex (see also Figures 1 and 2). The 64 corresponding concepts are listed in Table 1.

ID	From Concept ID	Articulation	To Concept ID
Hackel (1889) versus Small (1933) – Figure 5			
1	1	==	13
2	2	<	13
3	2	>	14
4	2	>	15
5	2	==	14 + 15
6	3	==	14
7	4	<	14
8	5	<	14
9	4 + 5	==	14
10	6	==	15
11	7	==	15
12	8	==	16
13	9	<	16
14	10	<	16
15	11	<	16
16	12	<	16
17	9 + 10 + 11 + 12	==	16
Small (1933) versus Blomquist (1948) – Figure 6			
18	13	==	17
19	14	==	18
20	15	==	20
21	16	>	21
22	16	>	22
23	16	>	23
24	16	==	21 + 22 + 23
25	14		19
26	15	<	19
27	16	>>	19
Blomquist (1948) versus Hitchcock & Chase (1950) – Figure 7			
28	17	==	24
29	18	==	25
30	19	>>	26
31	20	<	26
32	20	==	27
33	21	==	28
34	22	<	30
35	22		26
36	23	>>	26
37	23	>	29
38	23	>>	30
Hitchcock & Chase (1950) versus RAB (1968) – Figure 8			
39	24	==	31
40	25	<	32
41	26	<	32

42	30	<	32
43	25 + 26 + 30	==	32
RAB (1968) versus Godfrey & Wooten (1979) – Figure 9			
44	31	==	33
45	32	>	34
46	32	>	35
47	32	>	38
48	32	==	34 + 35 + 38
Godfrey & Wooten (1979) versus Campbell (1983) – Figure 10			
49	33	==	39
50	34	==	41
51	34	>	42
52	34	>	43
53	34	==	42 + 43
54	34	<	40
55	35	>>	40
56	35		41
57	35	>>	48
58	36	<	40
59	36	>	44
60	36	>	45
61	36	>	46
62	36	>	47
63	36	==	45 + 46 + 47
64	34 + 36	==	40
65	37		40
66	37	>	50
67	37	>	51
68	37	>	52
69	37	==	50 + 51 + 52
70	38	<	48
71	38	==	49
72	37 + 38	==	48
Campbell (1983) versus Weakley (2006) – Figure 11			
73	39	==	53
74	40	>	54
75	40	>	57
76	40	==	54 + 57
77	41	==	54
78	42	==	55
79	43	==	56
80	44	<	57
81	47	<	57
82	44 + 47	==	57
83	45	<	58
84	46	<	58
85	45 + 46	==	58
86	47	==	59
87	48	>	60
88	48	>	61
89	48	>	64
90	48	==	60 + 61 + 64
91	49	==	60
92	50	<	61
93	50	==	62
94	51	<	61
95	50 + 51	==	61
96	52	==	64
Hitchcock & Chase (1950) versus Godfrey & Wooten (1979) – Figure 12			
97	24	==	33
98	25	==	34

99	26	><	35
100	26	>	36
101	26	><	37
102	26	>	38
103	27	==	36
104	28	==	38
105	29	<	37
106	30	<	37
107	29 + 30	==	37
108	27 + 29 + 30	==	35
Hackel (1889) versus Weakley (2006) – Figure 13			
109	1	==	53
110	2	>	54
111	2	>	57
112	2	==	54 + 57
113	3	==	54
114	4	==	55
115	5	==	56
116	6	==	57
117	6	>	58
118	6	>	59
119	6	==	58 + 59
120	7	==	57
121	8	>	60
122	8	>	61
123	8	>	64
124	8	==	60 + 61 + 64
125	9	==	60
126	10	<	61
127	10	==	62
128	11	<	61
129	11	==	63
130	10 + 11	==	61
131	12	==	64

Table 3

Assessments of taxonomic and nomenclatural resolution in nine pairwise comparisons of *Andropogon* classifications (T_1 and T_2 , respectively). See also Figures 5-13, and particularly the legend in Figure 5. Abbreviations: TCs: taxonomic concepts; ==: congruent (grey square); not ==: not congruent (green rectangle or yellow octagon); = Name: same names; ≠ Name: different names; – Name: non-unique name.

T_1 (TCs) T_2 (TCs)	# of Merge TCs ¹ == / not ==	# of == TCs / Max == TCs ² %	# of (== TCs & = Name) / Max == TCs ² %	# of (== TCs & ≠ Name) / # of == TCs ³ %	# of (not == TCs & – Name) / # of not == TCs %
1889 (12) 1933 (4)	10 3 / 7	3 / 3 100%	0 / 3 0%	3 / 3 100%	1 / 7 14.3%
1933 (4) 1948 (7)	7 2 / 5	2 / 3 66.7%	1 / 3 33.3%	1 / 2 50.0%	2 / 5 40%
1948 (7) 1950 (7)	9 3 / 6	3 / 6 50%	3 / 6 50%	0 / 3 0.0%	4 / 6 66.7%
1950 (7) 1968 (2)	6 0 / 6	0 / 1 0%	0 / 1 0%	0 / 0 –	1 / 6 16.7%
1968 (2) 1979 (6)	5 0 / 5	0 / 1 0%	0 / 1 0%	0 / 0 –	1 / 5 20%
1979 (6) 1983 (14)	16 2 / 14	2 / 5 40%	0 / 5 0%	2 / 2 100%	4 / 14 28.6%
1983 (14) 2006 (12)	15 9 / 6	9 / 11 81.8%	4 / 11 36.4%	5 / 9 55.6%	4 / 6 66.7%
1950 (7) 1979 (6)	8 3 / 5	3 / 5 60%	2 / 5 40%	1 / 3 33.3%	2 / 5 40%
1889 (12) 2006 (12)	13 8 / 5	8 / 11 72.7%	0 / 11 0%	8 / 8 100%	1 / 5 20%
Totals (9 merges)	89 30 / 59	30 / 46 65.2%	10 / 46 21.7%	20 / 30 66.7%	20 / 59 33.9%

¹ Excluding the top-level concept *Andropogon* sec. *auctorum* (i.e., the given, consistent 'upper' limit of the use case).

² The maximum number of possible congruent merge concepts is obtained by taking the number of input concepts in the taxonomy with the lesser number of concepts to be integrated in the merge and subtracting 1 (see above; the top-level concept is consistently held congruent).

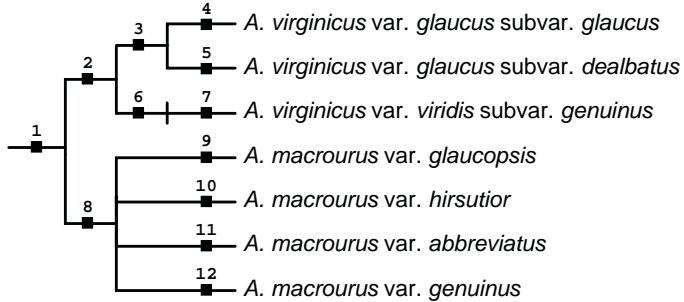
³ Actual number of congruent merge concepts.

Fig. 1

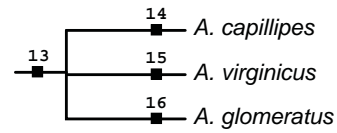
1	13	17	24	31	33	39	53
sec. Hackel (1889)	sec. Small (1933)	sec. Blomquist (1948)	sec. Hitchcock & C. (1950)	sec. RAD (1968)	sec. Godfrey & W. (1979)	sec. Campbell (1983)	sec. Weakley (2006)
<i>A. virginicus</i> var. <i>glaucus</i> subvar. <i>glaucus</i> 4	<i>A. capillipes</i> 14	<i>A. capillipes</i> 18	<i>A. capillipes</i> 25	<i>A. virginicus</i> 32	<i>A. capillipes</i> 34	<i>A. virginicus</i> var. <i>glaucus</i> "drylands variant" 42	<i>A. capillipes</i> var. <i>capillipes</i> 55
<i>A. virginicus</i> var. <i>glaucus</i> subvar. <i>dealbatus</i> 5	<i>A. capillipes</i>	<i>A. capillipes</i>	<i>A. capillipes</i>	<i>A. virginicus</i>	<i>A. capillipes</i>	<i>A. virginicus</i> var. <i>glaucus</i> "wetlands variant" 43	<i>A. capillipes</i> var. <i>dealbatus</i> 56
<i>A. virginicus</i> var. <i>viridis</i> subvar. <i>genuinus</i> 7	<i>A. virginicus</i> 15	<i>A. virginicus</i> var. <i>virginicus</i> 20	<i>A. virginicus</i> var. <i>virginicus</i> 27	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i> 36	<i>A. virginicus</i> var. <i>virginicus</i> "old-field variant" 45	<i>A. virginicus</i> var. <i>virginicus</i> 58
<i>A. virginicus</i> var. <i>viridis</i> subvar. <i>genuinus</i>	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i> "smooth variant" 46	<i>A. virginicus</i> var. <i>virginicus</i>
<i>A. virginicus</i> var. <i>viridis</i> subvar. <i>genuinus</i>	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i> var. <i>decipiens</i> 47	<i>A. virginicus</i> var. <i>decipiens</i> 59
<i>A. macrourus</i> var. <i>glaucopsis</i> 9	<i>A. glomeratus</i> 16	<i>A. virginicus</i> var. <i>glaucopsis</i> 21	<i>A. virginicus</i> var. <i>glaucopsis</i> 28	<i>A. virginicus</i>	<i>A. glaucopsis</i> 38	<i>A. glomeratus</i> var. <i>glaucopsis</i> 49	<i>A. glaucopsis</i> 60
<i>A. macrourus</i> var. <i>hirsutior</i> 10	<i>A. glomeratus</i>	<i>A. glomeratus</i> (?) 23	<i>A. virginicus</i> var. <i>hirsutior</i> 29	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>abbreviatus</i> 37	<i>A. glomeratus</i> var. <i>hirsutior</i> 50	<i>A. glomeratus</i> var. <i>hirsutior</i> 62
<i>A. macrourus</i> var. <i>abbreviatus</i> 11	<i>A. glomeratus</i>	<i>A. glomeratus</i>	<i>A. glomeratus</i> 30	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>abbreviatus</i>	<i>A. glomeratus</i> var. <i>glomeratus</i> 51	<i>A. glomeratus</i> var. <i>glomeratus</i> 63
<i>A. macrourus</i> var. <i>genuinus</i> 12	<i>A. glomeratus</i>	<i>A. virginicus</i> var. <i>tenuispathus</i> 22	<i>A. glomeratus</i>	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>abbreviatus</i>	<i>A. glomeratus</i> var. <i>pumilus</i> 52	<i>A. tenuispathus</i> 64

Fig. 2

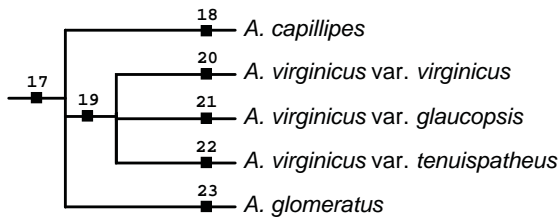
sec. Hackel (1889)



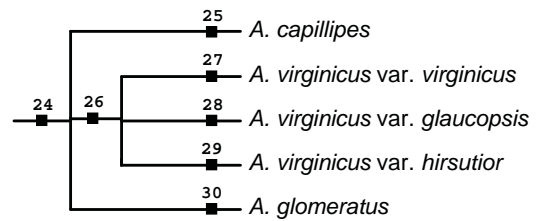
sec. Small (1933)



sec. Blomquist (1948)



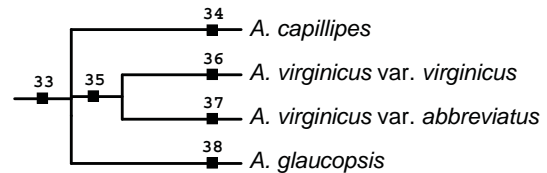
sec. Hitchcock & Chase (1950)



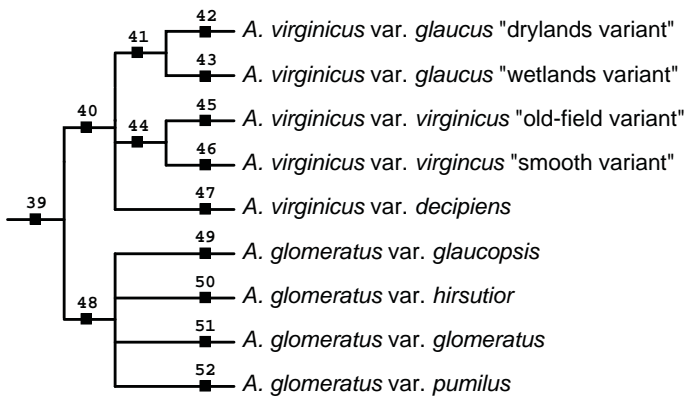
sec. RAB 1968



sec. Godfrey & Wooten (1979)



sec. Campbell (1983)



sec. Weakley 2006

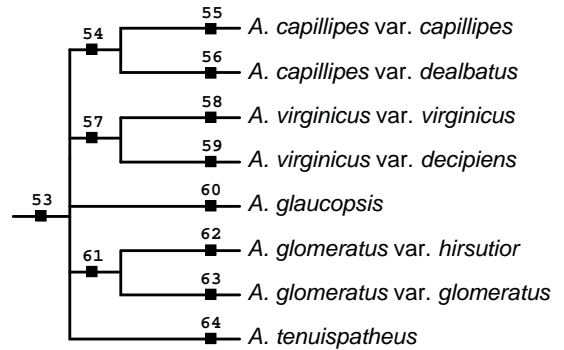


Fig. 3

taxonomy 1 Taxonomy1
(13 14 15 16)

taxonomy 2 Taxonomy2
(17 18 19 23)
(19 20 21 22)

articulation tw1 tw1
[1.13 equals 2.17]
[1.14 equals 2.18]
[1.15 equals 2.20]
[1.16 includes 2.21]
[1.16 includes 2.22]
[1.16 includes 2.23]
[1.16 r3sum 2.21 2.22 2.23]
[1.14 disjoint 2.19]
[1.15 is_included_in 2.19]
[1.16 overlaps 2.19]

Fig. 4

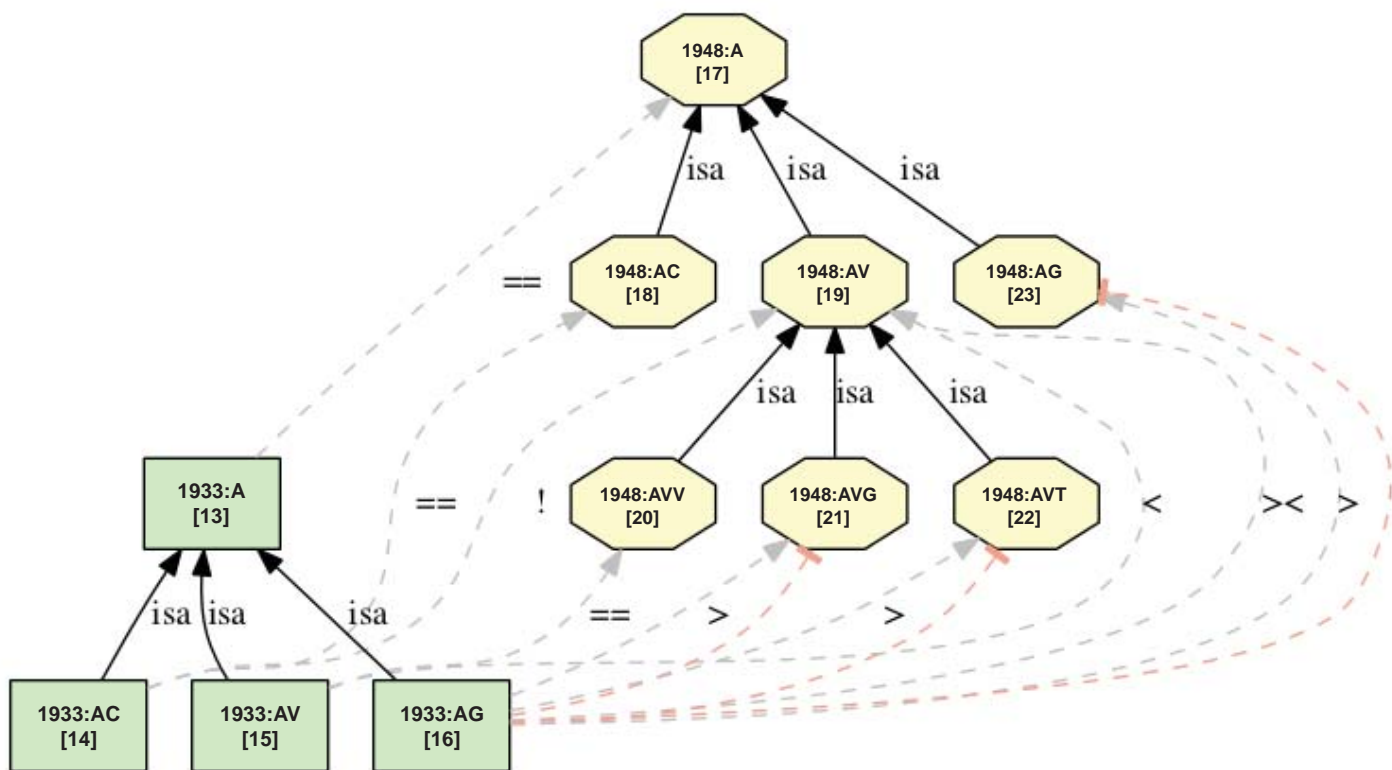


Fig. 5

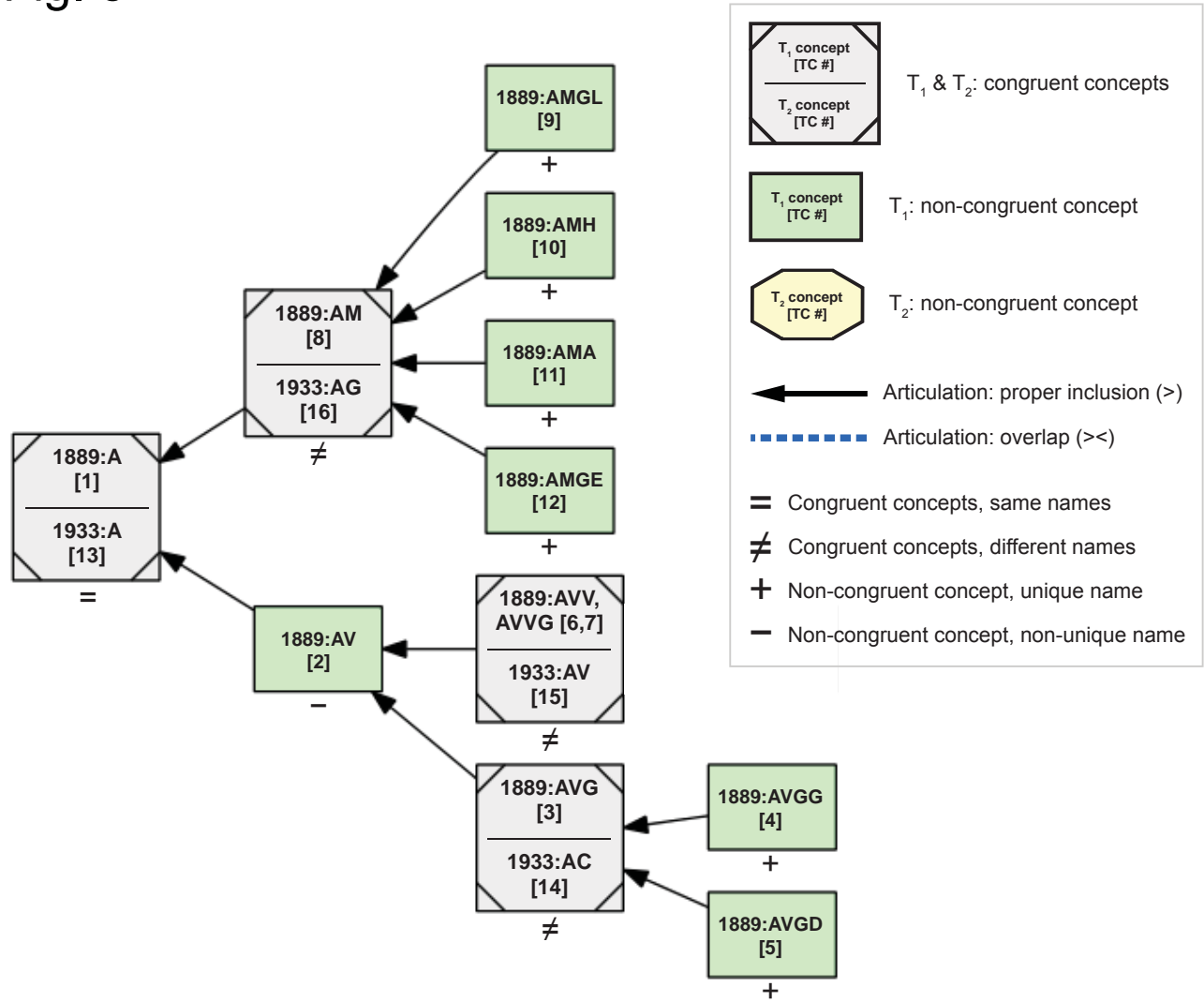


Fig. 6

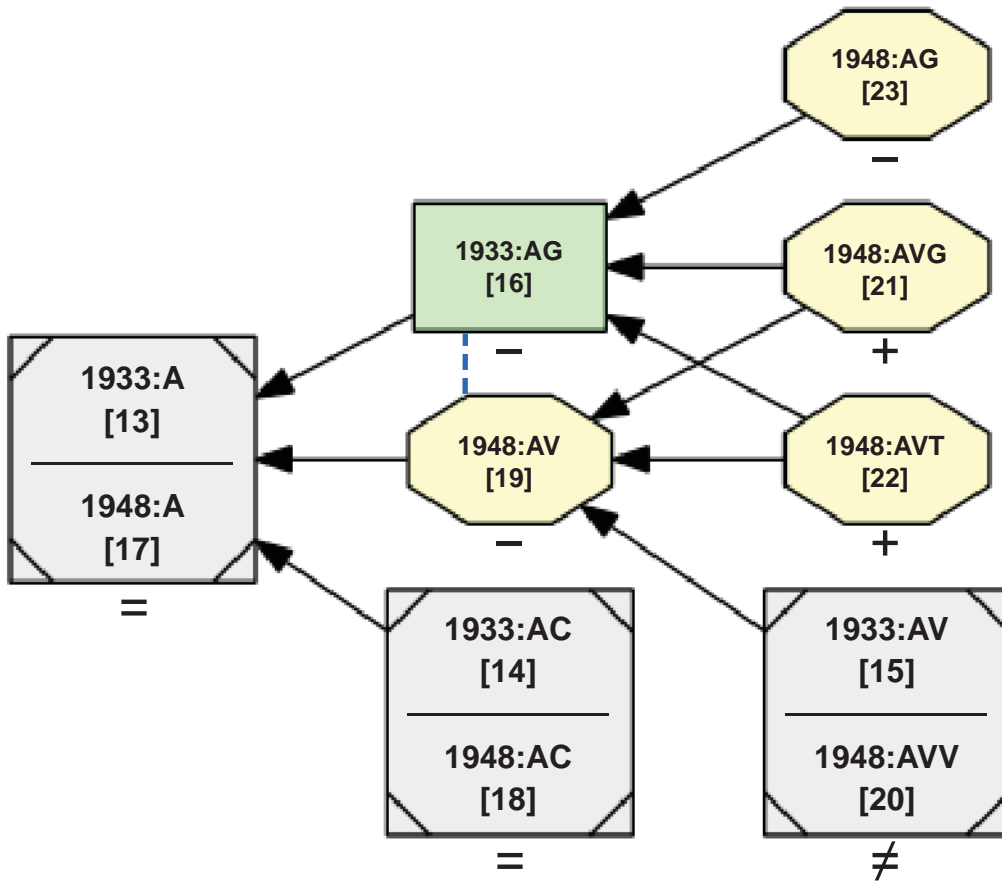


Fig. 7

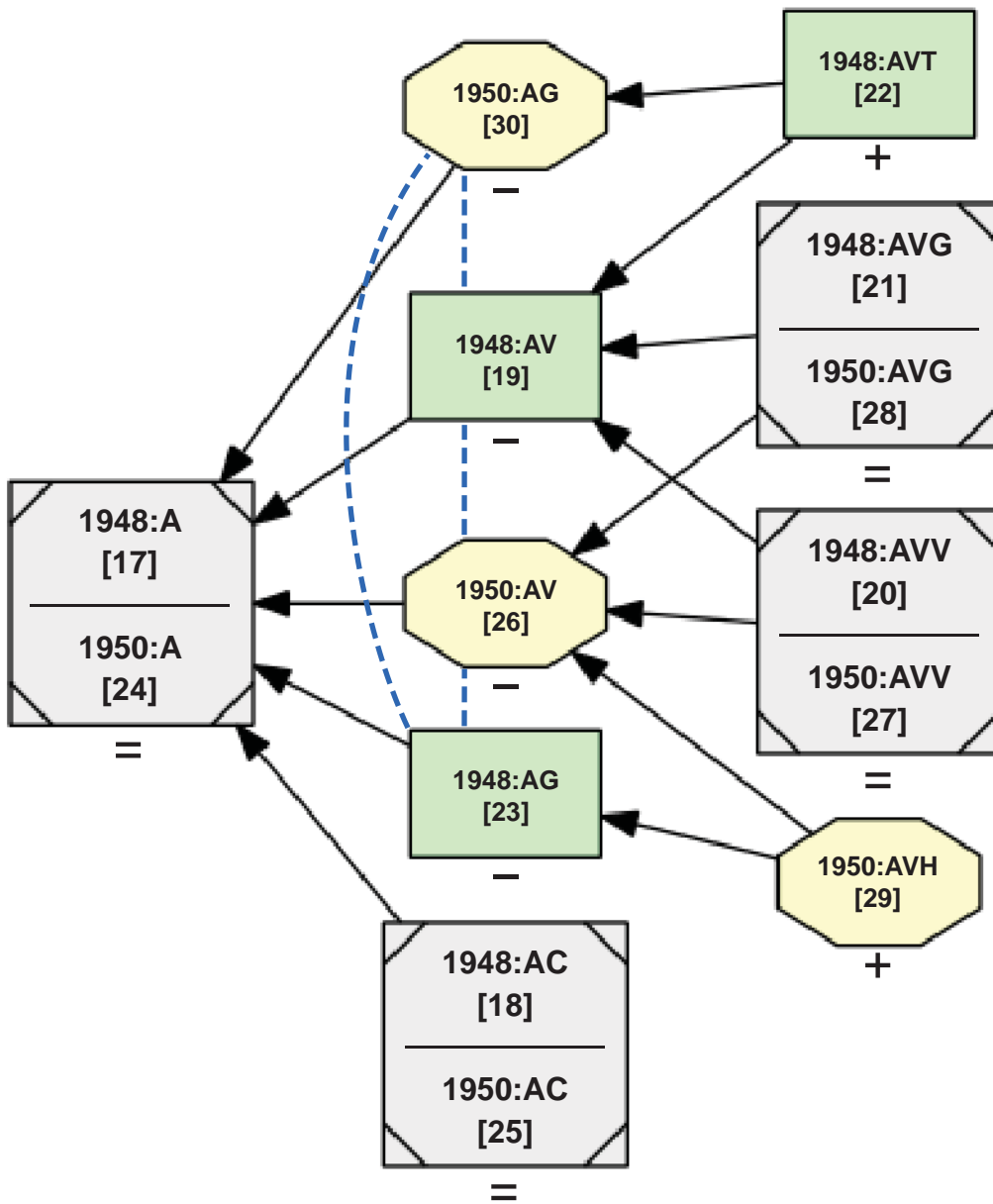


Fig. 8

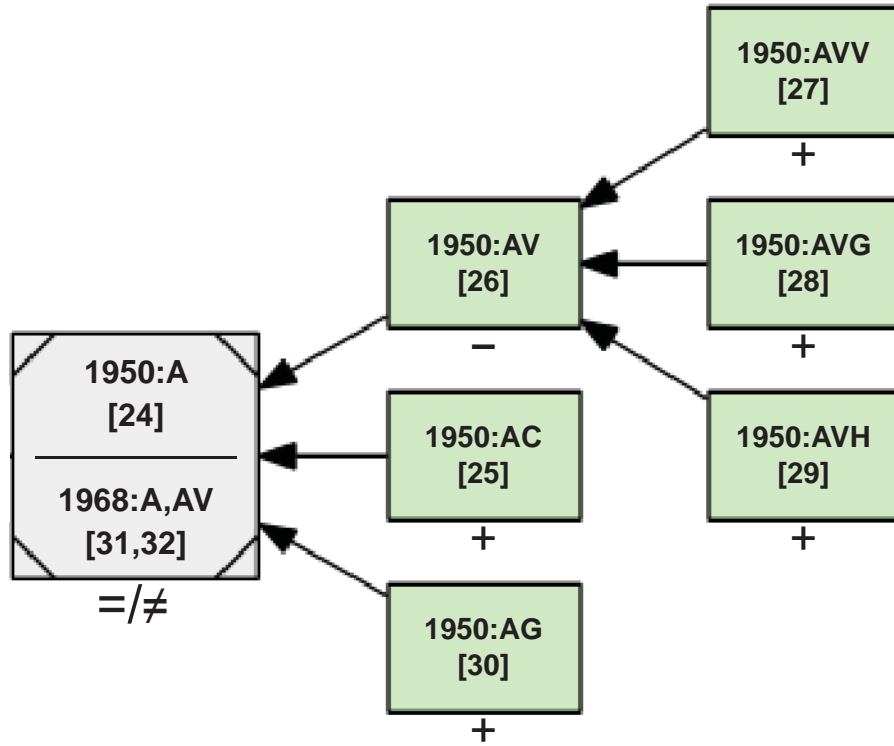


Fig. 9

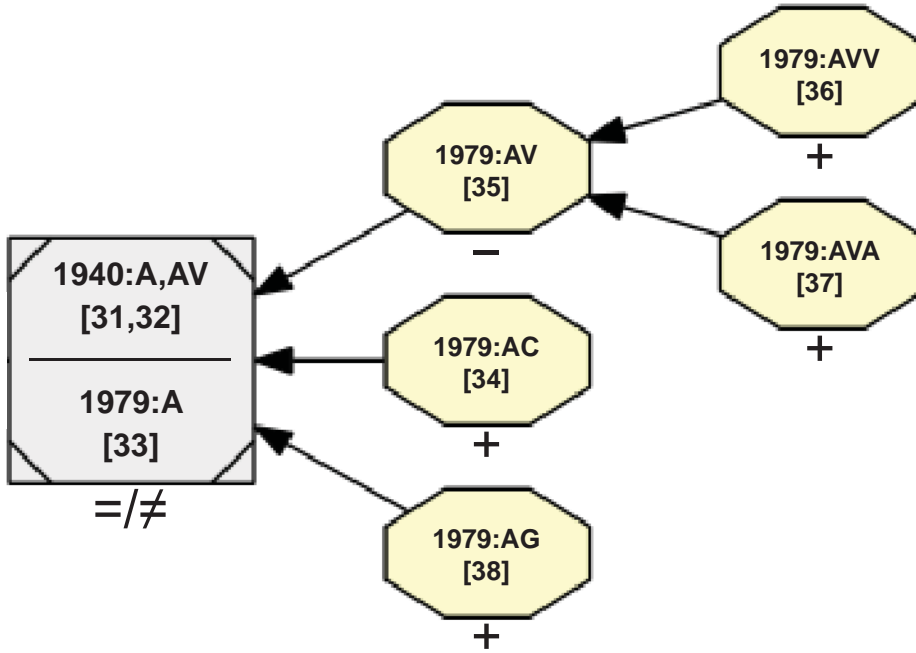


Fig. 10

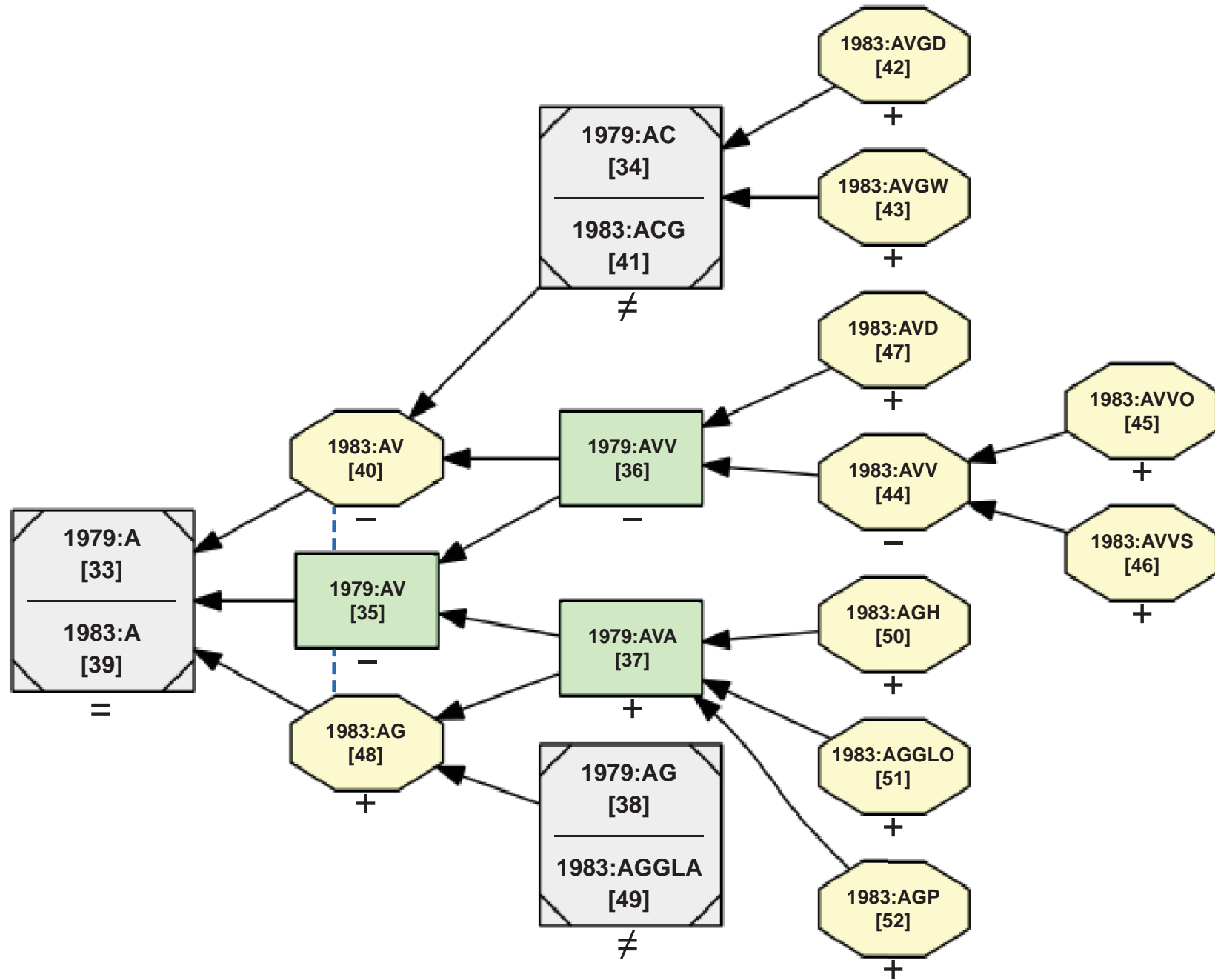


Fig. 11

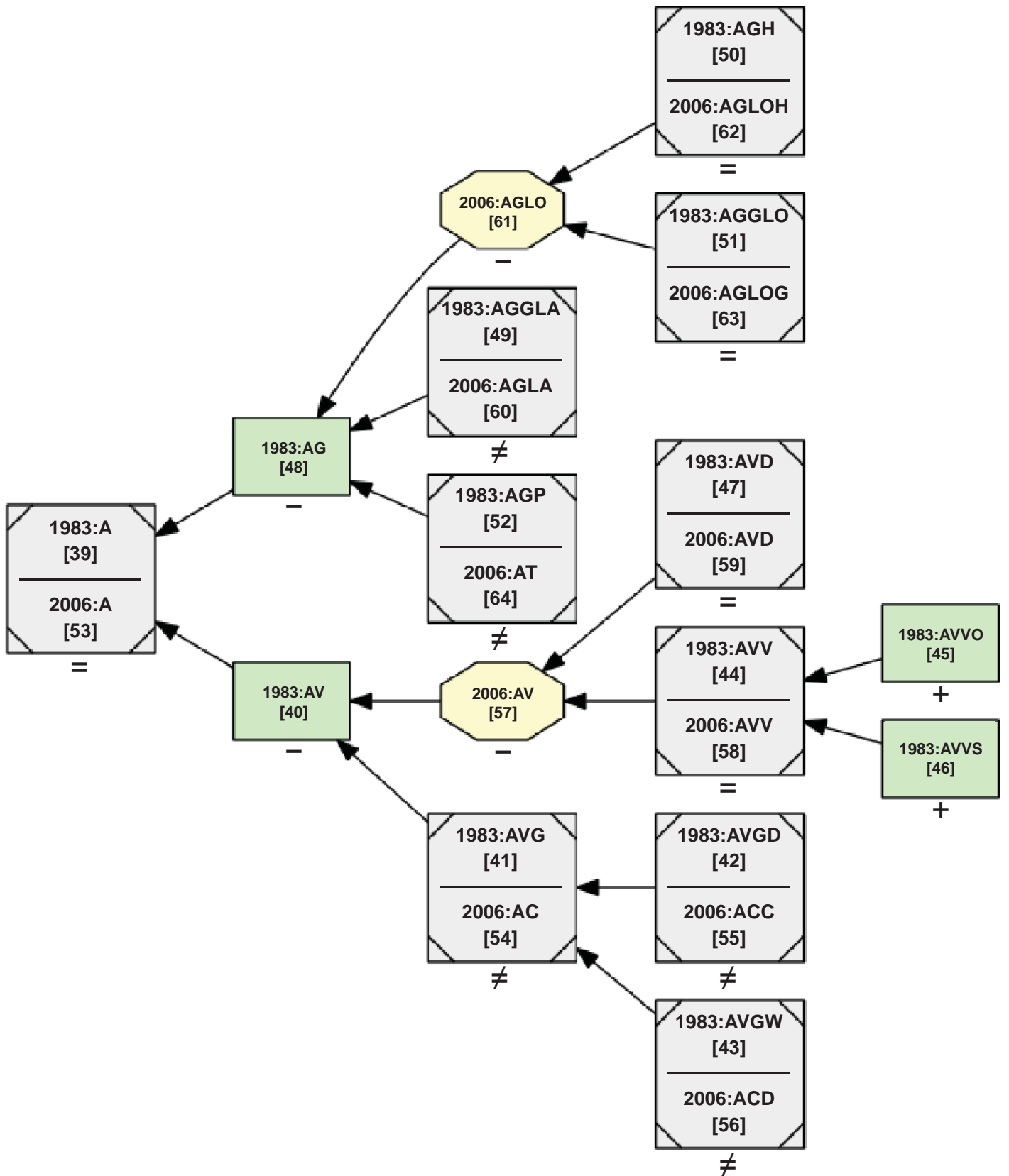


Fig. 12

