

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

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Abstract. This contribution introduces a novel, logic-based solution to the challenge of tracking the provenance of meanings across multiple biological taxonomies. The challenge arises due to limitations inherent in using type-anchored taxonomic names as identifiers of increasingly granular semantic differences being expressed in original and revised taxonomic classifications. We address the challenge through: (1) the use of taxonomic concept labels (thereby individuating name usages according to particular authors) that permit the assembly of alternative concept taxonomies; (2) sets of user-provided Region Connection Calculus articulations (RCC-5: congruence, proper inclusion, inverse proper inclusion, overlap, exclusion) among paired concepts represented in the alternative taxonomies; and (3) the use of an Answer Set Programming-based reasoning toolkit that ingests these and other taxonomic constraints to infer and visualize consistent multi-taxonomy alignments. The feasibility and utility of this approach are demonstrated with a use case involving pairwise alignments of 11 non-congruent classifications of Eastern United States grass entities variously assigned to the *Andropogon glomeratus-virginicus* 'complex' over an interval of 126 years. Derivative analyses of name/meaning identity reveal that, on average, taxonomic names are reliable identifiers of taxonomic identity for approximately 60% of the 127 merge regions obtained in 12 pairwise alignments. Name/meaning cardinality over the entire use case time interval ranges from 1/6 to 4/1, with only 1/36 names attaining the semantically ideal 1/1 ratio. We discuss the significance and scalability of the RCC-5 concept alignment approach in the context of building logically tractable solutions for identifying taxonomic provenance in biodiversity data and other Semantic Web environments.

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

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1. Introduction

This contribution introduces a novel, logic-based solution to the challenge of tracking the provenance of meanings across multiple biological taxonomies. The challenge arises due to limitations inherent in using taxonomic names as identifiers of increasingly granular semantic differences being expressed in original and revised classifications. We address the challenge through the use of *taxonomic concepts* [4,35], Region Connection Calculus (RCC-5) articulations [34,68], and an Answer Set Programming-based reasoning toolkit that infers consistent multi-taxonomy alignments [14,15]. The feasibility of this approach is demonstrated with a use case involving 11 non-congruent classifications of Eastern United States grass entities variously assigned to the *Andropogon glomeratus-virginicus* 'complex' over an interval of 126 years [35,90]. The taxonomy alignment approach is relevant specifically to the task of integrating name-based information in the biodiversity sciences [35,66,70], and more generally as a means of tracking concept provenance in the Semantic Web with RCC-5 articulations [18,23,88]. Our contribution reflects this balance by providing sufficient detail for biodiversity scientists while making connections to related research in the field of knowledge representation and reasoning [86].

2. Names as Identifiers of Taxonomic Meanings – Challenges and Solutions

Taxonomic names and nomenclatural relationships are necessary but not sufficient for integrating biodiversity data for the Semantic Web [4,35,55,69]. The reasons for this insufficiency are systemic and well known to contributors and users of such taxonomies [3,9,62,70]. Ultimately they are rooted in the way in which identity is established according to the rules of nomenclature that guide the re-/application of names to perceived groups [50,60]. Because biological classifications are (typically) meant to approximate natural, phylogenetic relationships, they are subject to adjustments whenever new evidence regarding the identity of taxonomic entities or relationships among these is brought forth by the latest systematic research [36]. For many organismal groups in the tree of life, systematists are not close to completing this process of adjustment. For instance, in the past 20 years the number of validly recognized species of primates has increased from 233 to 488 [72]. While such necessary taxonomic changes accumulate over

time, the *Codes* of nomenclature stipulate (*inter alia*) that name identity is grounded in the Principle of Typification [27,79]. This means that originally proposed and subsequently revised taxonomic groups receive the same valid name, or different names, based on the recurrently verifiable identity of individual type specimens (e.g., for taxa of the species rank) and individual type taxa (e.g., for taxa of the genus rank). According to the rules of nomenclature, types are to be designated at the respective earliest moments of baptizing names.

Typically both a type and a feature-based circumscription are provided when anchoring the meaning (referential extension) of a taxonomic name [28,34,36,92]. However, the former arbiter – i.e., the type identity – has special weight when dealing with alternative name/meaning assignments that become necessary when taxonomies undergo revisions. Another relevant, *Code*-mandated naming rule is the Principle of Priority [63], which states that in case of (again, type-centric) synonymy, the oldest available name remains the valid one. The vast majority of the 250+ year-old names of Linnaeus [74] are 'eternally validated' by this important Principle.

Application of the rules of nomenclature to changing classifications can create semantically complex networks of many-to-many relationships among valid and invalid names on one side, and circumscriptions on the other side [35,41,70]. Thus, in spite of the central role of *Code*-compliant names in interconnecting biodiversity data [65,66,74], these names have shortcomings as identifiers of granular differences between taxonomic perspectives that contributor and user communities adhere to at any given time. Sound knowledge representation in the biodiversity domain requires recognition of, and compensation for, these systemic insufficiencies [31,34,55].

Solutions to overcome the taxonomic name/meaning dissociation may take two major pathways. One option is to assemble single, comprehensive taxonomies for particular groups, with periodically updated versions [9,62,75]. This approach offers an immediate and valuable service to users. However in the longer term it often leads to multiple distinct perspectives being represented by earlier and later versions of the 'same' standard [5,36,85]. Thus in effect the unitary taxonomy turns into a temporal chain of partially incongruent taxonomies. Overlapping sets of names are reused from version to version with varying circumscriptions and no explicit tracking of taxonomic provenance [18]. In the end, unitary systems are likely to *promote* the proliferation of ambiguous name/meaning relationships.

Truly alternative – though also complementary – options to unitary classifications are being developed under the term "taxonomic concept approach". They share a convention, established in [4], to annotate taxonomic names *according to* (sec.) particular authors. An example of this convention is: *Andropogon virginicus* Linnaeus 1753 (name, name author, year) sec. Weakley 2015 (concept author, year) [90]. We refer to these combined name sec. author strings as *taxonomic concept labels*. The resolution gained by using such labels is critical – they permit the assembly of multiple alternative, internally coherent hierarchies where all concepts derived from one hierarchy can be connected via parent/child (*is_a*) relationships [35,80,83]. In a subsequent step, the hierarchies' entities can be aligned in reference to a variety of similarity indicators; including nomenclatural relationships, member composition, or diagnostic features [15,22,34,42,84].

Here we integrate concept-level annotations of alternative taxonomic perspectives with two additional workflow components: (1) user provision of an initial set of Region Connection Calculus (RCC-5) *articulations* among related concepts in each taxonomy, and (2) logical inference of additional articulations that are consistent with the input. The logically augmented sets of articulations are then translated into visualizations of merge taxonomies, also called *alignments*. The alignments resolve taxonomic identity with more granularity than possible with names and nomenclatural relationships alone, allowing human users and computers to understand and integrate information accordingly [42,81,82].

We apply the taxonomy alignment approach to the 11-classification *Andropogon glomeratus-virginicus* 'complex' use case (henceforth Andro-UC), using the novel Euler/X toolkit [13,14,15,16,17] to infer and visualize merge taxonomies. Before introducing the use case specifics, we first review the basic properties of the toolkit and draw parallels to related reasoning efforts.

3. Reasoning over Taxonomic Provenance with RCC-5 Articulations and the Euler/X Toolkit

The Euler/X toolkit is a successor of the CleanTax software [80,81,83]. The CleanTax prototype was originally built to deploy only First-Order Logic (FOL) reasoners [59]. Upgrades to Euler/X include new workflow support and analysis functions [16,17,80], and particularly the integration of Answer Set Programming (ASP) reasoners that are grounded

in Stable Model Semantics [38,39,57]. The taxonomy alignment problem is thereby modeled as a set of *constraints* (T_1, T_2, A, C), where: T_1, T_2 are the two taxonomies in need of alignment; A are the initial set of user-provided articulations; and C are additional relevant constraints (Figure 1A). Each input taxonomy (T_1, T_2) is separately represented from root to leaves through hierarchical parent/child (*is_a*) relationships that integrate the entailed concepts [83]. An example of the parent/child relationship is: *Andropogon virginicus* sec. Weakley (2015) is a parent of *Andropogon virginicus* "old-field variant" sec. Weakley (2015). The RCC-5 articulations vocabulary (A) includes five basic relationships that compare the referential extensions of taxonomic concept pairs; viz. congruence (\equiv), proper inclusion ($>$), inverse proper inclusion ($<$), overlap ($><$), and exclusion (\perp) [34,68]. For instance, *Andropogon capillipes* sec. Weakley (2015) $<$ *Andropogon capillipes* sec. Weakley (2006) expresses that the later (2015) concept has a narrower taxonomic circumscription than the earlier (2006) concept with the identical taxonomic name. Ambiguity can be asserted in RCC-5 using the disjunction "or", leading to a lattice of 32 possible articulations (R_{32}) that starts an empty set (\emptyset) at the bottom and ends with a maximally ambiguous set (\equiv or $>$ or $<$ or $><$ or \perp) at the top [42,80,81,83]. The set of constraints (C) applicable to taxonomy alignments are [83]: (1) *non-emptiness* – each concept has minimally one representing instance; (2) *sibling disjointness* – two child concepts of a parent concept are taxonomically exclusive of each other; and (3) *coverage* – parent concepts are completely circumscribed by the union of their children. For the present use case, all constraints are applied by default, but each can be relaxed globally, or locally, as appropriate [13].

The toolkit functions with relevance to the Andro-UC are as follows (Figure 1). (1) Visualization of each input taxonomy in the format of an *is_a* hierarchy, together with the set of user-provided articulations (Figure 1B). (2) Analysis of logical consistency – if the input constraints are jointly inconsistent (constraint over-specification) then no alignments are obtained. (3) Inference and representation of one or more consistent alignments, grounded in the consistent user-provided articulations and additional, logically implied articulations. Alignments are generated in two data formats: (a) as the set of *Maximally Informative Relations* (MIR [80]) which are interpretable by humans and machines, and (b) as merge taxonomy visualizations whose primary purpose is to aid human comprehension of taxonomic in-

/congruence among the input classifications and the constituent names (Figure 1C).

1A

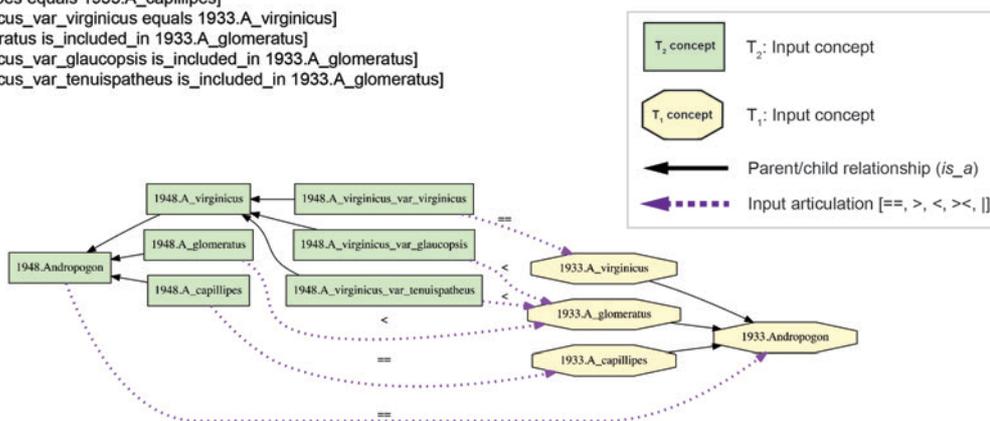
taxonomy 1948 Blomquist
 (Andropogon A_capillipes A_glomeratus A_virginicus)
 (A_virginicus A_virginicus_var_glaucopsis A_virginicus_var_tenuispatheus A_virginicus_var_virginicus)

taxonomy 1933 Small
 (Andropogon A_capillipes A_virginicus A_glomeratus)

articulation 1948-1933 Blomquist-Small
 [1948.Andropogon equals 1933.Andropogon]
 [1948.A_capillipes equals 1933.A_capillipes]
 [1948.A_virginicus_var_virginicus equals 1933.A_virginicus]
 [1948.A_glomeratus is_included_in 1933.A_glomeratus]
 [1948.A_virginicus_var_glaucopsis is_included_in 1933.A_glomeratus]
 [1948.A_virginicus_var_tenuispatheus is_included_in 1933.A_glomeratus]

1B

Nodes	
1933	4
1948	7
Edges	
isa_1933	3
isa_1948	6
Art.	6



1C

Nodes	
1933	1
1948	4
comb	3
Edges	
overlaps	1
input	9

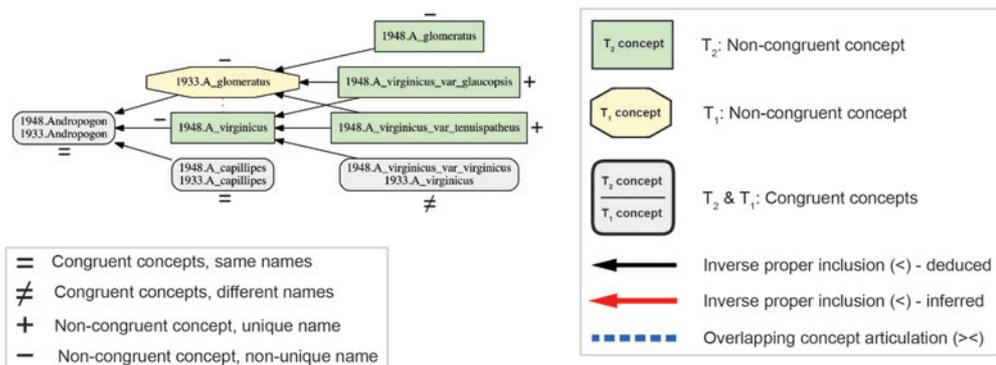


Fig. 1. Overview of taxonomy alignment input/output information for processing by the Euler/X toolkit, using the example of the Blomquist (1948) / Small (1933) alignment. (A) Input data format, showing the two input taxonomies and set of six user-provided input articulations (see also Appendix 1). (B) Input visualization (command: `--iv`), with legend (left) providing information on numbers of input concepts per taxonomy, *is_a* relationships, and RCC-5 articulations. (C) Merge taxonomy visualization (command: `-e mnpw --rcgo`), with legend (left) providing information on non-/congruent concepts and properly including/overlapping edges. Visualization conventions, including annotations of name/meaning identity (\equiv , \neq , $+$, $-$), are reused in Figures 4–6.

Additional toolkit functions include logic-based diagnosis and repair options in the case of inconsistent input, and visualizations of multiple alignments as aggregate and cluster views in the case of constraint under-specification [14,15]. The latter visualizations can inform interactive decision tree routines where the user is repeatedly prompted to resolve ambiguous

(disjunct) articulations, thereby reducing the number of possible word merges. Both sets of functions are intended to aid the user in achieving consistent, well-specified alignments. However, neither set of functions is needed to properly align the Andro-UC input, which already satisfies the criteria of consistency and sufficiency. We refer readers to other contributions

where these issues are discussed in more detail [16,17,32,33].

4. Relationship of the RCC-5 Concept Alignment Approach to Other Methods

To our knowledge, the specific combination of inferring consistent alignments of multiple biologically delimited taxonomies with RCC-5 articulations using Answer Set Programming reasoners has no immediate precedent in the Semantic Web domain. The logic foundations for this particular approach were developed in [15,42,83]. Whereas the modeling of an input taxonomy as an *is_a* hierarchy is well established [36,62,86], the remaining elements of the Euler/X toolkit appear to diverge from other frequently applied methods for matching ontologies or reasoning over concept provenance [18,21,23,51,76,86,88,93]. The use of RCC-5 articulations is arguably the most significant difference, and reflects the preference of domain scientists for expressing and inferring concept non-/congruence in reference to these spatial relationships [33,35,90]. In particular, biodiversity scientists are often faced with use cases where sets of taxonomic records or entities can either be relevant merged, or not, for information ingestion into subsequent analyses. This requirement, together with the notion that taxonomic boundaries are natural and empirically accessible [36], may selectively favor the deployment of RCC-5 over alternatives that utilize information from ontology classes and relationships to infer similarity ratios or percent matches among individual concepts and concept hierarchies [88]. The latter are highly appropriate for expressing "how semantically close?" two concept usages are. However, for the biodiversity scientist this begs an additional question [34]: "are the (minor) differences relevant enough to permit merging, or not?" In this context, RCC-5 provides direct, actionable, set theory-based information for resolving multi-taxonomy integration. The specific representation needs for biological taxonomies and derivations of FOL constraints are further discussed in [83].

The adherence to RCC-5 means that ambiguities in alignments are modeled through disjoint articulations, which may be present in the input articulations, output MIR, or both [32]. Disjoint articulations of the R_{32} lattice such as $A ==$ or $> B$ are readily modeled in ASP (or via RCC reasoners) but are more difficult to represent in OWL-DL. In particular, the ASP reasoners of the Euler/X toolkit [24,38] represent the RCC-5 input articulations using only the set operations of

union and subset relation, by subdividing the input concepts into polynomially many subconcepts or Euler regions [68]. The ASP reasoning process yields the subset relations of all subconcepts and reassembles these to constitute the input concepts and infer their respective RCC-5 relations, as further described in [13].

Parallel efforts to derive taxonomic concept provenance from textual descriptions through combinations of Natural Language Processing methods and phenotype ontologies are introduced in [22]. Other taxonomically focused query or integration applications for the Semantic Web that do not utilize RCC-5 include [9,12,62,69,84]. The extent to which the RCC-5 concept alignment approach is relevant to other provenance representation challenges in the Semantic Web remains underexplored.

5. Input and Alignment Conditions for the *Andropogon* Use Case

What motivates our choice of the *Andropogon* use case? The Andro-UC has been selected to demonstrate the feasibility and utility of the taxonomy alignment approach for several reasons. First among these is the availability of preexisting concept circumscriptions and articulations provided by one of the authors, Alan S. Weakley, who is an expert on the Flora of the Southern and Mid-Atlantic States [89,90]. An earlier version of the use case was published in [35] and included eight classifications ranging from 1889 to 2005. Three recent classifications are herein added to the Andro-UC, which now totals 11 classifications. The use case is furthermore suitable because it illustrates the extent to which names and meanings may dissociate over time as Code-compliant names are applied to variously incongruent classifications. The implications for integrating name- versus concept-annotated biodiversity data are thereby made clear. With only 100 concepts, the Andro-UC is relatively small. Its outer taxonomic boundaries are well defined and remain stable throughout the 126-year time interval. These properties allow us to present the corresponding alignment visualizations in their entirety and within the confines of this contribution. Additional comments on the general relevance of this use case and the applicability of our approach to other concept alignment challenges are offered in the Discussion.

5.1. Taxonomic particulars

The history of the Andro-UC is reviewed in [35,89,90]. The input classifications (T₁₋₁₁) are each reproduced according to the source publications (Figure 2). All input articulations were provided by the expert taxonomist in tabular format (Figure 3), which

readily facilitates translation in to RCC-5 relations. Strictly speaking, the Andro-UC concerns the "*A. virginicus-A. glomeratus* complex" as circumscribed in [90]. The use case is therefore much narrower in scope than the entire genus concept *Andropogon* sec. Clayton *et al.* (2013) [19], which includes more than 100 species (concepts) worldwide.

2	1	13	17	24	31	33
	sec. Hackel (1889)	sec. Small (1933)	sec. Blomquist (1948)	sec. Hitchcock & C. (1950)	sec. RAD (1968)	sec. Godfrey & W. (1979)
	<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> 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>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>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>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. 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. 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. 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. macrourus</i> var. <i>genuinus</i> 12	<i>A. glomeratus</i>	<i>A. virginicus</i> var. <i>tenuispatheus</i> 22	<i>A. glomeratus</i>	<i>A. virginicus</i>	<i>A. virginicus</i> var. <i>abbreviatus</i>

39	53	67	79	89
sec. Campbell (1983)	sec. Campbell (2003)	sec. Weakley (2006)	sec. BONAP (2014)	sec. Weakley (2015)
<i>A. virginicus</i> var. <i>glaucus</i> "drylands variant" 42	<i>A. virginicus</i> var. <i>glaucus</i> "drylands variant" 56	<i>A. capillipes</i> "drylands variant" 69	<i>A. capillipes</i> 80	<i>A. capillipes</i> 90
<i>A. virginicus</i> var. <i>glaucus</i> "wetlands variant" 43	<i>A. virginicus</i> var. <i>glaucus</i> "wetlands variant" 57	<i>A. capillipes</i> "wetlands variant" 70	<i>A. capillipes</i>	<i>A. dealbatus</i> 91
<i>A. virginicus</i> var. <i>virginicus</i> "old-field variant" 45	<i>A. virginicus</i> var. <i>virginicus</i> "old-field variant" 59	<i>A. virginicus</i> var. <i>virginicus</i> 72	<i>A. virginicus</i> var. <i>virginicus</i> 82	<i>A. virginicus</i> "old-field variant" 93
<i>A. virginicus</i> var. <i>virginicus</i> "smooth variant" 46	<i>A. virginicus</i> var. <i>virginicus</i> "smooth variant" 60	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i> var. <i>virginicus</i>	<i>A. virginicus</i> "smooth variant" 94
<i>A. virginicus</i> var. <i>virginicus</i> "deceptive variant" 47	<i>A. virginicus</i> var. <i>decipiens</i> 61	<i>A. virginicus</i> var. <i>decipiens</i> 73	<i>A. virginicus</i> var. <i>decipiens</i> 83	<i>A. virginicus</i> var. <i>decipiens</i> 95
<i>A. glomeratus</i> var. <i>glaucopsis</i> 49	<i>A. glomeratus</i> var. <i>glaucopsis</i> 63	<i>A. glaucopsis</i> 74	<i>A. glaucopsis</i> 84	<i>A. glaucopsis</i> 96
<i>A. glomeratus</i> var. <i>hirsutior</i> 50	<i>A. glomeratus</i> var. <i>hirsutior</i> 64	<i>A. glomeratus</i> var. <i>hirsutior</i> 76	<i>A. hirsutior</i> 85	<i>A. hirsutior</i> 97
<i>A. glomeratus</i> var. <i>glomeratus</i> 51	<i>A. glomeratus</i> var. <i>glomeratus</i> 65	<i>A. glomeratus</i> var. <i>glomeratus</i> 77	<i>A. glomeratus</i> var. <i>glomeratus</i> 87	<i>A. glomeratus</i> var. <i>glomeratus</i> 99
<i>A. glomeratus</i> var. <i>pumilus</i> 52	<i>A. glomeratus</i> var. <i>pumilus</i> 66	<i>A. tenuispatheus</i> 78	<i>A. glomeratus</i> var. <i>pumilus</i> 88	<i>A. tenuispatheus</i> 100

Fig. 2. Tabular representation and alignment of names and concepts for the 11 succeeding classifications of the Andro-UC, as provided by the expert user Weakley [35, 89,90]. Columns represent classifications whereas rows contain information on taxonomic name and concept identity. Cell shadings indicate congruent concept lineages. Consecutive concept numbers (1-100) are reused in Figure 3 for the purpose of comparison. See text for further details.

The respective classifications of the Andro-UC include, in chronological sequence (Figures 2 and 3): Hackel (1889) [48], Small (1933) [77], Blomquist (1948) [6], Hitchcock & Chase (1950) [49], Radford

et al. (1968) [67], herein abbreviated as "RAD (1968)", Godfrey & Wooten (1979) [44], Campbell (1983) [10], Campbell (2003) [11], Weakley (2006)

[89], Kartesz (2014) [53], herein referred to as "BONAP (2014)", and Weakley (2015) [90]. The tabular input alignment shown in Figure 3 encodes taxonomic congruence as a function of occupying the same row position and width. For instance, *A. capillipes* var. *capillipes* sec. Weakley (2015) (concept 90) \equiv *A. virginicus* var. *glaucus* subvar. *glaucus* sec. Hackel (1889) (concept 4). The exact articulation between paired concepts pertaining to different classifications can be 'read off' the table by tracing their

cell positions and vertical extensions – encoded with unique shadings – across the respective columns. The consistent column depth across the 11 classifications indicates that the taxonomic boundaries of the complex are congruent throughout. All taxonomic incongruences of the Andro-UC are restricted to differential subdivisions of entities recognized by various sources *within* jointly agreed-upon outer taxonomic confines.

3

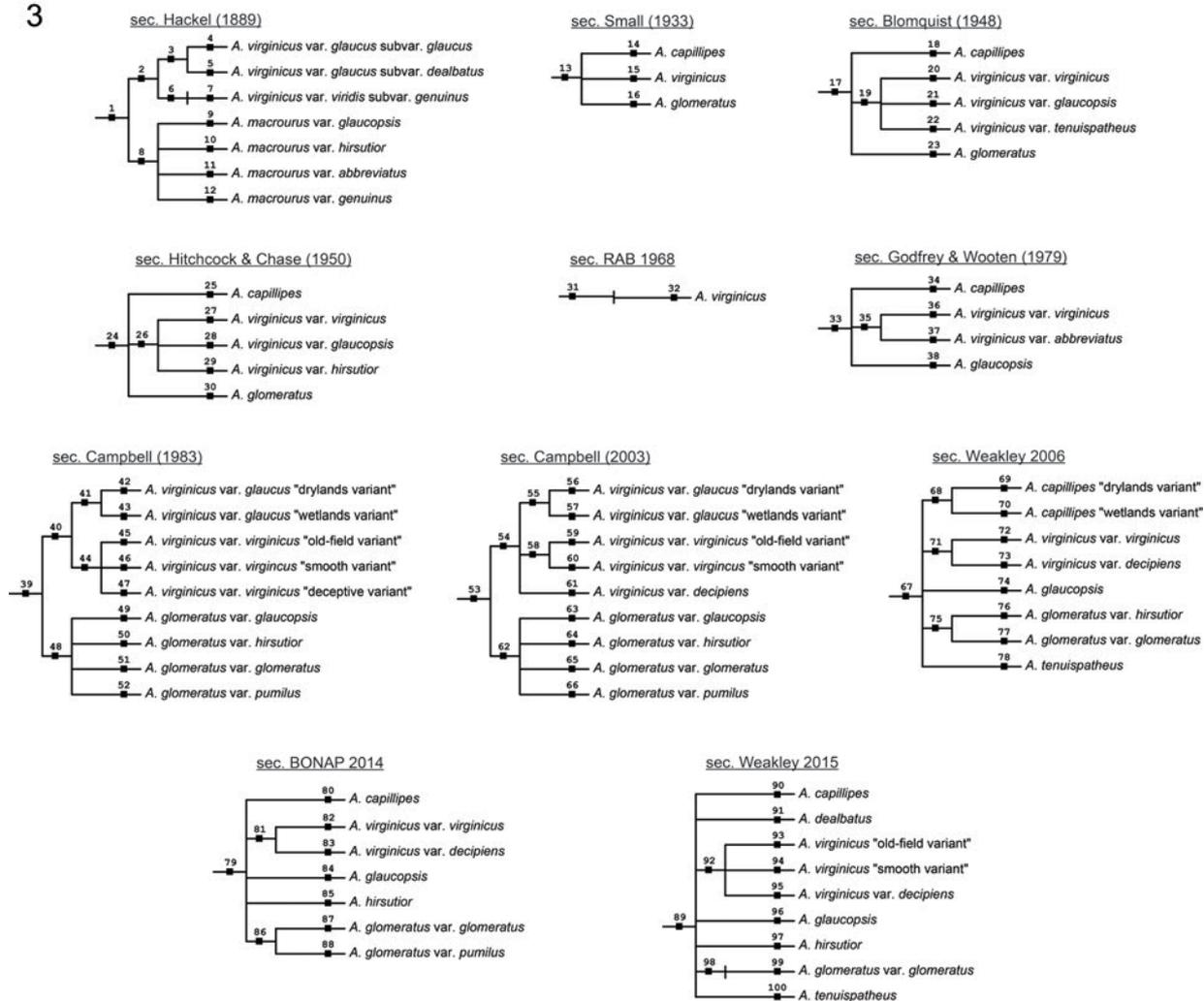


Fig. 3. Hierarchical, multi-level representations of the 11 input classifications of the Andro-UC (see also Appendix 1). Taxonomic name and concept identities (numbered from 1-100) as in Figure 2.

Another aspect of the input needing clarification is the representation of higher-ranked entities (compare Figures 2 and 3). These entities are not explicitly depicted in Figure 2 because the alignment table provi-

ded by Weakley emphasizes congruence among the narrowest taxonomic units of each classification. However, the higher-level entities are unambiguously implied by the nomenclatural conventions that guide

the source taxonomies, and are typically made explicit therein. For instance, the acceptance of two variety-level concepts *A. glomeratus* var. *hirsutior* sec. Weakley (2006) (concept 76) and *A. glomeratus* var. *glomeratus* sec. Weakley (2006) (concept 77) (Figure 2) also indicates the recognition of the species-level concept *A. glomeratus* sec. Weakley (2006) (concept 75) (Figure 3).

Here we opt to fully represent these implied higher-level taxonomic concepts to yield more comprehensive alignments containing up to four ranked levels (Figure 3). Where necessary we have added nominal (type-representing) taxonomic names and concepts to obtain comparable entities at each rank; e.g., *Andropogon virginicus* var. *viridis* sec. Hackel (1889) was added (concept 6) and is comparable to *Andropogon virginicus* var. *glaucus* sec. Hackel (1889) (concept 3) of the same rank and source classification.

5.2. Input configuration, workflow execution, and reproducibility

The Euler/X toolkit is open source and available at [14]. The software can be cloned on-line and then deployed on the desktop using the command-line interface. An overview of the toolkit's reasoning and visualization options is available through the command `euler --help`. Additional software dependencies include Python 2.X (toolkit coding language), the Answer Set Programming reasoners DLV [24] and Potassco (Gringo and claspD) [38], and the GraphViz software [37] for visualizing the input and output (merge) taxonomies (Figure 1). Additional detail regarding the creation, processing, and visualization of taxonomy alignments with the Euler/X toolkit is provided in [15,32,33].

The input conventions for labeling concepts and representing parent/child (*is_a*) relationships and articulations are in accordance with [31,32,33,34]. They are exemplified in Figure 1A for the 1948/1933 alignment. At present the Euler/X toolkit is limited to inferring pairwise taxonomy alignments. Hence we analyze and show alignment outcomes for the following ten linearly succeeding input configurations (Figures 4-6): 1933/1889 (Figure 4A), 1948/1933 (Figure 4B), 1950/1948 (Figure 4C), 1968/1950 (Figure 4D), 1979/1968 (Figure 4E), 1983/1979 (Figure 5B), 2003/1983 (Figure 5C), 2006/2003 (Figure 5D), 2014/2006 (Figure 6A), and 2015/2014 (Figure 6B). This chronological sequence is supplemented with two additional alignments; i.e., 1979/1950 (Figure 5A), which 'overcomes the resolution gap' generated

by the intermediate, coarse RAB (1968) classification that contains only one species-level concept (Figure 3); and 2015/1889 (Figure 6C), which represents the largest possible time interval between two taxonomies in the Andro-UC.

In configuring the 12 pairwise alignments we consistently represent the later (younger) taxonomy as T_2 and the earlier (older) taxonomy as T_1 [32]. This means that in all input and output visualizations (Figures 1, 4-6), concepts unique to T_2 are illustrated as green rectangles, whereas concepts unique to T_1 are shown as yellow octagons. Merge regions with multiple congruent concepts are rendered as grey rectangles with rounded corners (Figure 1C). We also follow the T_2/T_1 annotation sequence when specifying input articulations and output MIR. Lastly, we use the shorthand of [33] for taxonomic concept labels, where (e.g.) *Andropogon virginicus* var. *decipiens* sec. Weakley (2015) (concept 95) becomes "2015.A_virginicus_var_decipiens". The 12 input files (.txt format) for the Andro-UC are provided in Appendix 1.

All alignments were obtained using the command `"euler -i [input file name] -e mnpw --rcgo"` [13,14,15]. The `"-e mnpw"` stands for polynomial encoding (mn) of the input conditions for ASP reasoning, producing an output that includes all possible worlds (pw). The appended `"--rcgo"` produces reduced containment graphs (rcg), showing overlapping articulations (o). The command generates: (1) the input visualization (Figure 1A); (2) the set or output MIR that constitute the alignment (output in .csv format); and (3) visualizations (merge taxonomies) of the latter as GraphViz products (output in .pdf format).

The sets of Maximally Informative Relations (MIR) for each of the 12 alignments are provided in Appendix 2. In addition, and to ensure complete reproducibility, we have prepared the Andro-UC workflow as performed with the Euler/X toolkit as an experiment for reproduction at <http://recomputation.org/> [40]. This approach ensures full transparency and permanent accessibility of our data, tools, analyses, and products.

6. Analyses of Name/Meaning Dissociation

Analyses of taxonomic name/meaning identity are central to this contribution. In analyzing the performance of names as identifiers of taxonomic meanings in the Andro-UC, we provide three complementary groups of results [33,35,41]. First, we add simple

annotations to the visualized merge regions and taxonomies (Figures 1C, 4-6), as follows. (1) For regions of taxonomically congruent concepts (\equiv ; grey, rounded rectangles), we add either the symbol "=" or " \neq " to express that the corresponding taxonomic names (strings) are identical ($=$), or not (\neq). (2) For unique, non-congruent regions (*not* \equiv ; green rectangles, yellow octagons), we supply a "+" if the corresponding taxonomic names are *also unique* within the particular alignment, or a "-" if the names occur *elsewhere* (redundantly) in the alignment and thus have multiple incongruent meanings. Accordingly, an abundance of "=" and "+" symbols in the merge visualization would indicate that shared names denote congruent concepts whereas unique names denote concepts particular to only one classification. Both types of symbols ($=$, $+$) may be viewed as indicators of names performing reliably as identifiers of concepts. We refer to these as "reliable names". On the other hand, increasing occurrences of " \neq " and "-" symbols are indicative of "unreliable names", where nomenclatural stability or change are dissociated from taxonomic congruence or incongruence. We record the frequency of each symbol across the 12 alignments to obtain totals and percentages of nomenclatural and taxonomic identity, and of reliable/unreliable name ratios, as summarized in Table 1. The top-level concept (root) of the complex (sec. *auctorum*) was excluded from the counts and ratios because of its underspecified nomenclatural identity across treatments.

Second, we sort and analyze the output MIR of the 12 alignments (Appendix 2) to compute simple name/meaning relation analyses for the Andro-UC (Tables 2 and 3). For each alignment, we record the numbers of input concepts (T_2, T_1), input articulations (A), and MIR partitioned according to each of the RCC-5 articulations (Table 2). Again, MIR that articulate the root (complex) concepts are excluded from the counts. The quotient of (1) the number of congruent articulations (\equiv) in the merge and (2) the number of input concepts in the concept-poorer taxonomy – either T_2 or T_1 – provides an approximation of the relative congruence between two taxonomies [33]. If the ratio approaches 100% then the relative congruence is high, possibly in spite of differences in name usage. We furthermore resolve name/meaning identity of articulated concept pairs, based on the following ten combinatorial categories (Table 3): (1) two articulated concepts in T_2 and T_1 are either taxonomically congruent (\equiv) or not ($>$, $<$, $><$, $|$) [five options]; and (2) their corresponding names are either identical ($=$)

or not (\neq) [two options]. As before, we regard both the $\equiv / =$ and the $[>, <, ><, |] / \neq$ combinations as instances of reliable names [R], because either identical names denote congruence or non-identical names denote incongruence. In contrast, the remaining combinations – either \equiv / \neq or $[>, <, ><, |] / =$ – represent unreliable names [UR].

Third, we reinterpret the Weakley's input alignment as provided in Figure 2 to assess the performance of names as concept identifiers over the entire 1889-2015 time interval of the Andro-UC (i.e., not limited to pairwise comparisons). We adopt Remsen's [70] notion of *cardinality* to address two questions. First, how many usages and meanings are associated with each of the 36 unique taxonomic names (Table 4)? For instance, a name/meaning cardinality of 1/3 would indicate that an identical name was used at least in three classifications and associated with three reciprocally incongruent meanings. Second, how many (non-identical) names are associated with each of the 21 congruent sets (or lineages) of taxonomic meanings (Table 5)? For instance, a name/meaning cardinality of 3/1 would indicate that three non-identical names have been used to identify meanings across classifications that are taxonomically congruent. For the purpose of naming these apparent congruent sets, we select the most recent (youngest) taxonomic concept label that anchors an instance of the congruent meanings chain extending to concepts in one or more preceding classifications. An example is 2014.A.*capillipes* (youngest concept label, used to identify the entire congruent chain) \equiv 1889.A.*virginicus_var_glaucus* (oldest concept label used for an entity in the chain).

In addition to showing differences in name/meaning cardinality, Tables 4 and 5 also indicate whether certain names or concepts appear only once or more frequently in the Andro-UC, and whether their occurrences are continuous or interrupted (presence-absence-presence) along the 1889-2015 chain of classifications.

7. Results

7.1. Extent and origins of taxonomic incongruence

Due to the high precision of the input articulations (Figure 2; see also Appendix 1), each of the 12 input configurations yield a single, unambiguously articulated merge taxonomy (Figures 4-6). The 12 visualizations intuitively communicate that none of the alignments are entirely congruent, instead showing 2-

12 unique regions (compare Figures 5B and 5C) and an overall ratio of 56 congruent to 71 non-congruent regions (Table 1). While we cannot examine every

alignment of the Andro-UC in fine detail, we highlight phenomena that exemplify the extent and causes of taxonomic incongruence in this use case.

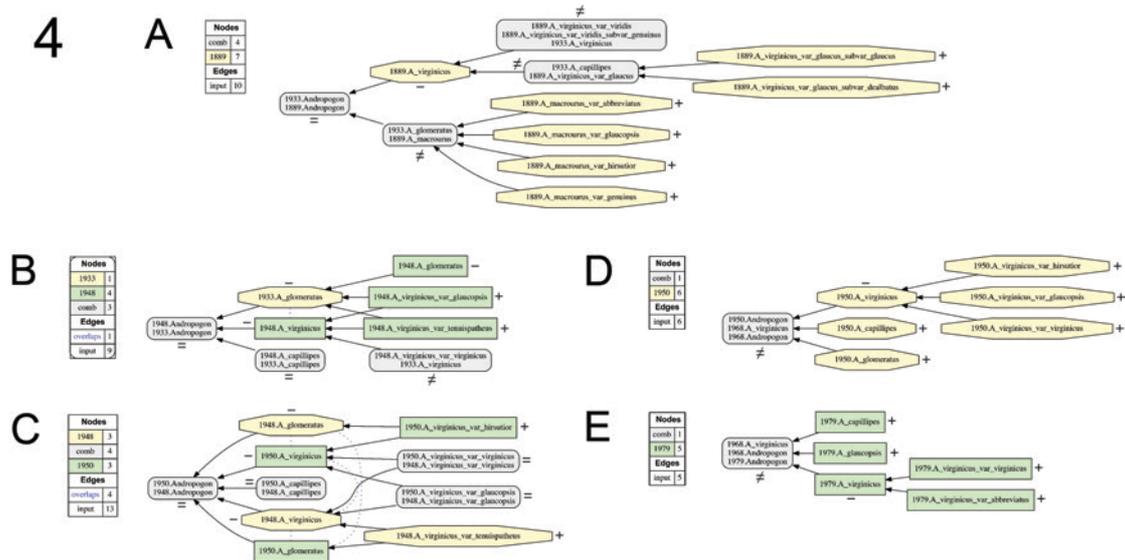


Fig. 4. Merge taxonomy visualizations for alignments 1-5 of the Andro-UC, 1889-1979. Representation conventions and annotations as in Figure 1C. (A) Small (1933) / Hackel 1889 alignment; (B) Blomquist (1948) / Small (1933) alignment; (C) Hitchcock & Chase (1950) / Blomquist (1948) alignment; (D) RAB (1968) / Hitchcock & Chase (1950) alignment; (E) Godfrey & Wooten (1979) / RAB (1968).

One cause for the apparent incongruence is unequal granularity or taxonomic concept resolution across the alignments. For instance, at the lowest taxonomic level, classifications authored from 1933 to 1979 recognize 1-5 concepts, whereas taxonomies published outside of this interval accept 7-9 concepts (Figures 2 and 3). Differences in granularity have the outcome that the more finely resolving taxonomy has one or more non-congruent (properly included) low-level concepts in comparison to its counterpart (e.g., Figures 4A and 5B). In the Andro-UC, this means that alignments of *any* alternative taxonomy to that of the most coarse-grained RAB (1968) system are necessarily only congruent with regards to the root-level concepts (Figures 4D and 4E), given that RAB (1968) recognize no taxonomic subdivisions within the complex. Indeed, when placed in the context of its immediate predecessor and successor (Figures 2, 4D, 4E, and 5A), the 1968 classification appears disruptive because the chain of taxonomic provenance between Hitchcock & Chase (1950) and Godfrey & Wooten (1979) is not replicated in RAB (1968).

In contrast, taxonomies produced in 1983 or later show relatively higher levels of congruence among the finest-degree concepts (Figures 5C, 5D, and 6).

Another way of scrutinizing this pattern is to say that, by and large, taxonomists publishing in the past 30 years have adopted Campbell's (1983) perspective on how finely one should differentiate entities within the complex. Incongruences among these 1983-2015 perspectives are mainly rooted in the authors' disagreements on how to name the finely resolved entities and integrate them into higher-level entities. Interestingly, Hackel's (1889) system already recognized seven low-level entities, and in that sense it is more congruent with contemporary perspectives (Figure 6C) than taxonomies published in the more taxonomically coarse-grained 1933-1979 interval.

In addition to unequal granularity, five of the 12 alignments show overlapping (><) articulations, most frequently involving species-level concepts. These articulations are challenging to represent without recourse to RCC-5 because they fracture the pattern of inverse/proper concept inclusion from tip- to root-level concepts [32,34,35]. An interesting case of overlap is the alignment of the 1950/1948 taxonomies (Figure 5C). Both Hitchcock & Chase (1950) and Blomquist (1948) recognize three identically named species-level concepts within in the complex, of which one is also taxonomically congruent

(1950.A_capillipes == 1948.A_capillipes). However, the authors' other two species-level concepts have four reciprocally overlapping articulations. Of particular note, due in part to its simplicity, is the articulation 1950.A_glomeratus >> 1948.A_glomeratus. Figure 2 illustrates that the overlap of these two concepts creates three merge regions: (1) the region congruent with 1950.A_virginicus_var_hirsutior, (2) the region

congruent with 1948.A_virginicus_var tenuispatheus, and (3) the region that actually constitutes the overlap. The latter region is not specifically recognized in either 1950/1948 input classification and therefore has no unique name assigned to it. Other authors, including Hackel (1889), have recognized and named the region (e.g., 1889.A_macrourus_var_abbreviatus; see Figure 2).

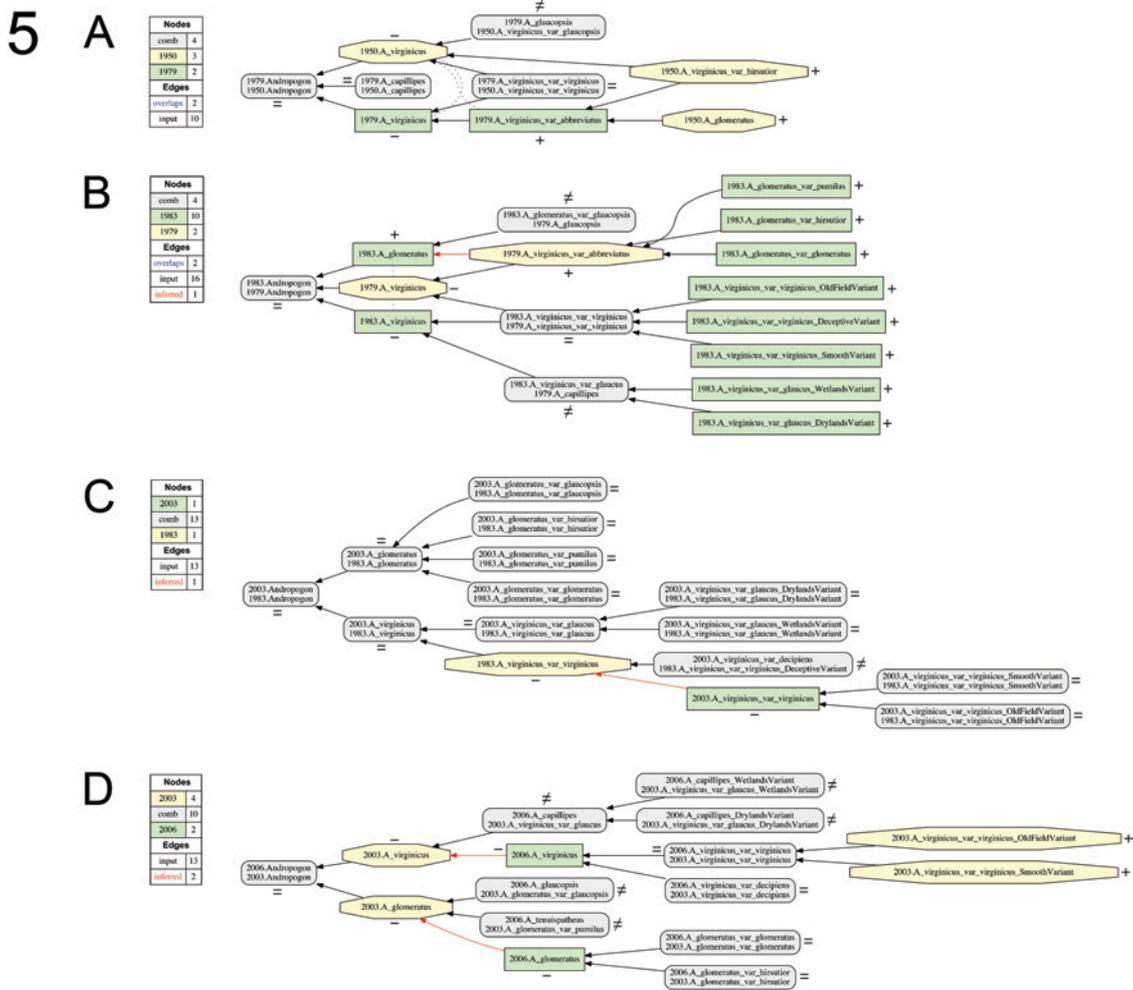


Fig. 5. Merge taxonomy visualizations for alignments 6-9 of the Andro-UC, 1950-2006. Representation conventions and annotations as in Figure 1C. (A) Godfrey & Wooten (1979) / Hitchcock & Chase (1950); (B) Campbell (1983) / Godfrey & Wooten (1979); (C) Campbell (2003) / Campbell (1983); (D) Weakley (2006) / Campbell (2003).

Generalizing the analysis of the 1950/1948 alignment, we observe that the overlap of two (or more) concepts may create *merge concept regions* for which there are no unique identities and names present in the respective input taxonomies. Nevertheless, reference to these merge regions is required to express the extent to which the concepts can be aligned with each

other. The Euler/X toolkit command `-e mncb` uniquely labels these merge concept regions, as described in detail in [32].

The aforementioned instances of differential resolution and overlapping concepts within the Andro-UC result in pairwise alignments with 5-15 merge regions (Table 1). Taking all 12 alignments in conjunction,

Table 1. Summary of taxonomic and nomenclatural identities of Euler regions across 12 merge visualizations for the Andro-UC (see Figures 4-6). Columns for each alignment show the number of merge regions (excluding the congruent parent region), ratio of congruent (==) versus (not ==) unique regions, percentage of congruent regions (% ==), ratio of identical (=) versus different (≠) names occupying the congruent regions (= / ≠), ratio of unique (+) versus non-unique (-) names occupying unique regions (+ / -), and ratio and percentage of reliable versus unreliable names (see text for explanation). Totals are percentages are provided for the cumulative values across all alignments.

Alignment	T ₂ / T ₁	Figure	Regions ¹	== / not ==	% ==	= / ≠	+ / -	Reliable / not	% Reliable
1	1933 / 1889	4A	10	3 / 7	30.0%	0 / 3	6 / 1	6 / 4	60.0%
2	1948 / 1993	4B	7	2 / 5	28.6%	1 / 1	2 / 3	3 / 4	42.9%
3	1950 / 1948	4C	9	3 / 6	33.3%	3 / 0	2 / 4	5 / 4	55.6%
4	1968 / 1950	4D	6	0 / 6	0.0%	0 / 0	5 / 1	5 / 1	83.3%
5	1979 / 1968	4E	5	0 / 5	0.0%	0 / 0	4 / 1	4 / 1	80.0%
6	1979 / 1950	5A	8	3 / 5	37.5%	2 / 1	3 / 2	5 / 3	62.5%
7	1983 / 1979	5B	15	3 / 12	20.0%	1 / 2	10 / 2	11 / 4	73.3%
8	2003 / 1983	5C	14	12 / 2	85.7%	11 / 1	0 / 2	11 / 3	78.6%
9	2006 / 2003	5D	15	9 / 6	60.0%	4 / 5	2 / 4	6 / 9	40.0%
10	2014 / 2006	6A	12	8 / 4	66.7%	6 / 2	2 / 2	8 / 4	66.7%
11	2015 / 2014	6B	13	6 / 7	46.2%	4 / 2	4 / 3	8 / 5	61.5%
12	2015 / 1889	6C	13	7 / 6	53.8%	0 / 7	5 / 1	5 / 8	38.5%
Totals	–	–	127	56 / 71	44.1%	32 / 24	45 / 26	77 / 50	60.6%

¹ Number of merge regions excludes the root/parent region ("*Andropogon*" sec. auctorum) whose name is held constant throughout.

Table 2. Summary of numbers of input concepts (T₂/T₁) and input articulations (A) for the 12 alignments of the Andro-UC, and of the Maximally Informative Relations (MIR) – totals and numbers of each type of RCC-5 articulation. Legend: Rel. == signifies relative congruence, i.e. the ratio of the number of == articulations in the merge divided by the number of input concepts in the concept-poorer taxonomy (either T₂ or T₁). Total for the relative congruence column shows the average percentage.

Alignment	Concepts T ₂	Concepts T ₁	Articulations	MIR ¹	==	>	<	>>		Rel. ==
1	4	12	8	33 (48)	4	6	2	0	21	100%
2	7	4	6	18 (28)	2	1	3	1	11	50.0%
3	7	7	7	36 (49)	3	3	3	4	23	42.9%
4	2	7	1	6 (14)	0	6	0	0	0	0.0%
5	7	2	1	5 (12)	0	0	5	0	0	0.0%
6	6	7	6	30 (42)	3	5	2	2	18	50.0%
7	14	6	10	65 (84)	3	4	15	2	41	50.0%
8	14	14	10	169 (196)	12	15	17	0	125	85.7%
9	12	14	10	143 (168)	9	10	13	0	111	75.0%
10	10	12	9	99 (120)	8	6	4	1	80	80.0%
11	12	10	10	99 (120)	7	2	10	0	80	70.0%
12	12	12	10	121 (144)	9	0	19	0	93	75.0%
Totals	106	107	88	824 (1025)	60	58	93	10	603	56.6%

¹ Number in parentheses includes all MIR that articulate the root/parent region ("*Andropogon*" sec. auctorum) which are otherwise excluded from the counts.

7.2. Quantification of name/meaning dissociation

Taxonomic names are reliable identifiers of taxonomic in-/congruence for 60.6% of 127 merge regions present in the 12 pairwise alignments of the Andro-UC (range: 38.5-83.3%) (Table 1). The highest reliability ratios are obtained for the 1968/1950 and 1979/1968 alignments which, not incidentally, include no congruent merge regions. Also not unexpected is the low (38.5%) reliable/unreliable names ratio for the 2015/1889 alignment (Figure 6C). In particular, 0/7 congruent concept regions of the 126

year-spanning alignment have reliable names; i.e., each of these regions is labeled by two non-identical names. However, taxonomic names in the Andro-UC do not necessarily perform better over short time intervals, or in alignments whose input taxonomies are closer to the present (2015). One example is the 2006/2003 alignment (Figure 5D), which has an undesirable 6/9 ratio (40.0%) of reliable/unreliable names.

Utilizing the 824 output MIR facilitates finer assessments of name/meaning dissociation (Table 3). Accordingly, among all 60 instances of pairwise taxonomic concept congruence (==) represented in the

Table 4. Continued.

#	Taxonomic name	1889	1933	1948	1950	1968	1979	1983	2003	2006	2014	2015	Usages	Meanings
15	<i>A. virginicus</i> var. <i>glaucus</i> "drylands variant"							1	1				2	1
16	<i>A. virginicus</i> var. <i>glaucus</i> "wetlands variant"							1	1				2	1
17	<i>A. virginicus</i> var. <i>virginicus</i> "old-field variant"							1	1				2	1
18	<i>A. virginicus</i> var. <i>virginicus</i> "smooth variant"							1	1				2	1
19	<i>A. capillipes</i> "drylands variant"									1			1	1
20	<i>A. capillipes</i> "wetlands variant"									1			1	1
21	<i>A. dealbatus</i>											1	1	1
22	<i>A. macrourus</i>	1											1	1
23	<i>A. macrourus</i> var. <i>abbreviatus</i>	1											1	1
24	<i>A. macrourus</i> var. <i>genuinus</i>	1											1	1
25	<i>A. macrourus</i> var. <i>glaucopsis</i>	1											1	1
26	<i>A. macrourus</i> var. <i>hirsutior</i>	1											1	1
27	<i>A. virginicus</i> "old-field variant"											1	1	1
28	<i>A. virginicus</i> "smooth variant"											1	1	1
29	<i>A. virginicus</i> var. <i>abbreviatus</i>						1						1	1
30	<i>A. virginicus</i> var. <i>glaucus</i> subvar. <i>dealbatus</i>	1											1	1
31	<i>A. virginicus</i> var. <i>glaucus</i> subvar. <i>glaucus</i>	1											1	1
32	<i>A. virginicus</i> var. <i>hirsutior</i>				1								1	1
33	<i>A. virginicus</i> var. <i>tenuispathus</i>			1									1	1
34	<i>A. virginicus</i> var. <i>virginicus</i> "deceptive variant"							1					1	1
35	<i>A. virginicus</i> var. <i>viridis</i>	1											1	1
36	<i>A. virginicus</i> var. <i>viridis</i> subvar. <i>genuinus</i>	1											1	1
Concepts per taxonomy / Cumulative totals		11	3	6	6	1	5	13	13	11	9	11	88	46

concept pairings with identical names (2 = / >, 9 = / <, 5 = / ><), and the other 145 have non-identical names. These types of name/meaning categorization yield an overall ratio of 781/43 reliable/unreliable names for the entire Andro-UC. The highest occurrences of unreliable names appear in the 1933/1889 (5 MIR),

2006/2003 (7 MIR), and 2015/1889 (10 MIR) alignments.

Quantification of name/meaning cardinality over the 126-year period of the Andro-UC reveals that half of the 36 taxonomic names have been used in multiple treatments whereas the other half are particular to

single treatments (Table 4). Cumulatively, the use case entails 88 name usages and 46 unique name/meaning combinations (ratio: 1.91:1). Only one name – *A. virginicus* – is used in every classification. Three additional names – *A. capillipes*, *A. glomeratus*,

and *A. virginicus* var. *virginicus* – are used in 6-8 of the 11 input classifications; all other (32/36) names occur in less than half of them. Most, though not all, of the names with 2-4 usages appear in temporally consecutive taxonomies (ratio: 9/13).

Table 5. Analysis of taxonomic name/meaning cardinality across the Andro-UC, based on 85 occurrences of congruent concepts labeled with 1-4 taxonomic names. Each of the 21 (sets of) congruent concepts in the use case is labeled according to its most recent (latest) recognition, and concept lineages are ordered accordingly. Non-identical (sets of) names associated with each congruent concept lineage are numbered in reverse chronological order, i.e., starting with their identity in the 2015 taxonomy. See also Figure 1 and Table 4.

#	Taxonomic concept lineage (label)	1889	1933	1948	1950	1968	1979	1983	2003	2006	2014	2015	Congruences	Names
1	2015.A capillipes	4						3	3	2		1	5	4
2	2015.A dealbatus	4						3	3	2		1	5	4
3	2015.A virginicus	3 (4)	1	2	2		2	2		1	1	1	8	3 (4)
4	2015.A_virginicus OldFieldVariant							2	2			1	3	2
5	2015.A_virginicus SmoothVariant							2	2			1	3	2
6	2015.A_virginicus var decipiens							2	1	1	1	1	5	2
7	2015.A glaucopsis	4		3	3		1	2	2	1	1	1	9	4
8	2015.A hirsutior	4			3			2	2	2	1	1	7	4
9	2015.A_glomeratus var glomeratus	2						1	1	1	1	1 (2)	6	2 (3)
10	2015.A_tenuispatheus	4		3				2	2	1	2	1	7	4
11	2014.A capillipes	2	1	1	1		1	2	2	1	1		8	2
12	2014.A_virginicus var virginicus								1	1	1		3	1
13	2014.A glomeratus				1						1		2	1
14	2006.A glomeratus			1						1			2	1
15	2003.A virginicus	1						1	1				3	1
16	2003.A glomeratus	2	1					1	1				4	2
17	1979.A virginicus						1						1	1
18	1979.A_virginicus var abbreviatus						1						1	1
19	1968.A virginicus					1							1	1
20	1950.A virginicus				1								1	1
21	1948.A virginicus			1									1	1
Concepts per taxonomy / Cumulative totals		11	3	6	6	1	5	13	13	11	9	11	85	44 (46)

Not surprisingly, the most frequently used name – *A. virginicus* – also has the highest number of reciprocally non-congruent taxonomic meanings, with a name/meaning cardinality of 1/6 (Table 4). The period of 1933-1983 includes six directly succeeding classifications (Figure 2) – all of which promote different meanings of "*A. virginicus*". Only three additional names have more than one meaning in the Andro-UC; viz. *A. capillipes* (name/meaning cardinality = 1/2), *A. glomeratus* (1/4) and, again, *A. virginicus* var. *virginicus* (1/2).

The 88 name usages in the Andro-UC correspond to 21 semantically distinct sets or lineages of taxonomic concepts (Table 5). Of these, the lineage congruent with 2015.A_glaucopsis has the highest num-

ber of preceding elements, appearing in 9/11 classifications and in association with four non-identical names. Other concept lineages with abundant prior affirmations include 2015.A_virginicus (8 affirmations/4 non-identical names), 2014.A_capillipes (8/2), 2015.A_hirsutior (7/4), and 2015.A_tenuispatheus (7/4). On the other end of the scale there are five concepts whose meanings are unique to one classification (two authored in 1979; and one in 1968, 1950, and 1948, respectively).

The least favorable name/meaning cardinality for the 21 distinct meaning lineages in the Andro-UC is 4/1; meaning that four non-identical names are used to identify taxonomically congruent concepts. This ratio applies to six concepts and their respective pre-

decessors: 2015.A_capillipes, 2015.A_dealbatus, 2015.A_virginicus, 2015.A_glaucopsis, 2015.A_hirsutior, and 2015.A_tenuispatheus. Conversely, a cardinality of 1:1 is obtained in 9/21 instances, of which only four have more than one usage (Table 5).

The information compiled in Tables 4 and 5 provides an intuitive sense of how taxonomic names fare in the longer term as identifiers of meanings in the Andro-UC. Naturally the performance of names should be evaluated in the context of taxonomic stability. A high degree of taxonomy stability would be mirrored in a relative scarcity of empty cells in Table 5, because early concepts would have recurrent, congruent successors – either with identical or non-identical names – in the temporal chain starting in 1889 and ending in 2015. This is evidently not the case: only 85/231 cells (36.8%) have values in them, and 14/16 chains (87.5%) with two or more concepts are non-contiguous.

In spite of this background of seemingly perpetual taxonomic disagreement, identifiers could nevertheless (in principle) maintain a name/meaning cardinality of 1/1. This would be reflected in taxonomic names simultaneous having the score of 1 in the "Meanings" column of Table 4 ($N_{Table4} = 32$ corresponding names) and the score of 1 in the "Names" column of Table 5 ($N_{Table5} = 9$ corresponding names). However, in actuality, the intersection of these two sets of taxonomic names includes exactly *one* name – *A. virginicus* var. *abbreviatus*. This name, used exclusively in Godfrey & Wooten (1979), is the only one that requires neither integration into a taxonomic concept label (sec.) nor articulation with RCC-5 in order to reliably identify its associated meaning across the entire use case. The remaining 35/36 names used in the Andro-UC are either syntactically or semantically 'compromised' by having name/meaning cardinality relations *other than* 1/1. This outcome is also reflected in the accumulation of numbers greater than 1 along the columns of Tables 4 and 5.

In summary, even though names used in the Andro-UC act as identifiers of meanings with reliability ratios of 56.6% or higher in the local, pairwise alignments (Tables 1-3), their global reliability is such that > 97.2% diverge from an ideal name/meaning cardinality of 1/1. This assessment remains adequate even if taxonomic change is taken into account.

8. Discussion

We limit the discussion to the overarching theme of the performance of names as identifiers of taxonomic concepts, with emphasis on the new insights and products gained from our RCC-5 representation and reasoning approach, and the relevance of this approach to larger or less biological taxonomy-focused use cases.

8.1. Reasoning over taxonomic change with RCC-5: New knowledge products

The Andro-UC serves as a concise illustration of the knowledge products gained through the RCC-5 concept alignment approach, in relation to the traditional practice of identifying and integrating taxonomic meanings through names and nomenclatural relationships [66]. Critically, the approach requires an initial set of articulations provided by human users that satisfy criteria of logical consistency and proper resolution to yield well-specified alignments [32]. The Euler/X toolkit includes suites of logic-based modules – termed *inconsistency analysis* and *ambiguity reduction* – to interactively identify such sets of input articulations if the user's original input violates these requirements [13,16,17]. However, in the present use case (Table 2), the user-provided input readily meets the criteria, leading to unique, well-specified specific alignments in all 12 cases (Figures 4-6).

The newly inferred knowledge products for the Andro-UC include the output MIR, merge visualizations, and derivative name/meaning analyses. With regards to the MIR (Table 2; Appendix 2), the initial set of 88 user-provided articulations is logically expanded by the toolkit reasoners to entail 824 articulations (1025 articulations if the root-level concepts are included). This means that, for each paired alignment, we can now readily *query* the MIR to ascertain whether any two taxonomic concepts and ancillary information can be merged, or not [42,81,82]. In particular, articulations of congruence (\equiv) and exclusion (\perp) between two concepts are bilaterally actionable for the purpose of integrating concepts. Proper inclusion (\supset) and inverse proper inclusion (\subset) are least unilaterally actionable without ambiguity. Overlap ($\supset\subset$) is commonly the most challenging articulation over which to execute merge commands. However, in some instances overlap at more inclusive levels in the merge can be resolved into less ambiguous articulations at lower levels. For instance, the 2014/2006 alignment (Figure 6A) entails the articula-

tion 2014.A_glomeratus >< 2006.A_glomeratus at the level directly following the root. At the next lower level, the extent of the overlap is resolved: both concepts share congruent subsumed elements, and each also has congruent (albeit unequally named and ranked) regions that are unique to it. Biological data annotated at this lower level are therefore readily integrated, in spite of the higher-level overlap. In summary, the sets of output MIR constitute comprehensive, value-added, and machine-interpretable information that can drive the resolution (integration, separation) of paired taxonomic concepts with better granularity and reliability than taxonomic names alone [5,28,32,33,41].

The merge visualizations are directly based on, and thus isomorphic with, the output MIR [13,15,83]. Their primary value is to aid human comprehension of taxonomic concept provenance in an instructive, tree-based format. Visualization tools of taxonomic concept identity and relationship have advanced significantly over the past 20 years [3,4,15,45,46,94]. Nevertheless the Euler/X toolkit is the first platform to leverage RCC-5 relationships and logic reasoning to yield merge taxonomies that combine all relevant input constraints (T_1, T_2, A, C) into coherent, tree-like visualizations.

The cognitive utility of these merge taxonomies is apparent; compare (e.g.) Figures 1, 2 and 3 – all of which contain information on the alignment of the Blomquist (1948) and Small (1933) classifications. Figure 2, while highly adequate for the particular conditions of Andro-UC, is less well suited to represent articulations among concepts nested into many (three or more) taxonomic ranks or phylogenetic levels. The tabular representation is best suited for visualizing flattened hierarchies. The concept 1948.A_virginicus (# 19 in Figure 3), for instance, is challenging to represent in the table. Figure 3, in turn, shows properly nested entities for the 1948/1933 taxonomies (with up to three levels), but provides primarily named-based information regarding their taxonomic provenance. This might lead to taxonomically erroneous conclusions, such as 1948.A_glomeratus == 1933.A_glomeratus (correct articulation: <) or 1948.A_virginicus == 1933.A_virginicus (>), or 1948.A_virginicus | 1933.A_glomeratus (><). In other words, the isolated, temporally succeeding tree representations in Figure 3, though not uncommon in the systematic literature [7,78,91], are not as precise or reliable as the RCC-5 alignments.

In contrast, the merge visualizations (Figures 1, 4–6) simultaneously account for nomenclatural identities, multi-level tree hierarchies, and reasoner-

inferred taxonomic provenance information. Their interpretation is intuitive, as the relative proportion and position of grey squares versus green rectangles or yellow octagons provides an immediate sense of the extent and localization of taxonomic congruence and incongruence (compare, e.g., Figures 5B and 5C). Moreover, occurrences of (=, ≠, +, -) annotations for concepts represented throughout the merge topology reflect the degree to which the validly recognized names are suitable as identifiers of taxonomic identity.

8.2. Name/meaning dissociation in the Andro-UC: Building better identifiers for taxonomically annotated information

We assert that the complexity of name/meaning relationships in the Andro-UC (Figure 2) and resulting poor performance of names as identifiers of taxonomic identity (Table 1-5) are not particularly exceptional for the field of biological taxonomy (herein broadly defined to include phylogenetics). The problem is systemic. Inquiries into the long-term name/meaning provenance for particular organismal lineages are bound to reveal countless use cases in which names perform considerably better, or even worse, than in the Andro-UC [1,20,31,35,41,64,73,85]. To some degree the inadequacies of names as concept identifiers may be managed pragmatically through human social processes; for instance, through an adherence to conservative re-/naming practices or (so-called) standardized or unitary taxonomies [5,43,52,75,87]. Moreover, the cumulative insufficiencies are often mitigated by the ability of expert human speakers to *contextualize* name usages and thus reliably delimit their meanings [29,31,65]. However, none of these counteracting human practices alter the insight that the identities and relationships of valid and invalid taxonomic names are fundamentally type-driven, and therefore not designed to track fine differences in taxonomic meaning at more expansive levels (i.e., beyond type identity). Logic reasoners in particular struggle with modeling what "*Andropogon virginicus*" means 'under currently accepted conditions' [58], i.e., when the relevant context of the name usage is not made explicit. Something beyond type-anchored names is needed if taxonomic perspectives are to be translated into entities fit for representation and reasoning in the machine processing-driven Semantic Web.

In analogy to delimiting phenotypic features [30,71], reliable fixation of the referential extension

of taxonomic names for their broad reapplication is not merely a matter of *ostension*; i.e., of identifying select ingroup (type) exemplars. Such definitions invariably under-specify the intended name extension in many practical contexts (such as different floristic treatments in the Andro-UC), thereby 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*, and thus subject to the kinds of provenance relationships that theories experience in science in general. We maintain that reference to individual types is necessary [92] yet insufficient for playing the more expansive role of theory identifier or integrator. Consequently, using taxonomic concept labels and RCC-5 articulations [34] or other means of comparison [22] outperforms the traditional, Code-compliant practice of tracking concept provenance.

The above insufficiencies are nowhere more apparent than in cases of concept overlap. Whenever succeeding taxonomies include overlapping concepts, the differences are rooted in something other than the desired degree of resolution [25,61,64,73]. For instance, both Hitchcock & Chase (1950) and Blomquist (1948) concur that there are three identically named species-level concepts entailed in the *Andropogon* complex (Figure 4C). They also concur that 1950/1948.A_virginicus has three variety-level child concepts. In short, they agree on the level of granularity for resolving concepts at higher and lower taxonomic ranks. However, they simultaneously disagree on the extent to which the available, type-anchored names reach out to respectively perceived, and necessarily more inclusive, taxonomic entities – where the latter are presumed (more precisely: theorized) to be evolutionary entities that are causally sustained in nature [8]. As a result of this differential inference of extra-type taxonomic boundaries, the referential extensions of four 1950/1948 species-level concepts overlap in complex ways (Figure 4C). One can expect such overlap to become more frequent at higher taxonomic levels where the performance of names as identifiers of taxonomic provenance becomes exceedingly poor [32,33,35].

Identifiers whose meanings change inadvertently or even unascertainably from one taxonomy to the next are suboptimal vehicles for integrating biodiversity data. The herein demonstrated alignment approach paves the way for building better taxonomic concept identifiers and provenance resolution services.

8.3. Scalability of the RCC-5 concept alignment approach and relevance to other Semantic Web domains

How scalable is the RCC-5 concept alignment approach within the field of biological taxonomy, and how relevant is it to other Semantic Web domains? Generally speaking, reasoning over taxonomic change with RCC-5 remains in its infancy [15,32,33,42,83]. New informatics research, more computationally 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 Andro-UC brings out some of the potential for reasoning over taxonomic provenance while leaving much room for further work. In particular, the 11 classifications of the Andro-UC lend themselves to 55 possible pairwise comparisons, of which only 12 are presented here (Figures 4-6). This omission is deliberate; future versions of the reasoning toolkit should be developed to align more than two input taxonomies simultaneously. In doing so, the reasoners would make use of transitive relationships such as "if concept $A = B$ and $B = C$ then $A = C$ ". We can then ask to what extent the ten chronologically succeeding and two additional alignments (Figures 5A and 6C) are *sufficient* for recovering the full set of 55 pairwise alignments, based primarily on transitive reasoning powers. Answers to such questions will have relevance for the scalability of this approach, and should inform the users' practice of providing input articulations.

The largest consistent use case processed to date with the Euler/X toolkit includes 483/317 input concepts (T_2/T_1) and 402 input articulations [33]. Using a custom RCC-5 reasoner, this use case can be resolved in less than 10 minutes on an individual laptop processor (S. Bowers, personal communication). However, large alignment use cases that entail multiple constraint over- or under-specifications are computationally complex. Resolving these use cases will require heuristic solutions that make use of reciprocally corresponding and hierarchically coherent concept subsets in each input taxonomy [13,16,17]. Nevertheless, we perceive that in the short term, generating adequate sets of input articulations will remain as the most significant obstacle for promoting the RCC-5 concept alignment approach.

Pathways to broader implementation should focus on integrating concept annotation conventions (name

sec. author), parent/child relationships, RCC-5 articulations, and reasoning and visualization services into existing, prominent biodiversity data platforms [2,34,35,47,54,56]. In particular, we envision solutions where organismal occurrence records are *identified* to non-identical yet well-circumscribed taxonomic concepts, and in turn the concepts are consistently and comprehensively articulated using RCC-5 alignment services. Such an infrastructure would permit biologically significant queries of the following types. (1) Return all records identified to the name *Andropogon virginicus* (optionally, with synonyms or algorithmically matched names). This query type corresponds to the current capability of many environments [9,66,69]. (2) Return all records identified to the concept *Andropogon virginicus* sec. Weakley (2015) and, alternatively, *Andropogon virginicus* sec. RAB (1968). Show the corresponding occurrence-based distribution maps. (3) Translate all identifications of occurrence records to Weakley (2015)-endorsed concepts into their corresponding identifications to BONAP (2014)-endorsed concepts (see Figure 6B). (4) Highlight 'problem records' that are identifiable to multiple non-congruent concepts in the set of aligned classification standards used to carry out identifications. (5) Show records in this target region as identified according to the most, or least, granular concept-level taxonomy. (6) For any set of records and biological data identified to any pair of concepts, assess whether the records and data can be integrated based on the reasoner-inferred set of MIR.

The above queries (2)-(6) all utilize taxonomic provenance information encoded via RCC-5 articulations. We submit that such articulations and the underlying reasoning services are urgently needed to build more semantically powerful and scalable biodiversity data portals. The particular strengths of RCC-5 in this context include explicitness, consistency, direct machine-interpretability, and above all flexibility in processing diverse forms of taxonomic concept input ranging from minimally structured lists of names (i.e., taxonomic concept labels) to phylogenies and monographic revisions [32,33,35].

Where suitable, this approach can be complemented by existing methods for representing concept similarity and drift in Semantic Web environments that exploit (*inter alia*) Natural Language Processing methods and relationships used in OWL-DL ontologies [12,22,26,36,69,76,88]. Within this larger context of *ontology matching*, the RCC-5 concept alignment approach is generally relevant to use cases where many of the classificatory practices and reasoning constraints of taxonomies apply [83]. This

means that Semantic Web applications that need to consistently align and visualize multiple, hierarchically structured sets of concepts with coverage and disjoint siblings may benefit from exploring the RCC-5 alignment approach as well.

Appendices

Appendix 1. Set of 12 Euler/X toolkit input data files for all alignments produced in the Andro-UC (Figures 4-6). Each file is saved in .txt format and contains annotations and instructions for run commands to yield the alignments and visualizations shown in the corresponding figures.

Appendix 2. Set of 12 Euler/X toolkit output Maximally Informative Relations (MIR) for the input data files provided in Appendix 1. Each output file is saved in .csv format. The MIR files form the basis for analyses of name/meaning relations (Tables 2-3).

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