EULER/X: A Toolkit for Logic-based Taxonomy Integration

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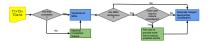
Sep 12, 2013

Outline

Introduction



► EULER/X Workflow



Summary

⇒ Andropogon spp. in the Carolinas, from Hackel 1889 to Weakley 2005

| Weakley 2005 | C. Campbell (1983, FNA 2003) | Godfrey & Wooten 1979 | RAB 1968 | Hitchcock & Chase 1950 | Blomquist 1948 | Small 1933 | Hackel 1889 |
|--|---|-----------------------------------|---------------|----------------------------------|-------------------------------------|--------------------|--|
| Andropogon capillipes var. capillipes | A. virginicus var. glaucus "drylands variant" | A. capillipes | A. virginicus | A. capillipes | A. capillipes | A. capillipes | A. virginicus var. glaucus subvar. glaucus |
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| Andropogon virginicus var. virginicus | A. virginicus var. virginicus "smooth variant" | A. virginicus var. virginicus | A. virginicus | A. virginicus var. virginicus | A. virginicus var. virginicus | A. virginicus | A. virginicus var. viridis subvar. genuinus |
| Andropogon virginicus var. decipiens | A. virginicus var. decipiens | A. virginicus var. virginicus | A. virginicus | A. virginicus var. virginicus | A. virginicus var. virginicus | A. virginicus | A. virginicus var. viridis subvar. genuinus |
| Andropogon glaucopsis | A. glomeratus var. glaucopsis | A. glaucopsis | A. virginicus | A. virginicus var. glaucopsis | A. virginicus var. glaucopsis | A. glomeratus | A. macrourus var. glaucopsis |
| Andropogon glomeratus var. hirsutior | A. glomeratus var. hirsutior | A. virginicus var. abbreviatus | A. virginicus | A. virginicus var. hirsutior | ? | A. glomeratus | A. macrourus var. hirsutior |
| Andropogon glomeratus var. glomeratus | A. glomeratus var. glomeratus | A. virginicus var. abbreviatus | A. virginicus | A. glomeratus | A. glomeratus | A. glomeratus | A. macrourus var. abbreviatus |
| Andropogon tenuispatheus | A. glomeratus var. pumilus | A. virginicus var. abbreviatus | A. virginicus | A. glomeratus | A. virginicus var. tenuispatheus | A. glomeratus | A. macrourus var. genuinus |
| 5 species, 8 vars. | 2 species, 7 vars (+ 2 informal "variants") | 3 species, 4 vars. | 1 species | 3 species, 5 vars. | 3 species, 5 vars. | 3 species, 3 vars. | 2 species, 7 vars. |

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⇒ Individual columns represent past classifications of Andropogon.

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⇒ Individual rows represent equivalent taxonomic entities, (almost) regardless of their name labels.

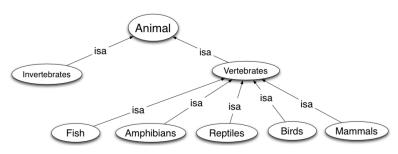
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- ⇒ Name/synonymy relationships are not sufficiently granular to capture this evolution of taxonomic views of Andropogon species.

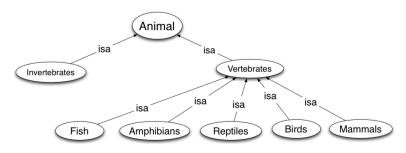
Taxonomy & Taxonomic Constraints

A **taxonomy** is a set of biological taxa (concepts) in an *ISA* hierarchy with taxonomic constraints:



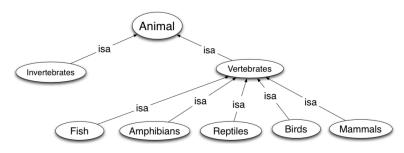
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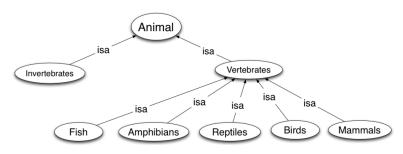
Non-Emptiness: Birds $\neq \emptyset$

A **taxonomy** is a set of biological taxa (concepts) in an *ISA* hierarchy with *taxonomic constraints*:



- Non-Emptiness: Birds ≠ ∅
- Sibling-Disjointness: Birds ∩ Fish = ∅

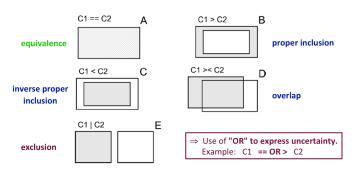
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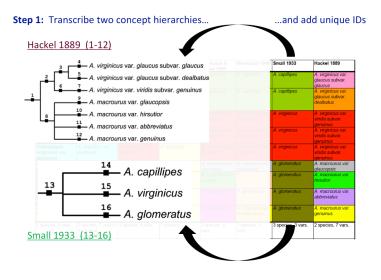


- Non-Emptiness: Birds ≠ ∅
- Sibling-Disjointness: Birds ∩ Fish = ∅
- Coverage: Animal = Invertebrates ∪ Vertebrates

RCC-5 Relations

Region Connection Calculus (RCC) [Ran92] abstractly describes regions(or their topological spaces) by their possible relations to each other. In EULER/X, we articulate a set of RCC-5 relations between different taxa



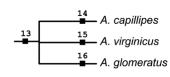


Step 2: Create a table with all concept labels

Hackel 1889 (1-12)



Small 1933 (13-16)



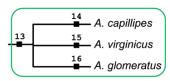
| ID | Name_Simple | According_To | Rank |
|----|--|--------------|------------|
| 1 | Andropogon | Hackel 1889 | Genus |
| 2 | Andropogon virginicus | Hackel 1889 | Species |
| 3 | Andropogon virginicus var. glaucus | Hackel 1889 | Variety |
| 4 | Andropogon virginicus var. glaucus subvar. glaucus | Hackel 1889 | Subvariety |
| 5 | Andropogon virginicus var. glaucus subvar. dealbatus | Hackel 1889 | Subvariety |
| 6 | Andropogon virginicus var. viridis | Hackel 1889 | Variety |
| 7 | Andropogon virginicus var. viridis subvar. genuinus | Hackel 1889 | Subvariety |
| 8 | Andropogon macrourus | Hackel 1889 | Species |
| 9 | Andropogon macrourus var. glaucopsis | Hackel 1889 | Variety |
| 10 | Andropogon macrourus var. hirsutior | Hackel 1889 | Variety |
| 11 | Andropogon macrourus var. abbreviatus | Hackel 1889 | Variety |
| 12 | Andropogon macrourus var. genuinus | Hackel 1889 | Variety |
| 13 | Andropogon | Small 1933 | Genus |
| 14 | Andropogon capillipes | Small 1933 | Species |
| 15 | Andropogon virginicus | Small 1933 | Species |
| 16 | Andropogon glomeratus | Small 1933 | Species |

Step 2: Create a table with all concept labels

Hackel 1889 (1-12)



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| ID | Name_Simple | According_To | Rank |
|----|--|--------------|------------|
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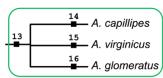
Step 3: Create a table with corresponding parent/child relationships ('is α ')

Hackel 1889 (1-12)

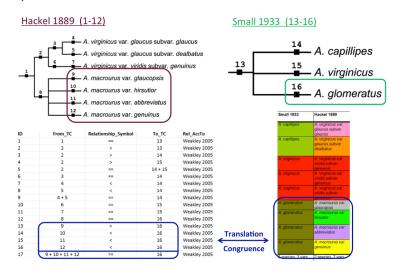


| ID | From_TC | Relationship | To_TC |
|----|---------|--------------|-------|
| 1 | 1 | is parent of | 2 |
| 2 | 2 | is parent of | 3 |
| 3 | 3 | is parent of | 4 |
| 4 | 3 | is parent of | 5 |
| 5 | 2 | is parent of | 6 |
| 6 | 6 | is parent of | 7 |
| 7 | 1 | is parent of | 8 |
| 8 | 8 | is parent of | 9 |
| 9 | 8 | is parent of | 10 |
| 10 | 8 | is parent of | 11 |
| 11 | 8 | is parent of | 12 |
| 12 | 13 | is parent of | 14 |
| 13 | 13 | is parent of | 15 |
| 14 | 13 | is parent of | 16 |

Small 1933 (13-16)



Step 4: Create a table with a suitable set of articulations



Challenges when connecting two taxonomies

- Input of articulations (Goal: achieve a complete and consistent mappings)
 - ► Taxonomic experts will not input ∞ articulations
 - Taxonomic experts will miss relevant articulations
 - Taxonomic experts could posit logically inconsistent articulations

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- Getting a merged taxonomy based on the input taxonomies and articulations
- "EULER/X Toolkit" is being developed to explore solutions to these challenges

EULER/X: X stands for its underlying reasoner

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EULER/FO: underlying reasoner Prover9/Mace4

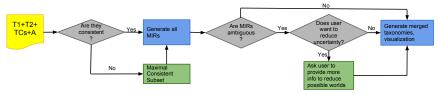
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- EULER/FO: underlying reasoner Prover9/Mace4
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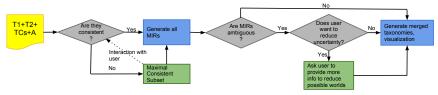
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- EULER/PyRCC: underlying reasoner PyRCC8

EULER/X Workflow



Overview of the EULER/X workflow

EULER/X Workflow

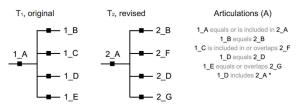


Overview of the EULER/X workflow

EULER/X Command Line Interface

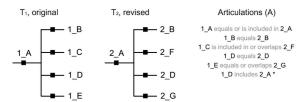
```
0 0
                               New Event 8-28-13 - sh - hash - 97×30
sh-3.2$ euler -help
Usage: euler [options]
Options:
  --version
                       show program's version number and exit
  -h, --help
                       show this help message and exit
                       verbose mode
  -v
  -p PROJECTNAME
                       project name
                       input file
  -i INPUTFILE
  -r INPUTDIR
                       input directory, by default ./
  -o OUTPUTDIR
                      output directory, by default ./
  -e ENCODE
                       encoding, e.g. mnpw, drpw, dlpw, etc.
  -b DL
                       dl encodina spare parameter
  --reasoner=REASONER
                      choose a reasoner
  --cc
                       consistency check only
  --dc
                       disable coverage
                       turn on uncertainty reduction
  ---
  --ie
                       inconsistency explanation
  --countmir
                       count # of occurance for each of rcc5
  --rcgo
                      Reduced containment graphs with overlaps
  --pwcluster
                       output the distance between pairwise possible world
  --simpcluster
                       simplify the possible world cluster
                       no output
                      artifitial example generator
  -n NARY
                      N-nary, used with -q
  -m NNODES
                      #nodes, used with -a
  -d DEPTH
                      depth, used with -q
  -t RELATION
                      artifitial articulaiton rel. used with -a
sh-3.2$
```

Synthetic Example



Two succeeding taxonomies (T_1, T_2) and a set of expert-asserted input articulations (A) among respective taxonomic concepts.

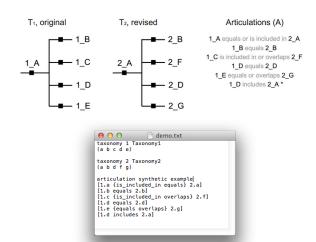
Synthetic Example



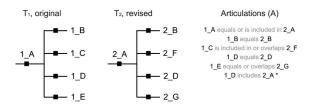
Two succeeding taxonomies (T_1, T_2) and a set of expert-asserted input articulations (A) among respective taxonomic concepts.

Objective: Get a merged taxonomy (or several possible merged taxonomies)

EULER/X Input



Consistency Checking / Inconsistency Repairing



```
Input is inconsistent!!
Remedial measure: remove [1.d includes 2.a]
Articulation <1.d includes 2.a> is inconsistent with [<1.a fis_included_in equals} 2.a>. <1.b ea
uals 2.b>, <1.c {is_included_in overlaps} 2.f>, <1.d equals 2.b>, <1.e {equals overlaps} 2.g>]
```

EULER/X points out that articulation "1_D includes 2_A" is inconsistent with other articulations and should be removed.

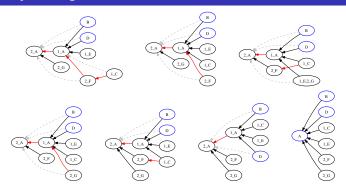


Taxonomy Merge

```
McChen - sh - bash - 150×43
         Possible morld 1: {1.d'="2.d, 1.b"="2.b, 1.d"<'2.a, 1.c"<"2.a, 1.b"<"2.a, 1.a"<"2.a, 1.a"<"2.a, 1.a">"2.b, 1.a">"2.b, 1.d"<'2.f, 1.e"><"2.f, 1.e"><"2.
         .f, 1.a"><'2.g, 1.c"><"2.g, 1.c"><"2.f, 1.d"|"2.f, 1.d"|"2.g, 1.d"|"2.b, 1.e"|"2.b, 1.e"|"2.b, 1.c"|"2.b, 1.c"|"2.b, 1.c"|"2.b, 1.b"|"2.b, 1.b"|"2.d, 1.b"|"2.d, 1.b"|"2.d, 1.c"|"2.a, 1.c"<"2.a, 1.e"<"2.a, 1.a"<"2.a, 1.a">"2.b, 1.a">"2.b, 1.a">"2.b, 1.d"<"2.a, 1.c"<"2.a, 1.b"<"2.a, 1.e"<"2.a, 1.a"<"2.a, 1.a">"2.a, 1.a">"2.b, 1.a"
g, 1.6"><2.g, 1.6"><2.f, 1.6"|"2.f, 1.6"|"2.f, 1.6"|"2.g, 1.6"|"2.b, 1.6"|"2.
         , 1.e^><².c, 1.c^><²2.g, 1.c^><²2.f, 1.d^!^2.f, 1.d^!^2.f, 1.d^!^2.b, 1.e^!^2.b, 1.e^!^2.b, 1.c^!^2.b, 1.c^!^2.b, 1.b^!^2.b, 1.b^!^2.b, 1.b^!^2.g, 1.b^!^2.f}.
Possible world 6: {1.d^=^2.d, 1.b^=^2.b, 1.d^<²2.a, 1.c^<²2.a, 1.c^<²2.a, 1.c^<²2.a, 1.e^<²2.a, 1.e^<²2.a, 1.a^>²2.b, 1.d^>²2.b, 1.d^>²2.b, 1.d^>²2.d, 1.e^><²2.b, 1.e^><²2.b, 1.e^><²2.a, 1.e^<²2.a, 1.e^<²2.a, 1.e^<²2.a, 1.e^>²2.a, 1.e^>²2.b, 1.d^>²2.b, 1.d^>²2.b, 1.e^><²2.b, 1.e^><²2.b, 1.e^><²2.a, 1.e^>²2.a, 1.e^>²2.a, 1.e^>²2.a, 1.e^>²2.b, 1.e
              . 1.e"><"2.a, 1.a"><"2.a, 1.d"|"2.f, 1.d"|"2.a, 1.d"|"2.a, 1.d"|"2.b, 1.e"|"2.b, 1.e"|"2.b, 1.c"|"2.b, 1.c"|"2.b, 1.c"|"2.a, 1.b"|"2.a, 1.b"|"2.a, 1.b"|"2.f;
    sh-3,2$ more demo_mir.csv
    1.a,2.a,{-, <}
    1.a,2.d,>
1.a,2.g,{>, ><}
1.a,2.f,{>, ><}
    1.c,2.a,<
1.c,2.b,!
1.c,2.g,{|, ><|
1.c,2.f,{<, ><|
1.e,2.g,{-, ><}
1.e,2.f,{!, ><}
    1.d.2.a.<
1.d.2.d.=
1.d,2.g,!
1.d,2.f,!
         sh=3.25
```



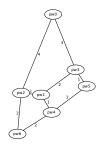
Taxonomy Merge



Set of possible worlds (pw0, pw1, ..., pw6) resulting from the repaired input example



Visual clustering of similar possible worlds



Visualization of possible worlds, where the distance between two possible worlds is the shortest distance traceable in the graph (e.g., the distance between worlds 5 and 6 is 4).



Uncertainty Reduction

sh-3.2\$ euler -i demo.txt -e mnpw --ur

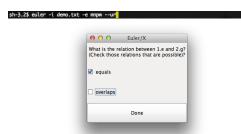


Uncertainty Reduction





Uncertainty Reduction

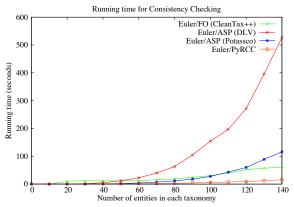


will give you only one possible world:



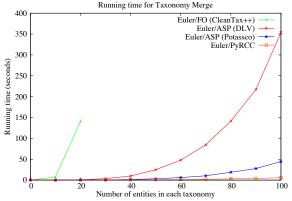
Demo – from end to end

Performance Results – Consistency Checking



Running time for consistency checking on synthetic taxonomies

Performance Results – Merging Taxonomies



Running time for merging taxonomies on synthetic taxonomies.

Performance Results – Summary

- How do different reasoner-based tools work?
 - EULER/FO: checks consistency by calling Mace4 once and then generates each mir by calling Prover9 (for m * n mir's assuming there are m, n entities in each taxonomy)
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- Merging Taxonomy
 - EULER/PyRCC > EULER/ASP (Potassco) >> EULER/ASP (DLV) >> EULER/FO (Prover9/Mace4)
 - Note: coverage constraints cannot be asserted using PyRCC8.

Comparison with Ontology Matching

| | Ontology Matching | Taxonomy Integration |
|--------|------------------------------|----------------------------|
| Input | ontologies (OWL, RDF), | taxonomies, articulations |
| | similarity / distance vector | & taxonomic constraints |
| | finding the matching | finding the relation |
| Output | between entities; | between entities; |
| | getting merged ontologies. | getting merged taxonomies. |

Related Work & Contribution

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- MoReTax
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 - prior work of EULER/FO

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Contribution

- Encodings
- Provenance
- Visualization
- The first real-life implementation of ASP in a domain

Encodings – Some ideas

1. Enumerate all the minterms (e.g. ABCD...):

```
%%% minterms
r(M):=\#int(M),M>=1,M<=\#maxint.
in(X, M) v out(X, M) := r(M), concept(X).
vr(M) v ir(M) := r(M).
```

Encode the constraints (including articulations) on the minterms:

```
%%% c1 b isa c1 a
ir(X) := in(c1_b, X), out(c1_a, X).
:- \#countX: vrs(X), in(c1_b, X), in(c1_a, X) = 0.
```

Decode according to the validity of the minterms:

```
hint(X, Y, 0) := concept(X), concept(Y), vr(R), in(X, R), out(Y, R).
hint(X, Y, 1) := concept(X), concept(Y), vr(R), in(X, R), in(Y, R).
hint(X, Y, 2) := concept(X), concept(Y), vr(R), out(X, R), in(Y, R).
rel(X, Y, "="): not hint(X, Y, 0), hint(X, Y, 1), not hint(X, Y, 2).
```

Thanks!