De-centralized but global: Redesigning biodiversity data aggregation for improved engagement and impact

Nico Franz, Ed Gilbert & Beckett Sterner

Biodiversity Knowledge Integration Center - Arizona State University

Keynote Session – June 10, 2019

3rd Annual Digital Data Conference – Yale University, New Haven, CO

0. Key message: Biodiversity informatics remains young and fresh; especially if we aim

to **incentivize experts/enthusiasts** in publishing high-quality, "data-intelligent" biodiversity data products.

0. Key message: Biodiversity informatics remains young and fresh; especially if we aim

to **incentivize experts/enthusiasts** in publishing high-quality, "data-intelligent" biodiversity data products.

1. "New at ASU" (and more generally): **The NEON Biorepository Data Portal** – a Darwin Core-based ecological monitoring and forecasting resource.

0. Key message: Biodiversity informatics remains young and fresh; especially if we aim

to **incentivize experts/enthusiasts** in publishing high-quality, "data-intelligent" biodiversity data products.

1. "New at ASU" (and more generally): The NEON Biorepository Data Portal – a Darwin Core-based ecological monitoring and forecasting resource.

2. Rethinking centralized biodiversity data aggregation: Diagnosis and components

of a de-centralized complement.

0. Key message: Biodiversity informatics remains young and fresh; especially if we aim

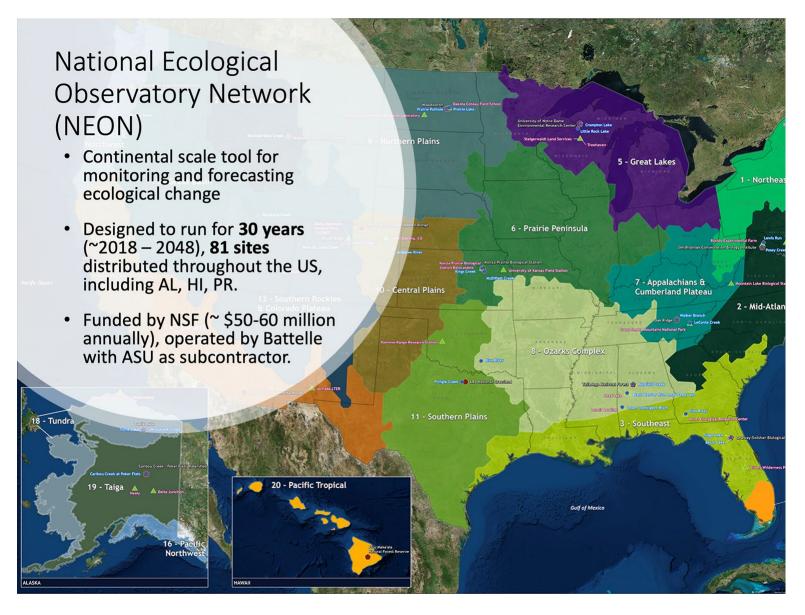
to **incentivize experts/enthusiasts** in publishing high-quality, "data-intelligent" biodiversity data products.

1. "New at ASU" (and more generally): The NEON Biorepository Data Portal – a Darwin Core-based ecological monitoring and forecasting resource.

2. Rethinking centralized biodiversity data aggregation: Diagnosis and components

of a de-centralized complement.

https://biorepo.neonscience.org





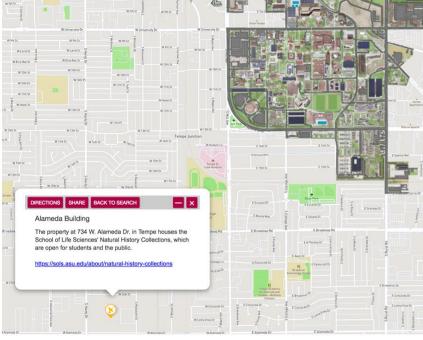


Domain facilities process samples and and send them to the NEON Biorepository at ASU.





Where are we located?



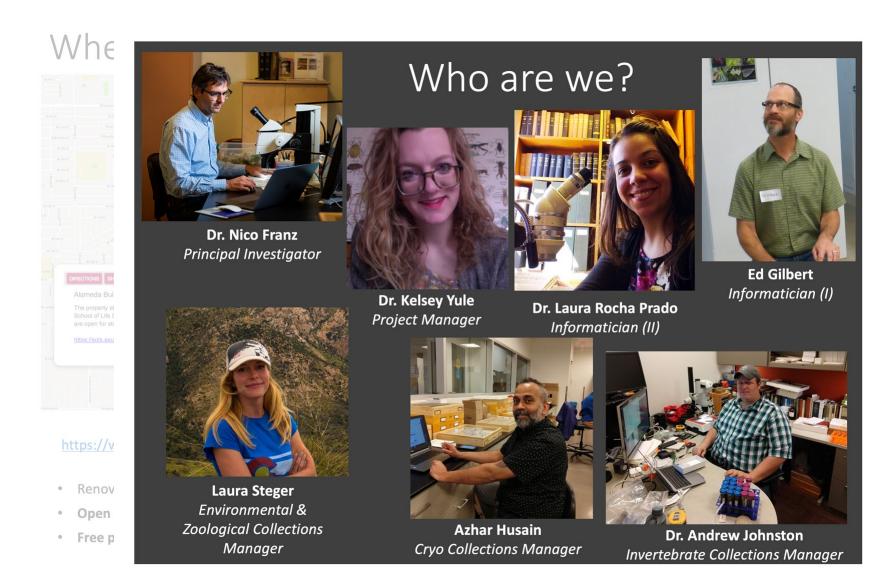


https://www.asu.edu/map/interactive/?id=120&mrklid=66206

- · Renovated and activated in the Fall of 2014.
- Open to the public (weekdays 9 am 5 pm).
- Free parking available right at entrance.

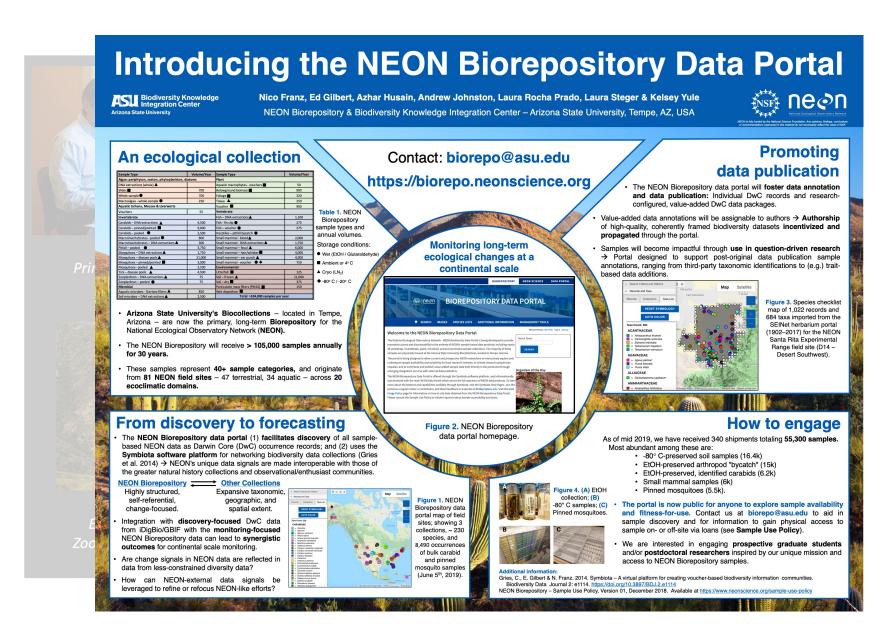






More information at Tuesday's poster session!

- Using the portal
- Access to samples
- New developments
 - Informatics
 - Research
- Prospective M.Sc./ Ph.D. applicants and postdocs

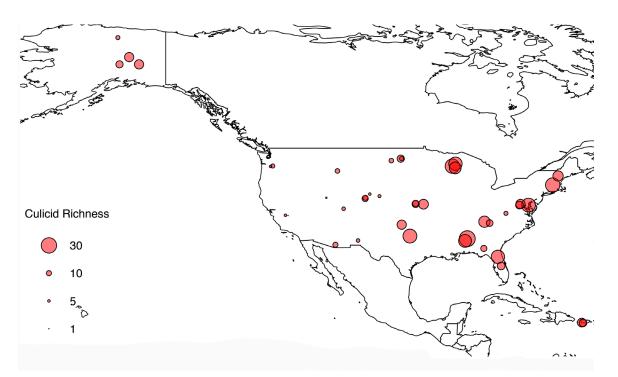


Early and broad

A short demonstration

https://biorepo.neonscience.org

[after a short BioRepo portal demo (Culicidae / SRER Plants)] *



Mosquito species richness per site, 2016–2017.

Change in species richness per site.

• NEON organismal sampling produces a unique, taxon-/region-/time-constrained, change-focused data signal.

^{*} Thanks to Dr. Kelsey Yule, NEON Biorepository @ ASU.

Rethinking centralized biodiversity data aggregation





Volume 2018 2018

Article Contents

Abstract

Introduction

No simple diagnosis for data quality deficiencies

Importance of trust for sustained use

Matching accountability to responsibility

Generation of novel systematic syntheses

Role of the DwC standard

Aggregation and authorship

Consequences of disenfranchizing taxonomic

Backbone-based data signal distortion: an example

An objection

Conclusion

Acknowledgements

Funding

To increase trust, change the social design behind aggregated biodiversity data 3

Nico M Franz ™, Beckett W Sterner

Database, Volume 2018, 2018, bax100, https://doi.org/10.1093/database/bax100 Published: 04 January 2018 Article history ▼

Split View

66 Cite

Permissions

Abstract

Growing concerns about the quality of aggregated biodiversity data are lowering trust in large-scale data networks. Aggregators frequently respond to quality concerns by recommending that biologists work with original data providers to correct errors 'at the source.' We show that this strategy falls systematically short of a full diagnosis of the underlying causes of distrust. In particular, trust in an aggregator is not just a feature of the data signal quality provided by the sources to the aggregator, but also a consequence of the social design of the aggregation process and the resulting power balance between individual data contributors and aggregators. The latter have created an accountability gap by downplaying the authorship and significance of the taxonomic hierarchies—frequently called 'backbones'—they generate, and which are in effect novel classification theories that operate at the core of datastructuring process. The Darwin Core standard for sharing occurrence records plays an under-appreciated role in maintaining the accountability gap, because this standard lacks the syntactic structure needed to preserve the taxonomic coherence of data packages submitted for aggregation, potentially leading to inferences that no individual source would support. Since high-quality data packages can mirror competing and conflicting classifications, i.e. unsettled systematic research, this plurality must be accommodated in the design of biodiversity data integration. Looking forward, a key directive is to develop new technical pathways and social incentives for experts to contribute directly to the validation of taxonomically coherent data packages as part of a greater, trustworthy aggregation process.

Issue Section: Perspective/Opinion

https://doi.org/10.1093/database/bax10

 Critique of monolithic aggregation designs.

Alignment of 5 taxonomic schemata (1922 – present)

Period of use Concept lineage 1 Concept lineage 2 Concept lineage 3 According to (sec.) 2009 - present Cleistesiopsis divaricata Cleistesiopsis oricamporum Cleistesiopsis bifaria Weakley (2015) Cleistesiopsis bifaria 2008 - present Cleistesiopsis divaricata Kartesz (2010) 3 USDA Plants (2012) 1993 - present Cleistes divaricata Cleistes bifaria 2 1946 - 1993 Cleistes div. var. divaricata Cleistes divaricata var. bifaria Fernald (1950) 1922 - 1991 Cleistes divaricata Radford AB (1968)

A. sec. Radford, Ahles & Bell (1968)



Distribution

divaric.

bifaria

R1 R2 R3 R4 oricamp.

bifaria

R1

R2

R3

R4



B. sec. Kartesz (2010) [BONAP]



--- W--I-I-- (2045)

Dist			
ifaria	divaric.	oricamp.	15
+	_	_	3
_	+	_	MISS
_	+	+	Jackso
_	_	+	0
		'	
			1

C. sec. weakley (2015)
= Cleistesiopsis bifaria = Cleistesiopsis divaricata = Cleistesiopsis oricamporum Charlotte Ch

Data transformation to conform with single taxonomic backbone

D. sec. SERNEC (2016) - RAW AGGREGATION

= Cleistes bifaria = Cleistes divaricata = Cleistes divaricata var. bifaria

Data package 2

=> Ingestion

= Cleistesiopsis bifaria

= Cleistesiopsis divaricata

= Cleistesiopsis oricamporum

ALABAMA



Distribution

 \oplus

"bifaria"

 \oplus

 $\widecheck{\oplus}$

+

(

R3

"divaric." | "oricamp."

Distribution

Aggregation yields

novel inferences of

sympatry (R1,R4)

& endemism (R2)

	bifaria	divaric.	oricamp
R1	((+)	-
R2	\oplus	Θ	_
R3	+	+	_
R4	((+)	(+)

E. sec. SERNEC (2016) - AGGREGATOR SYNTHESIS

Rethinking centralized biodiversity data aggregation (2)





Volume 2018 2018

Article Contents

Abstract

Introduction

No simple diagnosis for data quality deficiencies

Importance of trust for sustained use

Matching accountability to responsibility

Generation of novel systematic syntheses

Role of the DwC standard

Aggregation and authorship

Consequences of disenfranchizing taxonomic experts

Backbone-based data signal distortion: an example

An objection

Conclusion

Acknowledgements

Funding

To increase trust, change the social design behind aggregated biodiversity data 3

Nico M Franz ™, Beckett W Sterner

Database, Volume 2018, 2018, bax100, https://doi.org/10.1093/database/bax100

Published: 04 January 2018 Article history ▼

▶ PDF

■■ Split View

66 Cite

Permissions

Abstract

Growing concerns about the quality of aggregated biodiversity data are lowering trust in large-scale data networks. Aggregators frequently respond to quality concerns by recommending that biologists work with original data providers to correct errors 'at the source.' We show that this strategy falls systematically short of a full diagnosis of the underlying causes of distrust. In particular, trust in an aggregator is not just a feature of the data signal quality provided by the sources to the aggregator, but also a consequence of the social design of the aggregation process and the resulting power balance between individual data contributors and aggregators. The latter have created an accountability gap by downplaying the authorship and significance of the taxonomic hierarchies—frequently called 'backbones'—they generate, and which are in effect novel classification theories that operate at the core of datastructuring process. The Darwin Core standard for sharing occurrence records plays an under-appreciated role in maintaining the accountability gap, because this standard lacks the syntactic structure needed to preserve the taxonomic coherence of data packages submitted for aggregation, potentially leading to inferences that no individual source would support. Since high-quality data packages can mirror competing and conflicting classifications, i.e. unsettled systematic research, this plurality must be accommodated in the design of biodiversity data integration. Looking forward, a key directive is to develop new technical pathways and social incentives for experts to contribute directly to the validation of taxonomically coherent data packages as part of a greater, trustworthy aggregation process.

Issue Section: Perspective/Opinion

https://doi.org/10.1093/database/bax10
 0

- Critique of monolithic aggregation designs.
- Here we reformulate the issue in relation to the direction of data flow in hierarchical biodiversity data aggregation networks.

Rethinking centralized biodiversity data aggregation (2)





Volume 2018 2018

Article Contents

Abstract

Introduction

No simple diagnosis for data quality deficiencies

Importance of trust for sustained use

Matching accountability to responsibility

Generation of novel systematic syntheses

Role of the DwC standard

Aggregation and authorship

Consequences of disenfranchizing taxonomic experts

Backbone-based data signal distortion: an example

An objection

Conclusion

Acknowledgements

Funding

To increase trust, change the social design behind aggregated biodiversity data 3

Database, Volume 2018, 2018, bax100, https://doi.org/10.1093/database/bax100

Published: 04 January 2018 Article history ▼

<u></u> PDF

■■ Split View

66 Cite

te 👂 F

Permissions

Abstract

Growing concerns about the quality of aggregated biodiversity data are lowering trust in large-scale data networks. Aggregators frequently respond to quality concerns by recommending that biologists work with original data providers to correct errors 'at the source.' We show that this strategy falls systematically short of a full diagnosis of the underlying causes of distrust. In particular, trust in an aggregator is not just a feature of the data signal quality provided by the sources to the aggregator, but also a consequence of the social design of the aggregation process and the resulting power balance between individual data contributors and aggregators. The latter have created an accountability gap by downplaying the authorship and significance of the taxonomic hierarchies—frequently called 'backbones'—they generate, and which are in effect novel classification theories that operate at the core of datastructuring process. The Darwin Core standard for sharing occurrence records plays an under-appreciated role in maintaining the accountability gap, because this standard lacks the syntactic structure needed to preserve the taxonomic coherence of data packages submitted for aggregation, potentially leading to inferences that no individual source would support. Since high-quality data packages can mirror competing and conflicting classifications, i.e. unsettled systematic research, this plurality must be accommodated in the design of biodiversity data integration. Looking forward, a key directive is to develop new technical pathways and social incentives for experts to contribute directly to the validation of taxonomically coherent data packages as part of a greater, trustworthy aggregation process.

Issue Section: Perspective/Opinion

- https://doi.org/10.1093/database/bax10
 0
- Critique of monolithic aggregation designs.
- Here we reformulate the issue in relation to the direction of data flow in hierarchical biodiversity data aggregation networks.
- Then we outline a complementary solution that is **not centralized**, yet which can potentially reach **global** coverage.

Rethinking centralized biodiversity data aggregation (2)





Volume 2018 2018

Article Contents

Abstract

Introduction

No simple diagnosis for data quality deficiencies

Importance of trust for sustained use

Matching accountability to responsibility

Generation of novel systematic syntheses

Role of the DwC standard

Aggregation and authorship

Consequences of disenfranchizing taxonomic experts

Backbone-based data signal distortion: an example

An objection

Conclusion

Acknowledgements

Funding

To increase trust, change the social design behind aggregated biodiversity data 3

Database, Volume 2018, 2018, bax100, https://doi.org/10.1093/database/bax100

Published: 04 January 2018 Article history ▼

· ---

■■ Split View

66 Cite

Cite

Permissions

Abstract

Growing concerns about the quality of aggregated biodiversity data are lowering trust in large-scale data networks. Aggregators frequently respond to quality concerns by recommending that biologists work with original data providers to correct errors 'at the source.' We show that this strategy falls systematically short of a full diagnosis of the underlying causes of distrust. In particular, trust in an aggregator is not just a feature of the data signal quality provided by the sources to the aggregator, but also a consequence of the social design of the aggregation process and the resulting power balance between individual data contributors and aggregators. The latter have created an accountability gap by downplaying the authorship and significance of the taxonomic hierarchies—frequently called 'backbones'—they generate, and which are in effect novel classification theories that operate at the core of datastructuring process. The Darwin Core standard for sharing occurrence records plays an under-appreciated role in maintaining the accountability gap, because this standard lacks the syntactic structure needed to preserve the taxonomic coherence of data packages submitted for aggregation, potentially leading to inferences that no individual source would support. Since high-quality data packages can mirror competing and conflicting classifications, i.e. unsettled systematic research, this plurality must be accommodated in the design of biodiversity data integration. Looking forward, a key directive is to develop new technical pathways and social incentives for experts to contribute directly to the validation of taxonomically coherent data packages as part of a greater, trustworthy aggregation process.

Issue Section: Perspective/Opinion

- https://doi.org/10.1093/database/bax100
- Critique of monolithic aggregation designs.
- Here we reformulate the issue in relation to the direction of data flow in hierarchical biodiversity data aggregation networks.
- Then we outline a complementary solution that is not centralized, yet which can potentially reach global coverage.

Many collections remain offline.







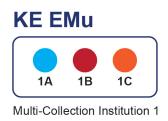


Other, individual collections, may have a web presence.



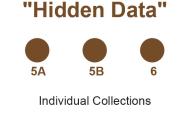
 Multi-collections software applications can bring institutional datasets on-line; yet this alone may not suffice to publish DwC-Archive data according to FAIR standards.

- Live Data Management
- No or Institional Aggregation
- IPT Needed for DwC-A Publishing (FAIR)

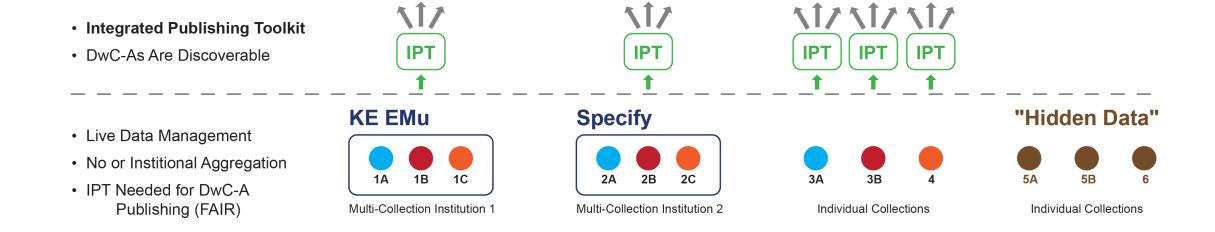




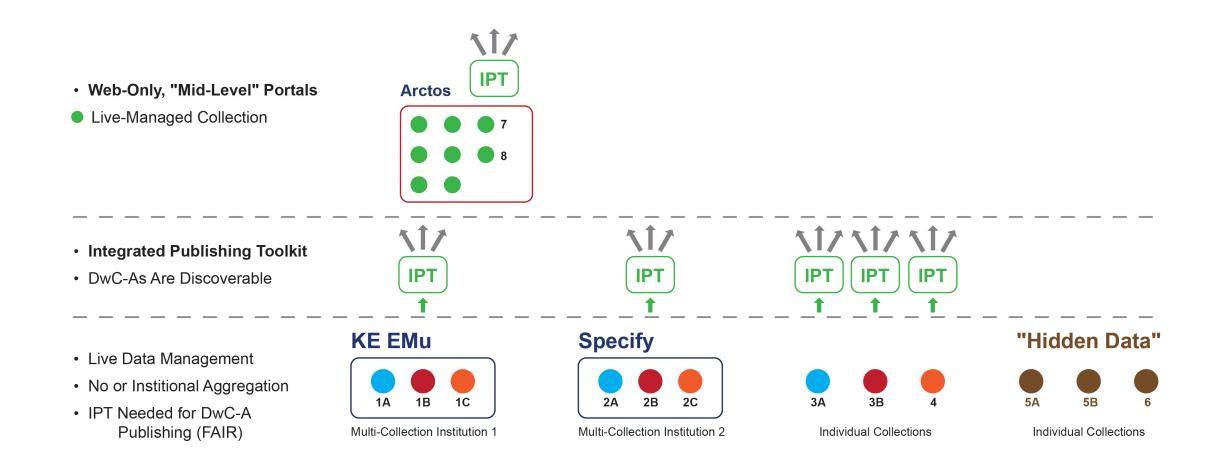




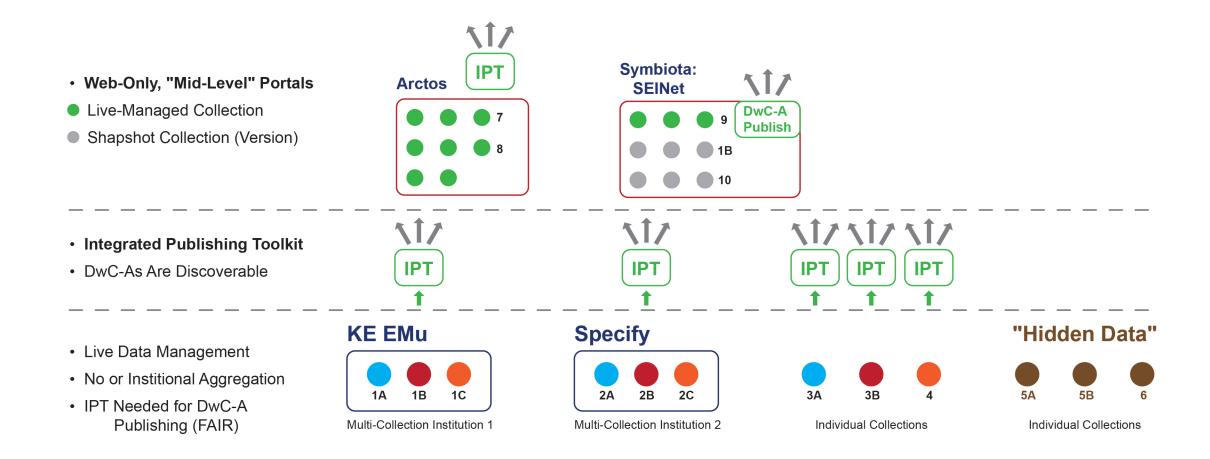
 The Integrated Publishing Toolkit (IPT) allows individual or multi-collection datasets to become discoverable as DwC-Archive packages to higher-level aggregators.



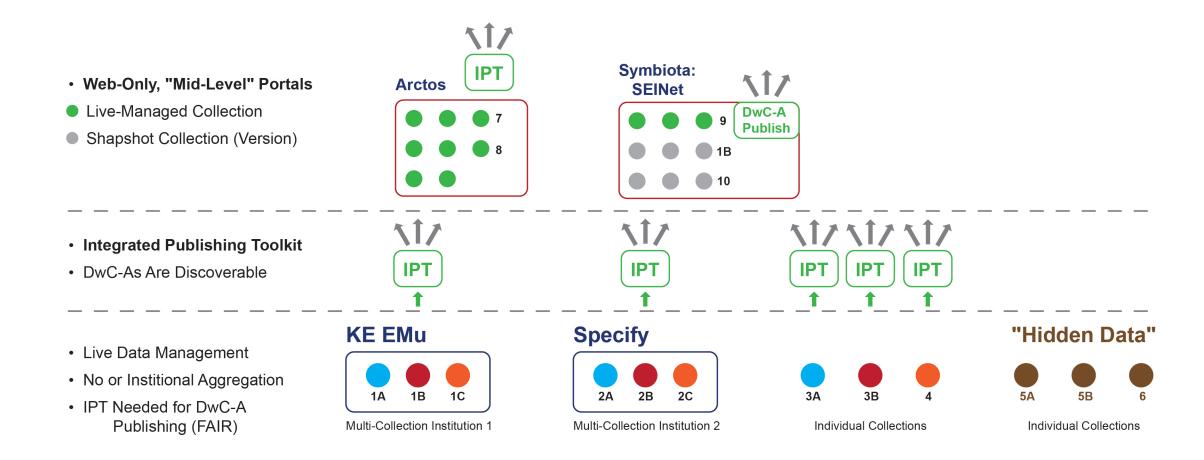
 There are also web-only, mid-level portal applications that support live collection management and can publish "up" through the (IPT).



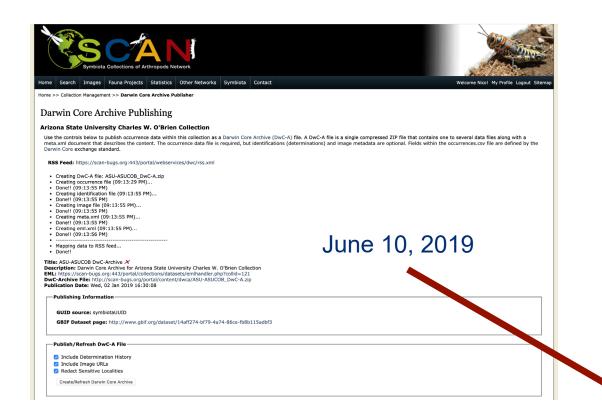
 Symbiota portals also support "snapshot collections" – i.e., periodical, manually triggered batch re-/uploads of static versions that are live-managed elsewhere.

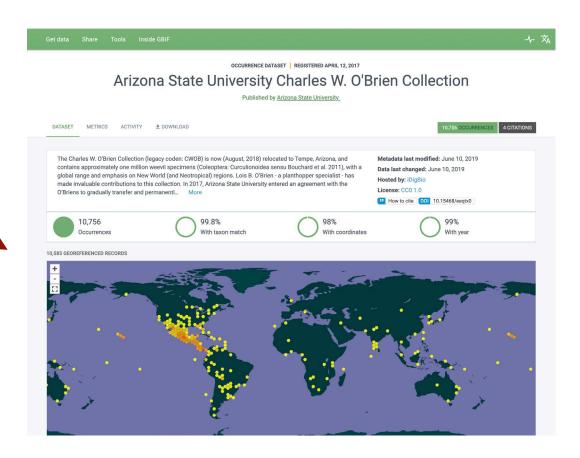


Symbiota portals also have a custom, fully built-in, IPT-analogous "Darwin Core Archive Publishing" module.

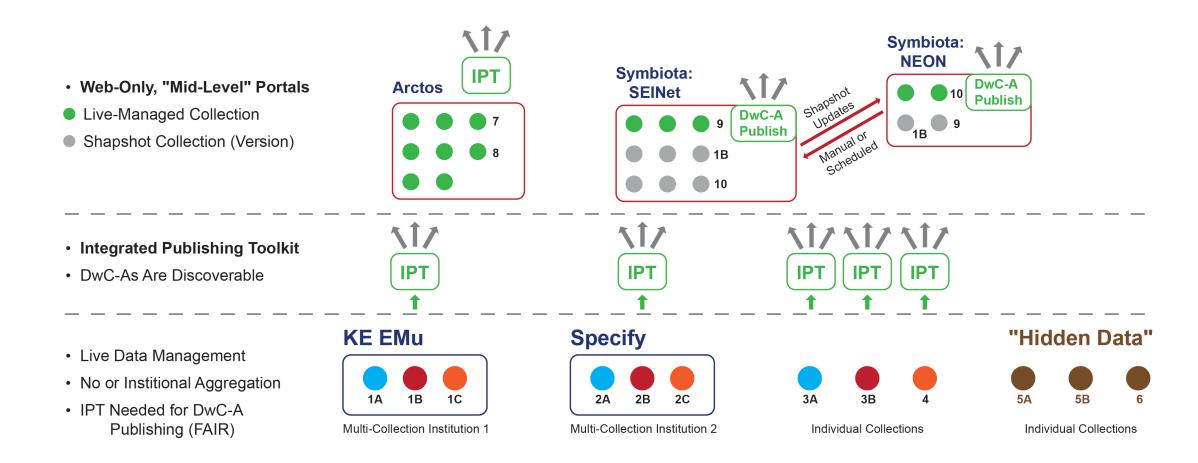


Example of Symbiota's DwC-A Publishing module (SCAN: ASUCOB)

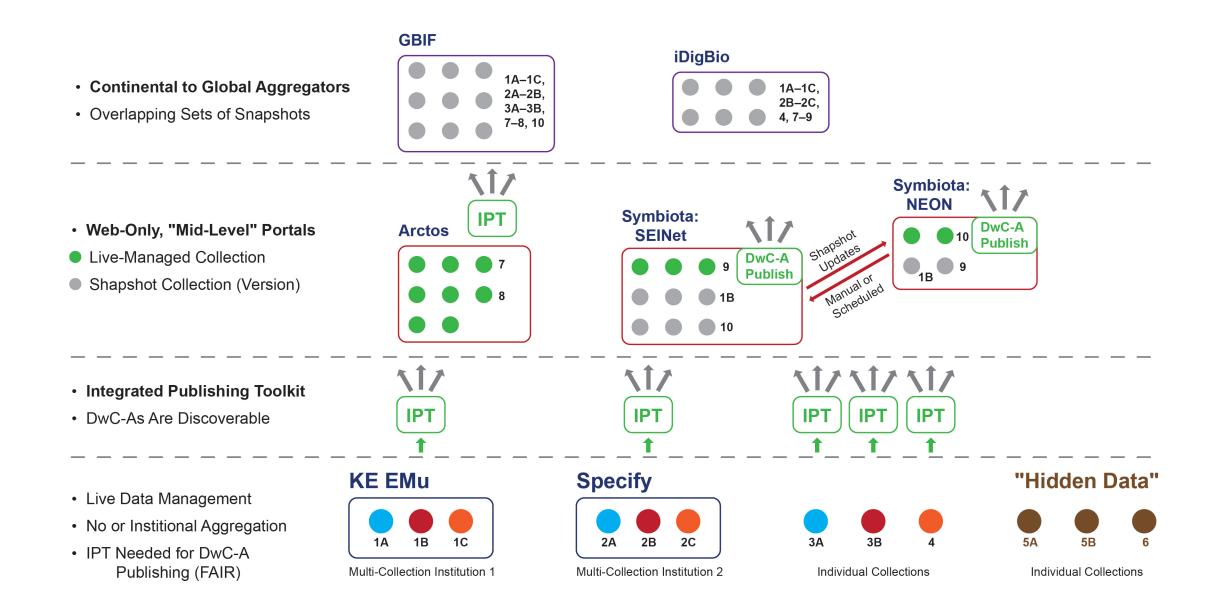




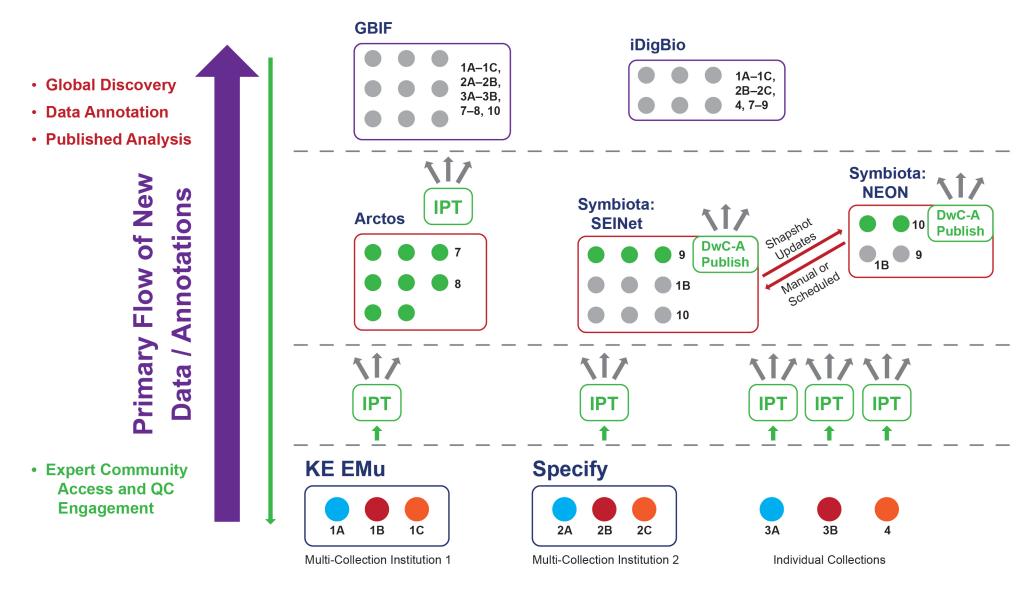
 Multiple, community-themed portals – each with unique live/snapshot collection profiles – can periodically receive reciprocal snapshot updates.



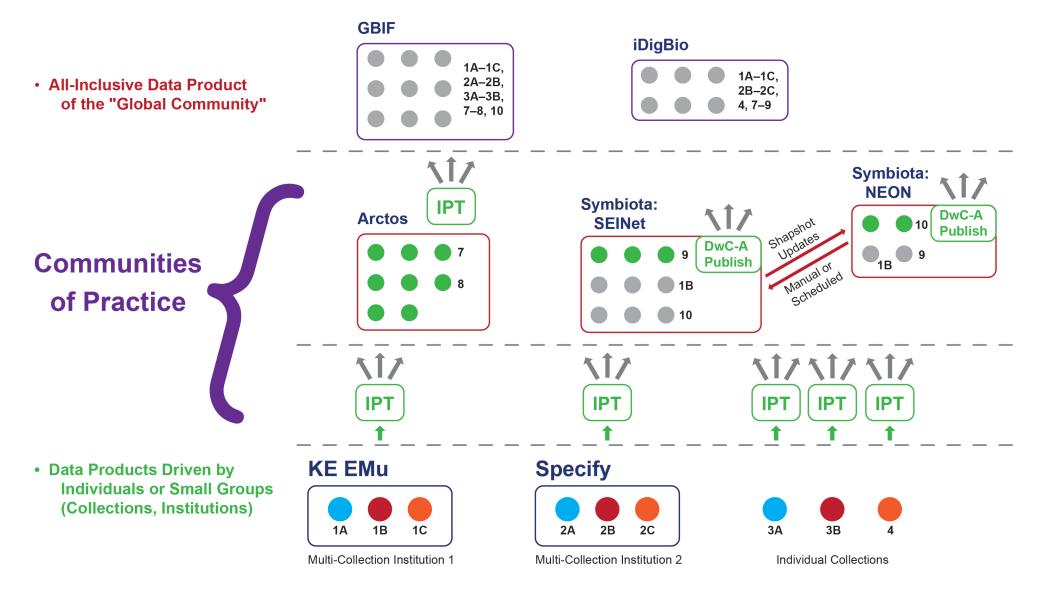
Highest-level aggregators typically only support collection snapshots!



This hierarchy sustains an imbalance in directional data flow: Annotations on global datasets are hard to pull downwards.



Moreover, by the time we reach the top, most **experts/enthusiasts no longer feel at home** (cf. Wenger 2000).

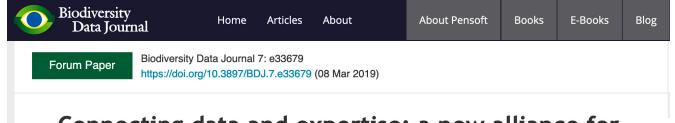


Wenger 2000: Communities of practice and social learning systems

 Table 2. Boundary Dimensions

	Coordination	Transparency	Negotiability
Engagement	What opportunities exist for joint activities, problem-solving, and discussions to both surface and resolve differences through action?	Do people provide explanations, coaching, and demonstrations in the context of joint activities to open windows on to each other's practices?	Are joint activities structured in such a way that multiple perspectives can meet and participants can come to appreciate each other's competences?
Imagination	Do people have enough understanding of their respective perspectives to present issues effectively and anticipate misunderstandings?	What stories, documents, and models are available to build a picture of another practice? What experience will allow people to walk in the other's shoes? Do they listen deeply enough?	Can both sides see themselves as members of an overarching community in which they have common interests and needs?
Alignment	Are instructions, goals, and methods interpretable into action across boundaries?	Are intentions, commitments, norms, and traditions made clear enough to reveal common ground and differences in perspectives and expectations?	Who has a say in negotiating contracts and devising compromises?

Community Access ⇔ Engagement ⇔ Quality ⇔ Trust ⇔ Use & Impact



Connecting data and expertise: a new alliance for biodiversity knowledge

▼ Donald Hobern, Brigitte Baptiste, Kyle Copas, Robert Guralnick, Andrea Hahn, Edwin van Huis, Eun-Shik Kim, Melodie McGeoch, Isayvani Naicker, Laetitia Navarro, Daniel Noesgaard, Michelle Price, Andrew Rodrigues, Dmitry Schigel, Carolyn A. Sheffield, John Wieczorek

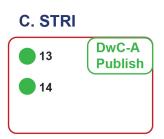
Abstract -

There has been major progress over the last two decades in digitising historical knowledge of biodiversity and in making biodiversity data freely and openly accessible. Interlocking efforts bring together international partnerships and networks, national, regional and institutional projects and investments and countless individual contributors, spanning diverse biological and environmental research domains, government agencies and non-governmental organisations, citizen science and commercial enterprise. However, current efforts remain inefficient and inadequate to address the global need for accurate data on the world's species and on changing patterns and trends in biodiversity. Significant challenges include imbalances in regional engagement in biodiversity informatics activity, uneven progress in data mobilisation and sharing, the lack of stable persistent identifiers for data records, redundant and incompatible processes for cleaning and interpreting data and the absence of functional mechanisms for knowledgeable experts to curate and improve data.

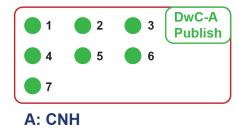
Designing for strong data communities

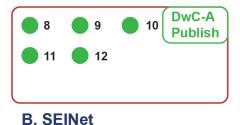
De-centralized, but global

 Independent, themed portal communities maintain live-managed collections.



- A: Consortium of Northeastern Herbaria
- B: [Southwest Environment Information Network]
- C: Smithsonian Tropical Research Institute



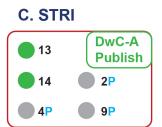


De-centralized, but global

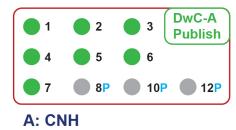
Partial, relevant collection snapshot subsets are represented.

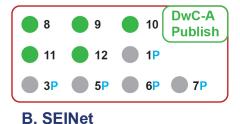
A-F = Portals | 1-20 = Collections (Partial)

- "Live-Managed" Collection
- "Shapshot" Collection (Vs.)



- A: Consortium of Northeastern Herbaria
- B: [Southwest Environment Information Network]
- C: Smithsonian Tropical Research Institute





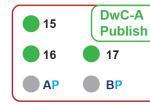
 Even partial, relevant portal snapshot subsets are ingestible, with provenance.

A-F = Portals | 1-20 = Collections (Partial)

- "Live-Managed" Collection
- "Shapshot" Collection (Vs.)



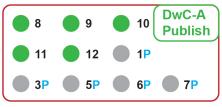
D. NEON



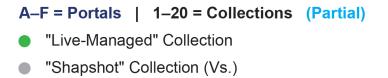
- A: Consortium of Northeastern Herbaria
- B: [Southwest Environment Information Network]
- C: Smithsonian Tropical Research Institute
- D: National Ecological Observatory Network

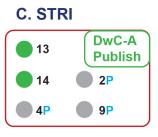


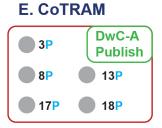
B. SEINet



Some research-themed portals may only include partial collection snapshots.









- A: Consortium of Northeastern Herbaria
- B: [Southwest Environment Information Network]
- C: Smithsonian Tropical Research Institute
- D: National Ecological Observatory Network
- E: Cooperative Taxonomic Resource for American Myrtaceae

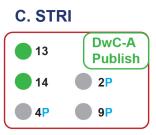


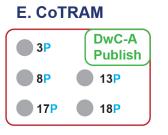


 Highly configurable portal-to-portal APIs negotiate the flow of data between live and snapshot collection instances.

 $A-F = Portals \mid 1-20 = Collections (Partial)$

- "Live-Managed" Collection = Direct Updates
- "Shapshot" Collection (Vs.) = API Updates







- A: Consortium of Northeastern Herbaria
- B: [Southwest Environment Information Network]
- C: Smithsonian Tropical Research Institute
- D: National Ecological Observatory Network
- E: Cooperative Taxonomic Resource for American Myrtaceae

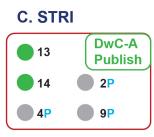


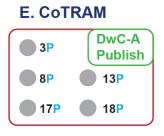
Portal-to-Portal

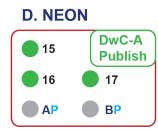
 As API services are optimized, the distinction between live and snapshot collection management increasingly falls away.

A-F = Portals | 1-20 = Collections (Partial)

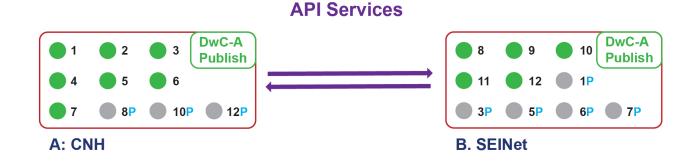
- "Live-Managed" Collection = Direct Updates
- "Shapshot" Collection (Vs.) = API Updates







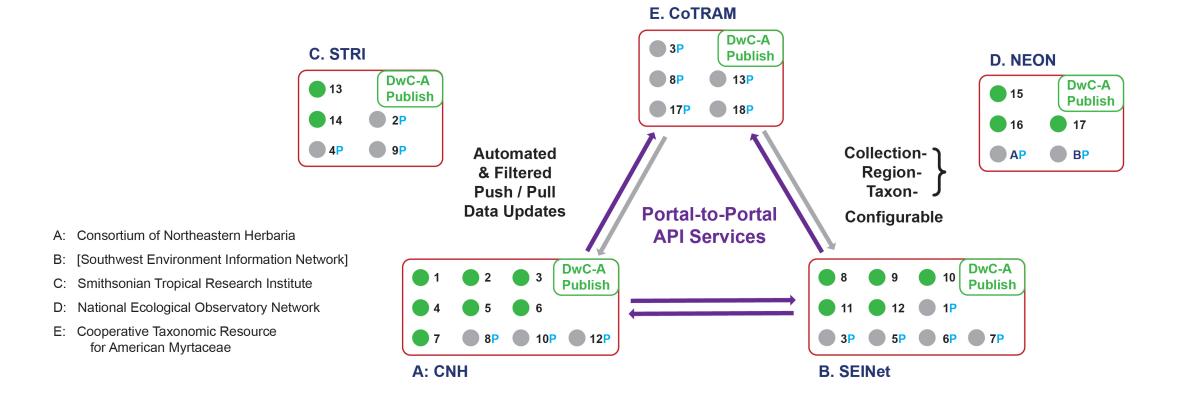
- A: Consortium of Northeastern Herbaria
- B: [Southwest Environment Information Network]
- C: Smithsonian Tropical Research Institute
- D: National Ecological Observatory Network
- E: Cooperative Taxonomic Resource for American Myrtaceae



Portal-to-Portal

 API service configurations include filtered, source-/sink-approval contingent data pushes and pulls.

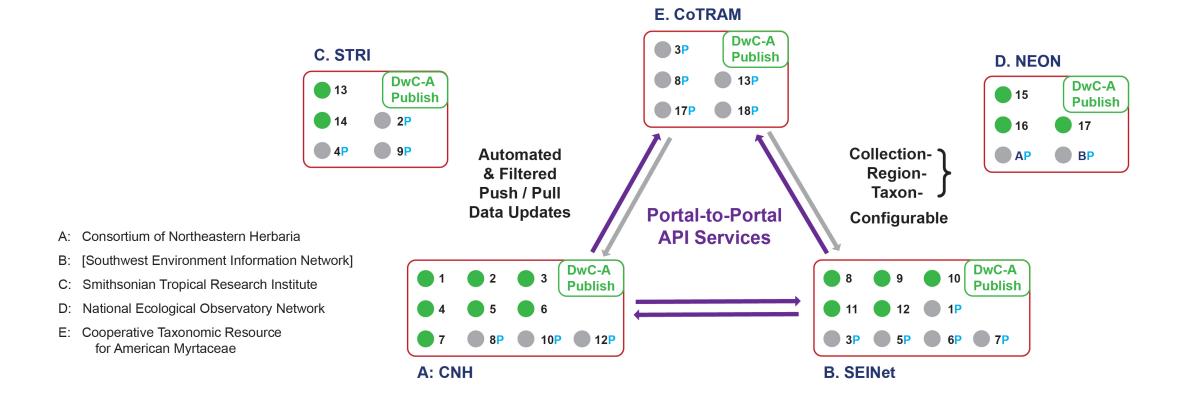
```
    A-F = Portals | 1-20 = Collections (Partial)
    "Live-Managed" Collection = Direct Updates
    "Shapshot" Collection (Vs.) = API Updates
```



 API service configurations allow filtered {collection, taxon, region, etc.), source-/sink-approval contingent data pushes and pulls.

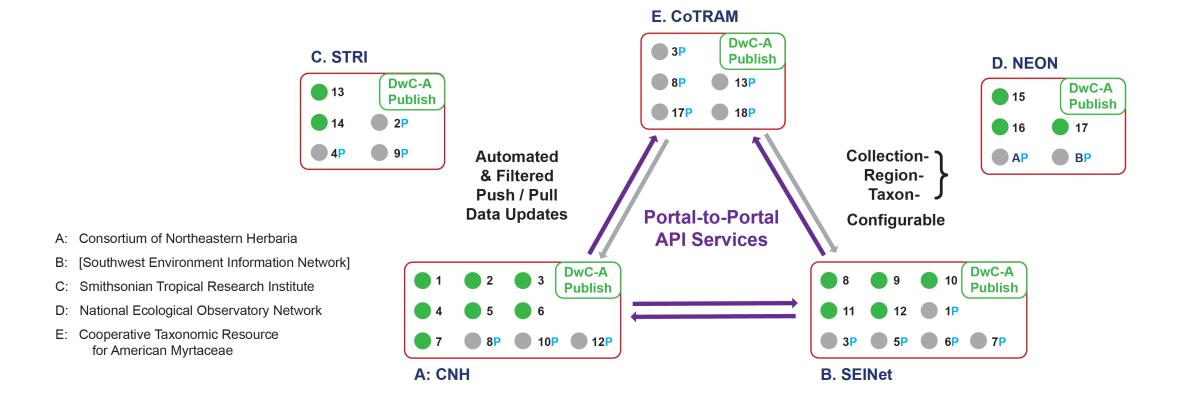
A-F = Portals | 1-20 = Collections (Partial)

- "Live-Managed" Collection = Direct Updates
- "Shapshot" Collection (Vs.) = API Updates



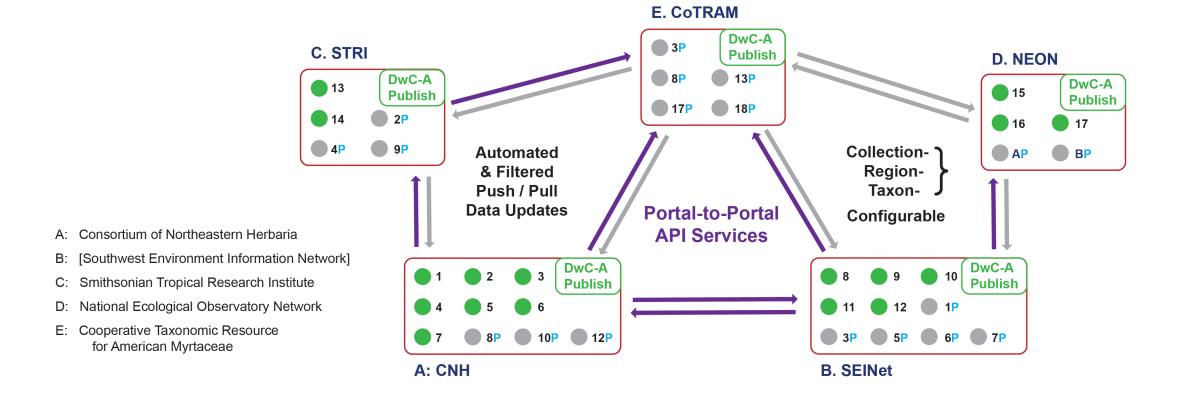
 Portal-to-portal API configurations become the "substrate" upon which the communities realize their "modes of belonging".

A-F = Portals | 1-20 = Collections (Partial)
 "Live-Managed" Collection = Direct Updates
 "Shapshot" Collection (Vs.) = API Updates



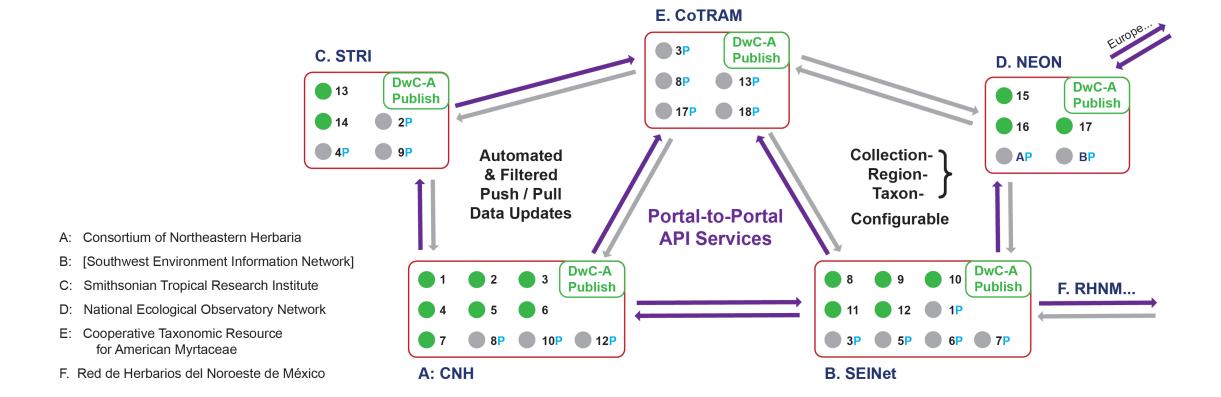
 The de-centralized network is broadly extensible between closely (high data flow) or remotely (low data flow) related communities.

A-F = Portals | 1-20 = Collections (Partial)
 "Live-Managed" Collection = Direct Updates
 "Shapshot" Collection (Vs.) = API Updates
 Higher- / Lower- volume data flow



 On the basis of a shared API service culture, a de-centralized data portal network can potentially grow to attain global coverage.

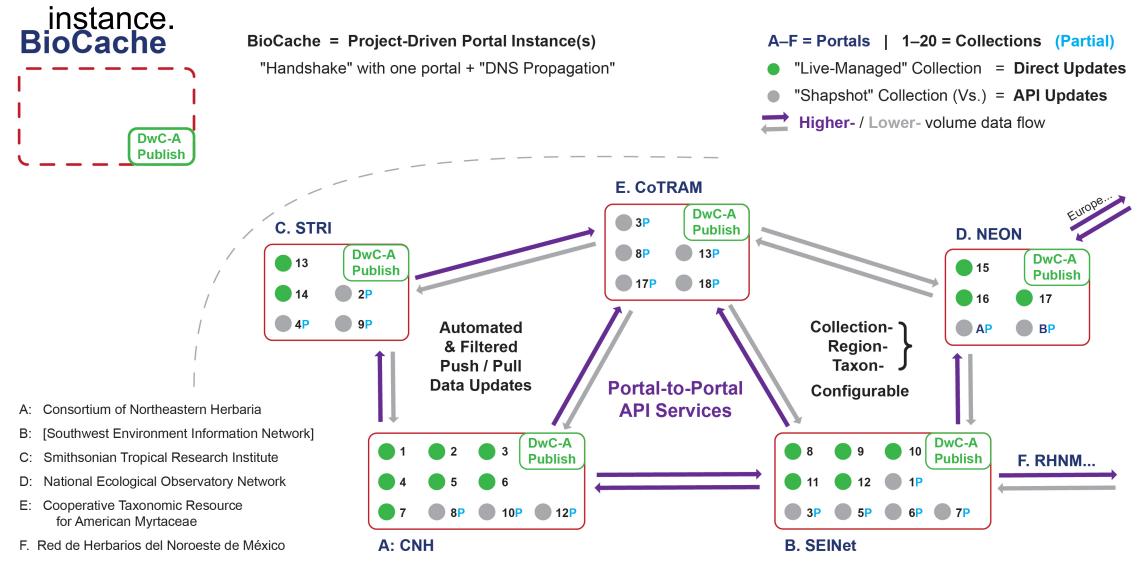
A-F = Portals | 1-20 = Collections (Partial)
 "Live-Managed" Collection = Direct Updates
 "Shapshot" Collection (Vs.) = API Updates
 Higher- / Lower- volume data flow



Designing for expert/enthusiast access

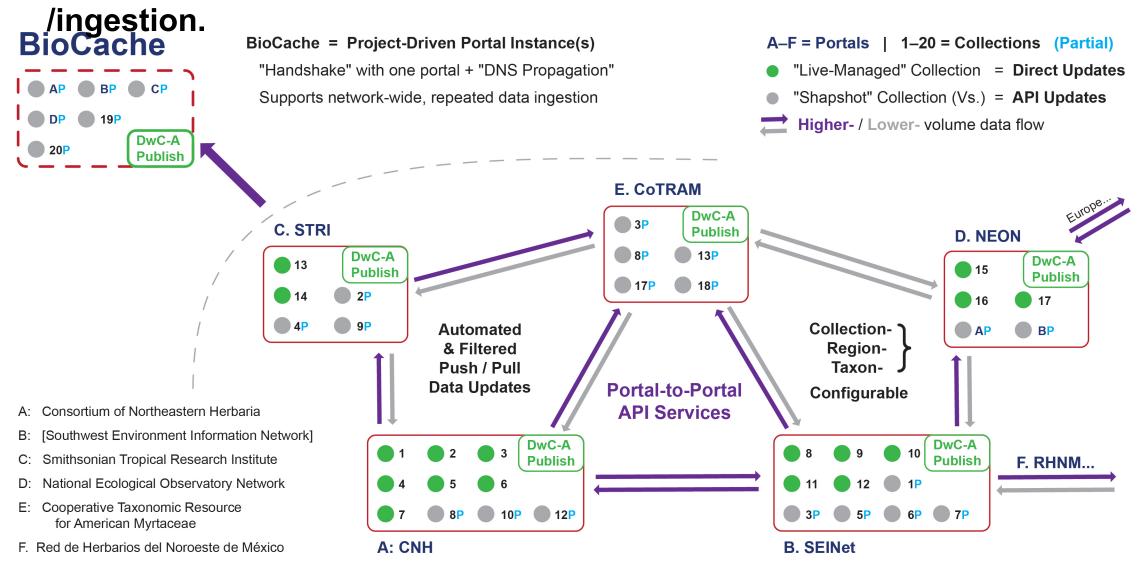
BioCache: Global access through custom research portal instances

Researchers create and register "via single handshake" a new portal



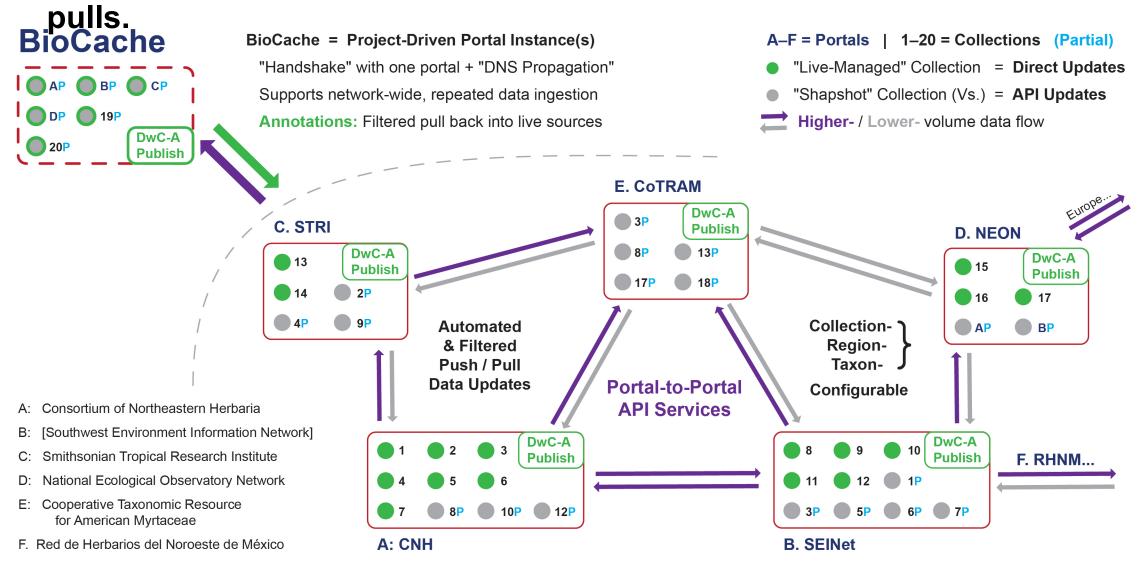
BioCache: Global access through custom research portal instances

Research instances enable repeatable, global data queries and re-



BioCache: Global access through custom research portal instances

Valued-added data can return to all (live) source collections via filtered



Stay tuned, it's underway

Taxonomic data intelligence for Darwin Core occurrences (3)



Controlling the taxonomic variable: Taxonomic concept resolution for a southeastern United States herbarium portal

▼ Nico Franz, Edward Gilbert, Bertram Ludäscher, Alan Weakley

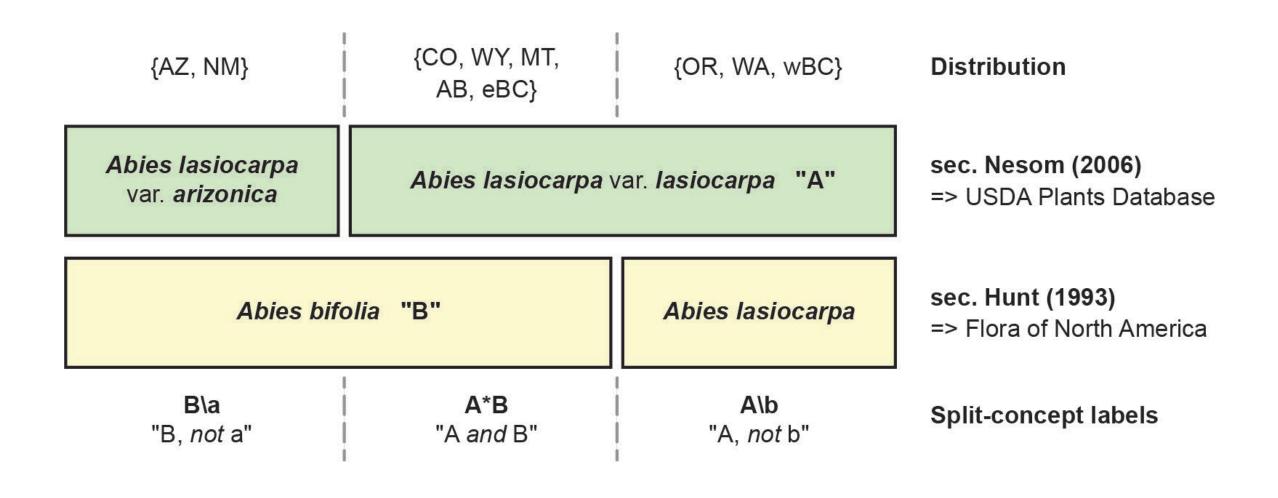
Executive summary -

Overview. Taxonomic names are imperfect identifiers of specific and sometimes conflicting taxonomic perspectives in aggregated biodiversity data environments. The inherent ambiguities of names can be mitigated using syntactic and semantic conventions developed under the taxonomic concept approach. These include: (1) representation of taxonomic concept labels (TCLs: name sec. source) to precisely identify name usages and meanings, (2) use of parent/child relationships to assemble separate taxonomic perspectives, and (3) expert provision of Region Connection Calculus articulations (RCC–5: congruence, [inverse] inclusion, overlap, exclusion) that specify how data identified to different-sourced TCLs can be integrated. Application of these conventions greatly increases trust in biodiversity data networks, most of which promote unitary taxonomic 'syntheses' that obscure the actual diversity of expert-held views. Better design solutions allow users to control the taxonomic variable and thereby assess the robustness of their biological inferences under different perspectives. A unique constellation of prior efforts – including the powerful Symbiota collections software platform, the Euler/X multi-taxonomy alignment toolkit, and the "Weakley Flora" which entails 7,000 concepts and more than 75,000 RCC–5 articulations – provides the opportunity to build a first full-scale concept resolution service for SERNEC, the SouthEast Regional Network of Expertise and Collections, currently with 60 member herbaria and 2 million occurrence records.

Intellectual merit. We have developed a multi-dimensional, step-wise plan to transition SERNEC's data culture from name- to concept-based practices. (1) We will engage SERNEC experts through annual, regional workshops and follow-up interactions that will foster buy-in and ultimately the completion of 12 community-identified use cases. (2). We will leverage RCC–5 data from the Weakley Flora and further development of the Euler/X logic reasoning toolkit to provide comprehensive genus- to variety-level concept alignments for at least 10 major flora treatments with highest relevance to SERNEC. The visualizations and estimated > 1 billion inferred concept-to-concept relations will effectively drive specimen data integration in the transformed portal. (3) We will expand Symbiota's taxonomy and occurrence schemas and related user interfaces to support the new concept data, including novel batch and map-based specimen determination modules, with easy output options in Darwin Core Archive format. (4) Through combinations of the new

- https://doi.org/10.3897/rio.2.e10610
- Engaging expert/enthusiast communities
 heed for pluralism and democracy for and among taxonomic perspectives in biodiversity data aggregation designs.

Alignment by Alan Weakley (http://herbarium.unc.edu/flora.htm)



Taxonomic data intelligence for Darwin Core occurrences (3)



Controlling the taxonomic variable: Taxonomic concept resolution for a southeastern United States herbarium portal

▼ Nico Franz, Edward Gilbert, Bertram Ludäscher, Alan Weakley

Executive summary -

Overview. Taxonomic names are imperfect identifiers of specific and sometimes conflicting taxonomic perspectives in aggregated biodiversity data environments. The inherent ambiguities of names can be mitigated using syntactic and semantic conventions developed under the taxonomic concept approach. These include: (1) representation of taxonomic concept labels (TCLs: name sec. source) to precisely identify name usages and meanings, (2) use of parent/child relationships to assemble separate taxonomic perspectives, and (3) expert provision of Region Connection Calculus articulations (RCC–5: congruence, [inverse] inclusion, overlap, exclusion) that specify how data identified to different-sourced TCLs can be integrated. Application of these conventions greatly increases trust in biodiversity data networks, most of which promote unitary taxonomic 'syntheses' that obscure the actual diversity of expert-held views. Better design solutions allow users to control the taxonomic variable and thereby assess the robustness of their biological inferences under different perspectives. A unique constellation of prior efforts – including the powerful Symbiota collections software platform, the Euler/X multi-taxonomy alignment toolkit, and the "Weakley Flora" which entails 7,000 concepts and more than 75,000 RCC–5 articulations – provides the opportunity to build a first full-scale concept resolution service for SERNEC, the SouthEast Regional Network of Expertise and Collections, currently with 60 member herbaria and 2 million occurrence records.

Intellectual merit. We have developed a multi-dimensional, step-wise plan to transition SERNEC's data culture from name- to concept-based practices. (1) We will engage SERNEC experts through annual, regional workshops and follow-up interactions that will foster buy-in and ultimately the completion of 12 community-identified use cases. (2). We will leverage RCC–5 data from the Weakley Flora and further development of the Euler/X logic reasoning toolkit to provide comprehensive genus- to variety-level concept alignments for at least 10 major flora treatments with highest relevance to SERNEC. The visualizations and estimated > 1 billion inferred concept-to-concept relations will effectively drive specimen data integration in the transformed portal. (3) We will expand Symbiota's taxonomy and occurrence schemas and related user interfaces to support the new concept data, including novel batch and map-based specimen determination modules, with easy output options in Darwin Core Archive format. (4) Through combinations of the new

- https://doi.org/10.3897/rio.2.e10610
- Engaging expert/enthusiast communities
 heed for pluralism and democracy for and among taxonomic perspectives in biodiversity data aggregation designs.
- Spatial reasoning tools (RCC-5) can help attain consistent and comprehensive taxonomic meaning mappings
 intelligence for data integration across evolving or conflicting views.

Taxonomic data intelligence for Darwin Core occurrences (3)



Controlling the taxonomic variable: Taxonomic concept resolution for a southeastern United States herbarium portal

▼ Nico Franz, Edward Gilbert, Bertram Ludäscher, Alan Weakley

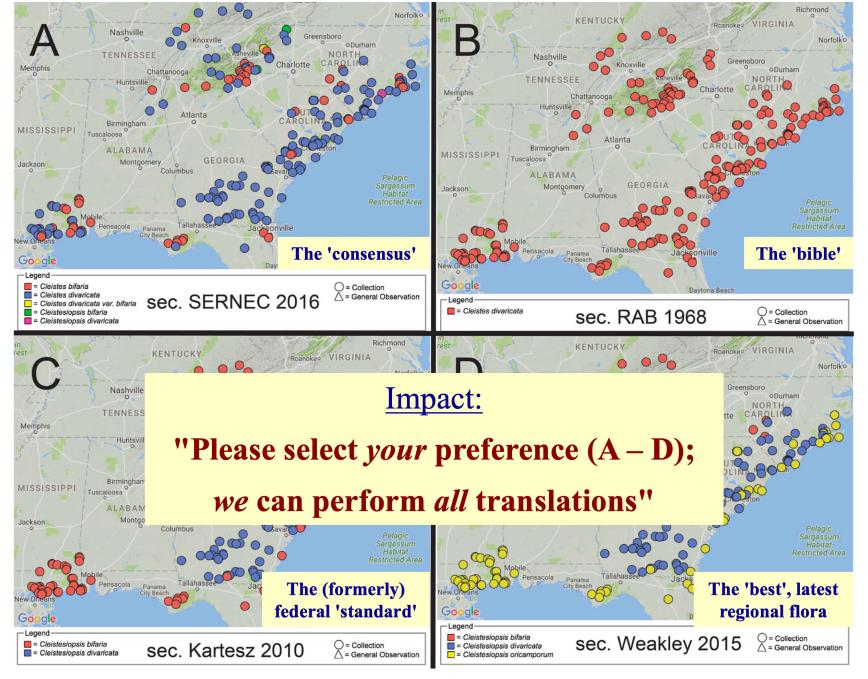
Executive summary -

Overview. Taxonomic names are imperfect identifiers of specific and sometimes conflicting taxonomic perspectives in aggregated biodiversity data environments. The inherent ambiguities of names can be mitigated using syntactic and semantic conventions developed under the taxonomic concept approach. These include: (1) representation of taxonomic concept labels (TCLs: name sec. source) to precisely identify name usages and meanings, (2) use of parent/child relationships to assemble separate taxonomic perspectives, and (3) expert provision of Region Connection Calculus articulations (RCC–5: congruence, [inverse] inclusion, overlap, exclusion) that specify how data identified to different-sourced TCLs can be integrated. Application of these conventions greatly increases trust in biodiversity data networks, most of which promote unitary taxonomic 'syntheses' that obscure the actual diversity of expert-held views. Better design solutions allow users to control the taxonomic variable and thereby assess the robustness of their biological inferences under different perspectives. A unique constellation of prior efforts — including the powerful Symbiota collections software platform, the Euler/X multi-taxonomy alignment toolkit, and the "Weakley Flora" which entails 7,000 concepts and more than 75,000 RCC–5 articulations — provides the opportunity to build a first full-scale concept resolution service for SERNEC, the SouthEast Regional Network of Expertise and Collections, currently with 60 member herbaria and 2 million occurrence records.

Intellectual merit. We have developed a multi-dimensional, step-wise plan to transition SERNEC's data culture from name- to concept-based practices. (1) We will engage SERNEC experts through annual, regional workshops and follow-up interactions that will foster buy-in and ultimately the completion of 12 community-identified use cases. (2). We will leverage RCC–5 data from the Weakley Flora and further development of the Euler/X logic reasoning toolkit to provide comprehensive genus- to variety-level concept alignments for at least 10 major flora treatments with highest relevance to SERNEC. The visualizations and estimated > 1 billion inferred concept-to-concept relations will effectively drive specimen data integration in the transformed portal. (3) We will expand Symbiota's taxonomy and occurrence schemas and related user interfaces to support the new concept data, including novel batch and map-based specimen determination modules, with easy output options in Darwin Core Archive format. (4) Through combinations of the new

- https://doi.org/10.3897/rio.2.e10610
- Engaging expert/enthusiast communities
 heed for pluralism and democracy for and among taxonomic perspectives in biodiversity data aggregation designs.
- Spatial reasoning tools (RCC-5) can help attain consistent and comprehensive taxonomic meaning mappings
 intelligence for data integration across evolving or conflicting views.

. Dialogical informaco become vebus



Source: Franz et al. 2016. Controlling the taxonomic variable: [...]. RIO Journal. doi:10.3897/rio.2.e10610

Project remains pending, but look!

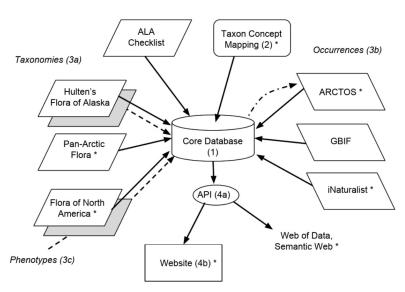
"Taxonomically intelligent data integration for a new Flora of Alaska"

Blog 1: Project roadmap

Posted by <u>Cam</u> on 2018-08-17

Hi! Welcome to this development blog, this website, and this project. Steffi and I were so pleased to get this NSF funding — many, many thanks to the ABI panelists, the four reviewers, and to NSF and US taxpayers.

In this blog, I'll lay out the main steps in the development of the informatics infrastructure. (For a general overview of the project, see here.) Here is an overview diagram:



The software and data elements to be constructed and integrated are:

1. A core database: a standard MySQL (MariaDB) database, running on a web-hosting platform (<u>Dreamhost</u>). Over the years I've played with many database paradigms, including XML databases (<u>ExistDB</u>) and graph databases (e.g., <u>4store</u>, <u>Allegrograph</u>,





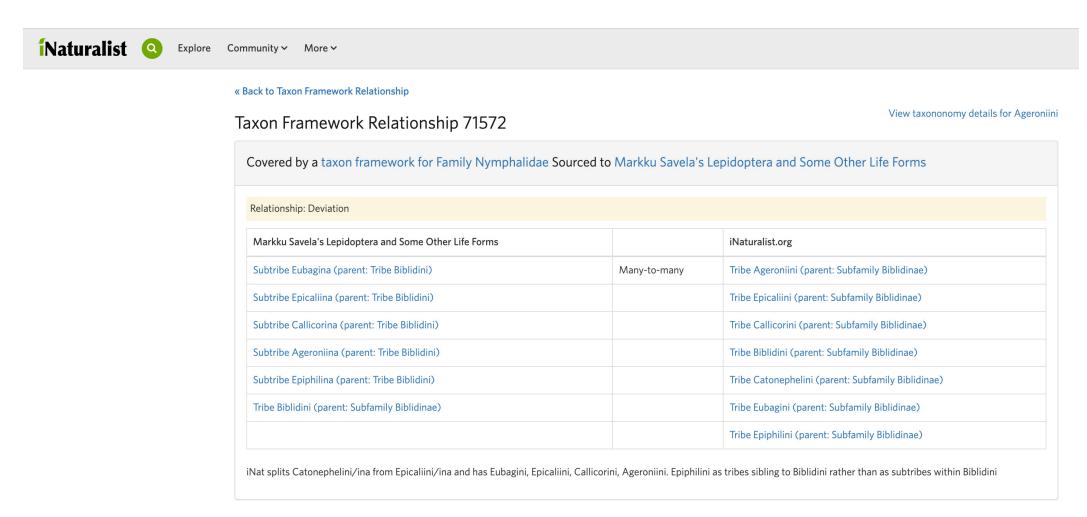
- NSF DBI 1759964
- PIs Ickert-Bond & Webb
- Reconciling Hulten, FNA & Pan-Arctic Flora
- See http://alaskaflora.org/

iNaturalist is mostly there already

Taxon Framework Relationships About Taxon Frameworks Taxon Frameworks help us describe 'what we mean' by a taxon. Taxon Framework Relationships are mappings between taxa on iNaturalist.org (internal taxa) and taxa on sources (external taxa) associated with a Taxon Framework. Read more Relationship Taxon Framework Relationship 332324 match one-to-one alternate position many-to-many many-to-one Covered by a taxon framework for Class Magnoliopsida Sourced to Plants of the World Online one-to-many not external Relationship: Match not internal Plants of the World Online iNaturalist.org Taxon framework taxon Species Trapa hyrcana (parent: Genus Trapa) Species Trapa hyrcana (parent: Genus Trapa) Internal taxon (including descendants) Type taxon name Taxon Framework Relationship 332323 External taxon (including children) Covered by a taxon framework for Class Lycopodiopsida Sourced to Plants of the World Online Internal taxon rank Relationship: Deviation Plants of the World Online iNaturalist.org External taxon rank any Species Lycopodium obtusifolium (parent:) One-to-one Species Phlegmariurus obtusifolius (parent: Genus Phlegmariurus) Added by We follow PPG I in recognizing Phlegmariurus as a segregate of Huperzia. Start typing someone's na Active Either \$ Taxon Framework Relationship 332322 Clear filters Covered by a taxon framework for Class Lycopodiopsida Sourced to Plants of the World Online Relationship: Deviation Plants of the World Online iNaturalist.org

https://www.inaturalist.org/taxon_framework_relationships

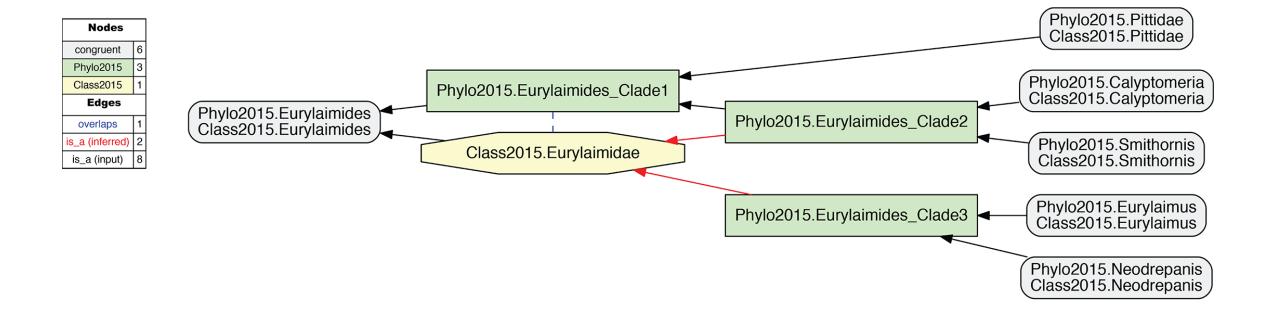
iNaturalist is mostly there already



Downstream deviations for Epicaliini 1

https://www.inaturalist.org/taxon_framework_relationships

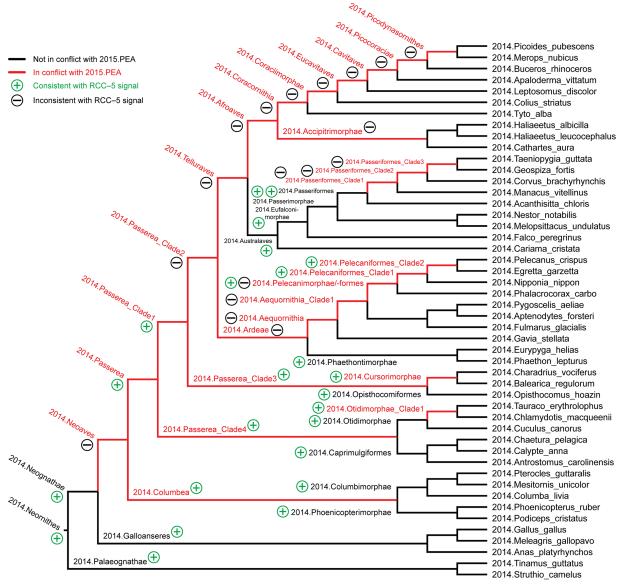
Recent addition: Concept alignment for phylogenomic trees



Franz, N.M. et al. 2019. Verbalizing phylogenomic conflict: [...]. https://doi.org/10.1371/journal.pcbi.1006493

Reliable theories of multi-tree node congruence require expert

judgment "Synthesis" OpenTree vs. RCC-5



Franz, N.M. et al. 2019. Verbalizing phylogenomic conflict: [...]. https://doi.org/10.1371/journal.pcbi.1006493

Hopeful conclusions

Key message: Biodiversity informatics remains young and fresh; especially if we aim

to **incentivize experts/enthusiasts** in publishing high-quality, "data-intelligent" biodiversity data products.

Hopeful conclusions

Key message: Biodiversity informatics remains young and fresh; especially if we aim

to **incentivize experts/enthusiasts** in publishing high-quality, "data-intelligent" biodiversity data products.

There are many grassroots or federally supported projects in this domain that **express**

enthusiasm for, and confidence in, a strong future for new, high-volume,

perpetually **data-restructuring systematic research**; driving our evolving

views of relations between DwC datasets and biological knowledge.

Hopeful conclusions

Key message: Biodiversity informatics remains young and fresh; especially if we aim

to **incentivize experts/enthusiasts** in publishing high-quality, "data-intelligent" biodiversity data products.

There are many grassroots or federally supported projects in this domain that **express**

enthusiasm for, and confidence in, a strong future for new, high-volume,

perpetually data-restructuring systematic research; driving our evolving

views of relations between DwC datasets and biological knowledge.

If you have the neceion and stomach for that future inin us now!

Acknowledgments

 Gil Nelson, Alnycea Blackwell, Jillian Goodwin, and all other iDigBio and Yale Peabody organizers and sponsors of #Digidata 2019.

ASU Biocollections & NEON Biorepository team.

Euler/X team: Bertram Ludäscher, Shizhuo Yu, Jessica Cheng.

 If you wish to read one paper on aligning taxonomic concepts: https://doi.org/10.1093/sysbio/syw023

