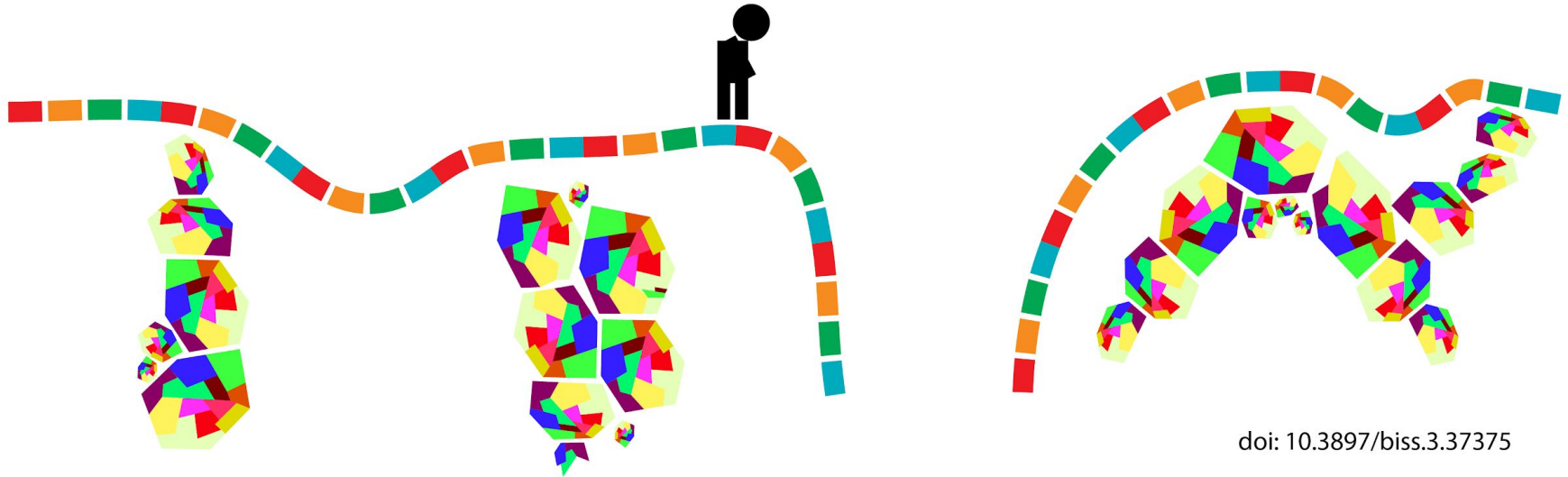


Are Software Standards Possible for Biodiversity, and What Would They Mean to the Fractured Landscape of Biodiversity Virtual Research Environments?

Biodiversity Next, 2019

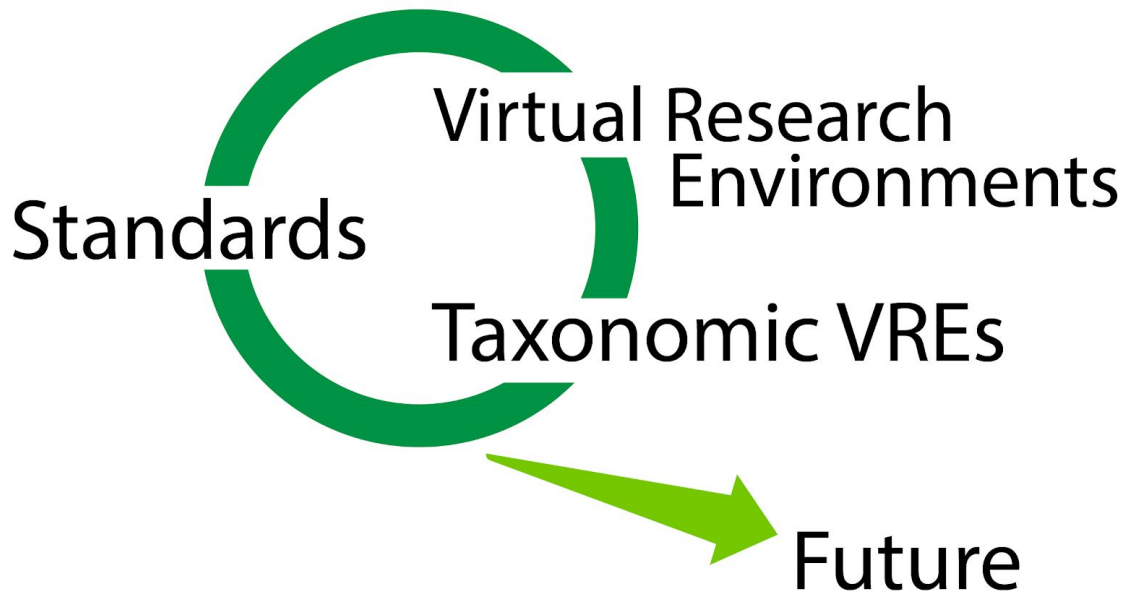
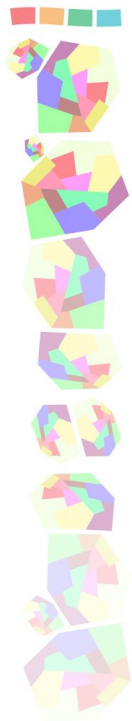
Matt Yoder



doi: 10.3897/biss.3.37375

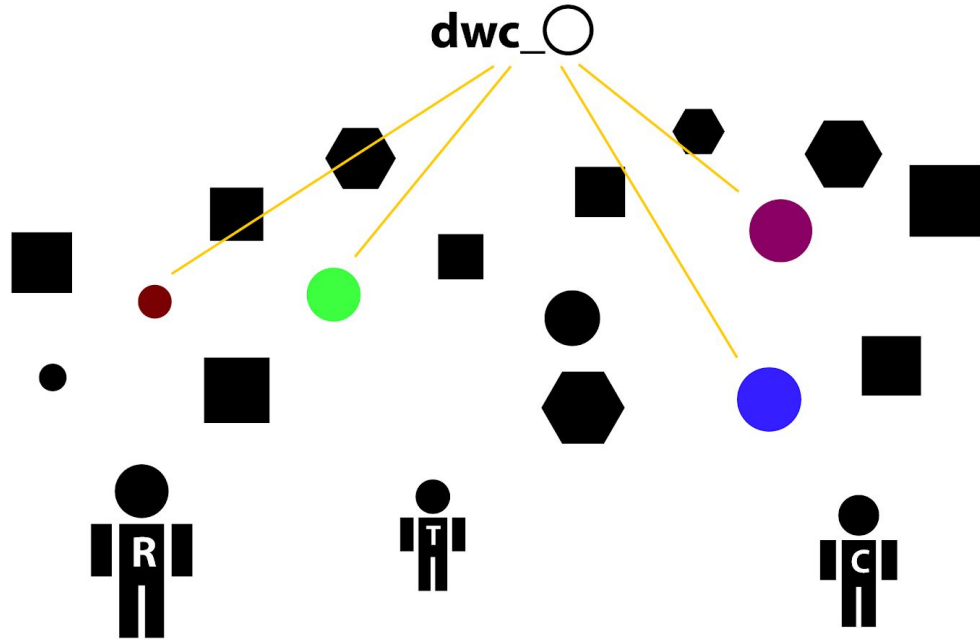
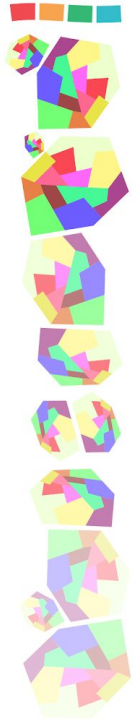


Outline





How do standards come to be?

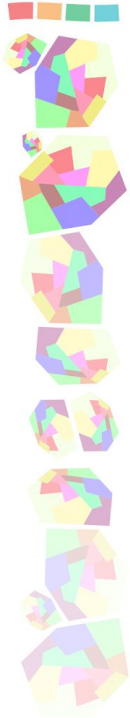


FFT:

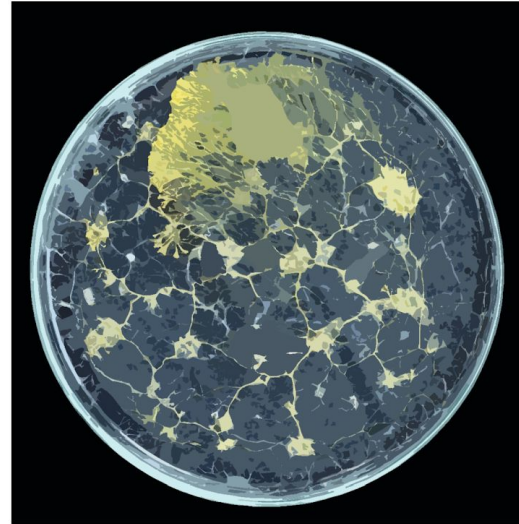
Standards are born from diversity.



Standard what?!



1 DWC field - sex
12,000 Distinct values!?!?!?



720- yes! 12k? Likely not.
The Blob, derived from image by Paris Museum

FFT:

https://github.com/tdwg/dwc-qa/blob/master/data/idigbioDistinctValues/iDigBio_distinct_sex_01-03-17.csv - **Thanks iDigDeb!**



... no standard applications either



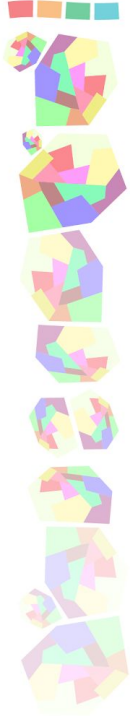
```
Paradox
- View Ask Report Create Modify Image Forms Tools Scripts Exit
Full form, 2 pages
Cited name: Epidinocarsis lopezi 1964
(De Santis)
(subg. subsp. )
TAXONOMIC STATUS Reference: NoyesHa984 : 273 Author:
Status: NC for Apoanagyrus lopezi De Santis
Apoana lopezD ( )
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KEYWORDS
Reference: BaarenBaNe996 : 710-720 Keyword: Ad
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HOSTS
Reference: GoergeNe990_ : 317-326 Comment: ZR Lab record?:
Associate: Phenacoccus manihoti Matille-Ferrero HePs
Relationship: PRH Common Name? Reliability: 12810
Parasitoid Type: Notes:
Phenacoccus manihoti Matille-Ferrero HePs 12810
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Region: F Country: State: Lab record?: Bc Notes:
116 of 232 1-M
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FFT:

Some VREs are nearing 3 decades old



“Taxonomic” VREs

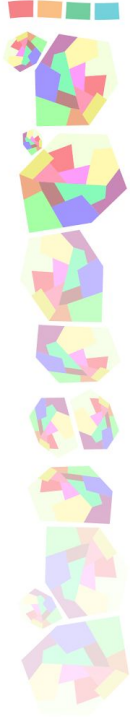


For the purposes of discussion integrate at least 4 of these things:

- manage specimens and generate material examined sections
- track complex taxonomic nomenclature, exporting publication ready catalogs
- create keys and interactive keys
- include image databases
- capture matrix data to produce phylogenies or generate taxon descriptions
- contain built in reference managers
- track collecting events, localities, field-notes
- track type specimens
- create anatomy ontologies
- act as endpoints for URIs
- ...much more*

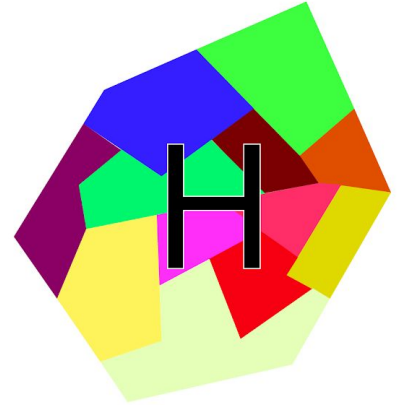


Integrated hypotheses are the foundations of biology



...

<aha!>

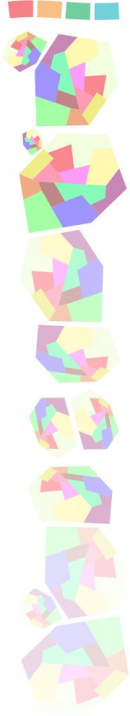


FFT:

Taxonomists are truly remarkable integrators.



Taxonomic VREs are lifetime companions



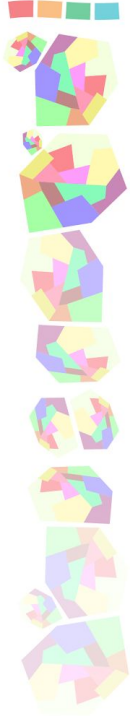
a taxonomic VRE can take

30 years to build

10 years to migrate



Origin of the Taxonomic VRE



CMS model

Wiki model

DWC model

Relational model

Open source Web

Closed Desktop



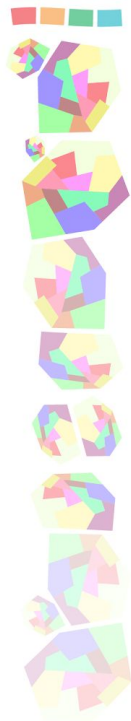
**ALL
BUILT
BY
TAXONOMISTS**

FFT:

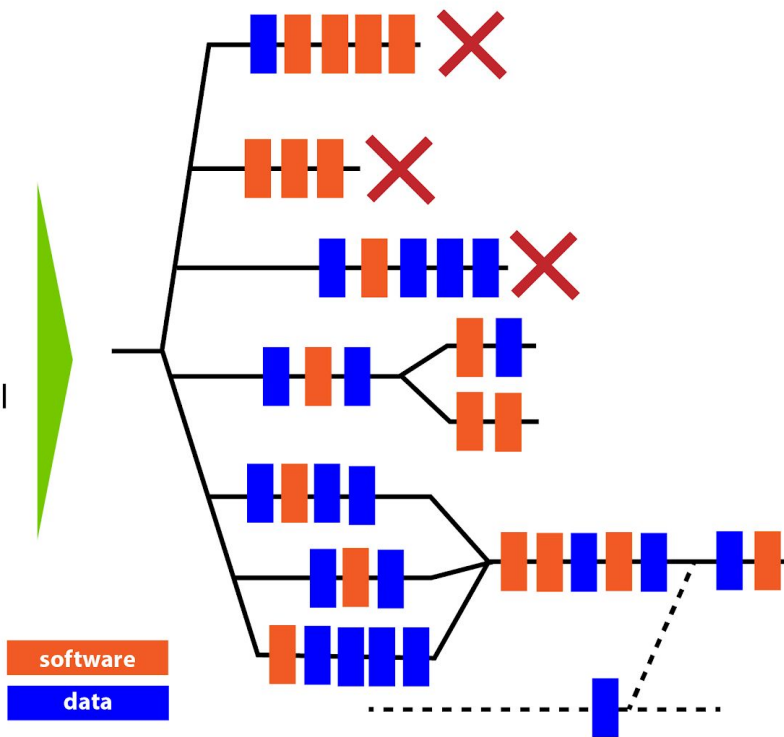
Where do taxonomists find time to do taxonomy?



Taxonomic VRE “speciation” and evolution



CMS model
Wiki model
DWC model
Relational model
Open source Web
Closed Desktop

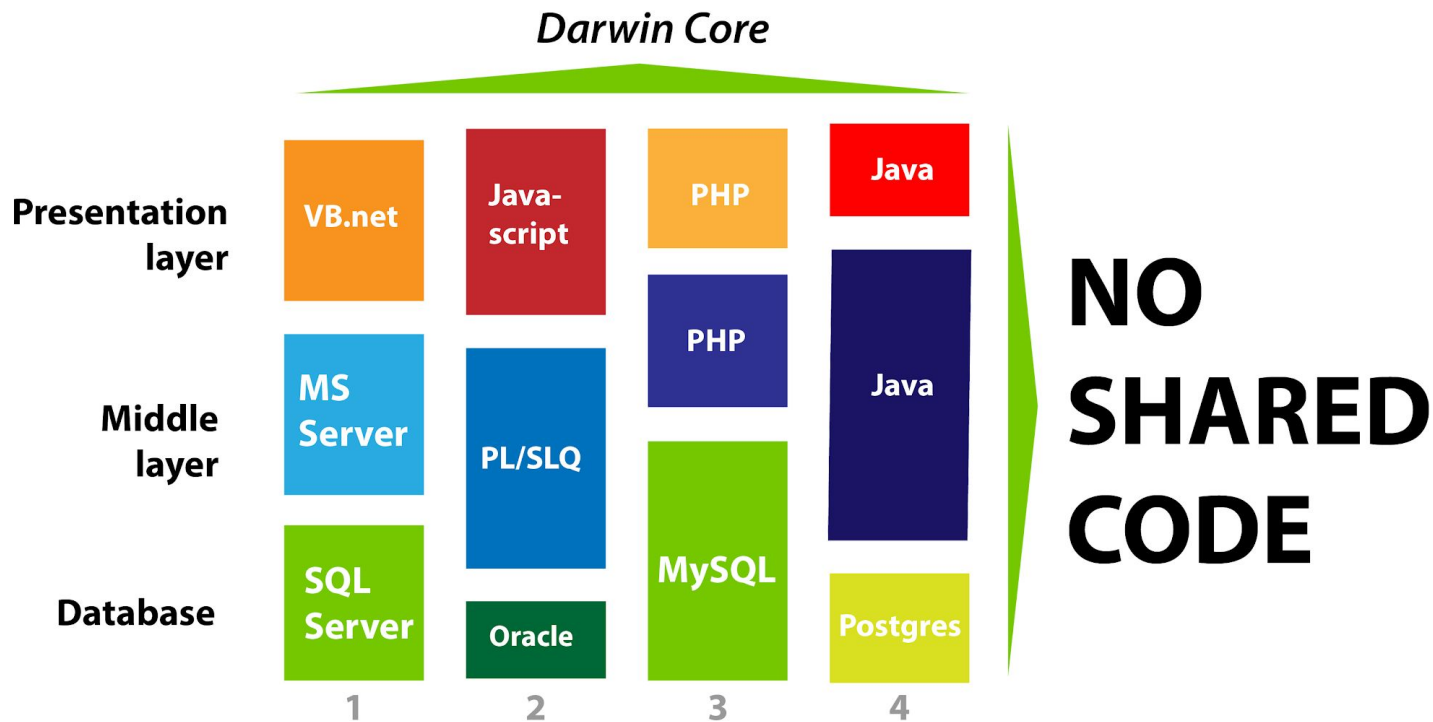


Proprietary
Unused
Unmaintained
Forked
Adapting

FFT: What would the software/data “tree” that optimizes science/innovation look like?



The fractured landscape of taxonomic VREs



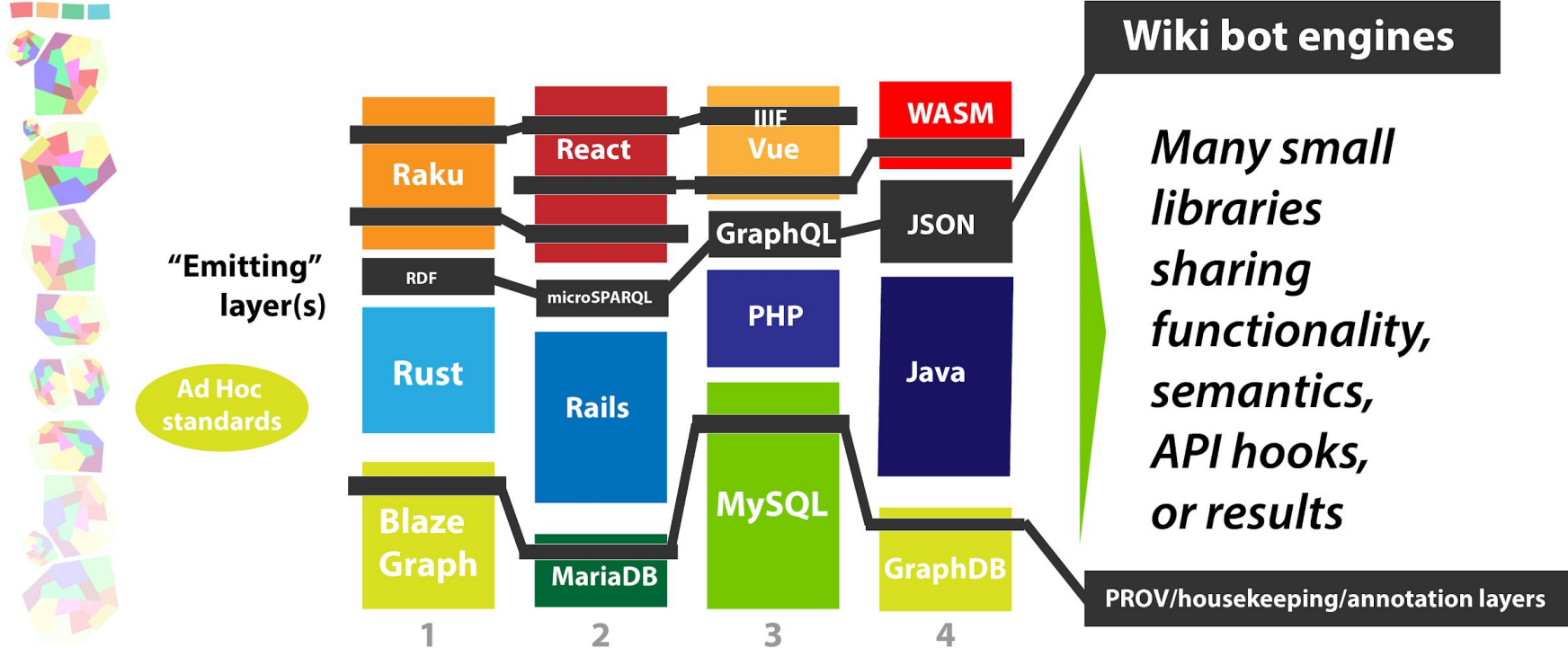
FFT:

That's a lot of software engineering.



Fusing fractures with (standard?)

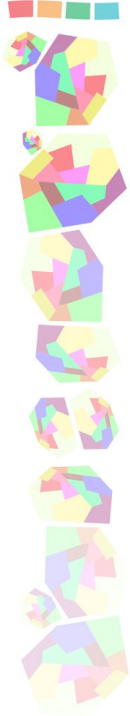
Shared code



FFT: Artisanal development with gene sharing prevents mono-culture, i.e. at-risk software.



10 Principles for better VREs



1 - Facilitate scientific processes

unapologetically an expert system

2 - Does computer stuff well

3 - Embrace iteration

4 - Proactive

facilitate discovery

predict next steps / anticipate needs

guide you to error correction

5- Live bearing (= "Born Digital")

6- Meaning > Efficiency > Appearance

7- Has cumulative outcomes (learns)

8- Intrusion decreases and
augmentation increases with use

9- Task delegating

10- Answer competency questions

FFT:

Is a Wiki a VRE? A reference manager? A georeferencing utility?



Application 1st consequences for standards

Not ratified until implemented (hopefully 2x)

Standard building opportunities galore:

Functional testing

Software widget/library

e.g. Label printing widget

Combinatoric validations

if A and B linked, then need C

Accessibility (human)

Competency questions (link question to standard to application)

e.g. tool is not enough to publish a valid new species

Gold standards

FFT:

Science is iterative, therefore standard development is as well.



David Shorthouse

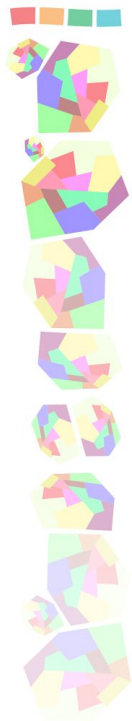
@dpsSpiders

Does your web-based biodiversity informatics project do functional testing with seleniumhq.org? Make a video! [#BiodiversitySelenium](https://twitter.com/BiodiversitySelenium)

2:49pm · 6 Jul 2017 · Twitter for Mac



Gradual exposure via familiar spaces ...



Semantic traits!!!!


Citation metrics!!! resolvable identifiers SLAM

Collaboration! WASM VR Machine learning

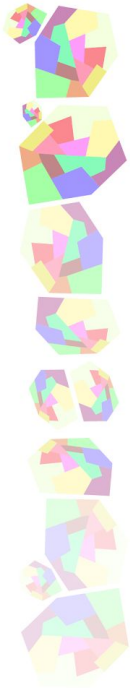
Minimum information Citizen science SEQUENCE EVERYTHING!

Wiki-data graph database Virtual museums

? triple stores JSON-LD LSIDs

 SPARQL endpoints Distributed systems

Essential biodiversity variables **FAIR**



TaxonWorks

FFT:

This is a cliff hanger.



Thanks



TaxonWorks collaborators (see homepage)



Biodiversity Next attendees that lent an ear



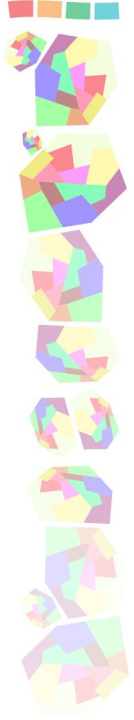
Species File Group



NSF ABI-1356381: “Collaborative Research: ABI Innovation: Rapid prototyping of semantic enhancements to biodiversity informatics platforms”, <https://doi.org/10.5281/zenodo.1409244>



... we're hiring (UI/UX, community manager)



1



Still here? Fine, some recommendations that were cut:

Plan for immediate obsolescence, every feature your VRE has an out, at least in concept

Force collaboration

Write more javascript and scripting languages, given your user's a fighting chance of affecting change.

Write more APIs.

Coding user roles, constraints and restrictions means you like dictators.

Invest in new taxonomists, give them new tools.

Don't worry about it (the impending Apocalypse), describe your species, digitize your specimens, and drink a warm drink.

Who needs standards if R savvy students feast on JSON?

Data aggrivators become data aggregtators when applications fix problems before they escape.