SPNHC 2022, Edinburgh 5th-10th June 2022

Workshop Title:

Application of BIOfid tools for extracting data from biodiversity literature

Length of Workshop

Half Day (9th June 2022)

Institutions:

(1) University Library Johann Christian Senckenberg, Frankfurt am Main, Germany
(2) Senckenberg Gesellschaft für Naturforschung, Frankfurt am Main, Germany
(3) Department of Computer Science and Mathematics, Goethe University Frankfurt, Frankfurt am Main, Germany

Workshop Facilitators:

Dr. Gerwin Kasperek (1),
Giuseppe Abrami (3)
Dr. Christine Driller (2)
Dr. Andy Lücking (3)
Prof. Dr. Alexander Mehler (3)
Carlos Alberto Martínez-Muñoz (2)
Dr. Adrian Pachzelt (1)

Content:

In an ideal world, extraction of machine-readable data and knowledge from natural-language biodiversity literature would be done automatically, but not so currently. The BIOfid project has developed some tools that can help with important parts of this highly demanding task, while certain parts of the workflow cannot be automated yet. BIOfid focuses on the 20th century legacy literature, a large part of which is only available in printed form. In this workshop, we will present the current state of the art in mobilisation of data from our corpus, as well as some challenges ahead of us. Together with the participants, we will exercise or explain the following tasks (some of which can be performed by the participants themselves, while other tasks currently require execution by our specialists with special equipment): Preparation of text files as an input; pre-processing with TextImager/TextAnnotator; semi-automated annotation and linking of named entities; generation of output in various formats; evaluation of the output. The workshop will also provide an outlook for further developments regarding extraction of statements from natural-language literature, with the long-term aim to produce machine-readable data from literature that can extend biodiversity databases and knowledge graphs.

Main Message:

The BIOfid project has developed tools that can help with important parts of the workflows necessary to mobilise data from biodiversity literature. In this workshop, we will demonstrate the current state of the art and some challenges ahead of us. Together with the participants, we will exercise or explain several tasks necessary to mobilise this kind of data.

Audience:

The workshop is aimed at researchers in the field of biodiversity who want to mobilize data from the literature for IT-based analysis, as well as developers working on similar issues.

Application of BIOfid tools for extracting data from biodiversity literature

BIOfid Team

University Library Johann Christian Senckenberg, Frankfurt am Main

Text Technology Lab, Goethe University, Frankfurt am Main

Senckenberg Society for Nature Research, Frankfurt am Main

Workshop Agenda

1. Introduction to BIOfid
2. BIOfid Web-Interface
3. Natural Language Processing-Pipeline (Hands-on)
4. XML
5. Java-Pipeline (Hands-on)
6. – Break –
7. Colab (Hands-on)
8. Semantic Role Labeling
9. Survey
10. Discussion

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Three partners behind BIOfid

University Library Johann Christian Senckenberg

- comprehensive collection of biodiversity literature (printed & digital)
- service provider for nation-wide supply of literature

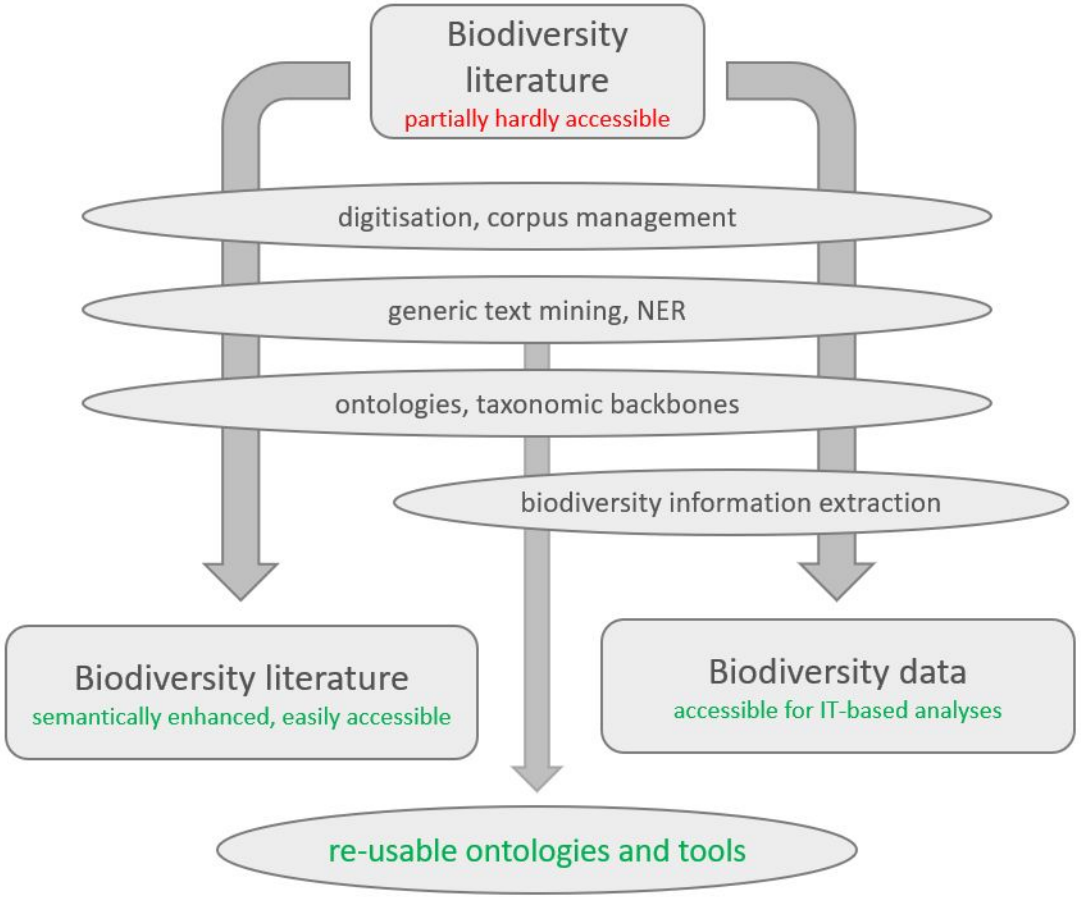
Senckenberg Society for Nature Research

- one of the leading German institutions in biodiversity research
- expertise in biodiversity informatics

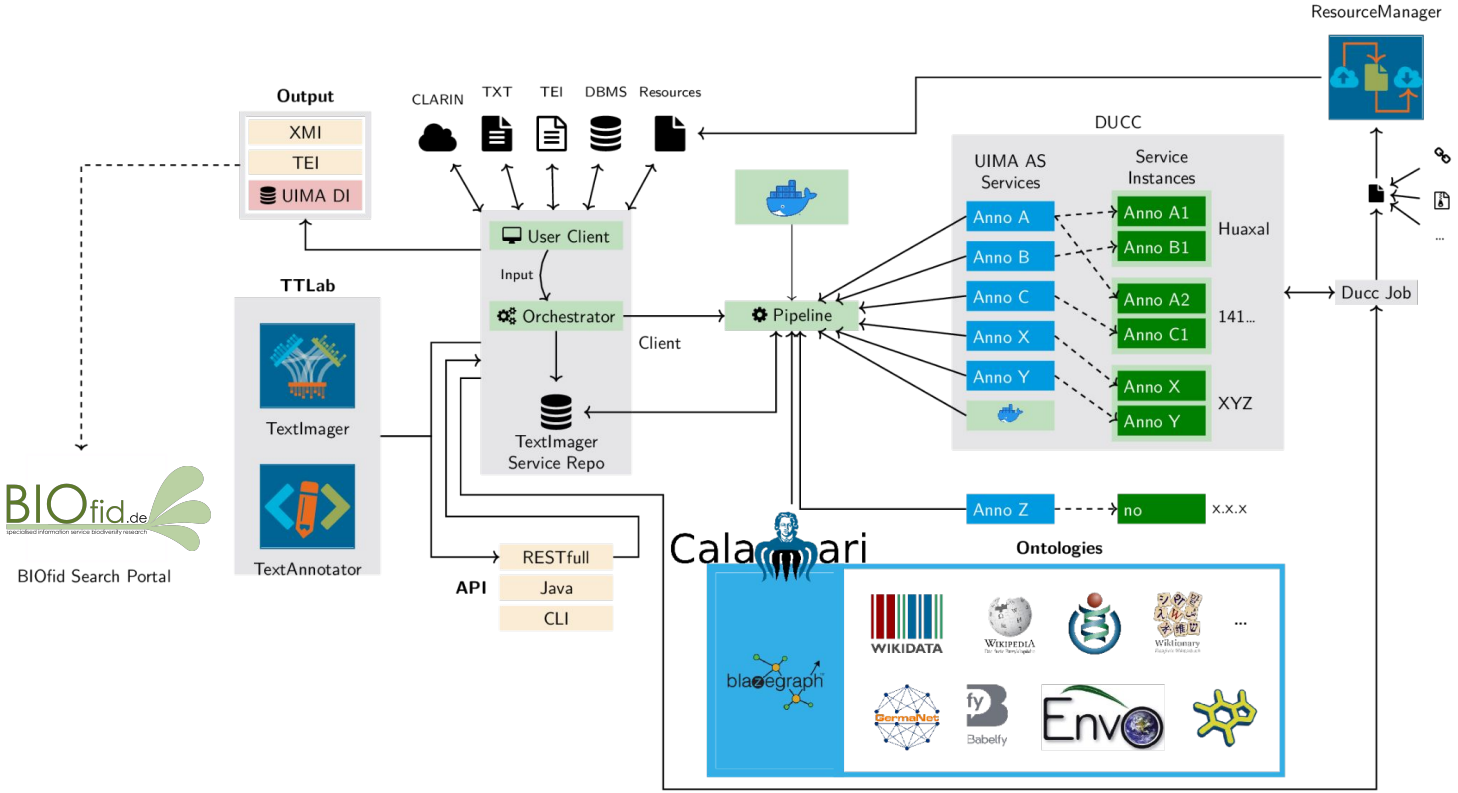
Text Technology Lab, Goethe University, Frankfurt am Main

- excellent team for automated analysis and synthesis of structures and content of natural-language texts

How to make biodiversity literature more accessible



Procedures and data flows, somewhat more detailed…



Central European focus

BIOfid has a Central European focus - in particular German-speaking regions.

BIOfid (phase 1 & 2) is focussed on certain taxonomic groups - mainly higher plants, birds, butterflies, but also myriapods, insects…

But, in the end, BIOfid will provide services relevant to other regions and/or taxonomic groups as well.

Digitisation of printed literature

UB JCS has largest collection of print biology literature in Central Europe…
and strives to make large parts available on-line

- “German Botanical Journals, 1753–1914”
  project completed 2013, ca. 180 titles
  https://sammlungen.ub.uni-frankfurt.de/botanik?lang=en
- 20th century biodiversity literature from Central Europe
  ongoing part of BIOfid project; in-copyright-materials
  https://sammlungen.ub.uni-frankfurt.de/biodiv?lang=en
- further digitalisation acitivities
  (e.g. “Sammlung Deutscher Drucke 1801-1870”)

… whenever possible, content shall also be incorporated in BHL

Building a BIOfid corpus

One of BIOfid's aims: extraction of biodiversity data from literature (focus Central Europe, vascular plants, birds, butterflies)
-> enabling more efficient IT-based analyses

Corpus will be assembled from various sources:

- digitised content from UB JCS
- content digitised elsewhere but *lacking* free licenses
- content digitised elsewhere *with* free licenses / PD
- born-digital content from OA journals

Domain-specific ontologies

Ontologies are needed as a basis for semantically enhancing the literature, but

- not enough depth in existing ontologies
- not enough coverage of German terms in existing ontologies

-> development and expansion of ontologies as a BIOfid task

some examples:

- LepAO - Lepidoptera Anatomy Ontology
- ChilAO - Chilopoda Anatomy Ontology
- GTO - GBIF Taxonomy Ontology
- ENVO - Environment Ontology

Further BIOfid services

There's more… (but not part of today's workshop):

- open access journal platform (OJS)
- digitisation on demand (including copyright clearance for orphaned works)
- supply of printed literature via document delivery or ILL
- FID licenses for electronic content (restricted to Germany: *JSTOR Global Plants*; *Birds of the World*; *Brill e-books*)

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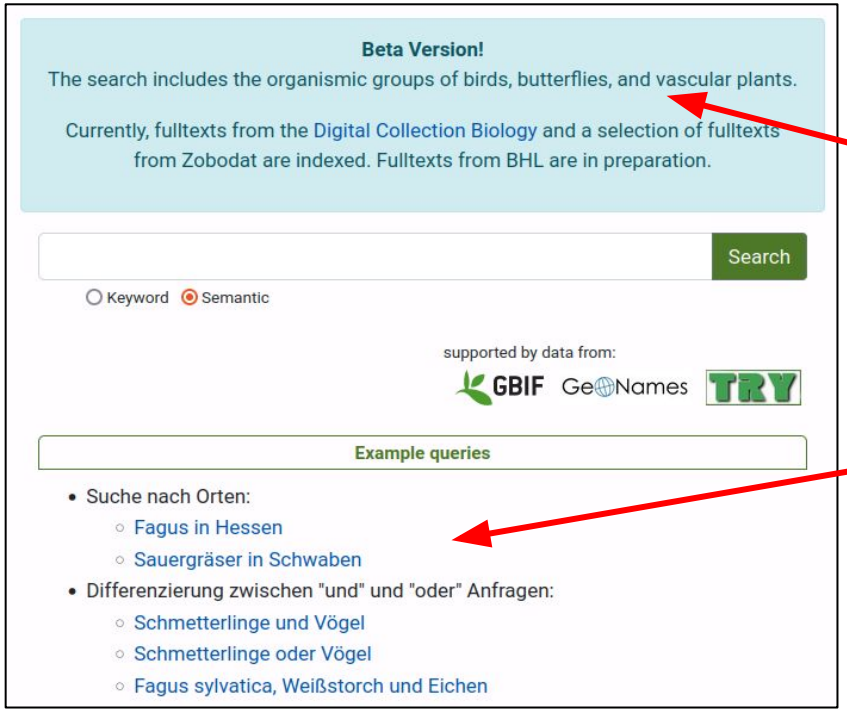
BIOfid Search Web-Interface

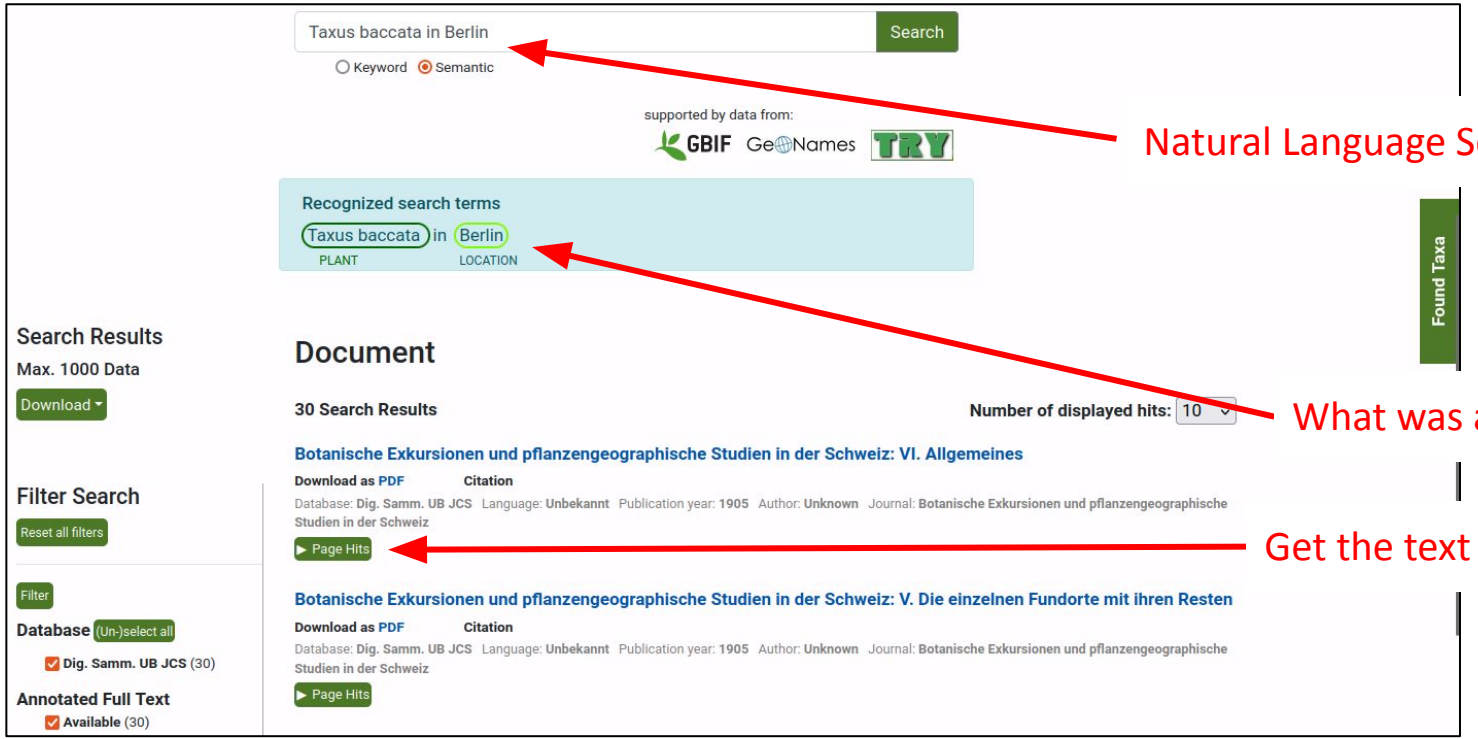
https://www.biofid.de/search/



Restricted taxa only!

Example Queries
(only in German)

BIOfid Search Web-Interface

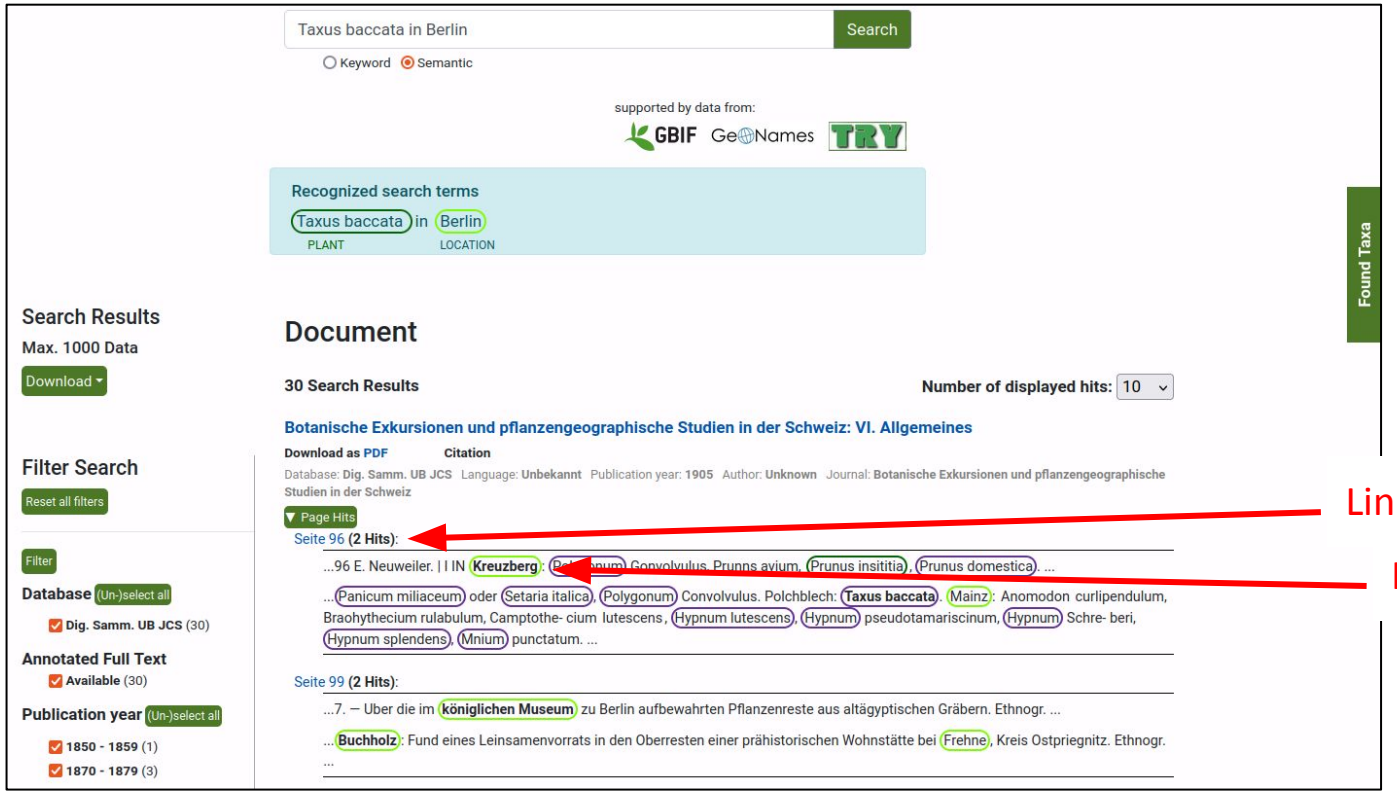


Natural Language Search

What was actually recognized

Get the text annotations

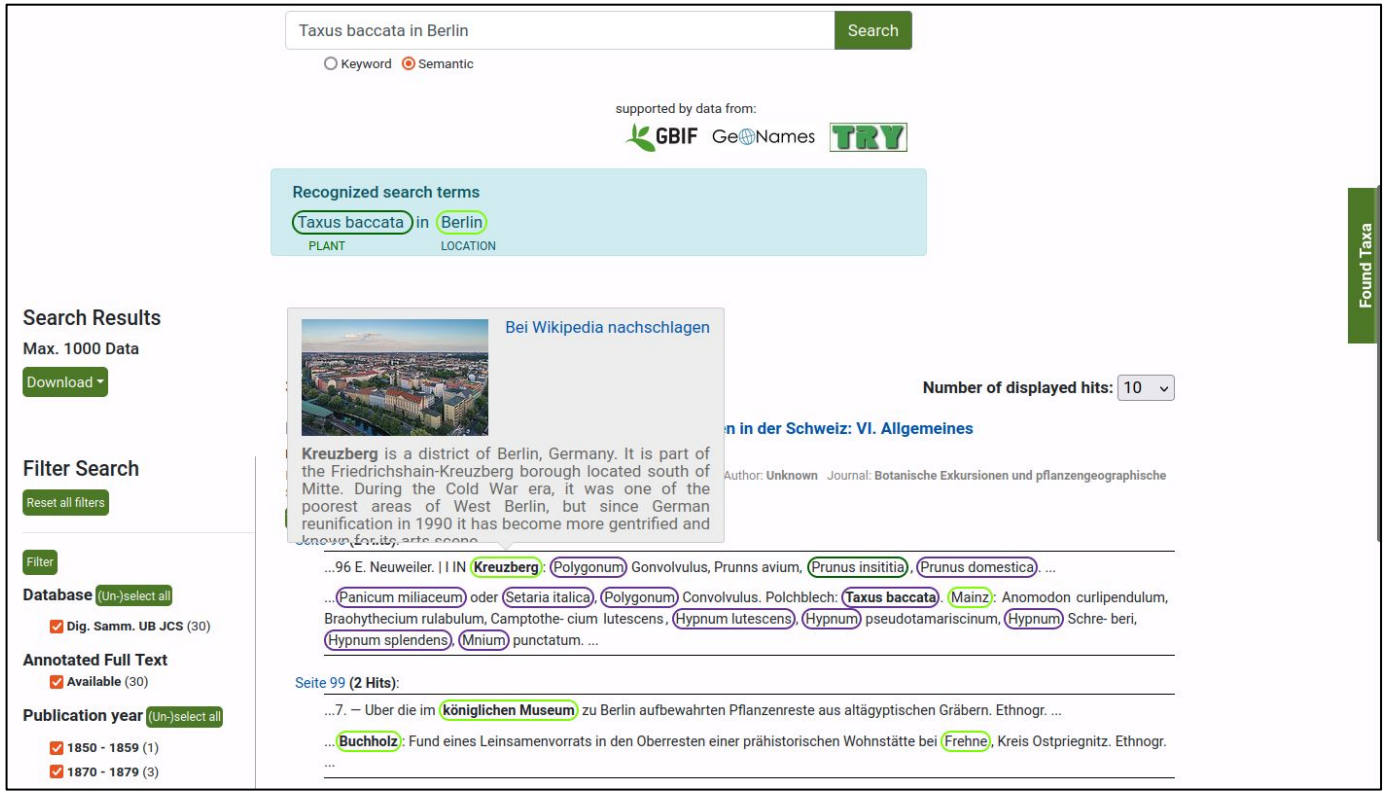
BIOfid Search Web-Interface



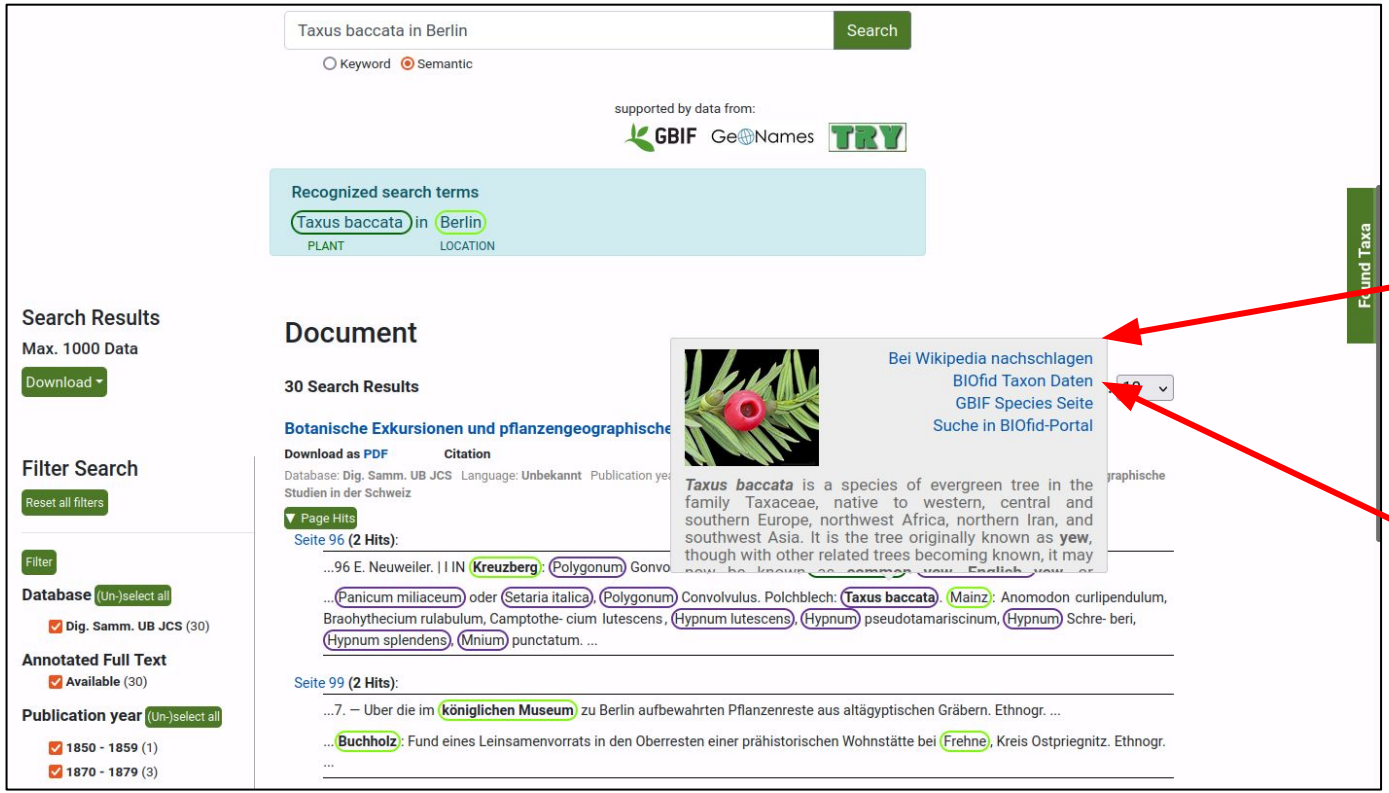
Link to the digitized page

Interactive annotations!!

BIOfid Search Web-Interface



BIOfid Search Web-Interface



Annotation context information

BIOfid URI

BIOfid Search Web-Interface

BIOfid URI: https://www.biofid.de/bio-ontologies/Tracheophyta/gbif/5284517

Taxus baccata L.

Group	Property	Value
Systematics	Kingdom	Plantae
	Phylum	Tracheophyta
	Class	Pinopsida
	Order	Pinales
	Family	Taxaceae
	Genus	Taxus
	Scientific Name	Taxus baccata L.
	Name Author	L.
	Label	Taxus baccata
	Taxon Rank	species (en)
	Vernacular Name	Eibe (de)
	Vernacular Name	Beereneibe (de)
	Vernacular Name	Europäische Eibe (de)
	Vernacular Name	Gemeine Eibe (de)
	Vernacular Name	Gewöhnliche Eibe (de)
	Vernacular Name	yew (en)
	Vernacular Name	Common yew (en)
	Vernacular Name	English yew (en)
	Vernacular Name	European yew (en)
	Vernacular Name	Yew (en)
	Vernacular Name	if (fr)
	Vernacular Name	if commun (fr)
	Taxonomic Status	accepted
	Parent Name	Taxus
Traits	flower color	yellow
Metadata	TRY-Species ID	53526
Misc	Type	GBIF Taxon
	Is in BIOfid Literature Corpus	True
	Type	flower yellow
	Type	Named Individual
	Type	Named Individual

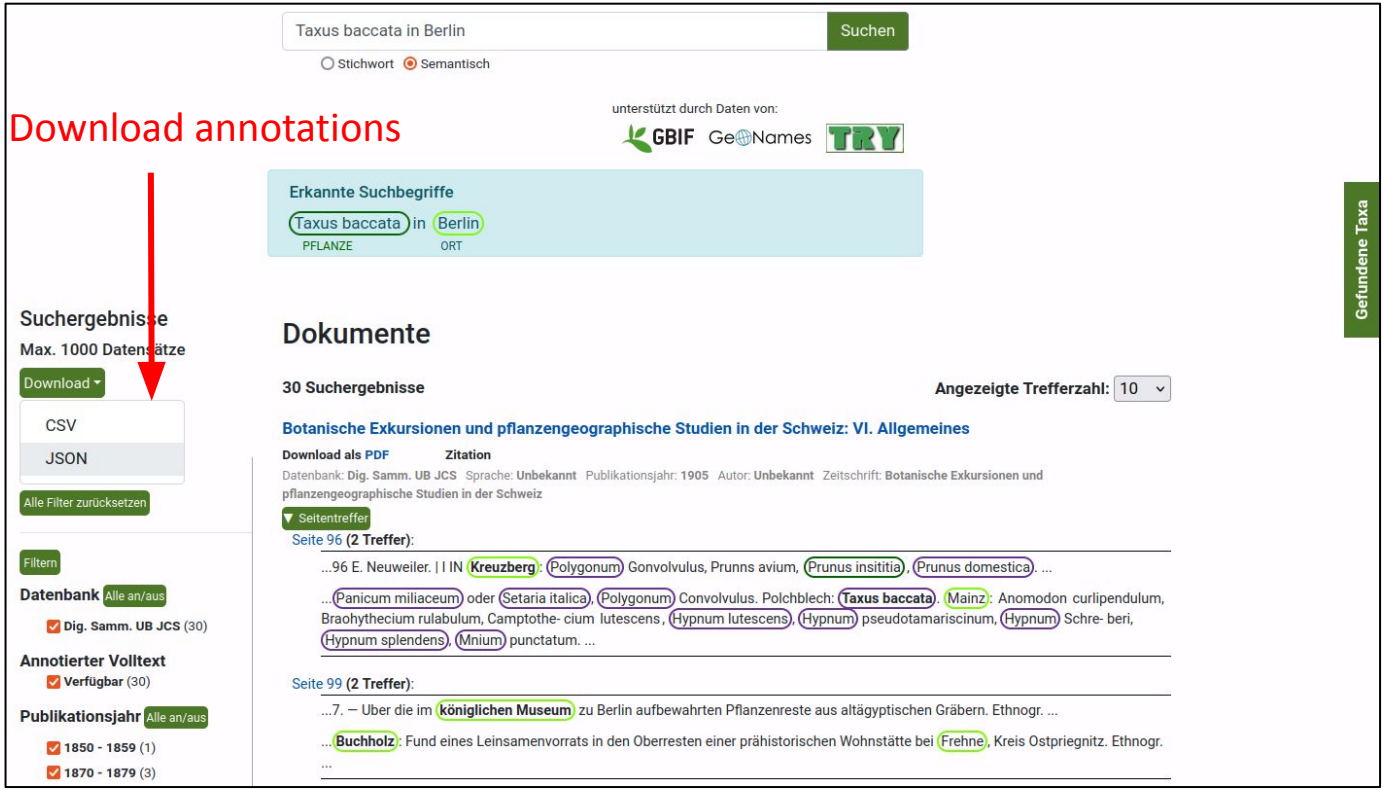
What your browser sees


```
title:                "Taxus baccata L."
uri:                  "https://www.biofid.de/bio-ontologies/Tracheophyta/gbif/5284517"
data:
  0:
    predicate:
        type:         "uri"
      value:          "https://www.biofid.de/bio-ontologies#has_petal_color"
    object:
        type:         "uri"
        value:        "http://purl.obolibrary.org/obo/PATO_0000324"
    objectLabel:
        type:         "literal"
        value:        "yellow"
    predicateLabel:
        type:         "literal"
        value:        "flower color"
  1:
    predicate:
        type:         "uri"
        value:        "https://dwc.tdwg.org/terms/#class"
    object:
        type:         "uri"
      value:          "https://www.biofid.de/bio-ontologies/Tracheophyta/gbif/194"
    objectLabel:
        type:         "typed-literal"
        datatype:     "http://www.w3.org/2001/XMLSchema#string"
        value:        "Pinopsida"
```


What your crawler sees

SCAN ME

BIOfid Search Web-Interface



BIOfid JSON Download Data

…{
"Authors": "Unbekannt",
"Journal": "Botanische Exkursionen und pflanzengeographische Studien in der Schweiz",
"PublicationYear": 1905,
"Source": "",
"TextExtracts": [
{
"Label": "Seite 96",
"Page URL": "https://sammlungen.ub.uni-frankfurt.de/4439682?query=taxus%20baccata%20kreuzberg",
"TextAnnotations": [
"<em class=\"location_place\" id=\"15c6369f95\" wikidata=\"http://www.wikidata.org/entity/Q308928\">Kreuzberg",
"<em biofid-uri-0=\"https://www.biofid.de/bio-ontologies/Tracheophyta#GBIF_5284517\"
biofid-uri-1=\"https://www.biofid.de/bio-ontologies/Tracheophyta#GBIF_8235017\"
biofid-uri-2=\"https://www.biofid.de/bio-ontologies/Tracheophyta#GBIF_8343790\" class=\"taxon facet biofid-included\" id=\"6b204fa5c2\"
wikidata=\"http://www.wikidata.org/entity/Q179729\">Taxus baccata"
]
},
{
"Label": "Seite 99",
"Page URL": "https://sammlungen.ub.uni-frankfurt.de/4439685?query=buchholz%20k%C3%B6niglichen%20museum",
"TextAnnotations": [
"<em class=\"location_place\" id=\"4b084ae4ac\" wikidata=\"http://www.wikidata.org/entity/Q156722\">k\u00f6niglichen Museum",
"<em class=\"location_place\" id=\"22d5d33242\" wikidata=\"http://www.wikidata.org/entity/Q675015\">Buchholz"
]
}
],
"Title": "VI. Allgemeines",
"URL": "http://sammlungen.ub.uni-frankfurt.de/botanik/periodical/pageview/5027912"
}, ...

BIOfid Text Annotation Demo Part I

Google Collab: https://t1p.de/biofid-annotation

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Demo

1. Go to http://spnhc2022.texttechnologylab.org and upload text file

Demo

Example file:
https://sammlungen.ub.uni-frankfurt.de/botanik/content/rpage/4162821

I am pleased to think that the study of the Rhizocephala began in Naples in 1787, when Cavolini (1) published his volume "Sulla generazione dei Pesci e dei Granchi". Although his view of the adult Sacculina as a morbid growth produced by the crab to surround a deposit of the eggs of a parasite is only of historic interest, we may admire the fortune and merit of the Neapolitan naturalist in recognizing the Crustaceous nature of the parasite through its Nauplius larvae, and also in discovering the Cryptoniscus larva of a parasite of the Sacculina, which he rightly referred to the Isopoda, under the name Oniscus squilliformis. His work was ignored till 1854, and unsurpassed till 1862.

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XML

1. Understanding the output file: Stand-off annotation
2. Separating primary data (“the text”) from annotations. Why?
3. Inline annotation and discontinuous constituents
   E.g. “look up” is an English verb, but: “I looked it up.”
   <pos=noun>I</pos>
   <pos=verb>looked</pos>
   <pos=pron>it</pos>
   <pos=??>up</pos> (?? could be verb prefix, but connection to verb lost [e.g., if more than one verb in sentence])
   <pos=punct>.</pos>
4. Related problem: inline annotation and several annotations for the same input → “crossing annotation spans”

XML

1. Understanding the output file: Markables, Indices, Features

markable:	I		a	m		p	l	e	a	s	e	d		t	o	
index:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
	s0 e1		s2 e4			start=5 end=12										

feature:

```
<pos value="ppron" begin="0" end="1" id="100"/>
<lemma value="be" begin="2" end="4" id="201"/>
<verb_complex value="be pleased" begin="2" end="12"
id="990"/>
```

XML

1. Different ways and formats, we use UIMA CAS and XMI (https://uima.apache.org/d/uimaj-current/apidocs/org/apache/uima/cas/CAS.html)
2. *Unstructured Information Management Architecture* (UIMA) , includes the
   - CAS (*Common Analysis System*) for creating and handling the data that annotators manipulate
   - CAS includes the type system which defines two kinds of entities, *types* and *features*.
3. Open standard format: XMI (*XML Metadata Interchange*)
4. Let's have a look at the sections of the output file

XML

1. Loading name spaces to regiment elements in a unique way
   `<xmi:XMI xmlns:xmi="http://www.omg.org/XMI" …`
2. The “document element” (near top): `<tcas:DocumentAnnotation begin="0" end="691" language="en" sofa="1" xmi:id="8"/>`
3. …and its link to the input string (close to bottom): `<cas:Sofa mimeType="text" sofaID="_InitialView" sofaNum="1" sofaString="I am pleased to think …`
4. … which is our *Subject of Analysis* (sofa)

XML

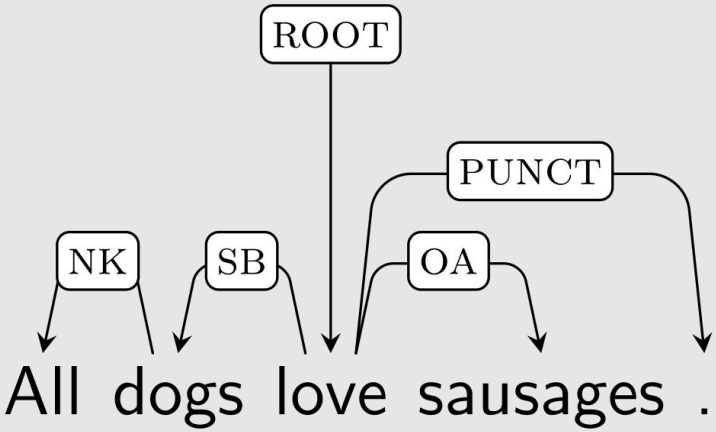
1. Annotations are added in terms of the *Markable–Index–Feature*-Model
2. Tokens (i.e., “single words”): `<type6:Token xmi:id="165" sofa="1" begin="16" end="21" lemma="4423" pos="2737" morph="6048" order="0"/>`
   - This is “think”, begins at index 16, ends at index 21 and belong to sofa 1 (our document)
   - important: “think” becomes unique with the ID “189”
   - it is also linked to other feature layers: lemma, morph(ology), part of speech (pos)
3. So, what’s “think”’s part of speech? Follow the pos-ID: `<pos:POS_VERB xmi:id="2737" sofa="1" begin="16" end="21" PosValue="VB" coarseValue="VERB"/>`

XML

1. Various layers build according to this model: besides lemmas, morphology and POS, the single sentences are distinguished and receive a syntactic annotation in terms of dependency structure.
2. E.g.: `<type6:Sentence begin="632" end="684" sofa="1" xmi:id="73"/>`
3. “I am pleased to think [...]”: “think” depends on “pleased”, which is the govenor in syntax (ID 149): `<dependency:Dependency xmi:id="9685" sofa="1" begin="16" end="21" Governor="125" Dependent="165" DependencyType="XCOMP" flavor="basic"/>`

Excursus: Dependency Structure

1. Dependency: syntactic relation between *words*: a governor or head and its dependent
2. Binary tree with labelled edges
3. Simple example: *All dogs love sausages*.



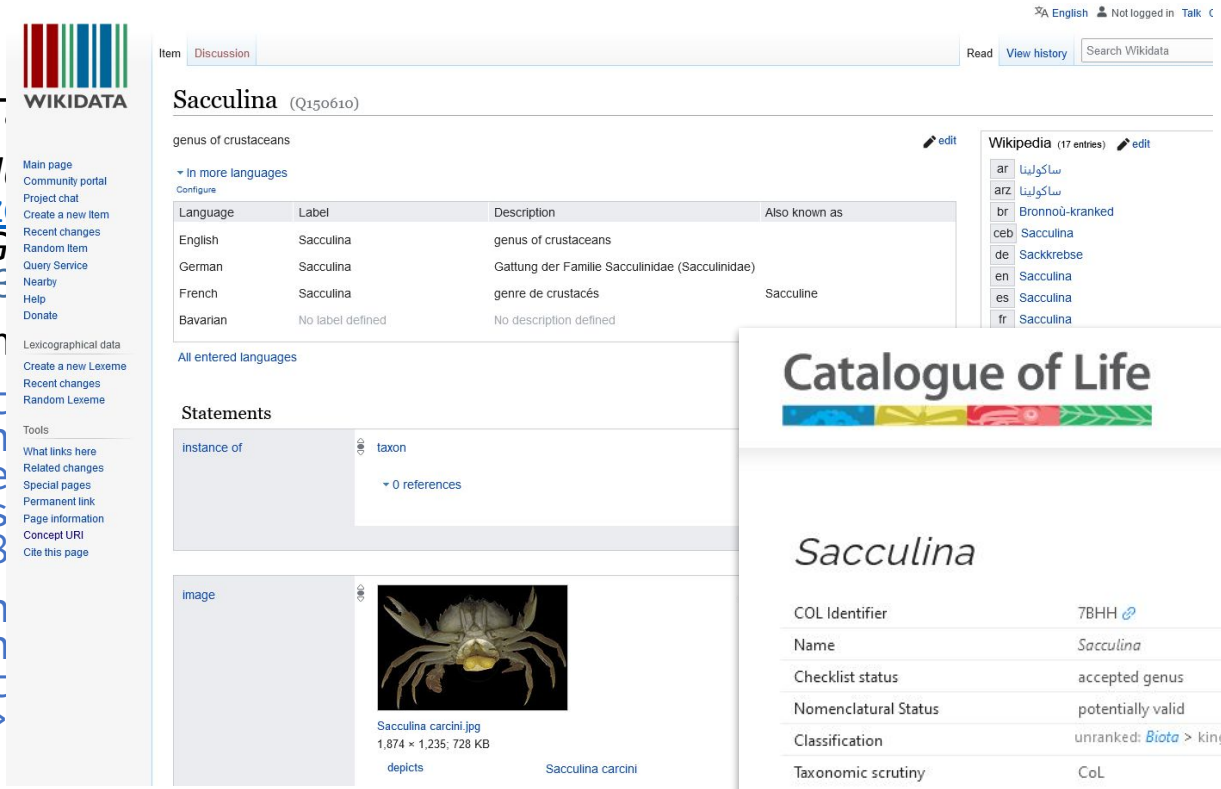
- Root: head of sentence (main verb)
- SB: subject
- OA: accusative object
- NK: noun kernel (part of noun phrase)
- PUNCT: punctuation

Named Entities

1. Finally: Taxa!
2. *Global Names Finder* (gnfinder; Mozzherin, Myltsev & Zalavadiya, https://zenodo.org/record/6537485) und "*Taxon Gazetteer*" (Ahmed, Stoeckel, Driller, Pachzelt & Mehler, DOI: 10.18653/v1/K19-1081)
3. "Sacculina":
   - `Gazetteer: <type19:Taxon xmi:id="12004" sofa="1" begin="197" end="206" value="http://www.wikidata.org/entity/Q150610, https://www.biofid.de/bio-ontologies/Tracheophyta%23GBIF_7297853"/>`
   - `gnfinder: <type19:Taxon xmi:id="12318" sofa="1" begin="197" end="206" value="Sacculina" identifier="https://www.catalogueoflife.org/data/taxon/7BHH"/>`

Named Entities

1. Finally: T
2. *Global N*
   https://z
   "Taxon G
   10.18653
3. "Sacculin
   - Gazet
     begin
     value
     https
     72978
   - gnfin
     begin
     ident
     HH"/>



Views

1. *Views*: list of elements that belong to a “view”: `<cas:View members="8 13 25 37 49 61 …`
2. This way, different “views” (e.g. annotations) can be associated with the same source text
3. Single annotators can also be tracked via *fingerprints* (home-made function)

Conclusion: Versatile, flexible and portable format

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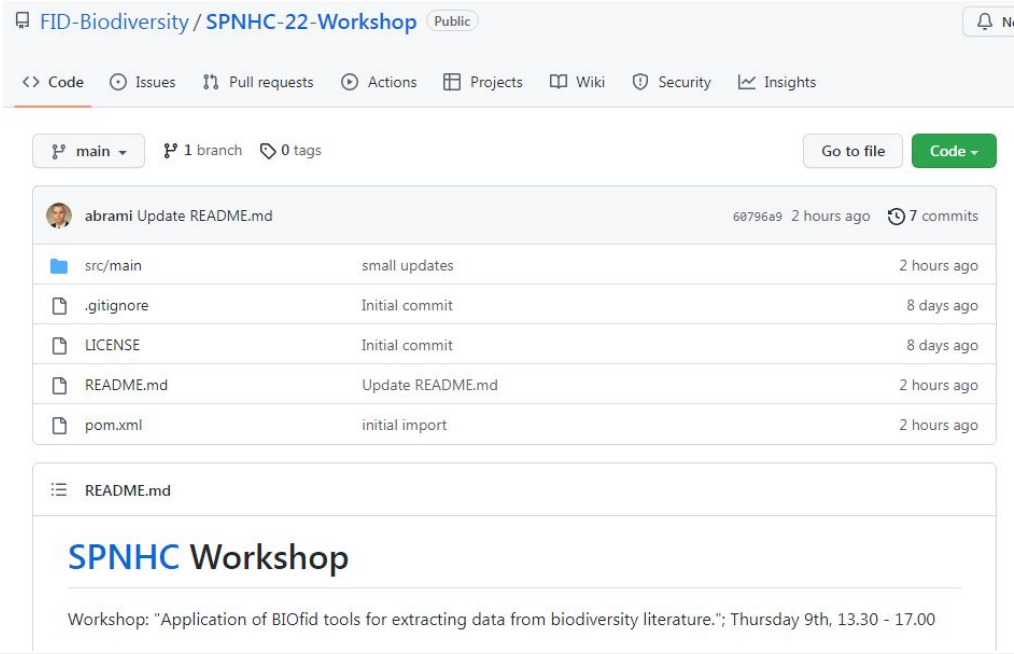
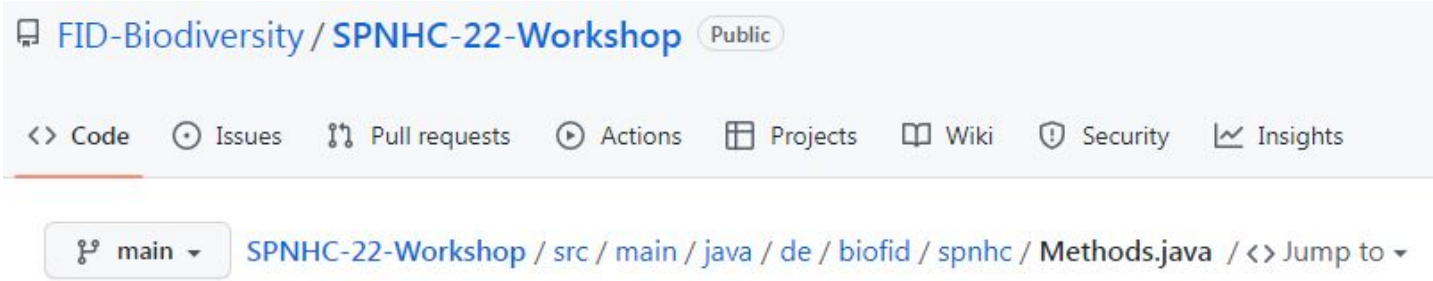
Java pipeline

1. Website-Pipeline is available as github project at https://github.com/FID-Biodiversity/SPNHC-22-Workshop
2. requires Java SDK version 11
3. clone from github
4. open in IntelliJ (https://www.jetbrains.com/idea/)
5. build your own pipeline



Java pipeline

1. The workshop project provides four tools: SpaCy, BIOfid's HeidelTime extension, GeoNames tagger, GNFinder
2. Go to Methods.java:



3. Select the tools you want (line 76):

```
75
76          pCas = processNLP.process(sContent, NLP.getSpacy(), NLP.getHeidelTimeBioFID(), NLP.getGeoNames(), NLP.getGNFinder());
77
```

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BIOfid Text Annotation Demo Part II

Google Collab: https://t1p.de/biofid-annotation

BIOfid API - Context Analysis

https://www.biofid.de/api/v1/getTermContext?term=https://www.biofid.de/bio-ontologies/Tracheophyta/gbif/5284517

Returns the most common co-occurrences for taxa and locations in the text:

BIOfid API - Context Analysis

https://www.biofid.de/api/v1/getTermContext?term=https://www.biofid.de/bio-ontologies/Tracheophyta/gbif/5284517

Returns the most common co-occurrences for taxa and locations in the text:

Taxa

1.	Taxus baccata L.	(278 cooccurrences)
2.	Taxus baccata Thunb.	(270)
3.	Taxus baccata Hook.	(270)
4.	Plantae	(220)
…		
7.	Quercus L.	(122)
8.	Carex L.	(118)
…		
32.	Daphne mezereum L.	(99)
…		
51.	Juniperus communis L.	(87)
…		
73.	Viburnum opulus L.	(84)

BIOfid API - Context Analysis

https://www.biofid.de/api/v1/getTermContext?term=https://www.biofid.de/bio-ontologies/Tracheophyta/gbif/5284517

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…		
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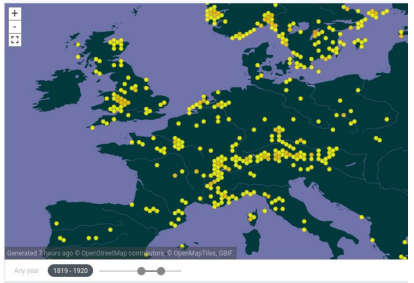
…		
32.	Daphne mezereum L.	(99)
…		
51.	Juniperus communis L.	(87)
…		
73.	Viburnum opulus L.	(84)

Locations

1.	Central Eastern Alps	(6)
2.	Limestone Alps	(5)
3.	Ford	(5)
4.	Corridor	(5)
5.	Left Bank of the Rhine	(5)
6.	Lesnoje (Russia)	(5)
7.	Zirl (Austria)	(5)
8.	South West Germany	(5)
9.	Saint Pierre and Miquelon	(5)
10.	Komsomolsk (Russia)	(5)
11.	…	



GBIF Data 1819-1920

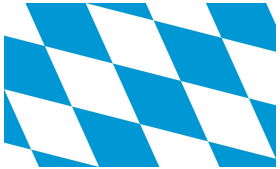
BIOfid API - Context Analysis

Base URL: https://www.biofid.de/api/v1/getTermContext

Ways to query

By String Term

https://www.biofid.de/api/v1/getTermContext?term=**zygaenidae**



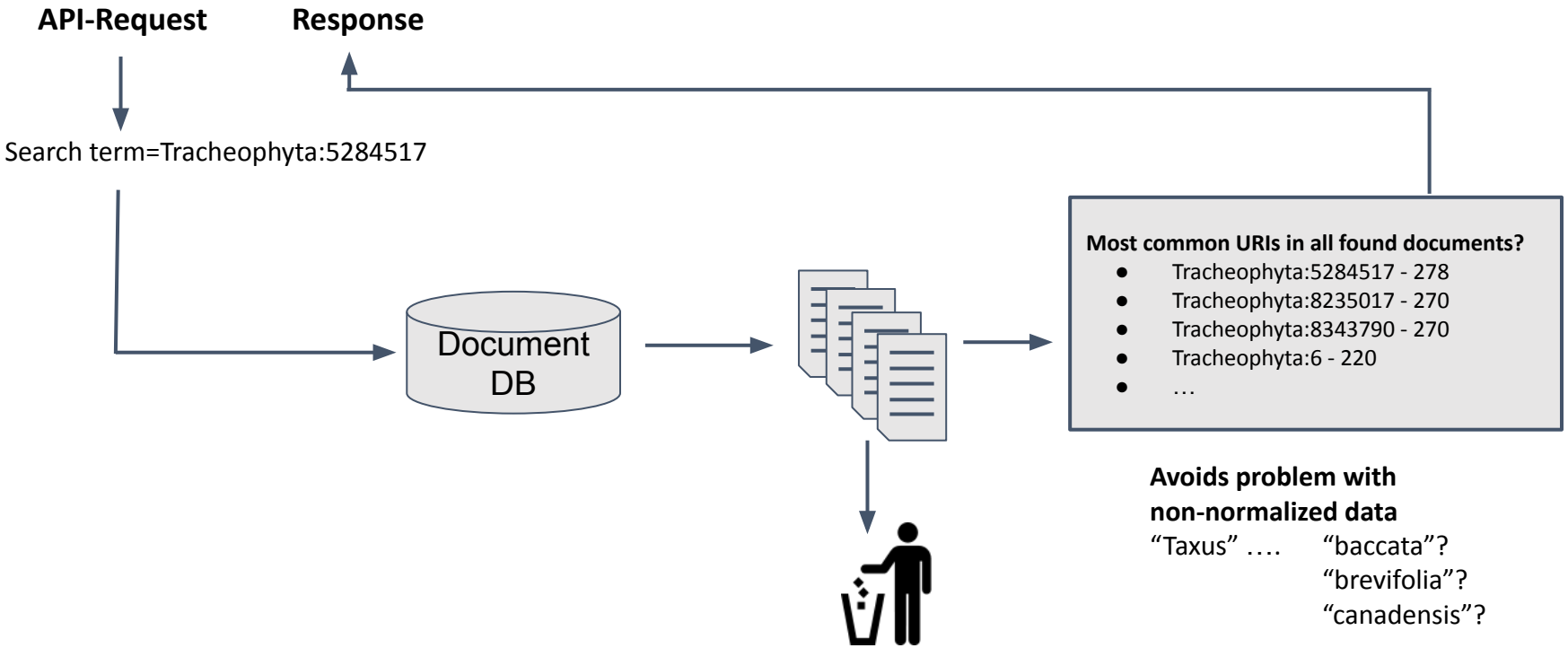
By Wikidata URI

https://www.biofid.de/api/v1/getTermContext?term=**http://www.wikidata.org/entity/Q980**

By BIOfid URI

https://www.biofid.de/api/v1/getTermContext?term=**https://www.biofid.de/bio-ontologies/Tracheophyta/gbif/5284517**

BIOfid API - Context Analysis



BIOfid API - Context Analysis

Advantages of the Context Analysis

- Aggregate the information pieces (“signals”) from hundreds of manuscripts
- Although a specific interaction is never mentioned, the CA reveals it

The power of normalized data!

Make a Context Analysis yourself

Google Collab: https://t1p.de/biofid-context

Workshop Agenda

1. Introduction to BIOfid
2. BIOfid Web-Interface
3. Natural Language Processing-Pipeline (Hands-on)
4. XML
5. Java-Pipeline
6. – Break –
7. Colab (Hands-on)
8. Semantic Role Labeling
9. Survey
10. Discussion

SRL: Semantic Role Labeling

1. From named entities to relations, and in a systematic manner.
2. Approach: assigning participant roles to syntactic arguments.
3. Simple example (repeated): *All dogs love sausages*.
   - Relation: *loving*
   - "Lover": *all dogs*
   - "Loved": *sausages*
4. Not: *Sausages love all dogs.*

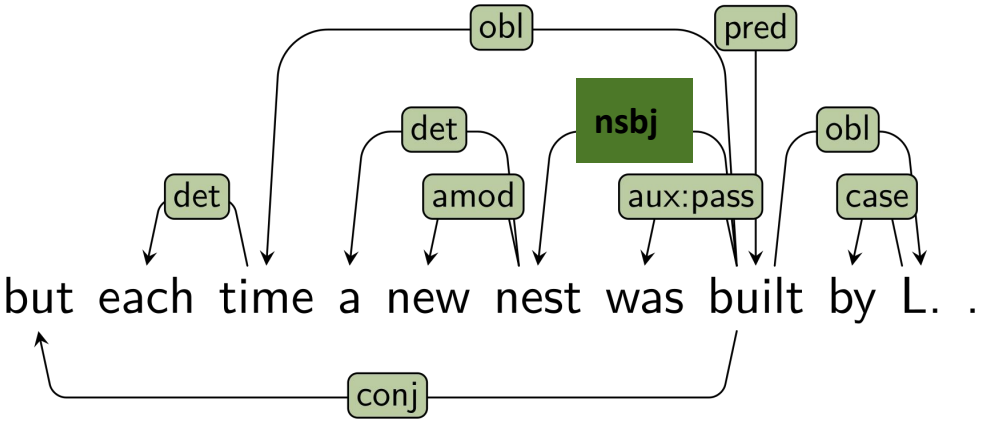
SRL

1. Representations in computational linguistics:
   - Positional: love(*all dogs*, *sausages*) ≠ love(*sausages*, *all dogs*)
   - Verb specific: [relation = *love*, lover = *all dogs*, loved = *sausages*]
   - General: [relation = *love*, agent = *all dogs*, patient = *sausages*]
   - Abstract: [relation = *love*, ARG0 = *all dogs*, ARG1 = *sausages*]
2. PropBank (Bonial et al. 2015): abstract approach

ARG0	proto-agent	ARG3	starting point, benefactive, attribute
ARG1	proto-patient	ARG4	ending point
ARG2	instrument, benefactive, attribute	modifiers	modals, location, time, negation, purpose, ...

SRL: (Dependency) Syntax is not enough

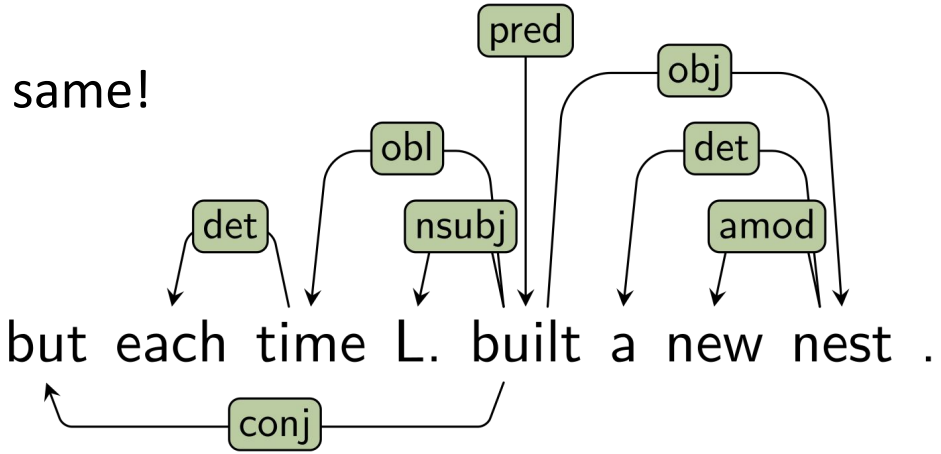
1. Real world example:
   “[...] jedesmal aber wurde ein neues Nest gebaut” [von *Lantus exeubitor L.*] (BIOFid 4523122)
   [...] *but each time a new nest was built [by Lantus exeubitor L.]*
2. Right: Dependencies (UD)
3. Roles:
   - relation: *building*
   - builder: *Lantus exubitor L.* (oblique argument)
   - built: *new nest* (direct object)



https://universaldependencies.org, UD

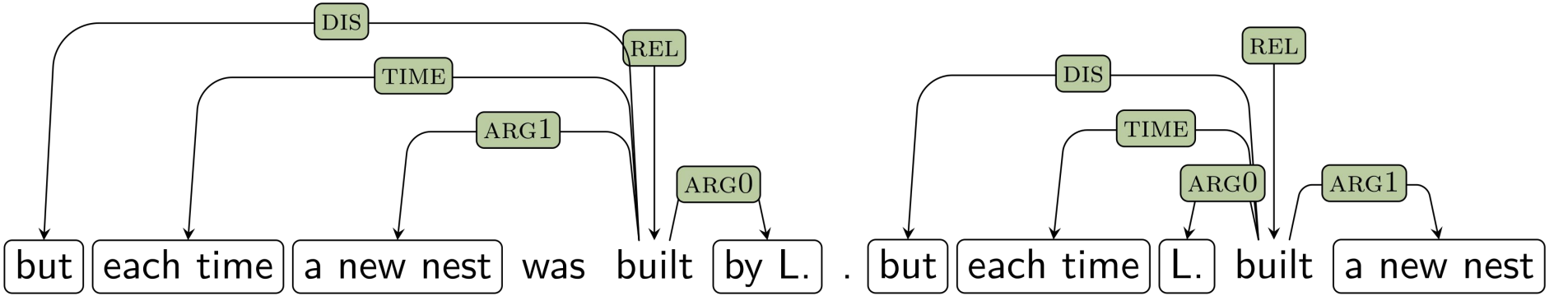
SRL: (Dependency) Syntax is not enough

1. Active voice: jedesmal aber baute L. ein neues Nest.
   but each time L. built a new nest
2. quite different syntactic structure: *Lantus exubitor L.* is n(ominal)subj(ect)
3. .. but semantic roles remain the same!



SRL

1. example annotations for our sample sentence
2. But: works reasonably well for English, but not (yet) for German -> **ongoing work for next edition**



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BIOfid-Survey

https://t1p.de/biofid-survey

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