

Mobilizing Bat1K through versioned, machine readable and automatically generated data publications.

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Guiding Questions

How to keep track of Bat1k data corpus?

How to cite specific versions of the Bat1k data corpora?

How to share specific versions of the Bat1k data corpora?

Reuse, reuse, reuse.

- ▶ Darwin Core Archive -> GBIF, GloBI
- ▶ Taxonomic Alignment Tools ¹ -> align with specific versions MDD, NCBI Taxonomy
- ▶ Signed Data Citations ²

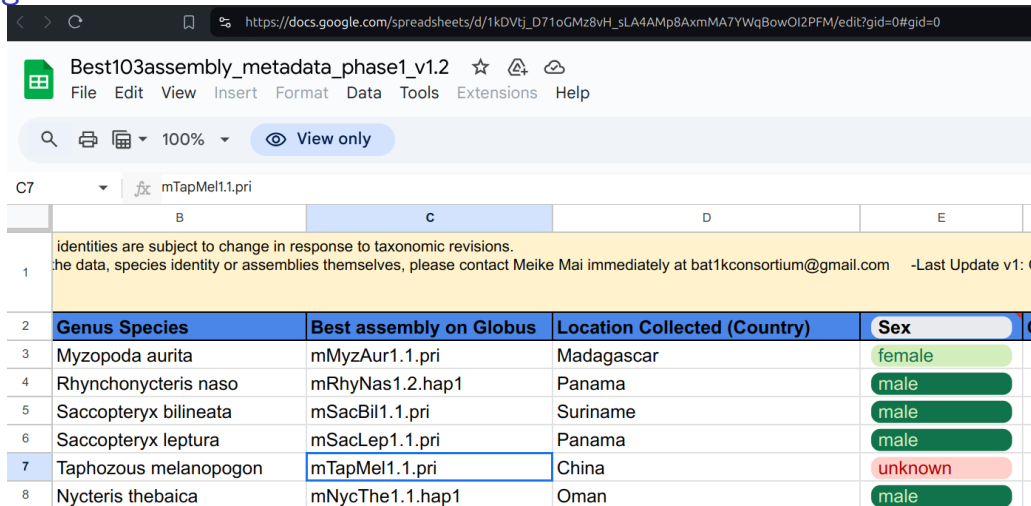
¹<https://github.com/globalbioticinteractions/nomer>

²Elliott M.J., Poelen, J.H. & Fortes, J.A.B. (2023) Signing data citations enables data verification and citation persistence. *Sci Data*. <https://doi.org/10.1038/s41597-023-02230-y>
hash://sha256/f849c870565f608899f183ca261365dce9c9f1c5441b1c779e0db49df9c2a19d

At NASBR 2025

Jorrit -> Ariandna -> Sonja -> Meike -> Bat1k data

Google Sheet



Best103assembly_metadata_phase1_v1.2

File Edit View Insert Format Data Tools Extensions Help

100% View only

C7 mTapMel1.1.pri

	B	C	D	E
1	Identities are subject to change in response to taxonomic revisions. If you have any questions about the data, species identity or assemblies themselves, please contact Meike Mai immediately at bat1kconsortium@gmail.com -Last Update v1: C			
2	Genus Species	Best assembly on Globus	Location Collected (Country)	Sex
3	Myzopoda aurita	mMyzAur1.1.pri	Madagascar	female
4	Rhynchonycteris naso	mRhyNas1.2.hap1	Panama	male
5	Saccopteryx bilineata	mSacBil1.1.pri	Suriname	male
6	Saccopteryx leptura	mSacLep1.1.pri	Panama	male
7	Taphozous melanopogon	mTapMel1.1.pri	China	unknown
8	Nycteris thebaica	mNycThe1.1.hap1	Oman	male

Figure 1: Best103assembly_metadata_phase1_v1.2 accessed at https://docs.google.com/spreadsheets/d/1kDVtj_D71oGMz8vH_sLA4AMp8AxmMA7YWqBowOI2PFM on 2024-10-27.

Google Sheet -> Versioned, Machine Readable Data Package

```
preston track\  
  --message "BatLit genome index"\  
https://docs.google.com/spreadsheets/d/1kDVtj\_D71oGMz8vH\_sLA4AMp8AxmMA7YWql  
  | sha256sum
```



Taxonomic Alignment through Nomer - Find (mis-)Alignments

```
cat bat1k.tsv\  
| nomer append\  
--properties $(echo 'nomer.schema.input=[{"column":0,"type":"externalId"}'  
| grep NONE\  
| cut -f2
```

Lasiurus ega

Hipposideros swinhoii


Next Steps

- ▶ Versioned Bat1K -> DwC-A - Add meta.xml and eml.xml to describe schema according to Darwin Core Archive to enable:
 - ▶ Indexing by GBIF as bat occurrences through vouchered specimen/genome
 - ▶ Indexing by GloBI as bat<>human interactions evidenced by vouchered specimen/genomes to enable automated data reviews ⁴

⁴Geiselman, Cullen K. & Sarah Younger. 2020. Bat Eco-Interactions Database. www.batbase.org
<https://github.com/globalbioticinteractions/batbase/archive/9c65cfeee1a054f9db8cd8bf6892017fd1b3c840.zip>
2024-10-25T22:39:59.352Z 6755e9ff065849a8a7472858e98b62458fab93e4c20006f823e844a3ee77f5f2 see
also <https://depot.globalbioticinteractions.org/reviews/globalbioticinteractions/batbase/>

Take Aways

- ▶ track, version and package original data
- ▶ implement automated data review workflow
- ▶ implement automated data product workflow

 <https://depot.globalbioticinteractions.org/reviews/globalbioticinteractions/batbase/>

A Review of Biotic Interactions and Taxon Names Found in globalbioticinteractions/batbase

by Nomer and Elton, two naive review bots

review@globalbioticinteractions.org

<https://globalbioticinteractions.org/contribute>

<https://github.com/globalbioticinteractions/batbase/issues>

2024-10-26

Abstract

Life on Earth is sustained by complex interactions between organisms and their environment. These biotic interactions can be captured in datasets and published digitally. We present a review process of such an openly accessible digital interactions dataset of known origin, and discuss its outcome. The dataset under review, named globalbioticinteractions/batbase, is 5.24KiB in size and contains 16,491 interaction with 7 unique types of associations (e.g., preysOn) between 601 primary taxa (e.g., *Carollia perspicillata*) and 3,483 associated taxon (e.g., *Lepidoptera*). The report includes detailed summaries of interactions data as well as a taxonomic review from multiple catalogs.