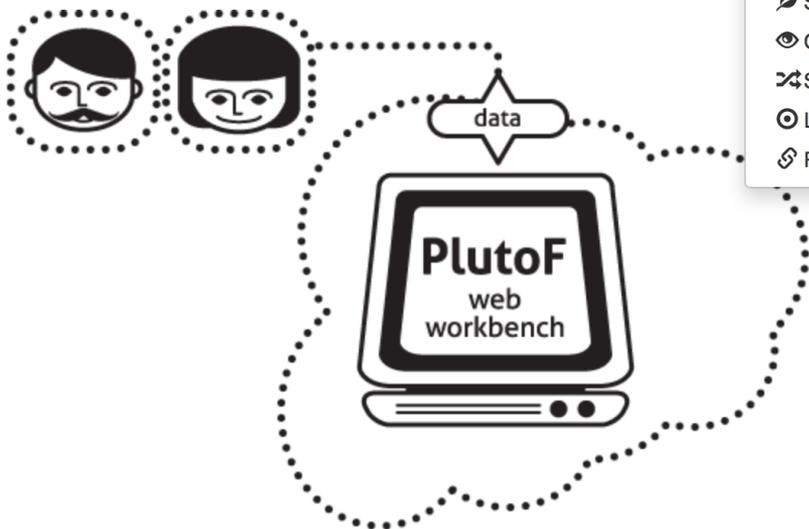# Publishing datasets with DOI-s in PlutoF cloud

Urmas Kõljalg

Natural History Museum, University of Tartu, Estonia

Tartu, 23rd of October, DataCite conference

PlutoF – Cloud Database and Computing Services

https 🔒 dev.plutof.ut.ee | Reader

PlutoF | 📖 Studies | 👤 Persons | ▲ References | Laboratory ▾ | ▦ Taxon Occurrences ▾ | 🔖 Clipboard | 🔧 Settings | ⮞ Logout

🍃 Specimens
👁 Observations
🔀 Sequences
◎ Living Culture
🔗 Reference-Based

Welcome to PlutoF

PlutoF provides cloud database and computing services for the taxonomical, ecological, phylogenetical, etc. research. The purpose of the platform is to provide synergy through common modules for the classifications, taxon names, analytical tools, etc.

It allows to address integrated questions in ecology and coevolution of taxa. Different types of the species occurrences, viz. preserved specimens, DNA sequences, human observations, references can be stored in PlutoF as well. PlutoF has no restrictions on taxon and geographic coverage and therefore can be used for the databasing interacting taxa.

It also includes collection management module. Few examples of the public web outputs from PlutoF are Estonian eBiodiversity (http://elurikkus.ut.ee), and molecular key for fungi (http://unite.ut.ee).

Feedback

PlutoF
NATARC

- Create, Manage, Store, Share and Publish your biodiversity datasets

- on observations, collections, monitoring, DNA, metagenomics, multimedia, etc.

Registrated users

2012   > 800
2013   > 1200
2014   > 1500

From nearly 40 countries

PlutoF cloud - statistics of use

Year	Unique visits	Pageviews	Average time of use
2013	17 623	644 378	30 min 59 sec
2012	19 353	737 576	30 min 1 sec

PlutoF - distribution of visits by country, in 2013

Estonia	USA	United Kingdom	Sweden	Finland	total of countries
14 183	1 398	423	352	166	36

specimen

observation

dna

habitat

taxonomy
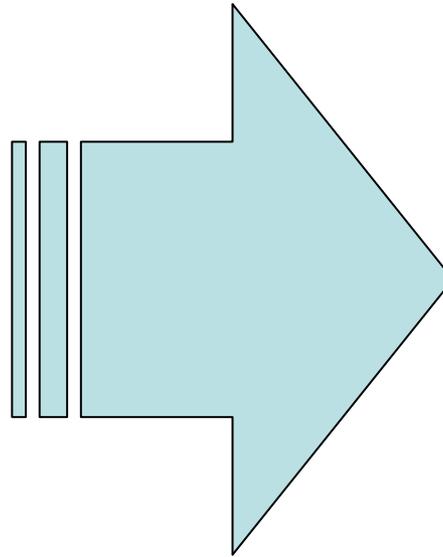
data mobilisation

Creator of datasets
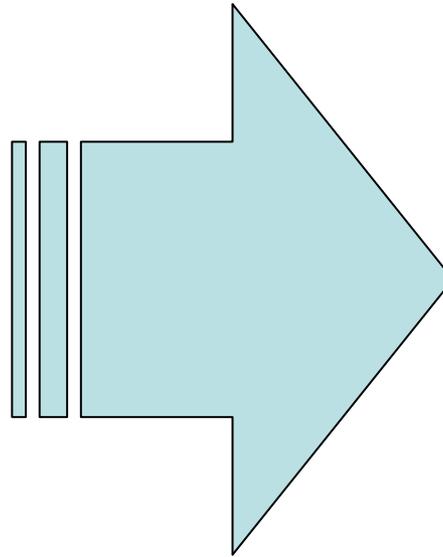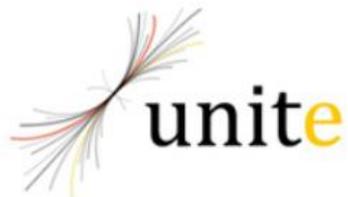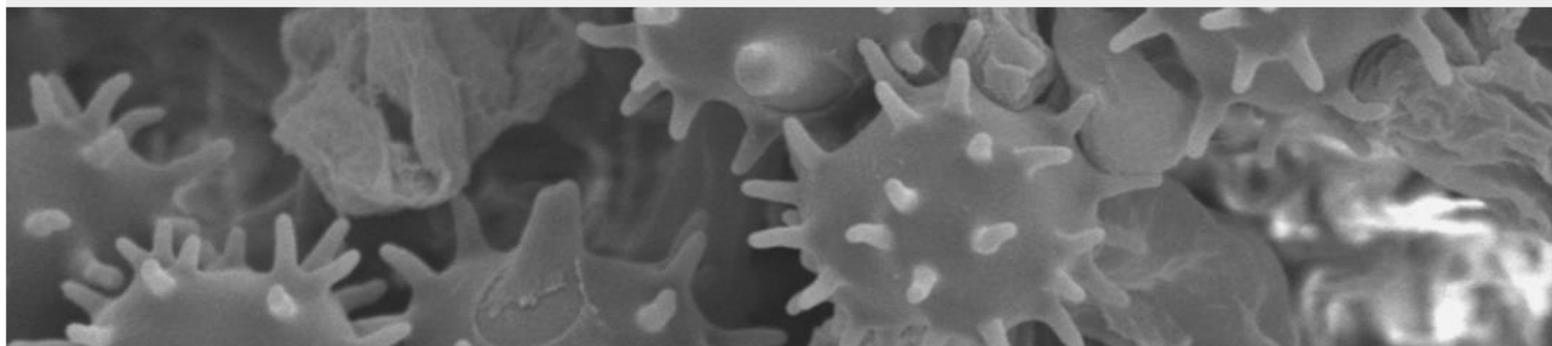
UNITE community

Curated rDNA ITS datasets from any biological sample (specimen, living specimen, soil, water, air, medical, etc.)

Global key for the DNA based fungal species

Unified system for the DNA based fungal species linked to the classification
Ver. 5.0

unite

Username •••••••• Log in

Current version: **5.0**; Release date: 18.12.2012 (**read more**)
Number of UNITE fungal Species Hypotheses: **52 481** (based on 98% threshold value, see also SH statistics below)
Number of fungal ITS sequences in current version (UNITE+INSD): **352 622**

UNITE provides unified way how you delimit, identify, communicate and work with DNA based Species Hypotheses (SH). All SHs are connected to the taxon name and classification. Read **Kõljalg et al. 2013** paper for the description of the system.

What is Species Hypothesis?

Species Hypothesis – any species level group of individuals that share a given set of observed characters. **Read more**

Click to enlarge

What are reference and representative sequences?

Reference sequence (RefS) – serves as a name anchor for the Species Hypothesis and is chosen by the expert. **Read more**

Click to enlarge

UNITE Community

Members
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UNITE list

News

Oct. 14, 2013 **UNITE homepage updated: Unified system for the DNA based fungal species (ver. 5.0) released.**

Species Hypotheses statistics (ver 5.0)

User statistics

QIIME

qiime.org

Reader

e-Teatmik | GeoNames | MapRestServiceApi – EDIT | Ramírez-Lóp...Thelephora | .: B H L E U R O P E :. | Find Coordinates | From the Cov...of Sciences | Acta Botanic...anica (ABY)

TDWG: Confer... | Merelabor :: Copy | www.earthobs... | High Level Qu... | Tartu Ülikooli... | UNITE – citing | Towards a uni... | QIIME

Fork me on GitHub

Quantitative Insights Into Microbial Ecology

qiime

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What is QIIME?

QIIME (pronounced "chime") stands for Quantitative Insights Into Microbial Ecology. QIIME is an open source software package for comparison and analysis of microbial communities, primarily based on high-throughput amplicon sequencing data (such as SSU rRNA) generated on a variety of platforms, but also supporting analysis of other types of data (such as shotgun metagenomic data). QIIME takes users from their raw sequencing output through initial analyses such as OTU picking, taxonomic assignment, and construction of phylogenetic trees from representative sequences of OTUs, and through downstream statistical analysis, visualization, and production of publication-quality graphics. QIIME has been applied to single studies based on billions of sequences from thousands of samples.

Code

QIIME is open source software. You can find the code under public revision control in our GitHub repository. You can find related projects under the QIIME organization on GitHub. We're very interested in community contributions and feedback. Use pull requests to contribute code or documentation, and our issue tracker to report bugs or request new features.

Getting started with QIIME

The quickest way to get started using QIIME is with the EC2 image or the VirtualBox. The QIIME overview tutorial is a good first analysis to run. In this tutorial you'll download a small data set and work through a series of commands that will introduce you to QIIME's most commonly used features and analyses.

PlutoF

NATARC

How to communicate DNA based species in research papers?

DOI?

Boletus luridus | SH326509.06FU

Distance to the closest SH (read more): 0.5%
No of sequences in SH: 20

Placement in the fungal classification (read more):
Fungi; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Boletales;
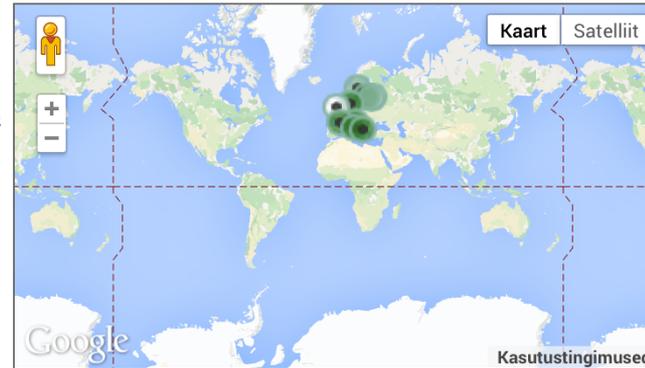Boletaceae; Boletus
Links to taxon name in: Index Fungorum; MycoBank; NCBI

Reference sequence: UDB000648
Chosen by: Andrew F.S. Taylor
Date: 2013-12-04 07:05:15

Large map (incl. map info)

	Sequence ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa ▾		Clustering based on: Full ITS
more |	KC734544		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more |	KC734542		Boletus (Boletus luridus)	Italy				TGACCTGCGGAAGGACATTATCGAATT
more |	**UDB015166**	**Boletus luridus**		Estonia	Fruitbody			--------------------TCGAATT
more |	**UDB013674**			Estonia	Ectomycorrhiza	Tilia		--------------GGAAGGATCATTATCGAATT
more |	**UDB015762**	**Boletus luridus**		Estonia	Fruitbody			--------------------TCGAATT
more |	JQ685714		Boletus (Boletus luridus var luridus)	Montenegro				--------------------TCGAATT
more |	JQ685715		Boletus (Boletus luridus var luridus)	Montenegro				--------------GAAGGATCATTATCGAATT
more |	**UDB000655**	**Boletus luridus**		Sweden	Fruitbody			--------------------TCGAATT
more |	**UDB002401**	**Boletus luridus**		Great Britain	Fruitbody			---------------------GAATT
more |	AY278766		Boletus (Boletus luridus)					---------AAGGATCATTATCGAATT
more |	AY278765		Boletus (Boletus luridus)					---------AAGGATCATTATCGAATT
more |	**UDB000648**	**Boletus luridus**		Great Britain	Fruitbody		RefSeq	--------------------TCGAATT
more |	AJ889930		Boletus (Boletus luridus)	Denmark	Fruitbody	Fagus sylvatica		--------------------TCGAATT
more |	**UDB000077**	**Boletus luridus**		Denmark	Fruitbody			--------------------TCGAATT
more |	EF644121		Boletaceae (uncultured Boletus)	Austria	Ectomycorrhiza	Populus tremula		--------------------TCGAATT
more |	EF644104		Boletus (Boletus luridus)	Austria	Fruitbody	Populus tremula		---------------ATCATTATCGAATT
more |	JF907793		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more |	AF465183		Boletales (uncultured Boletaceae)	France	Ectomycorrhiza			--------------------TCGAATT
more |	JF907802		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more |	JF907789		Boletus (Boletus caucasicus)	Italy				----------CGGAAGGATCATTATCGAATT

1.5% — 2%
1% — 2.5%
0.5% — 3%

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Uncultured ectomycorrhiza (Boletus) isolate 26 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: EF644121.1

FASTA   Graphics   PopSet

Go to: ⌄

```
LOCUS       EF644121                582 bp    DNA     linear   ENV 01-OCT-2008
DEFINITION  Uncultured ectomycorrhiza (Boletus) isolate 26 18S ribosomal RNA
            gene, partial sequence; internal transcribed spacer 1, 5.8S
            ribosomal RNA gene, and internal transcribed spacer 2, complete
            sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION   EF644121
VERSION     EF644121.1  GI:157284042
KEYWORDS    ENV.
SOURCE      uncultured Boletus
  ORGANISM  uncultured Boletus
            Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
            Agaricomycetes; Agaricomycetidae; Boletales; Boletineae;
            Boletaceae; environmental samples.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Krpata,D., Peintner,U., Langer,I., Fitz,W.J. and Schweiger,P.
  TITLE     Ectomycorrhizal communities associated with Populus tremula growing
            on a heavy metal contaminated site
  JOURNAL   Mycol. Res. 112 (PT 9), 1069-1079 (2008)
   PUBMED   18692376
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Krpata,D., Peintner,U., Langer,I., Fitz,W. and Schweiger,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-2007) Institute of Microbiology, University
            Innsbruck, Technikerstrasse 25, Innsbruck 6020, Austria
FEATURES             Location/Qualifiers
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                     /isolate="26"
                     /isolation_source="ectomycorrhizal root tips of Populus
                     tremula growing in heavy metal contaminated site near
```

Change region shown ▾

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Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

LinkOut to external resources ▲
SILVA LSU Database

[SILVA]

SH326509.06FU

[UNITE]

related identifed ITS sequences

[emerencia]

Related information ▲
Related Sequences

PopSet

PubMed

Taxonomy

Recent activity ▲
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Uncultured ectomycorrhiza (Boletus) isolate 26 18S ribosomal RNA gene, partial Nucleotide

See more...

Boletus luridus | SH326509.06FU

Distance to the closest SH (read more): 0.5%
No of sequences in SH: 20

Placement in the fungal classification (read more):
Fungi; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Boletales;
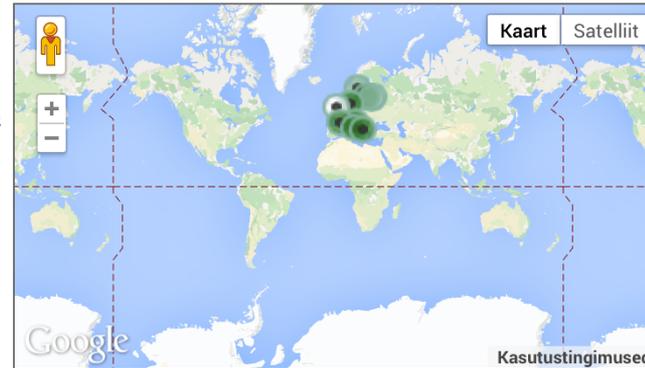Boletaceae; Boletus
Links to taxon name in: Index Fungorum ; MycoBank ; NCBI

Reference sequence: UDB000648
Chosen by: Andrew F.S. Taylor
Date: 2013-12-04 07:05:15

Large map (incl. map info)

			1.5%		2%	
			1%		2.5%	
			0.5%		3%	

	Sequence ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa ▾		Clustering based on: Full ITS
more |	KC734544		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more |	KC734542		Boletus (Boletus luridus)	Italy				TGACCTGCGGAAGGACATTATCGAATT
more |	UDB015166	Boletus luridus		Estonia	Fruitbody			--------------------TCGAATT
more |	UDB013674			Estonia	Ectomycorrhiza	Tilia		-------------GGAAGGATCATTATCGAATT
more |	UDB015762	Boletus luridus		Estonia	Fruitbody			--------------------TCGAATT
more |	JQ685714		Boletus (Boletus luridus var luridus)	Montenegro				--------------------TCGAATT
more |	JQ685715		Boletus (Boletus luridus var luridus)	Montenegro				-------------GAAGGATCATTATCGAATT
more |	UDB000655	Boletus luridus		Sweden	Fruitbody			--------------------TCGAATT
more |	UDB002401	Boletus luridus		Great Britain	Fruitbody			---------------------GAATT
more |	AY278766		Boletus (Boletus luridus)					---------AAGGATCATTATCGAATT
more |	AY278765		Boletus (Boletus luridus)					---------AAGGATCATTATCGAATT
more |	UDB000648	Boletus luridus		Great Britain	Fruitbody		RefSeq	--------------------TCGAATT
more |	AJ889930		Boletus (Boletus luridus)	Denmark	Fruitbody	Fagus sylvatica		--------------------TCGAATT
more |	UDB000077	Boletus luridus		Denmark	Fruitbody			--------------------TCGAATT
more |	EF644121		Boletaceae (uncultured Boletus)	Austria	Ectomycorrhiza	Populus tremula		--------------------TCGAATT
more |	EF644104		Boletus (Boletus luridus)	Austria	Fruitbody	Populus tremula		-------------ATCATTATCGAATT
more |	JF907793		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more |	AF465183		Boletales (uncultured Boletaceae)	France	Ectomycorrhiza			--------------------TCGAATT
more |	JF907802		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more |	JF907789		Boletus (Boletus caucasicus)	Italy				-------------CGGAAGGATCATTATCGAATT

Accession code of the SH:

SH326509.06FU

is resolved with unique uri (stable identifier):

http://unite.ut.ee/sh/SH326509.06FU

Species Hypothesis pages version 6 (release date: pre-release)

Boletus luridus | SH326509.06FU

Distance to the closest SH (read more): 0.5%
No of sequences in SH: 20

Placement in the fungal classification (read more):
Fungi; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Boletales;
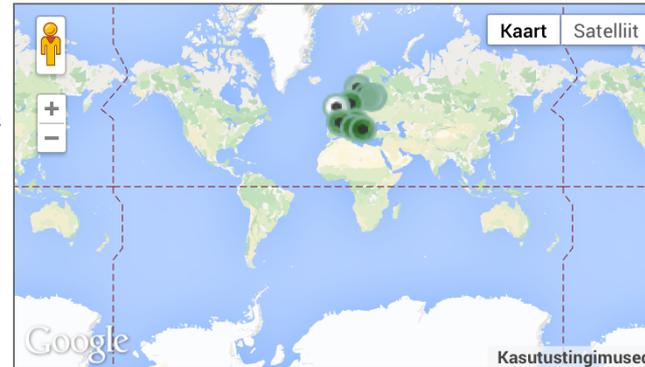Boletaceae; Boletus
Links to taxon name in: Index Fungorum; **MycoBank**; **NCBI**

Reference sequence: UDB000648
Chosen by: Andrew F.S. Taylor
Date: 2013-12-04 07:05:15

Large map (incl. map info)

Kaart | Satelliit

1.5% — 2%
1% — 2.5%
0.5% — 3%

	Sequence ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa ▾		Clustering based on: Full ITS
more	KC734544		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
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more	**UDB000077**	**Boletus luridus**		Denmark	Fruitbody			--------------------TCGAATT
more	EF644121		Boletaceae (uncultured Boletus)	Austria	Ectomycorrhiza	Populus tremula		--------------------TCGAATT
more	EF644104		Boletus (Boletus luridus)	Austria	Fruitbody	Populus tremula		----------------ATCATTATCGAATT
more	JF907793		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more	AF465183		Boletales (uncultured Boletaceae)	France	Ectomycorrhiza			--------------------TCGAATT
more	JF907802		Boletus (Boletus luridus)	Italy				--------------------TCGAATT
more	JF907789		Boletus (Boletus caucasicus)	Italy				----------------CGGAAGGATCATTATCGAATT

PlutoF cloud (UNITE)

DNA based species

are Open Access

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Thank you!