Sommersemester 2025
Vertiefte Bestimmungsübungen an Tieren (MEES003/C3)

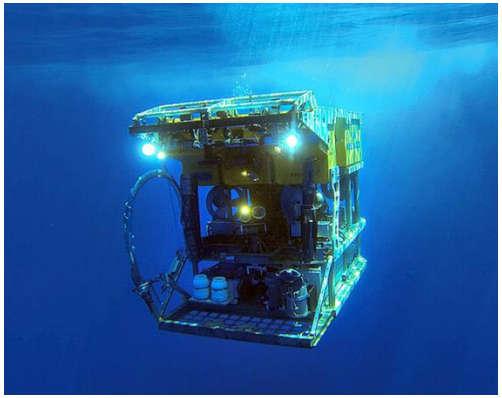
Environmental DNA (eDNA) Metabarcoding Analysis

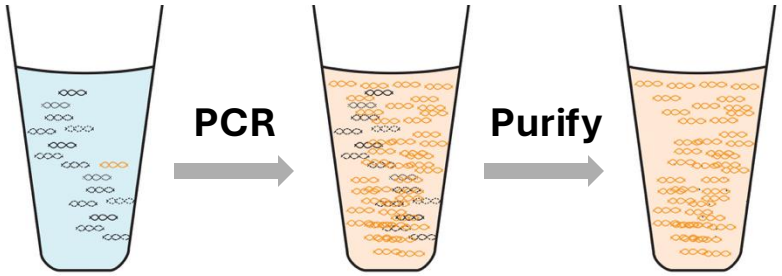
Day 3

Shumpei Yamakawa

Day1, 2:
eDNA Metabarcoding for identifying animals living in a pond near Halle

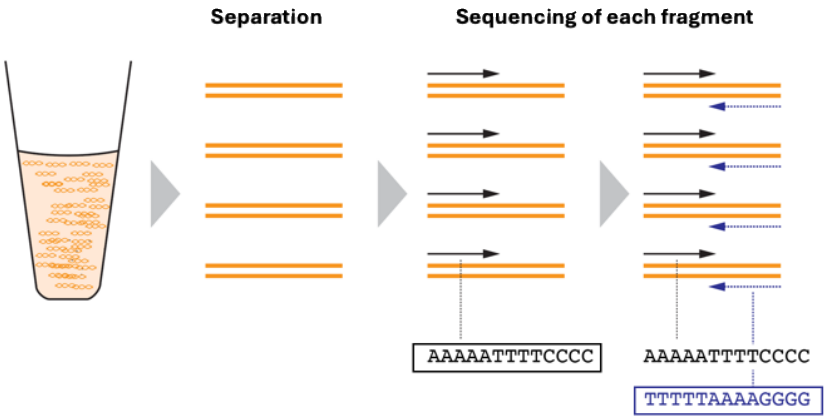
Day3: Metabarcoding analysis in different samples and a public dataset





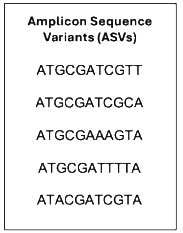
Send to the company or institute…

NGS analysis



Receive the sequencing data

Data processing



126 variants

Annotation

Analysis/Annotation

Publication

MOLECULAR ECOLOGY RESOURCES

RESOURCE ARTICLE | Full Access

Comparing iDNA from mosquitoes and flies to survey mammals in a semi-controlled Neotropical area

Bruno H. Saranholi, Karen G. Rodriguez-Castro, Carolina S. Carvalho, Samira Chahad-Ehlers, Carla C. Gestich, Sónia C. S. Andrade, Patrícia D. Freitas, Pedro M. Galetti Jr

First published: 03 August 2023 | https://doi.org/10.1111/1755-0998.13851 | Citations: 4

Handling Editor: Sebastien Calvignac-Spencer

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Abstract

Ingested-derived DNA (iDNA) from insects represents a powerful tool for assessing vertebrate diversity because insects are easy to sample, have a diverse diet and are

Data deposition

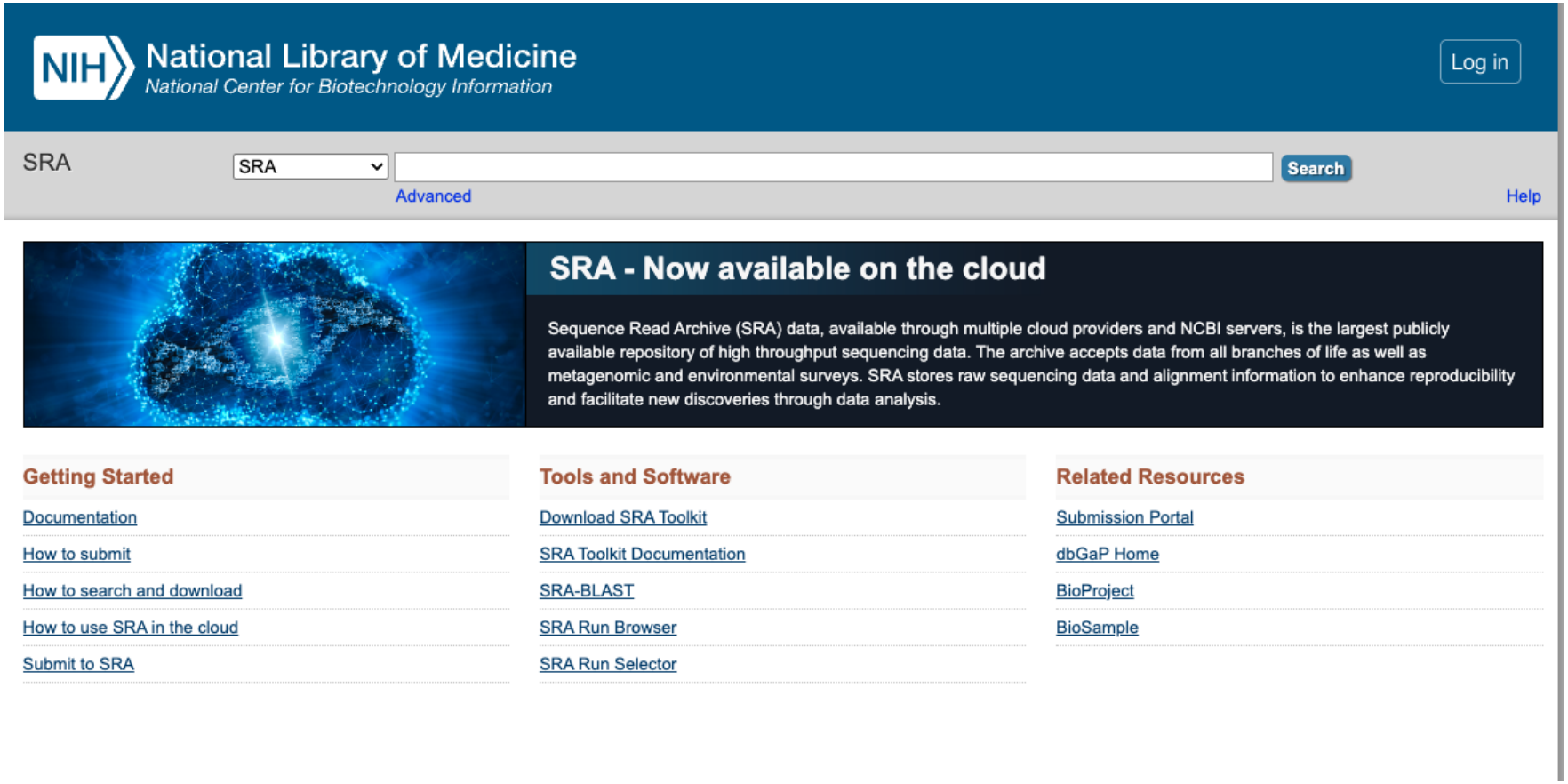
Open Research

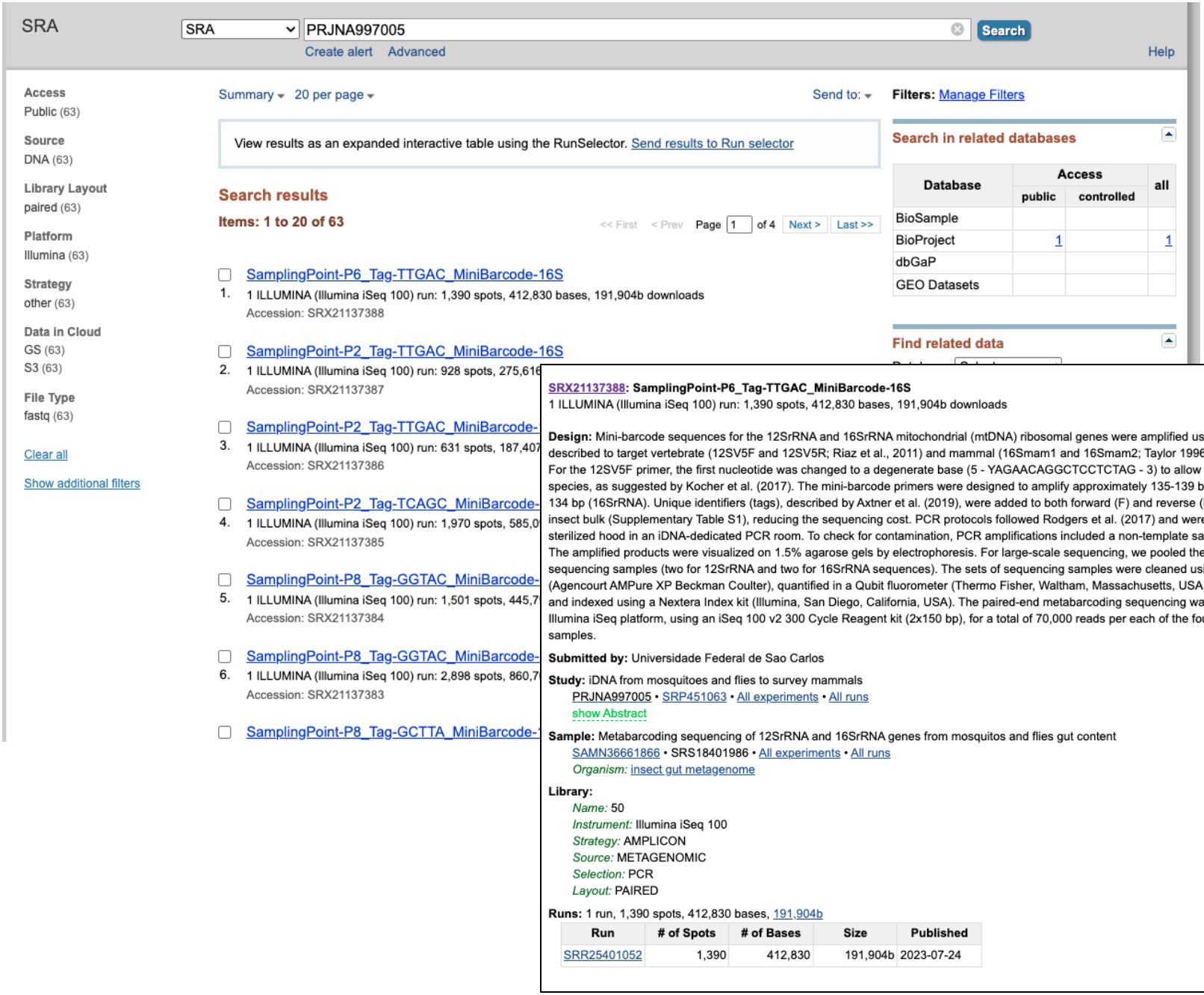
DATA AVAILABILITY STATEMENT

Raw sequence data are available in the NCBI BioProject and in the Sequence Read Archive repository under Accession number PRJNA997005.

SRA: Sequence Read Archive

https://www.ncbi.nlm.nih.gov/sra




SRA
SRA
PRJNA997005
Search
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DNA (63)
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fastq (63)
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View results as an expanded interactive table using the RunSelector. Send results to Run selector
Search results
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1. SamplingPoint-P6_Tag-TTGAC_MiniBarcode-16S
1 ILLUMINA (Illumina iSeq 100) run: 1,390 spots, 412,830 bases, 191,904b downloads
Accession: SRX21137388
2. SamplingPoint-P2_Tag-TTGAC_MiniBarcode-16S
1 ILLUMINA (Illumina iSeq 100) run: 928 spots, 275,616
Accession: SRX21137387
3. SamplingPoint-P2_Tag-TTGAC_MiniBarcode-
1 ILLUMINA (Illumina iSeq 100) run: 631 spots, 187,407
Accession: SRX21137386
4. SamplingPoint-P2_Tag-TCAGC_MiniBarcode-
1 ILLUMINA (Illumina iSeq 100) run: 1,970 spots, 585,0
Accession: SRX21137385
5. SamplingPoint-P8_Tag-GGTAC_MiniBarcode-
1 ILLUMINA (Illumina iSeq 100) run: 1,501 spots, 445,7
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1 ILLUMINA (Illumina iSeq 100) run: 2,898 spots, 860,7
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Search in related databases
Database
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public
controlled
all
BioSample
BioProject 1 1
dbGaP
GEO Datasets
Find related data
SRX21137388: SamplingPoint-P6_Tag-TTGAC_MiniBarcode-16S
1 ILLUMINA (Illumina iSeq 100) run: 1,390 spots, 412,830 bases, 191,904b downloads
Design: Mini-barcode sequences for the 12SrRNA and 16SrRNA mitochondrial (mtDNA) ribosomal genes were amplified using primers previously described to target vertebrate (12SV5F and 12SV5R; Riaz et al., 2011) and mammal (16Smam1 and 16Smam2; Taylor 1996) species, respectively. For the 12SV5F primer, the first nucleotide was changed to a degenerate base (5 - YAGAACAGGCTCCTCTAG - 3) to allow binding in more mammal species, as suggested by Kocher et al. (2017). The mini-barcode primers were designed to amplify approximately 135-139 bp (12SrRNA) and 130-134 bp (16SrRNA). Unique identifiers (tags), described by Axtner et al. (2019), were added to both forward (F) and reverse (R) primers to mark each insect bulk (Supplementary Table S1), reducing the sequencing cost. PCR protocols followed Rodgers et al. (2017) and were carried out within an UV-sterilized hood in an iDNA-dedicated PCR room. To check for contamination, PCR amplifications included a non-template sample as negative control. The amplified products were visualized on 1.5% agarose gels by electrophoresis. For large-scale sequencing, we pooled the samples in four sets of sequencing samples (two for 12SrRNA and two for 16SrRNA sequences). The sets of sequencing samples were cleaned using magnetic beads (Agencourt AMPure XP Beckman Coulter), quantified in a Qubit fluorometer (Thermo Fisher, Waltham, Massachusetts, USA), normalized to 50 ng/l, and indexed using a Nextera Index kit (Illumina, San Diego, California, USA). The paired-end metabarcoding sequencing was performed on an Illumina iSeq platform, using an iSeq 100 v2 300 Cycle Reagent kit (2x150 bp), for a total of 70,000 reads per each of the four sets of sequencing samples.
Submitted by: Universidade Federal de Sao Carlos
Study: iDNA from mosquitoes and flies to survey mammals
PRJNA997005 • SRP451063 • All experiments • All runs
show Abstract
Sample: Metabarcoding sequencing of 12SrRNA and 16SrRNA genes from mosquitos and flies gut content
SAMN36661866 • SRS18401986 • All experiments • All runs
Organism: insect gut metagenome
Library:
Name: 50
Instrument: Illumina iSeq 100
Strategy: AMPLICON
Source: METAGENOMIC
Selection: PCR
Layout: PAIRED
Runs: 1 run, 1,390 spots, 412,830 bases, 191,904b
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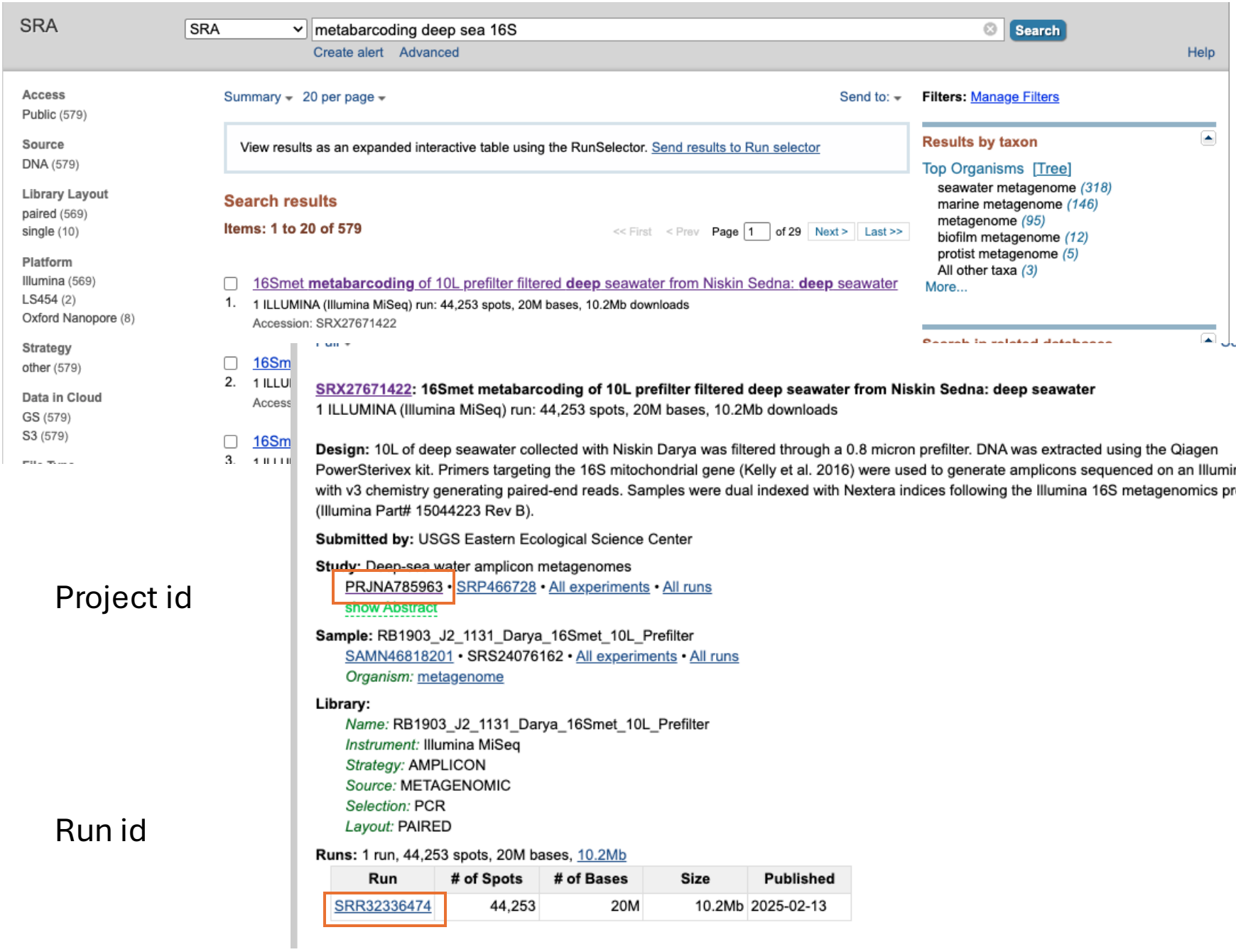
# of Spots
# of Bases
Size
Published
SRR25401052
1,390
412,830
191,904b
2023-07-24



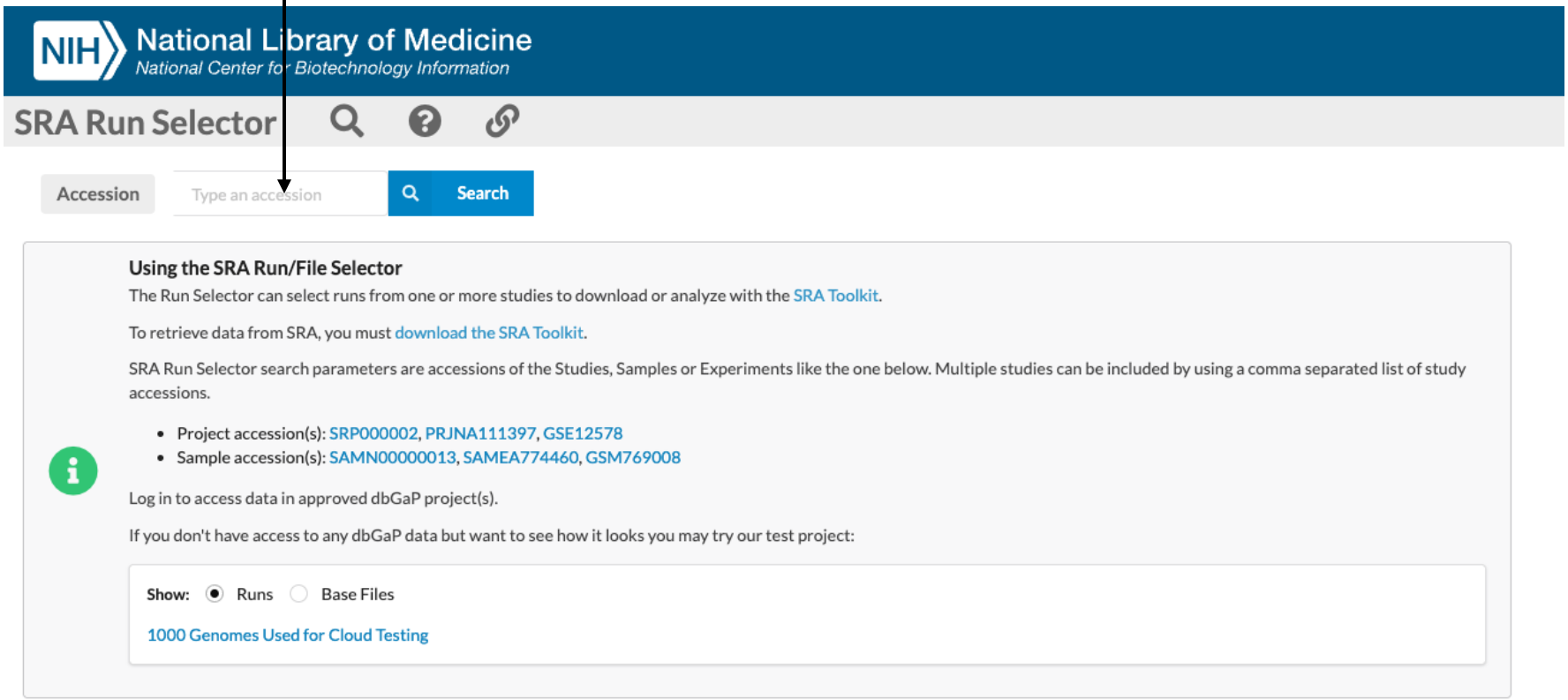
Project id

Run id

Details of the analysis may be found in SRA Run selector

https://www.ncbi.nlm.nih.gov/Traces/study/

PRJNA785963



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	Run	BioSample	AvgSpotLen	Bases	Bytes	Collection_Date	Depth	env_broad_scale	env_local_scale	Experiment	filter_material	filter_pore_size	lat_lon	Library Name	Niskin_name	nucl_acid_ext
1	SRR26406384	SAMN37846936	330	177.21 M	64.81 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112076	Sterivex	0.2	32.97398 N 75.91420 W	RB1903_J2_1137_Darya_18S_1L_Sterivex_run2	Darya	Sterivex filters were extracted using the
2	SRR26406385	SAMN37846935	337	214.81 M	78.93 Mb	2019-04-25	948m	oceanic epipelagic zone biome	oceanic epipelagic zone biome	SRX22112075	Prefilter	0.8	33.91893 N 75.83331 W	RB1903_J2_1135_Sedna_18S_10L_Prefilter_run2	Sedna	Prefilters were extracted using the Qiag
3	SRR26406386	SAMN37846934	337	148.81 M	52.73 Mb	2019-04-23	298m	oceanic epipelagic zone biome	oceanic epipelagic zone biome	SRX22112074	Sterivex	0.2	35.67351 N 74.79731 W	RB1903_J2_1133_Darya_18S_1L_Sterivex_run2	Darya	Sterivex filters were extracted using the
4	SRR26406387	SAMN37846933	337	208.12 M	82.07 Mb	2019-04-17	516m	oceanic epipelagic zone biome	oceanic epipelagic zone biome	SRX22112073	Prefilter	0.8	31.76121 N 79.19059 W	RB1903_J2_1130_Sedna_18S_10L_Prefilter_run2	Sedna	Prefilters were extracted using the Qiag
5	SRR26406388	SAMN37806937	325	75.21 M	31.91 Mb	2019-04-11	731m	oceanic epipelagic zone biome	oceanic epipelagic zone biome	SRX22112071	Sterivex	0.2	31.88915 N 77.36567 W	RB1903_J2_1128_Darya_18S_1L_Sterivex	Darya	Sterivex filters were extracted using the
6	SRR26406389	SAMN37807008	128	54.81 M	26.77 Mb	2019-10	Surface	laboratory	laboratory	SRX22112070	Prefilter	0.8	NA	Lab_extraction_ctl_cox1_10L_Prefilter	NA	Prefilters were extracted using the Qiag
7	SRR26406390	SAMN37807006	116	20.56 M	9.59 Mb	2019-09	Surface	laboratory	laboratory	SRX22112068	Sterivex	0.2	NA	Lab_extraction_ctl_cox1_1L_Sterivex	NA	Sterivex filters were extracted using the
8	SRR26406391	SAMN37807005	98	1.39 M	444.34 kb	2019-09	Surface	laboratory	laboratory	SRX22112067	Sterivex	0.2	NA	Lab_extraction_ctl_18S_1L_Sterivex	NA	Sterivex filters were extracted using the
9	SRR26406392	SAMN37807004	122	83.54 M	40.02 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112066	Prefilter	0.8	NA	RB1903_Postcruise_ctl_Sedna_cox1_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag
10	SRR26406393	SAMN37807003	486	140.44 M	61.83 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112065	Prefilter	0.8	NA	RB1903_Postcruise_ctl_Darya_cox1_10L_Prefilter	Darya	Prefilters were extracted using the Qiag
11	SRR26406394	SAMN37807002	178	85.94 M	42.97 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112064	Sterivex	0.2	NA	RB1903_Postcruise_ctl_Sedna_cox1_1L_Sterivex	Sedna	Sterivex filters were extracted using the
12	SRR26406395	SAMN37807001	453	126.22 M	56.91 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112063	Sterivex	0.2	NA	RB1903_Postcruise_ctl_Darya_cox1_1L_Sterivex	Darya	Sterivex filters were extracted using the
13	SRR26406396	SAMN37807000	328	7.93 M	3.75 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112062	Prefilter	0.8	NA	RB1903_Postcruise_ctl_Sedna_18S_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag
14	SRR26406397	SAMN37806999	344	59.25 M	23.99 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112061	Prefilter	0.8	NA	RB1903_Postcruise_ctl_Darya_18S_10L_Prefilter	Darya	Prefilters were extracted using the Qiag
15	SRR26406398	SAMN37806936	527	88.92 M	39.52 Mb	2019-04-09	Surface	laboratory	laboratory	SRX22112060	Prefilter	0.8	NA	RB1903_Precruise_ctl_Sedna_cox1_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag
16	SRR26406399	SAMN37806998	256	2.24 M	1.21 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112059	Sterivex	0.2	NA	RB1903_Postcruise_ctl_Sedna_18S_1L_Sterivex	Sedna	Sterivex filters were extracted using the
17	SRR26406400	SAMN37806997	334	123.26 M	52.10 Mb	2019-04-30	Surface	laboratory	laboratory	SRX22112058	Sterivex	0.2	NA	RB1903_Postcruise_ctl_Darya_18S_1L_Sterivex	Darya	Sterivex filters were extracted using the
18	SRR26406401	SAMN37807007	106	13.05 k	71.31 kb	2019-10	Surface	laboratory	laboratory	SRX22112069	Prefilter	0.8	NA	Lab_extraction_ctl_18S_10L_Prefilter	NA	Prefilters were extracted using the Qiag
19	SRR26406402	SAMN37806996	557	83.35 M	38.04 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112057	Prefilter	0.8	32.97398 N 75.91420 W	RB1903_J2_1137_Sedna_cox1_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag
20	SRR26406403	SAMN37806995	560	87.98 M	39.08 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112056	Prefilter	0.8	32.97398 N 75.91420 W	RB1903_J2_1137_Darya_cox1_10L_Prefilter	Darya	Prefilters were extracted using the Qiag
21	SRR26406404	SAMN37806994	551	128.02 M	54.97 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112055	Sterivex	0.2	32.97398 N 75.91420 W	RB1903_J2_1137_Sedna_cox1_1L_Sterivex	Sedna	Sterivex filters were extracted using the
22	SRR26406405	SAMN37806993	572	140.78 M	60.97 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112054	Sterivex	0.2	32.97398 N 75.91420 W	RB1903_J2_1137_Darya_cox1_1L_Sterivex	Darya	Sterivex filters were extracted using the
23	SRR26406406	SAMN37806992	339	105.31 M	46.46 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112053	Prefilter	0.8	32.97398 N 75.91420 W	RB1903_J2_1137_Sedna_18S_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag
24	SRR26406407	SAMN37806991	336	142.59 M	62.05 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112052	Prefilter	0.8	32.97398 N 75.91420 W	RB1903_J2_1137_Darya_18S_10L_Prefilter	Darya	Prefilters were extracted using the Qiag
25	SRR26406408	SAMN37806990	331	90.97 M	39.27 Mb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112051	Sterivex	0.2	32.97398 N 75.91420 W	RB1903_J2_1137_Sedna_18S_1L_Sterivex	Sedna	Sterivex filters were extracted using the
26	SRR26406409	SAMN37806989	417	314.85 k	212.07 kb	2019-04-29	2571m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112050	Sterivex	0.2	32.97398 N 75.91420 W	RB1903_J2_1137_Darya_18S_1L_Sterivex	Darya	Sterivex filters were extracted using the
27	SRR26406410	SAMN37806935	573	140.50 M	58.58 Mb	2019-04-09	Surface	laboratory	laboratory	SRX22112049	Prefilter	0.8	NA	RB1903_Precruise_ctl_Darya_cox1_10L_Prefilter	Darya	Prefilters were extracted using the Qiag
28	SRR26406411	SAMN37806988	515	118.75 M	50.08 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112048	Prefilter	0.8	32.49361 N 76.19091 W	RB1903_J2_1136_Sedna_cox1_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag
29	SRR26406412	SAMN37806987	542	111.85 M	48.85 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112047	Prefilter	0.8	32.49361 N 76.19091 W	RB1903_J2_1136_Darya_cox1_10L_Prefilter	Darya	Prefilters were extracted using the Qiag
30	SRR26406413	SAMN37806986	506	124.07 M	53.07 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112046	Sterivex	0.2	32.49361 N 76.19091 W	RB1903_J2_1136_Sedna_cox1_1L_Sterivex	Sedna	Sterivex filters were extracted using the
31	SRR26406414	SAMN37806985	516	114.24 M	48.19 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112045	Sterivex	0.2	32.49361 N 76.19091 W	RB1903_J2_1136_Darya_cox1_1L_Sterivex	Darya	Sterivex filters were extracted using the
32	SRR26406415	SAMN37806984	338	112.99 M	49.98 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112044	Prefilter	0.8	32.49361 N 76.19091 W	RB1903_J2_1136_Sedna_18S_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag
33	SRR26406416	SAMN37806983	334	82.92 M	35.20 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112043	Prefilter	0.8	32.49361 N 76.19091 W	RB1903_J2_1136_Darya_18S_10L_Prefilter	Darya	Prefilters were extracted using the Qiag
34	SRR26406417	SAMN37806982	332	106.40 M	46.41 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112042	Sterivex	0.2	32.49361 N 76.19091 W	RB1903_J2_1136_Sedna_18S_1L_Sterivex	Sedna	Sterivex filters were extracted using the
35	SRR26406418	SAMN37806981	326	91.25 M	39.24 Mb	2019-04-28	2164m	oceanic bathypelagic zone biome	oceanic bathypelagic zone biome	SRX22112041	Sterivex	0.2	32.49361 N 76.19091 W	RB1903_J2_1136_Darya_18S_1L_Sterivex	Darya	Sterivex filters were extracted using the
36	SRR26406419	SAMN37806980	543	124.43 M	53.76 Mb	2019-04-25	948m	oceanic epipelagic zone biome	oceanic epipelagic zone biome	SRX22112040	Prefilter	0.8	33.91893 N 75.83331 W	RB1903_J2_1135_Sedna_cox1_10L_Prefilter	Sedna	Prefilters were extracted using the Qiag

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ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1133_Darya_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1133_Darya_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1133_Cedna_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1133_Cedna_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1128_Cedna_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1130_Cedna_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1128_Cedna_16Smet_1L_Sterivex	mitochondrial 16S

Runs: 1 run, 1,390 spots, 412,830 bases, 191,904b

Run	# of Spots	# of Bases	Size	Published
SRR25401052	1,390	412,830	191,904b	2023-07-24

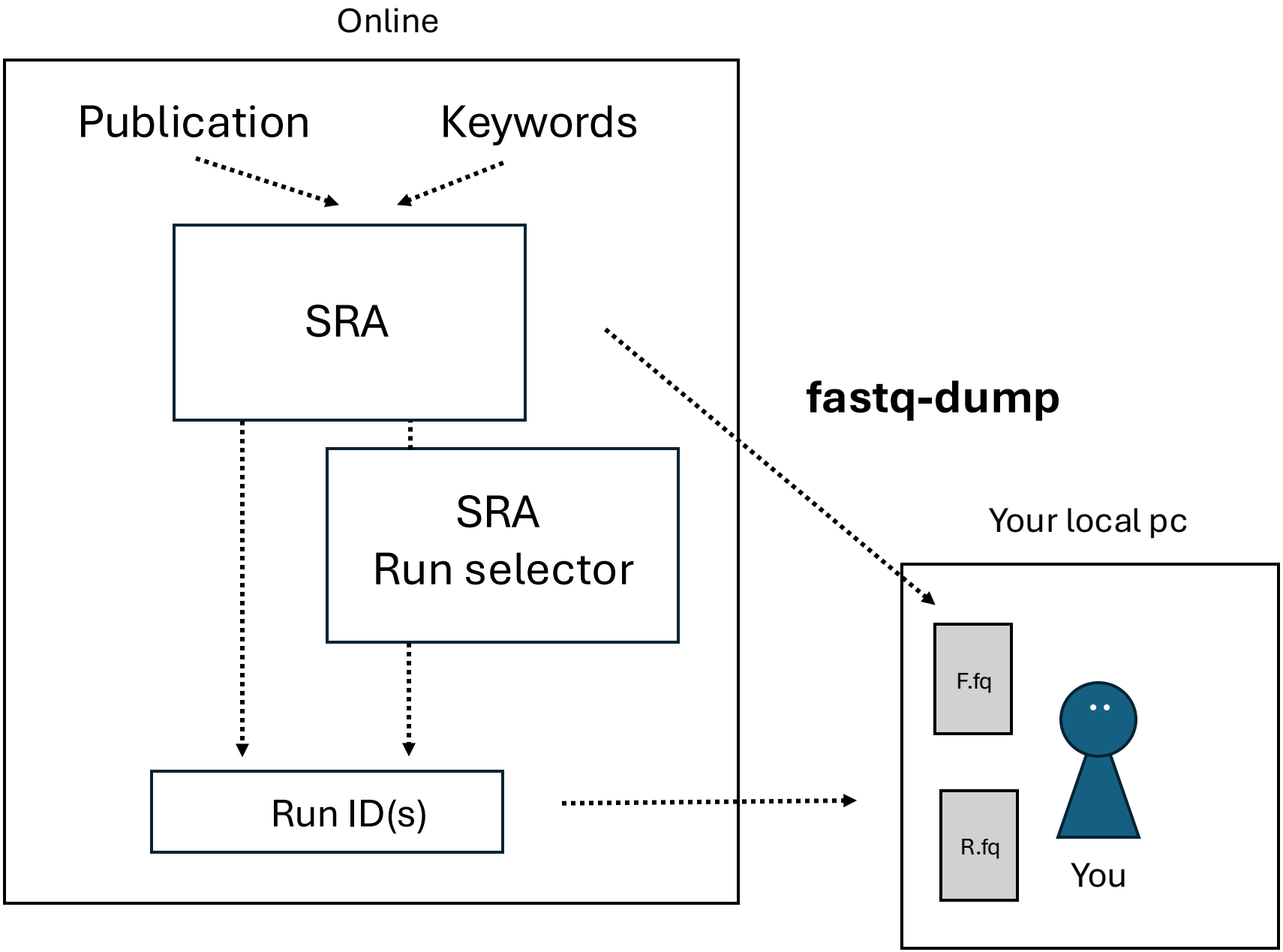
Download fastq files from SRA

Find the BioProject ID and search for it in the SRA Run Selector (https://www.ncbi.nlm.nih.gov/Traces/study/) to find the run ID.

```
fastq-dump --gzip --split-files ***RUN ID***
```

```
shumpei_yamakawa@cs-918058803005-default:~$ fastq-dump --gzip --split-files SRR3233649
0
Read 83944 spots for SRR32336490
Written 83944 spots for SRR32336490
shumpei_yamakawa@cs-918058803005-default:~$ ls
a  b  c  ncbi-blast-2.16.0+  New_directory1  R  README-cloudshell.txt  sratoolkit.3.2.
1-ubuntu64  SRR32336490_1.fastq.gz  SRR32336490_2.fastq.gz  test  test2  test_meta
```

-> Go to the same analysis


Online
Publication
Keywords
SRA
SRA
Run selector
Run ID(s)
fastq-dump
Your local pc
F.fq
R.fq
You

Tasks:

(Remaining Day2) Sample6 and Sample7

Analysis of public datasets 1

- **example 1: deep sea samples**
- **example 2: mosquito/fry samples**

Analysis of public datasets 2

- **find and analyze the datasets in SRA**

Example 1: Deep-sea water amplicon metagenomes. PRJNA785963

OCEAN EXPLORATION

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DEEP SEARCH: DEEP Sea Exploration to Advance Research on Coral/Canyon/Cold seep Habitats

Home / Expeditions / DEEP SEARCH / Mission Logs / September 22

DEEP SEARCH 2017 Comes to an Early End, but the Project Is Just Beginning

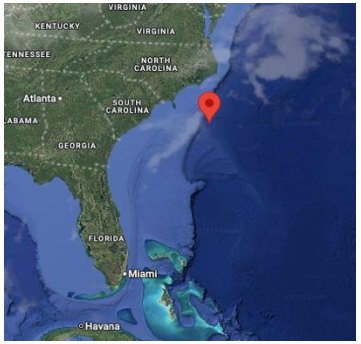
By Caitlin Adams, NOAA Office of Ocean Exploration and Research, Web Coordinator
September 22, 2017

The two Niskin bottles used to collect deep-sea water samples are mounted to the bottom of ROV *Jason* and can be triggered by the ROV's manipulator arms. *Image courtesy of DEEP SEARCH 2019 - BOEM, USGS, NOAA.* Download larger version (jpg, 704 KB).

Ex.) SRR32336490

Sea water (depth 2,571 m)

16s rRNA amplicon / metazoa



Example 2

MOLECULAR ECOLOGY RESOURCES

RESOURCE ARTICLE | Full Access

Comparing iDNA from mosquitoes and flies to survey mammals in a semi-controlled Neotropical area

Bruno H. Saranholi, Karen G. Rodriguez-Castro, Carolina S. Carvalho, Samira Chahad-Ehlers, Carla C. Gestich, Sónia C. S. Andrade, Patrícia D. Freitas, Pedro M. Galetti Jr

First published: 03 August 2023 | https://doi.org/10.1111/1755-0998.13851 | Citations: 4

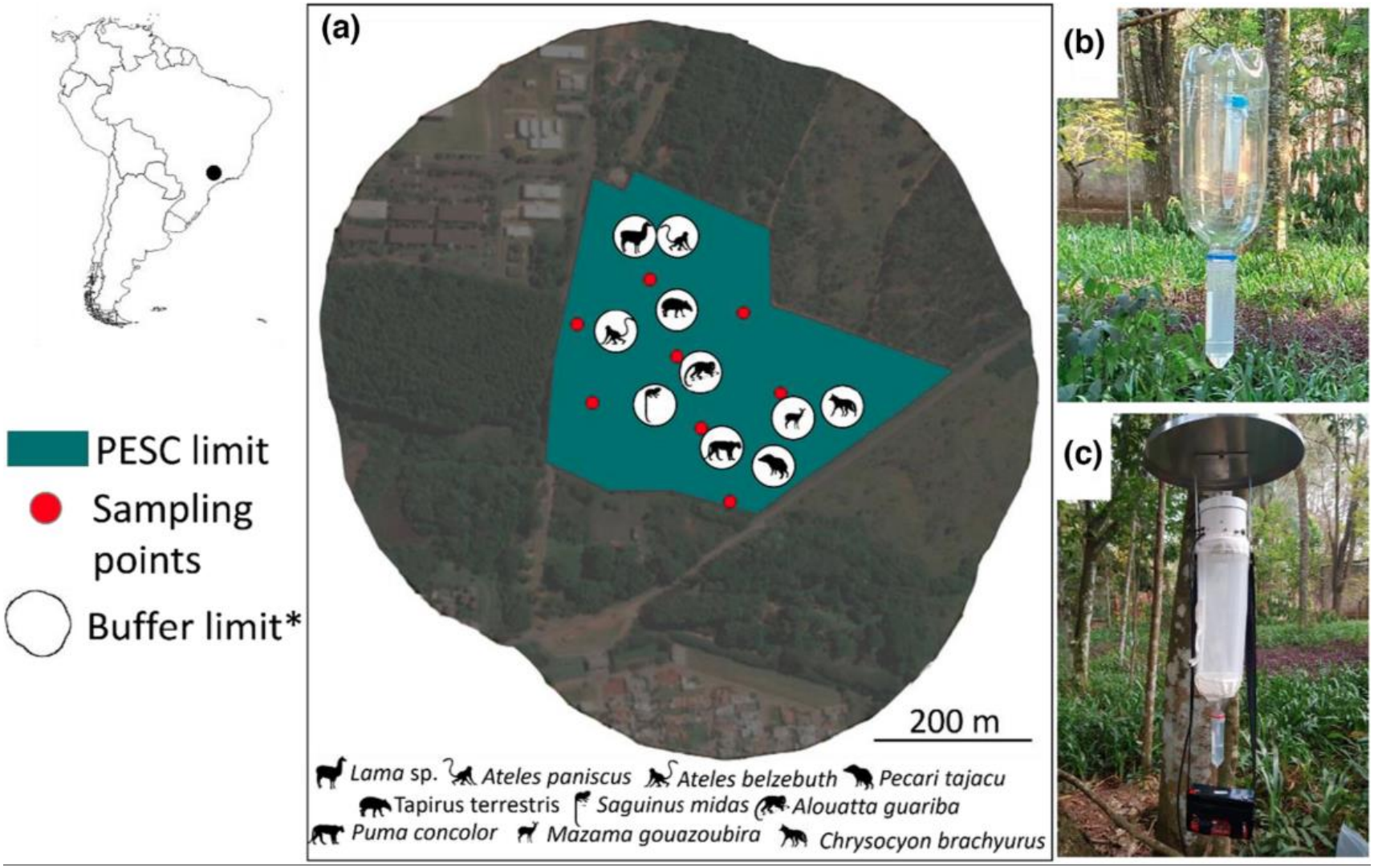
Handling Editor: Sebastien Calvignac-Spencer

Abstract

Ingested-derived DNA (iDNA) from insects represents a powerful tool for assessing vertebrate diversity because insects are easy to sample, have a diverse diet and are

Metabarcoding

Distribution of animals?



Amplified 16s rrna sequences (vertebrates)

Parque Ecológico de São Carlos
(Zoo and nature park)

Ex)

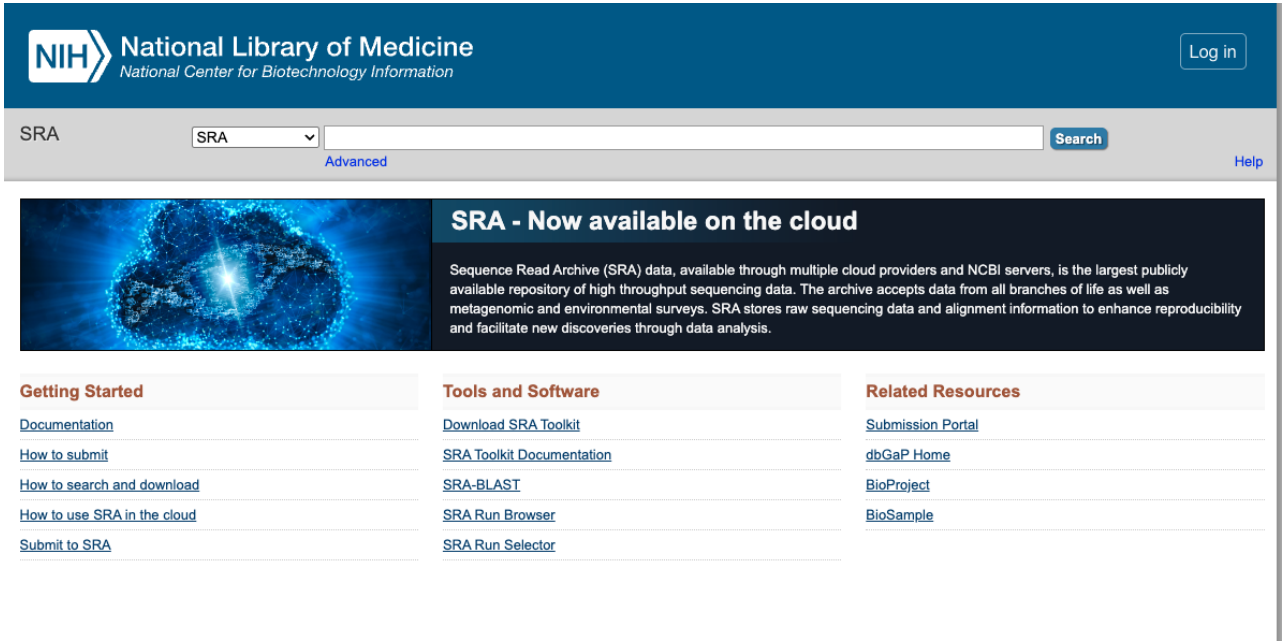
Hematophagous mosquito

SRR25401090

Saprophagous fly

SRR25401082

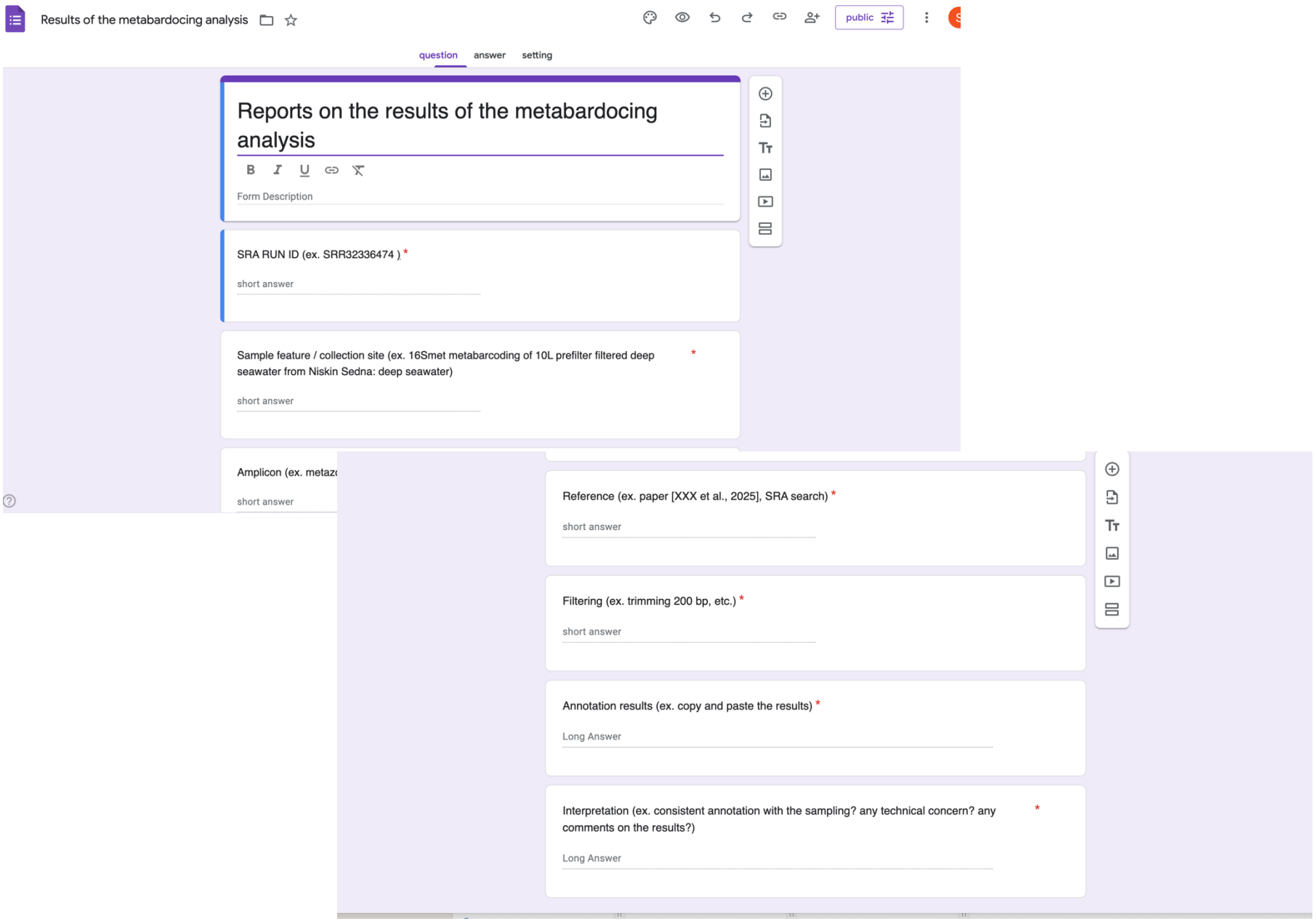
Analysis of public datasets




```
#####
Results

Abandance: total 31661 reads
16 species was identified

Phylum            Class    Species          blast_tophit     blast_ident     abundance       seqs
-------------------------------------------------------------------------------------------------
Arthropoda        Branchiopoda     Daphnia longispina       JN874595.1      97.521  128     seq63
Arthropoda        Branchiopoda     Eubosmina cf.    EU650685.1      98.347  67      seq93
Arthropoda        Branchiopoda     Scapholeberis mucronata EF189615.1       98.326  33      seq114
Arthropoda        Branchiopoda     Simocephalus vetulus     LC382447.1      97.531  36      seq113
Arthropoda        Insecta Cloeon dipterum LC801945.1       96.680  43      seq109
Bryozoa Phylactolaemata Plumatella repens        DQ305341.1      98.438  31      seq115
Chordata          Actinopteri      Carassius auratus        DQ868870.1      99.674  59      seq101
Chordata          Actinopteri      Gasterosteus aculeatus   DQ027919.1      99.340  135     seq59
Chordata          Actinopteri      Leucaspius delineatus    NC_020357.1     99.342  68      seq92
Chordata          Actinopteri      Pseudorasbora interrupta         MN175390.1      99.342  5       seq125
Chordata          Amphibia         Bufo bufo        JN647011.1      99.669  202     seq54,seq100
Chordata          Amphibia         Pelophylax lessonae      MH105105.1      99.656  16      seq118
Chordata          Amphibia         Rana temporaria KC977158.1       100.000 96      seq80
Chordata          Aves     Gallinula chloropus      DQ485864.1      98.635  38      seq112
Chordata          Mammalia         Myocastor coypus         AF422886.1      99.281  4       seq126
Rotifera          Eurotatoria      Keratella quadrata       AF499046.1      99.010  4439    seq6,seq8,seq18,s
-------------------------------------------------------------------------------------------------

Output files are in Sample5_asv.csv_95
```

Amplicons need to be metazoan 16s rRNA for the customized scripts

https://docs.google.com/forms/d/e/1FAIpQLSfTs3waEgm2DijM044nAUQhnMFUr2IuhOSFIiwLmjz8MnwjGQ/viewform?usp=header



Tasks:

(Remaining Day2) Sample6 and Sample7

Analysis of public datasets 1

- **example 1: deep sea samples**
- **example 2: mosquito/fry samples**

Analysis of public datasets 2

- **find and analyze the datasets in SRA (at least one)**

-> Make a short report

https://docs.google.com/forms/d/e/1FAIpQLSfTs3waEgm2DijM044nAUQhnMFUr2IuhOSFIiwLmjz8MnwjGQ/viewform?usp=header