

Sommersemester 2025

Vertiefte Bestimmungsübungen an Tieren (MEES003/C3)

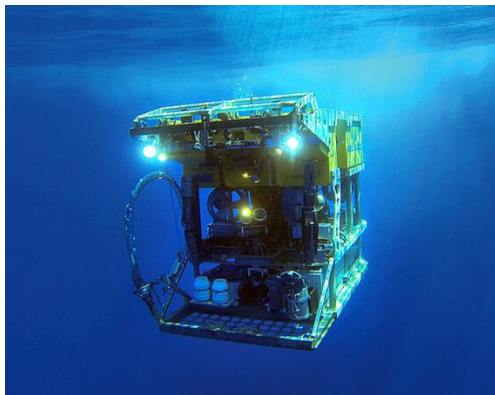
Environmental DNA (eDNA) Metabarcoding Analysis

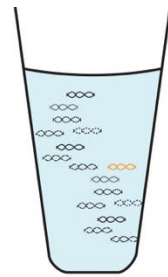
Day 3



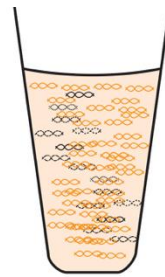
Day1, 2:
eDNA Metabarcoding for
identifying animals living in
a pond near Halle

Day3: Metabarcoding analysis in different samples and a public dataset

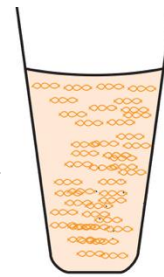




PCR



Purify



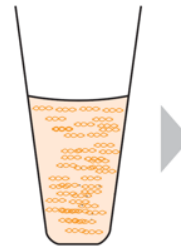
Send to the company or institute...



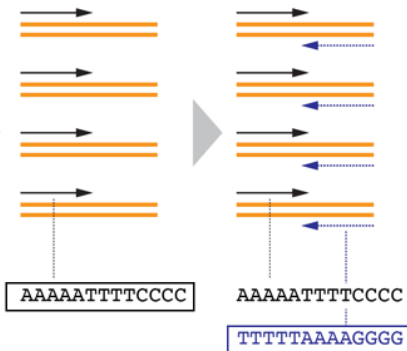
NGS analysis



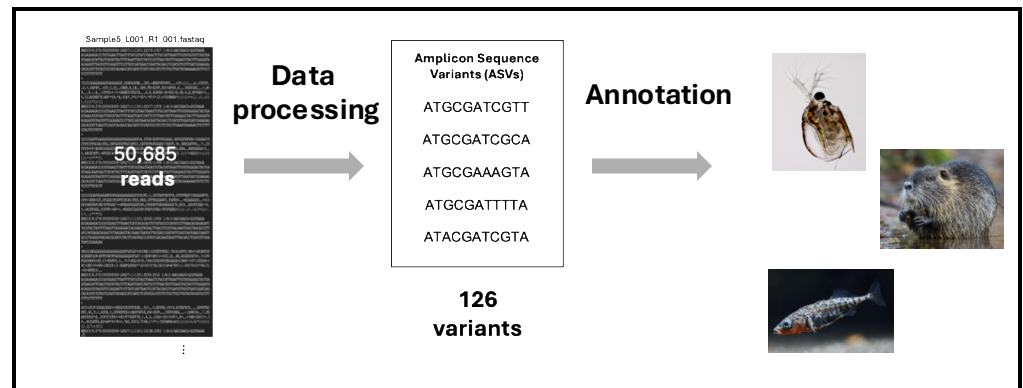
Separation



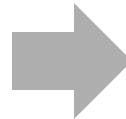
Sequencing of each fragment



Receive the sequencing data



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. Rodríguez-Castro, Carolina S. Carvalho, Samira Chahad-Ehlers, Carla C. Gestich, Sônia 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

SECTIONS

PDF TOOLS SHARE

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>



National Library of Medicine
National Center for Biotechnology Information

Log in

SRA

SRA ▼

[Advanced](#)

Search

[Help](#)



SRA - Now available on the cloud

Sequence Read Archive (SRA) data, available through multiple cloud providers and NCBI servers, is the largest publicly available repository of high throughput sequencing data. The archive accepts data from all branches of life as well as metagenomic and environmental surveys. SRA stores raw sequencing data and alignment information to enhance reproducibility and facilitate new discoveries through data analysis.

Getting Started

[Documentation](#)

[How to submit](#)

[How to search and download](#)

[How to use SRA in the cloud](#)

[Submit to SRA](#)

Tools and Software

[Download SRA Toolkit](#)

[SRA Toolkit Documentation](#)

[SRA-BLAST](#)

[SRA Run Browser](#)

[SRA Run Selector](#)

Related Resources

[Submission Portal](#)

[dbGaP Home](#)

[BioProject](#)

[BioSample](#)

Access

Public (63)

Source

DNA (63)

Library Layout

paired (63)

Platform

Illumina (63)

Strategy

other (63)

Data in Cloud

GS (63)

S3 (63)

File Type

fastq (63)

[Clear all](#)

[Show additional filters](#)

Summary 20 per page

Send to

Filters: [Manage Filters](#)

View results as an expanded interactive table using the RunSelector. [Send results to Run selector](#)

Search results

Items: 1 to 20 of 63

<< First < Prev Page 1 of 4 Next > Last >>

☐ [SamplingPoint-P6_Tag-TTGAC_MiniBarcode-16S](#)

1. 1 ILLUMINA (Illumina iSeq 100) run: 1,390 spots, 412,830 bases, 191,904b downloads
Accession: SRX21137388

☐ [SamplingPoint-P2_Tag-TTGAC_MiniBarcode-16S](#)

2. 1 ILLUMINA (Illumina iSeq 100) run: 928 spots, 275,616 bases, 135,904b downloads
Accession: SRX21137387

☐ [SamplingPoint-P2_Tag-TTGAC_MiniBarcode-16S](#)

3. 1 ILLUMINA (Illumina iSeq 100) run: 631 spots, 187,407 bases, 135,904b downloads
Accession: SRX21137386

☐ [SamplingPoint-P2_Tag-TCAGC_MiniBarcode-16S](#)

4. 1 ILLUMINA (Illumina iSeq 100) run: 1,970 spots, 585,040 bases, 135,904b downloads
Accession: SRX21137385

☐ [SamplingPoint-P8_Tag-GGTAC_MiniBarcode-16S](#)

5. 1 ILLUMINA (Illumina iSeq 100) run: 1,501 spots, 445,740 bases, 135,904b downloads
Accession: SRX21137384

☐ [SamplingPoint-P8_Tag-GGTAC_MiniBarcode-16S](#)

6. 1 ILLUMINA (Illumina iSeq 100) run: 2,898 spots, 860,740 bases, 135,904b downloads
Accession: SRX21137383

☐ [SamplingPoint-P8_Tag-GCTTA_MiniBarcode-16S](#)

Search in related databases

Database	Access		all
	public	controlled	
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](#)

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

SRA

SRA

metabarcoding deep sea 16S

Search

Create alertAdvanced

Help

Access

Public (579)

Source

DNA (579)

Library Layout

paired (569)

single (10)

Platform

Illumina (569)

LS454 (2)

Oxford Nanopore (8)

Strategy

other (579)

Data in Cloud

GS (579)

S3 (579)

Summary20 per page

Send to:Filters: Manage Filters

View results as an expanded interactive table using the RunSelector. Send results to Run selector

Search results

Items: 1 to 20 of 579

<< First < Prev Page 1 of 29 Next > Last >>

☐ 16Smet metabarcoding of 10L prefilter filtered deep seawater from Niskin Sedna: deep seawater

1. 1 ILLUMINA (Illumina MiSeq) run: 44,253 spots, 20M bases, 10.2Mb downloads

Accession: SRX27671422

☐ 16Sm

2. 1 ILLUMINA (Illumina MiSeq) run: 44,253 spots, 20M bases, 10.2Mb downloads

Accession: SRX27671422

☐ 16Sm

3. 1 ILLUMINA (Illumina MiSeq) run: 44,253 spots, 20M bases, 10.2Mb downloads

Accession: SRX27671422

SRX27671422: 16Smet metabarcoding of 10L prefilter filtered deep seawater from Niskin Sedna: deep seawater

1 ILLUMINA (Illumina MiSeq) run: 44,253 spots, 20M bases, 10.2Mb downloads

Design: 10L of deep seawater collected with Niskin Darya was filtered through a 0.8 micron prefilter. DNA was extracted using the Qiagen PowerSterivex kit. Primers targeting the 16S mitochondrial gene (Kelly et al. 2016) were used to generate amplicons sequenced on an Illumina MiSeq with v3 chemistry generating paired-end reads. Samples were dual indexed with Nextera indices following the Illumina 16S metagenomics protocol (Illumina Part# 15044223 Rev B).

Submitted by: USGS Eastern Ecological Science Center

Study: Deep-sea water amplicon metagenomes

PRJNA785963 • SRP466728 • All experiments • All runs

show Abstract

Sample: RB1903_J2_1131_Darya_16Smet_10L_Prefilter

SAMN46818201 • SRS24076162 • All experiments • All runs

Organism: metagenome

Library:

Name: RB1903_J2_1131_Darya_16Smet_10L_Prefilter

Instrument: Illumina MiSeq

Strategy: AMPLICON

Source: METAGENOMIC

Selection: PCR

Layout: PAIRED

Runs: 1 run, 44,253 spots, 20M bases, 10.2Mb

Run	# of Spots	# of Bases	Size	Published
SRR32336474	44,253	20M	10.2Mb	2025-02-13

Results by taxon

Top Organisms Tree

seawater metagenome (318)

marine metagenome (146)

metagenome (95)

biofilm metagenome (12)

protist metagenome (5)

All other taxa (3)

More...

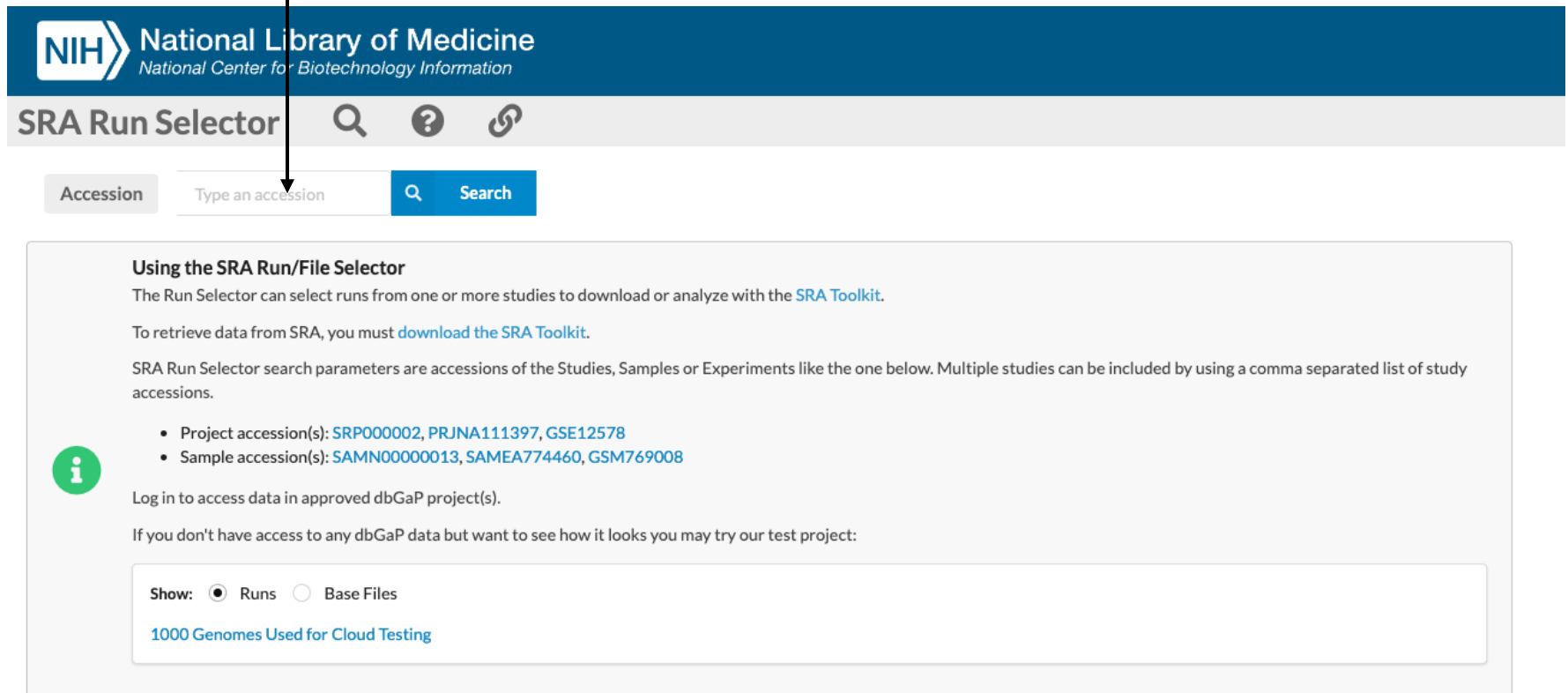
Search in related databases

Project id

Run id

Details of the analysis may be found in SRA Run selector
<https://www.ncbi.nlm.nih.gov/Traces/study/>

[PRJNA785963](#)



NIH National Library of Medicine
National Center for Biotechnology Information

SRA Run Selector

Accession


Using the SRA Run/File Selector

The Run Selector can select runs from one or more studies to download or analyze with the [SRA Toolkit](#).

To retrieve data from SRA, you must [download the SRA Toolkit](#).

SRA Run Selector search parameters are accessions of the Studies, Samples or Experiments like the one below. Multiple studies can be included by using a comma separated list of study accessions.

- Project accession(s): [SRP000002](#), [PRJNA111397](#), [GSE12578](#)
- Sample accession(s): [SAMN00000013](#), [SAMEA774460](#), [GSM769008](#)

 Log in to access data in approved dbGaP project(s).

If you don't have access to any dbGaP data but want to see how it looks you may try our test project:

Show: ☒ Runs ☐ Base Files

[1000 Genomes Used for Cloud Testing](#)

Found 125 Items			Search within results										Q		Clear				1	1	3	>
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	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	nuc_acid_ext					
<input type="checkbox"/>	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_185_1L_Sterivex_run2	Darya	Sterivex filters were extracted using the					
<input type="checkbox"/>	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_185_10L_Prefilter_run2	Sedna	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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_185_1L_Sterivex_run2	Darya	Sterivex filters were extracted using the					
<input type="checkbox"/>	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_185_10L_Prefilter_run2	Sedna	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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_185_1L_Sterivex	Darya	Sterivex filters were extracted using the					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	8	SRR26406391	SAMN37807005	98	1.39 M	444.34 kb	2019-09	Surface	laboratory	laboratory	SRX22112067	Sterivex	0.2	NA	Lab_extraction_ctl_185_1L_Sterivex	NA	Sterivex filters were extracted using the					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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_185_10L_Prefilter	Sedna	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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_185_10L_Prefilter	Darya	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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_185_1L_Sterivex	Sedna	Sterivex filters were extracted using the					
<input type="checkbox"/>	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_185_1L_Sterivex	Darya	Sterivex filters were extracted using the					
<input type="checkbox"/>	18	SRR26406401	SAMN37807007	106	13.05 k	71.31 kb	2019-10	Surface	laboratory	laboratory	SRX22112069	Prefilter	0.8	NA	Lab_extraction_ctl_185_10L_Prefilter	NA	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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_185_10L_Prefilter	Sedna	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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_185_10L_Prefilter	Darya	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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_185_1L_Sterivex	Sedna	Sterivex filters were extracted using the					
<input type="checkbox"/>	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_185_1L_Sterivex	Darya	Sterivex filters were extracted using the					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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					
<input type="checkbox"/>	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_185_10L_Prefilter	Sedna	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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_185_10L_Prefilter	Darya	Prefilters were extracted using the QIag					
<input type="checkbox"/>	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_185_1L_Sterivex	Sedna	Sterivex filters were extracted using the					
<input type="checkbox"/>	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_185_1L_Sterivex	Darya	Sterivex filters were extracted using the					
<input type="checkbox"/>	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					

17	18	19	20	21
	↕ ReleaseDate	↕ create_date	↕ Sample Name	Target_Gene
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1128_Darya_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1137_Darya_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1137_Darya_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1137_Cedna_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1137_Cedna_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1136_Darya_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1136_Darya_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1136_Cedna_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:04:00Z	RB1903_J2_1136_Cedna_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1135_Darya_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1135_Darya_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1128_Darya_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1135_Cedna_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1135_Cedna_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1134_Darya_16Smet_101L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:03:00Z	RB1903_J2_1134_Darya_16Smet_1L_Sterivex	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:02:00Z	RB1903_J2_1134_Cedna_16Smet_10L_Prefilter	mitochondrial 16S
ATCAYGT	2025-02-13	2025-02-13 17:04:00Z	RB1903_J2_1134_Cedna_16Smet_1L_Sterivex	mitochondrial 16S
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 SRR32336490
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

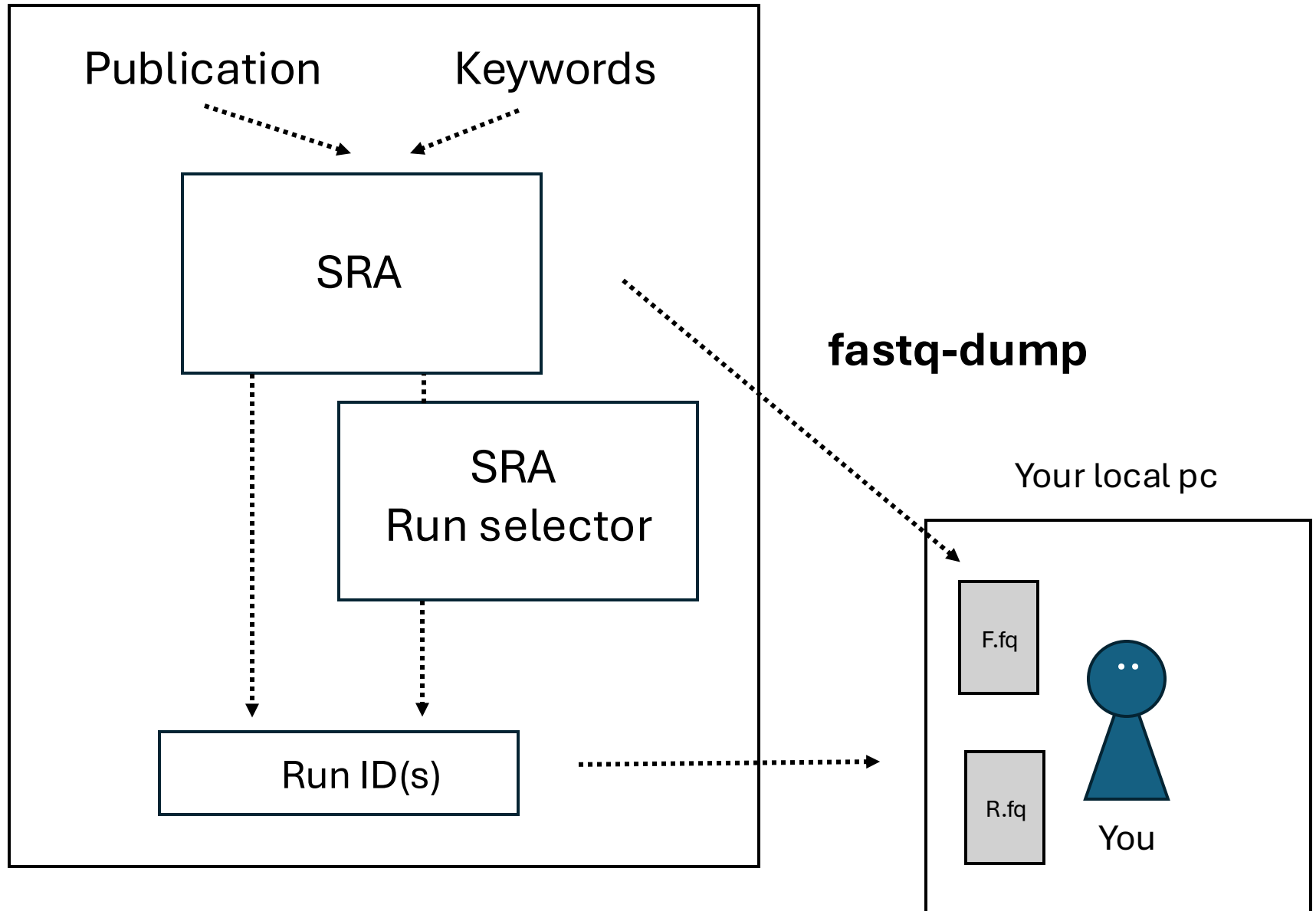
Your local pc

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](#)

[About](#) ▾[Expeditions](#) ▾[Science & Technology](#) ▾[Data & Products](#) ▾[Education](#) ▾[Multimedia](#) ▾[News](#) ▾

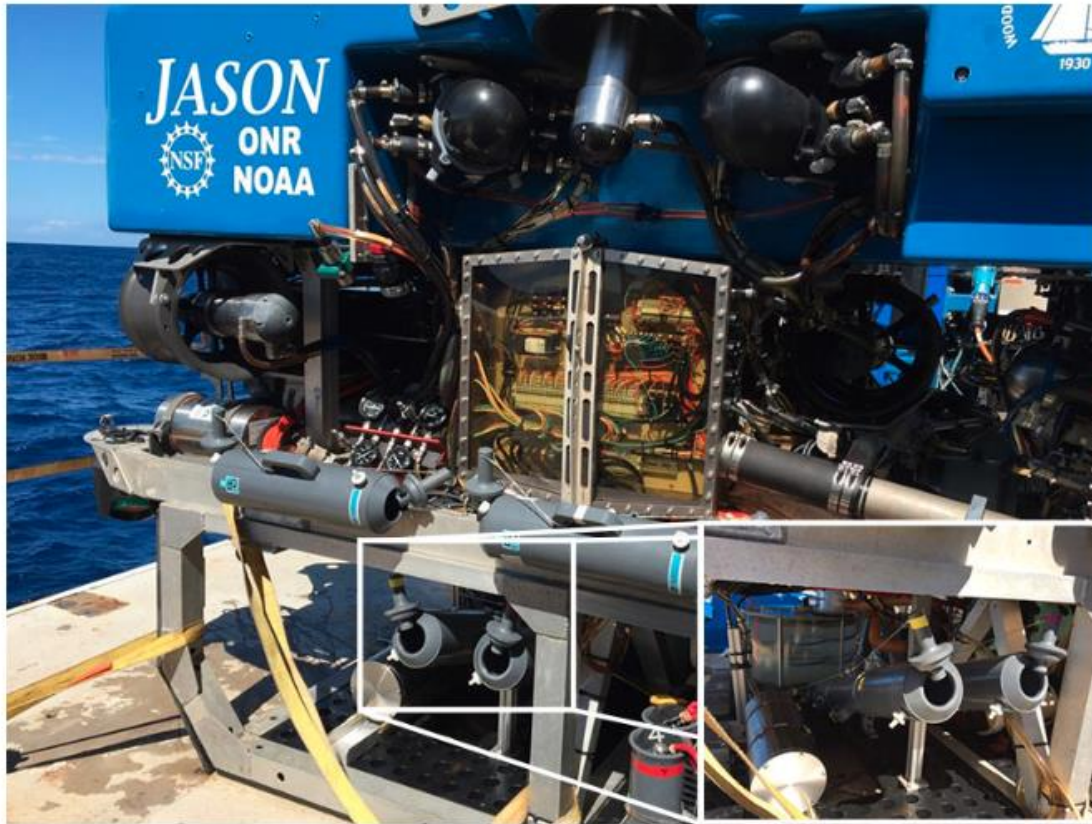
DEEP SEARCH: DEEP Sea Exploration to Advance Research on Coral/Canyon/Cold seep Habitats

[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



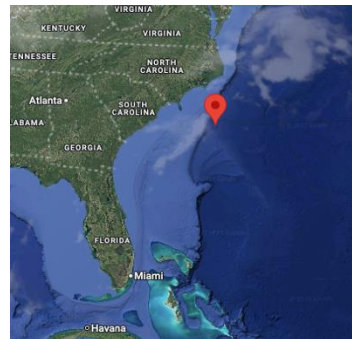


The two Niskin bottles used to collect deep-sea water samples are mounted to the bottom of ROV *Jason* and can be triggered by the ROV's manipulator arms. Image courtesy of DEEP SEARCH 2019 - BOEM, USGS, NOAA. [Download larger version \(jpg, 704 KB\)](#).

Ex.) SRR32336490

Sea water (depth 2,571 m)

16s rRNA amplicon / metazoa



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, Sônia 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

 SECTIONS

 PDF  TOOLS  SHARE

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

Example 2

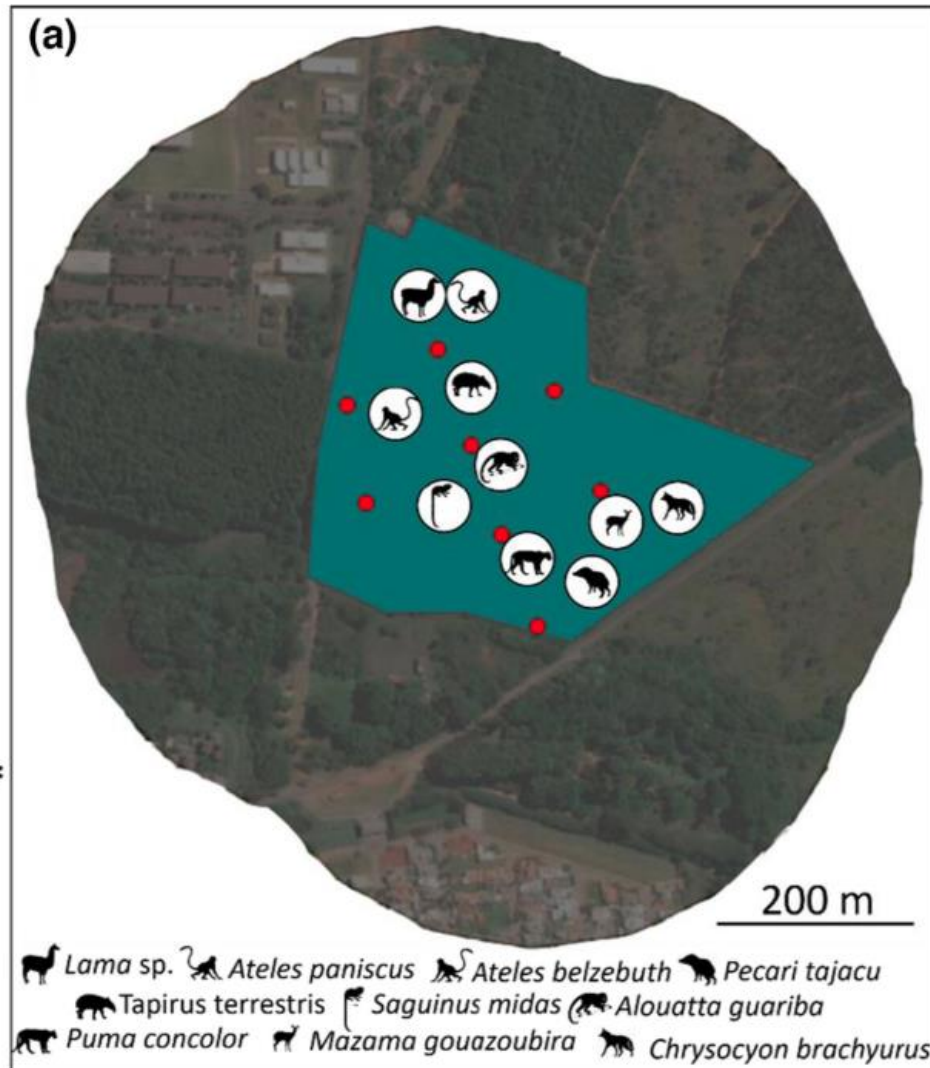




Metabarcoding

Distribution of animals?





Amplified 16s rna sequences (vertebrates)

Parque Ecológico de São Carlos
(Zoo and nature park)

Ex)

Hematophagous mosquito




SRR25401090

Saprophagous fly



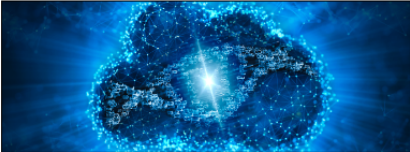
SRR25401082

Analysis of public datasets

 **National Library of Medicine**
National Center for Biotechnology Information

Log in

SRA [Advanced](#) [Help](#)



SRA - Now available on the cloud

Sequence Read Archive (SRA) data, available through multiple cloud providers and NCBI servers, is the largest publicly available repository of high throughput sequencing data. The archive accepts data from all branches of life as well as metagenomic and environmental surveys. SRA stores raw sequencing data and alignment information to enhance reproducibility and facilitate new discoveries through data analysis.

Getting Started

- [Documentation](#)
- [How to submit](#)
- [How to search and download](#)
- [How to use SRA in the cloud](#)
- [Submit to SRA](#)

Tools and Software

- [Download SRA Toolkit](#)
- [SRA Toolkit Documentation](#)
- [SRA-BLAST](#)
- [SRA Run Browser](#)
- [SRA Run Selector](#)

Related Resources

- [Submission Portal](#)
- [dbGaP Home](#)
- [BioProject](#)
- [BioSample](#)

```
#####
Results

Abundance: 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  Leucaspis 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 seq00
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

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**