



arnes



Primer ravnanja z biološkimi in biotehnološkimi podatki v okviru raziskovalnih projektov na NIB

dr. Marko Petek, NIB
Mreža znanja 2021, od 23. do 30. novembra

Raziskave na Oddelku za biotehnologijo in sistemsko biologijo

Delovni sklop: OMIKE

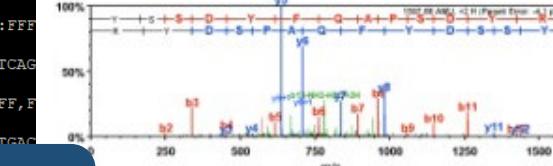
Vodja: prof. dr. Kristina Gruden



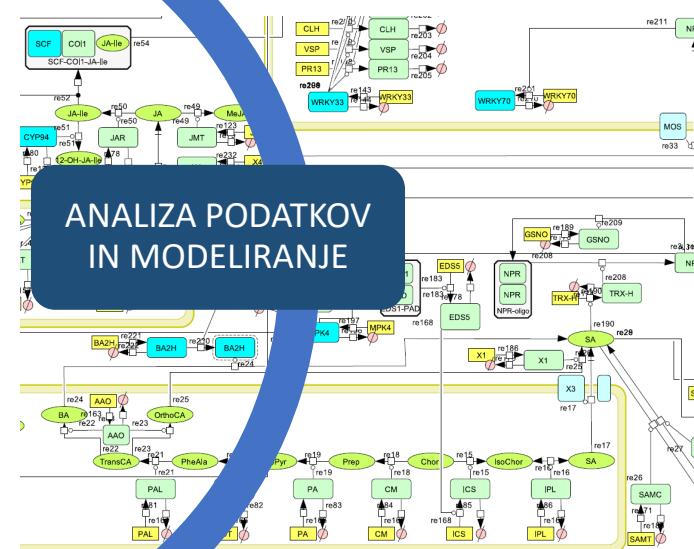
POTRJEVANJE HIPOTEZ S
FUNKCIJSKIMI ŠTUDIJAMI

```
@SRR12649980.1 1/1
NTGGCATGTCGGTGTATCAAGGCAACAGCACCATCAGGAATTCTCTC
+
#FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF:FFF
@SRR12649980.2 2/1
NTGGAGTAGTAAATGGTGTAGGCATAGGTCACTTCTCATTTCAGG
+
#F:FF, FF, F, FF, ::::::FFFFF:FFFF, F:, FFFF:F, FF::, FF, F
@SRR12649980.3 3/1
NGCTGGAGAACCTCCACCTGAATTAATTTAATTTAATTTAATTTAATTTA
+
#:FFF:::FFFFFFFFF
```

GENOMIKA,
TRANSKRIPTOMIKA,
PROTEOMIKA,
METABOLOMIKA, ...



ANALIZA PODATKOV
IN MODELIRANJE



POSTAVLJANJE
HIPOTEZ



Raziskovalni podatki na Oddelku za biotehnologijo in sistemsko biologijo

- Surovi podatki
- Metapodatki
- Vmesni in končni rezultati obdelave podatkov in modeliranja
- Publikacije (docx, pptx, pdf...)

Načrt ravnjanja s projektnimi podatki (“data management plan”)

	Synthetic biology constructs / Phytobricks	Transcriptomics	Metabolomics	Electroantennography	Plant phenotyping	Promoter transcriptional activity
Generated by	CSIC, EI, TUDA	NIB, EI	TUDA, CSIC	TUDA	CSIC, EI	CSIC
Format of generated data	GenBank	fastq, hdf5	DATA.MS, NMReDATA, Bruker data format, Shimadzu data format (qgd)	txt(ASCII), jpeg, eag	jpeg, txt(ASCII)	txt(ASCII), jpeg
Raw data storage at	CSIC, EI, TUDA, GeneBank	NIB, EI, SRA/ArrayExpress/ GEO	TUDA, CSIC, MetaboLights, MolCheck	TUDA, FAIRDOMHub	CSIC, EI, FAIRDOMHub	CSIC, FAIRDOMHub
Expected data size	< 1 GB	< 1800 GB	< 30 GB	< 5 GB	< 10 GB	< 1 GB
Analysed by	CSIC, EI, TUDA	NIB, EI	TUDA, CSIC	TUDA	CSIC, EI	CSIC
Analysed data storage at	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	GB Elements Database, FAIRDOMHub
Minimal information requirements	MIRIAM	MIAME	CIMR	MINI	MIAPPE	/
Standards, formats	Genebank, SBOL data and visual	MAGE-ML	mzML, mzQuantML, nmrML	NWB	/	/
Ontologies and vocabularies used	SBOL	GO, KEGG, InterPro, MapMan	CHEBI, KEGG, MapMan	OEN	PO, TO, CO	SBOL
SOPs stored at	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub
Scripts stored at	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub	FAIRDOMHub

Podatkovni repozitoriji

SPECIALIZIRANI REPOZITORIJI ZA SUROVE BIOLOŠKE PODATKE

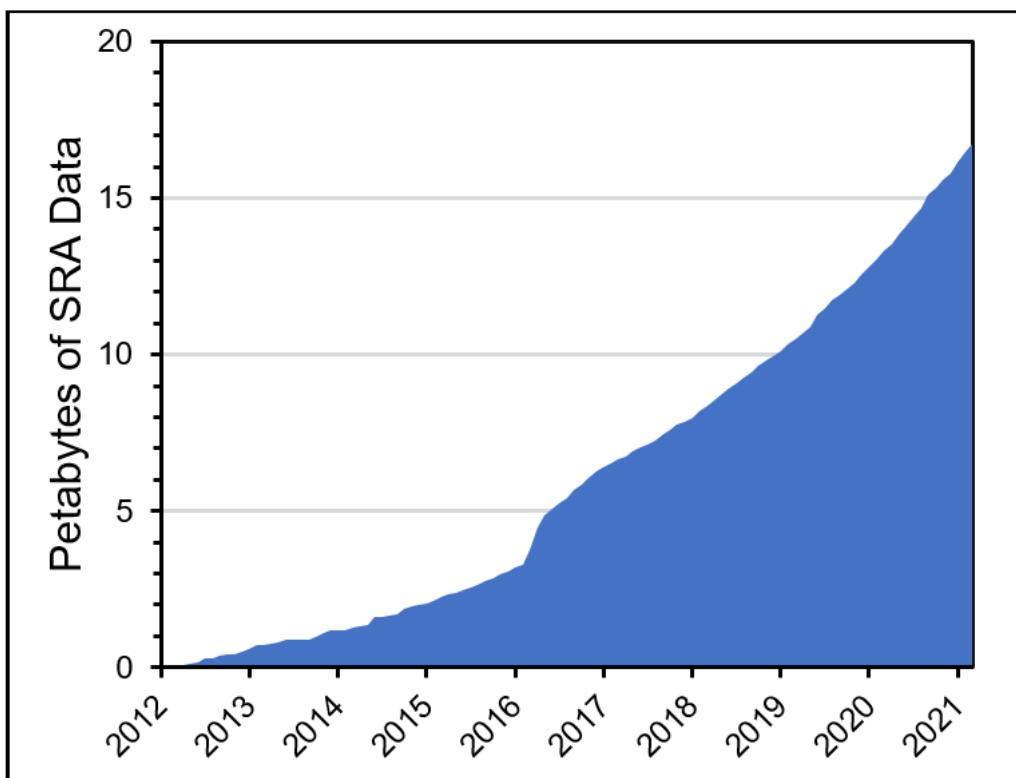


SPLOŠNI REPOZITORIJI ZA PODATKE



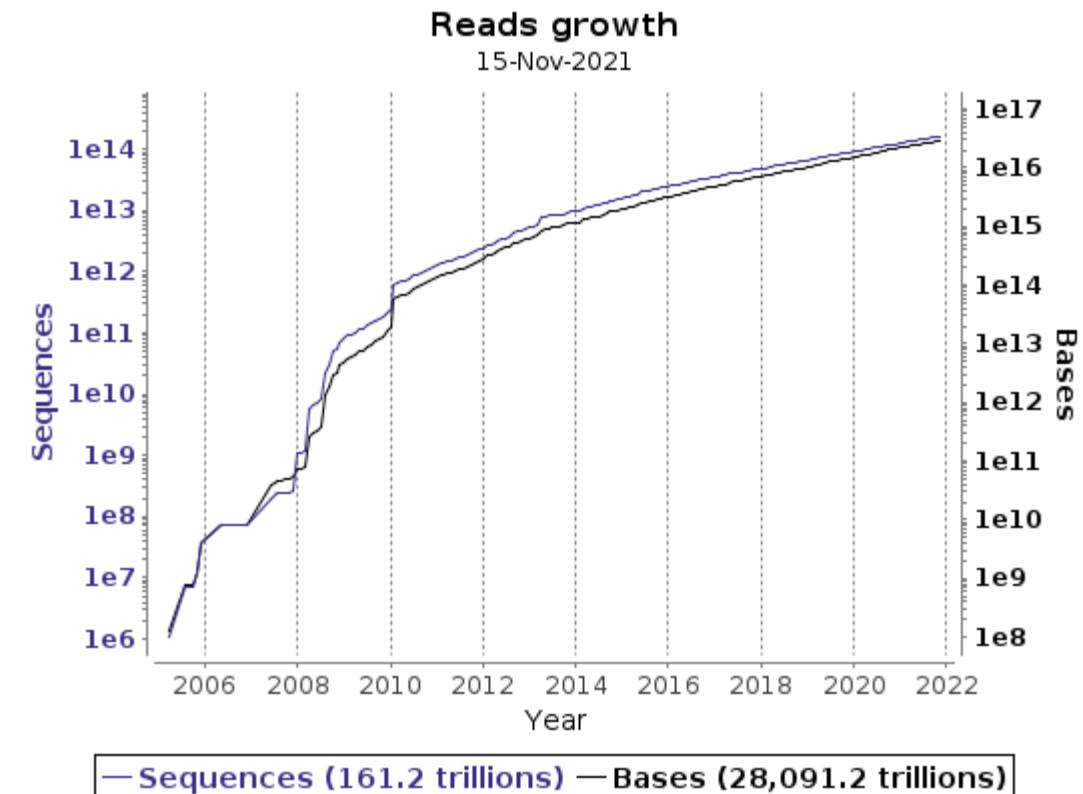
Podatkovni repozitoriji

Rast količine podatkov visokozmogljivostnega sekvenciranja DNA (in RNA):



Vir: NCBI Insights
(<https://ncbiinsights.ncbi.nlm.nih.gov/2021/08/09/espsss-workshop/#more-6180>)

ENA



Vir: EBI ENA
(<https://www.ebi.ac.uk/ena/browser/about/statistics>)

Deponiranje surovih podatkov v javne repozitorije

<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA400633>

Leptinotarsa decemlineata midgut RNASeq

The goal of the project was to investigate gene expression in Colorado potato beetle larval midguts reared (healthy) potato plants.

Accession	PRJNA400633
Data Type	Raw sequence reads
Scope	Multispecies
Publications	1. Published online: Schoville S et al., "A model species for agricultural pest genomics: the genome of Leptinotarsa decemlineata (Coleoptera: Chrysomelidae)", <i>Scientific Reports</i> , 2018;8(1)
Grants	"Biotechnology and Plant Systems Biology" (Grant ID P4-0165, Slovenian Research Agency)
Submission	Registration date: 29-Aug-2017 National Institute of Biology
Related Resources	<ul style="list-style-type: none"> Growth and defense trade-offs in multitrophic interaction between potato and its two major pests Using RNAi and SysBio approaches for validation of insecticide targets in CPB guts Colorado Potato Beetle Genome Project
Relevance	Agricultural

Project Data:

Resource Name	Number of Links
SEQUENCE DATA	
SRA Experiments	3
OTHER DATASETS	
BioSample	3

SRA Data Details

Parameter	Value
Data volume, Gbases	9
Data volume, Mbytes	7866

Study: Leptinotarsa decemlineata midgut RNASeq

Sample: Midguts of Leptinotarsa decemlineata larva reared continuously on potted non-infected (healthy) potato plants.

Library:

- Name: 21_HEALTHY
- Instrument: AB SOLID 4 System
- Strategy: RNA-Seq
- Source: TRANSCRIPTOMIC
- Selection: RANDOM
- Layout: SINGLE

Spot descriptor:

1 forward

Links:

Runs: 1 run, 95.9M spots, 4.8G bases, 3.8Gb

Run	# of Spots	# of Bases	Size	Published
SRR5989325	95,930,453	4.8G	3.8Gb	2017-09-24

Abstract:

The goal of the project was to investigate gene expression in Colorado potato beetle larval midguts reared on virus infected vs non-infected (healthy) potato plants.



**Kako na NIB-u ravnamo s
podatki preden jih deponiramo v
javnih repozitorijih?**

Kako na NIB-u ravnamo s podatki preden jih deponiramo v javnih repozitorijih?

- Surovi podatki
- Metapodatki



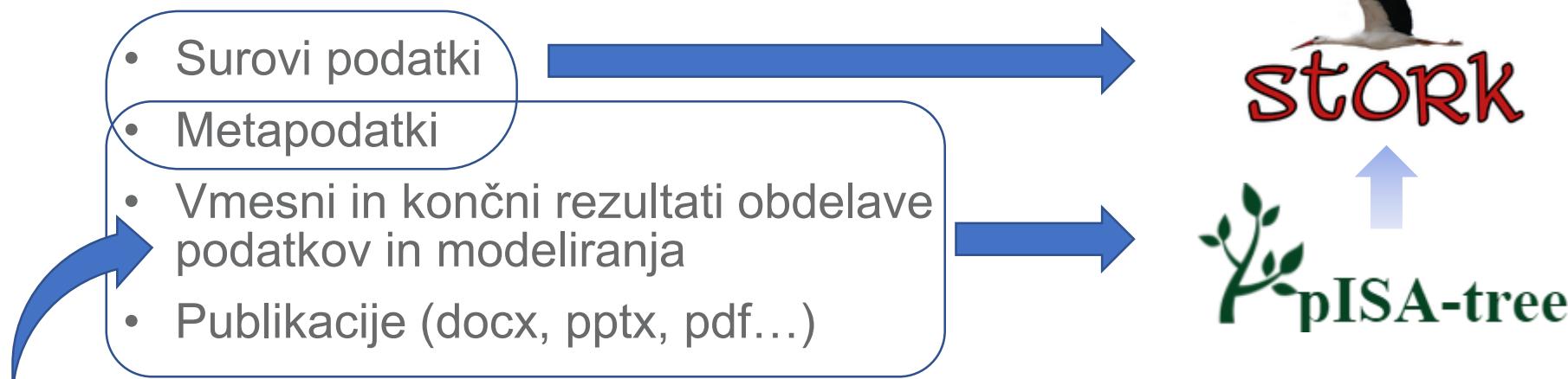
mrežni strežnik z
varnostno kopijo in
omejenim dostopom

- Vmesni in končni rezultati obdelave podatkov in modeliranja
- Publikacije (docx, pptx, pdf...)

Kako na NIB-u ravnamo s podatki preden jih deponiramo v javnih repozitorijih?



Kako na NIB-u ravnamo s podatki preden jih deponiramo v javnih repozitorijih?



mrežni strežnik z varnostno kopijo in omejenim dostopom

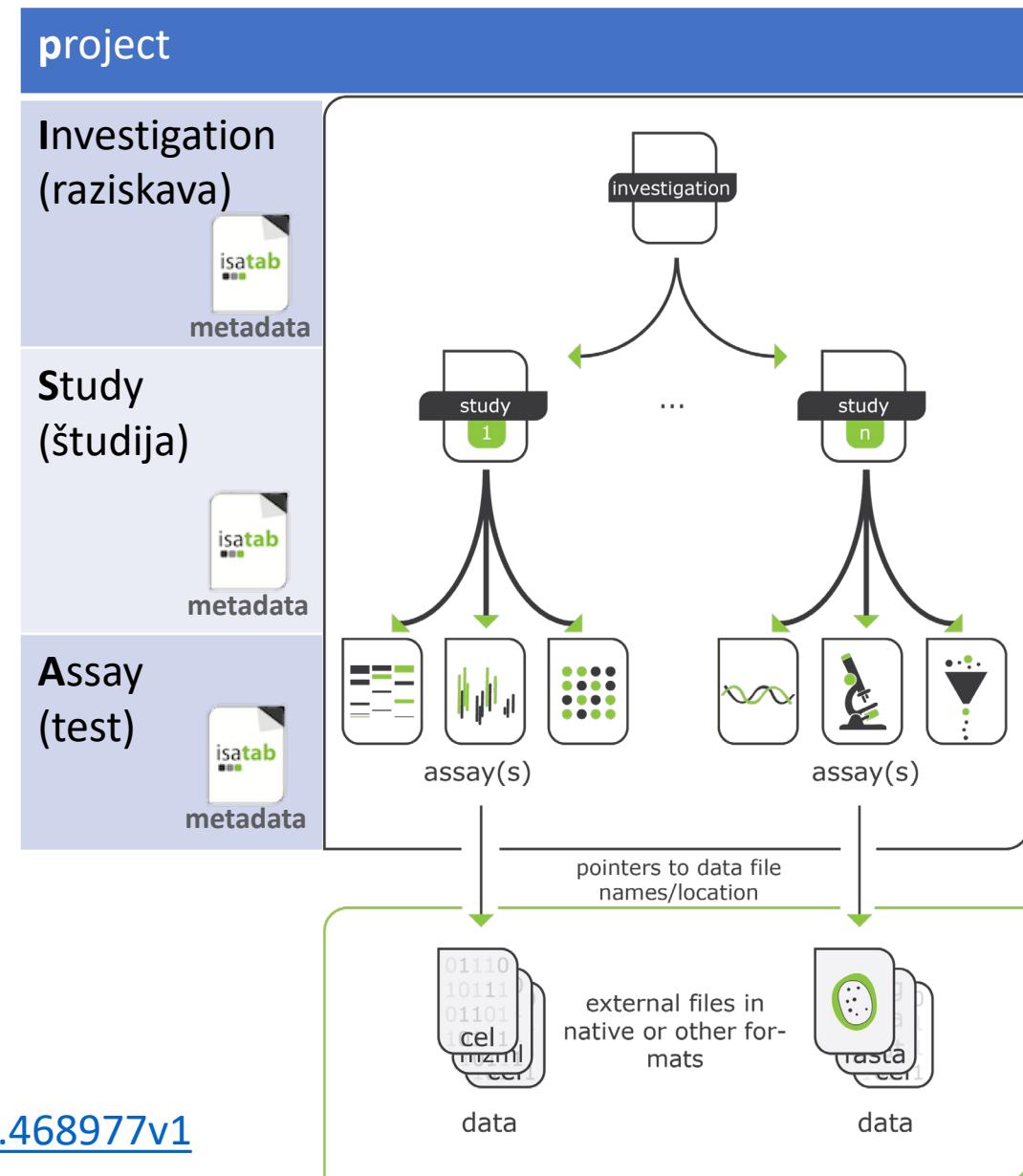
drugi mrežni strežnik z varnostno kopijo

pISA-tree

- Sistem za organizacijo projektnih podatkov (***.bat** skripte)
- Uporabljamo datotečne mape urejene v drevesno strukturo po **ISA standardu**
- metapodatkovne txt datoteke v **ISA-Tab formatu**

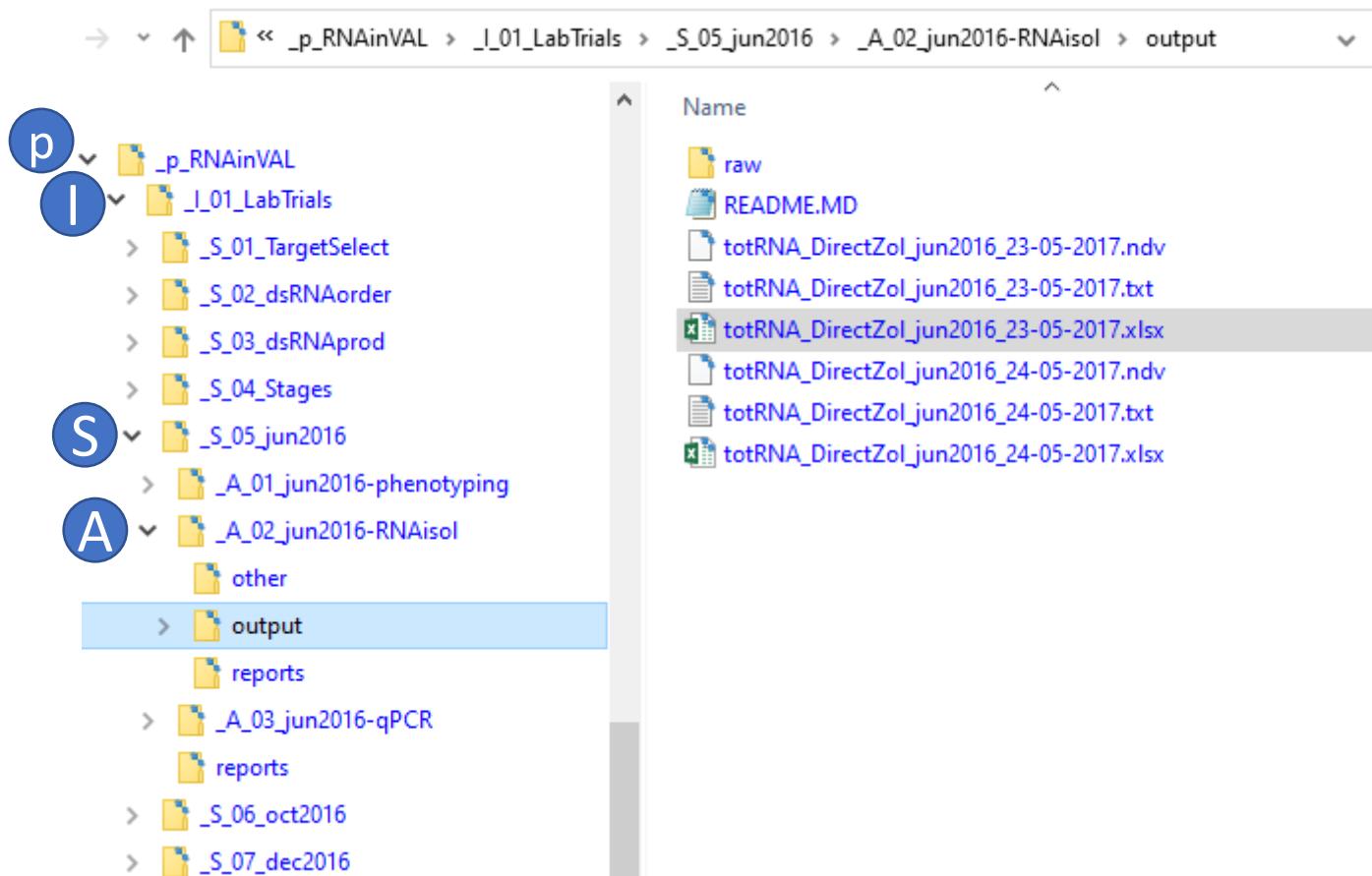
<https://github.com/NIB-SI/pISA-tree>

<https://www.biorxiv.org/content/10.1101/2021.11.18.468977v1>



Vir: <https://isa-tools.org/format/specification.html>

plSA-tree: primer lokalne strukture



pISA-tree: primer lokalne strukture

The screenshot shows a Windows File Explorer window with the following details:

- Path:** << _p_RNAinVAL > _L_01_LabTrials > _S_05_jun2016 > _A_02_jun2016-RNAisol
- File Explorer View:** Shows a tree view of folders and files. The folder `_A_02_jun2016-RNAisol` is selected.
- Content View:** A table showing the following files and their details:

Name	Date modified	Type	Size
other	13. 05. 2021 17:22	File folder	
output	13. 05. 2021 17:16	File folder	
reports	10. 05. 2021 16:27	File folder	
_ASSAY_METADATA.TXT	12. 11. 2021 15:33	Text Document	1 KB
analytes.xlsx	17. 05. 2021 10:34	Microsoft Excel Work...	16 KB
README.MD	10. 05. 2021 16:27	MD File	1 KB
showMetadata.bat	1. 04. 2020 14:26	Windows Batch File	1 KB
showTree.bat	1. 04. 2020 14:26	Windows Batch File	1 KB
xche		_ASSAY_METADATA.TXT - Notepad	

Notepad Content: The file `_ASSAY_METADATA.TXT` contains the following assay metadata:

```
Assay: _A_02_jun2016-RNAisol
Short Name: 02_jun2016-RNAisol
Assay Class: WET
Assay Type: RNAisol
Title: RNA isolation and pre-qPCR sample prep
Description: RNA isolation and sample preparation for qPCR
pISA Assay creation date: 2021-05-10
pISA Assay creator: Marko Petek
Lab manager: Marko Petek
Phenodata: ../../phenodata_20210113.txt
Featuredata:
RNA ID: $_RNA
Homogenisation protocol: handheld electric rotor-stator homogenization in tubes with Trizol
Date Homogenisation: 2017-04-26
Isolation Protocol: ZymoRNA
Date Isolation: 2017-04-26
Storage RNA: CU470
Dnase treatment protocol: Zymo DNase I
Dnase ID: $_DNase
Date DNase_treatment: 2017-05-10
Storage_DNase_treated: NA
Operator: Marko Petek, Katja Stare
cDNA ID: $_cDNA
DateRT: 2017-05-10
Notes:
Data:
```

pISA-tree --> FAIRDOMHub.org

- FAIRDOMHub
 - uporablja ISA format
 - na voljo večina licenc za odprto kodo in podatke (Creative Commons, Open Data Commons, ...)
 - omogoča pridobitev DOI za podatke
- Prenos v programskem okolju R s paketom seekr (<https://github.com/NIB-SI/seekr>)

← → ⌂ ⌂ fairdomhub.org/projects/252

FAIRDOM HUB Search i Search here... Search ⚙ Register Log in

_p_RNAinVAL

Overview

This project's main objective was to identify novel Colorado potato beetle gene targets for the development of specific RNAi insecticides and further validate prospective targets using transcriptomics. The work included gene selection, establishment of double-stranded RNA (dsRNA) production methodology and the evaluation of dsRNAs' insecticidal potential in CPB feeding laboratory and field trials.

Programme: NIBSys FAIRDOM PALS: No PALS for this Project
SEEK ID: <https://fairdomhub.org/projects/252> Project start date: 1st Nov 2014
Funding codes: Project end date: 31st Oct 2017

- Z4-7068

Public web page: <http://projects.nib.si/rnainval/>
Organisms: Leptinotarsa decemlineata

Related items

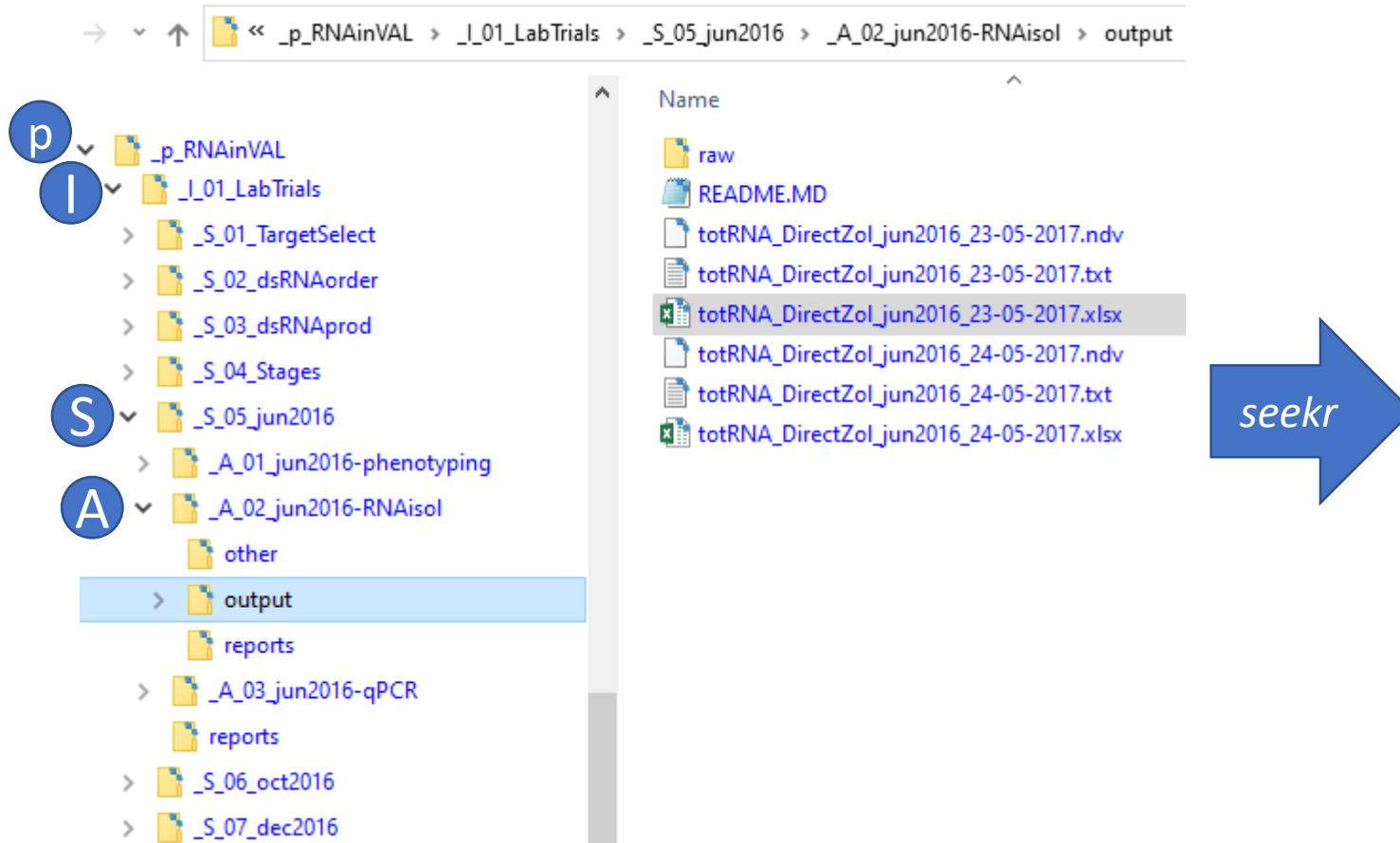
People (1) Programmes (1) Institutions (1) Investigations (3) Studies (18) Assays (60) Data files (351) Documents (1485)

NIBSys

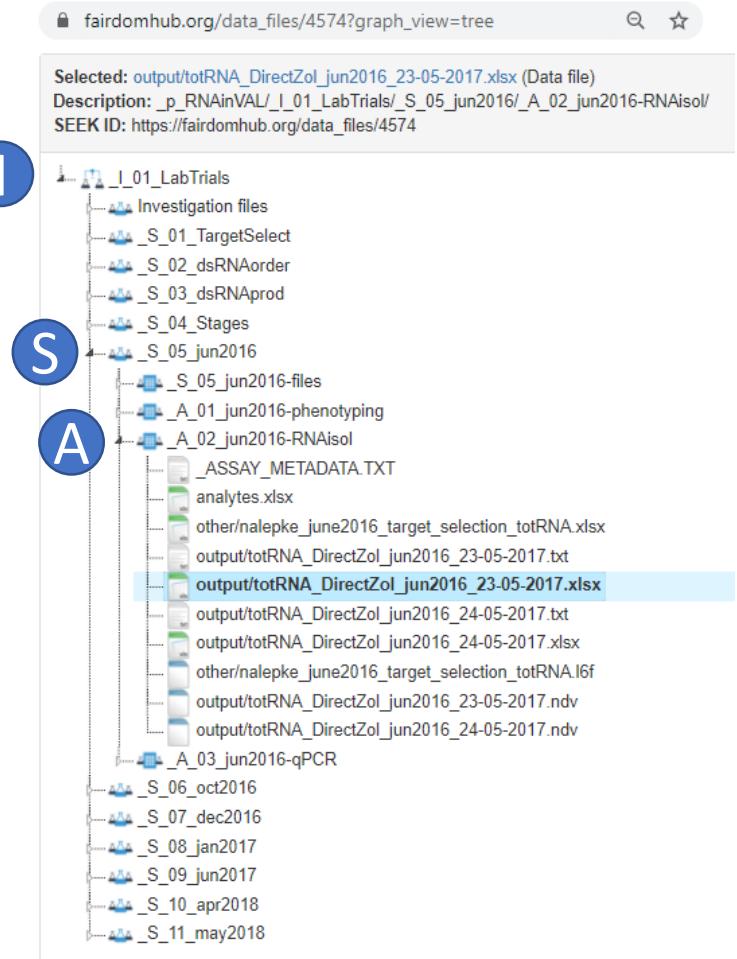
National Institute of Biology, Department of Biotechnology and Systems Biology projects

NIB Projects: Hyp - Spatiotemporal analysis of hypersensitive response to Potato virus Y in potato, pISA-tree, MOA - Multiomics analysis of potato response to Potato virus Y (PVY) infection, SUSPIRE - Sustainable Bioproduction of Pheromones for Insect Pest Control in Agriculture, INDIE - Biotechnological production of sustainable indole, _p_SIRT, ADAPT - Accelerated Development of multiple-stress tolerAnt PoTato, _p_RNAinVAL, tst, tst2
Web page: <http://www.nib.si/eng/index.php/departments/department-of-biotechnology-and-systems-biology>

plSA-tree -----> FAIRDOMHub.org



seekr



Zahvala



prof. dr. Kristina Gruden



doc. dr. Špela Baebler



dr. Tjaša Lukan



prof. dr. Andrej Blejec



dr. Živa Ramšak



Katja Stare



dr. Maja Zagorščak



dr. Anna Coll Rius



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Hvala za pozornost!