

# FAIR in reproduktibilni podatki na ustanovi s podporo orodja pISA-tree

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# Priprava podatkov za deljenje: princip FAIR

## FAIR Principles

Make your data:

- **F**indable
- **A**ccessible
- **I**nteroperable
- **R**eusable

### Findable

- Descriptive metadata
- Persistent Identifiers

### Accessible

- Determining what to share
- Participant consent and risk management
- Access status

### Interoperable

- XML standards
- Data Documentation Initiative
- CDISC

### Reusable

- Rights and licence models
- Permitted and non-permitted use

<http://datafairport.org/>



European Open  
Science Cloud

Big Data to  
Knowledge (BD2K)

FAIRDOM

# Kdaj podatki ustrezajo FAIR zahtevam?

## What is FAIR DATA?



Data and supplementary materials have sufficiently rich metadata and a unique and persistent identifier.

**FINDABLE**



Metadata and data are understandable to humans and machines. Data is deposited in a trusted repository.

**ACCESSIBLE**



Metadata use a formal, accessible, shared, and broadly applicable language for knowledge representation.

**INTEROPERABLE**



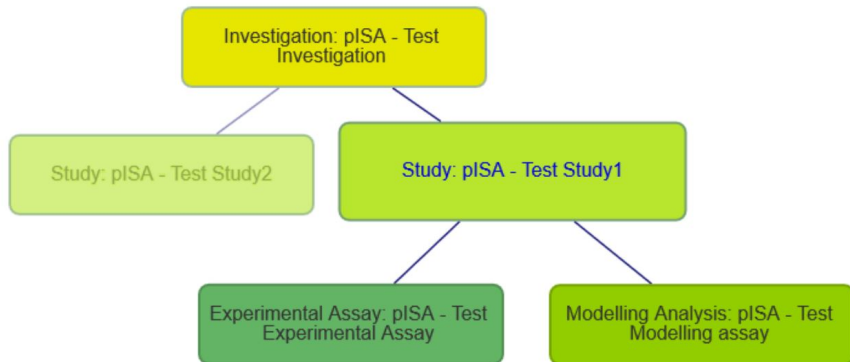
Data and collections have a clear usage licenses and provide accurate information on provenance.

**REUSABLE**

- Potreba po **lokalni organizaciji podatkov** v majhnih/srednje velikih raziskovalnih enotah.
- **Iskanje, izmenjava in ponovna raba podatkov** iz več poskusov.
- **Uporaba** in nadgradnja **načina dela, ki so ga raziskovalci že vajeni.**
- Zagotoviti **dovolj metapodatkov** za prenos podatkov v javne repozitorije.
- Uporaba metapodatkov **za potrebe ponovljivih analiz.**
- Spodbuditi uporabo **sistemov za spremljanje verzij** (npr. git in GitHub), kjer je to smiselno.

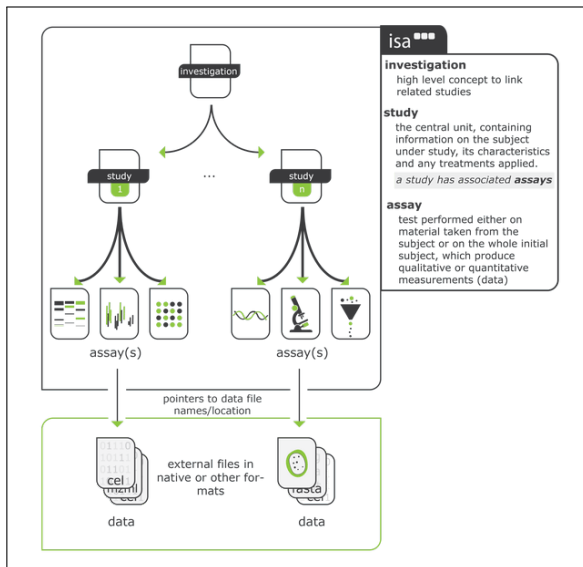
- **Drevesna struktura direktorijev**: LaTeX/texmf, R/paketi, ...
- Osebna drevesa direktorijev za pripravo ponovljivih statističnih poročil (R/Sweave/knitr/Rmarkdown/LaTeX in RStudio/WinEdt projekti).
- Raziskovalne korake lahko razdelimo v nivoje **p**roject/**I**nvestigation/**S**tudy/**A**ssay, kar je skladno z okvirom ISA (sami smo nivoje imenovali: Study/Experiment/Analysis).
- Čimmanj dodatnega dela, nezahtevna namestitvev.

Selected item: Study: pISA - Test Study1



<https://fairdomhub.org/>

# Struktura modela ISA-tab



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

## pISA-tree:

Drevesna struktura direktorijev  
skladna z okvirjem FAIRDOM/ISA

- **Temelji na datotečnem sistemu** (Windows, razširljivo na Linux).
- Projektno drevo direktorijev z vloženimi direktoriji za nivoje **p**roject/**I**nvestigation/**S**tudy/**A**ssay.
- '**make...**' ukazne datoteke za izdelavo poddreves za nivoje:
  - **makeProject.bat**
  - **makeInvestigation.bat**
  - **makeStudy.bat**
  - **makeAssay.bat**
- Predloge za 'metadata' datoteke posameznih nivojev **vzpodbujanje vnosa metapodatkov** (navadne datoteke s pari Ključ/Vrednost (Key/Value)).

▶ Skip tree representation



../\_p\_project

makeInvestigation.bat

../\_p\_project

makeInvestigation.bat

/\_I\_Investigation

makeStudy.bat

/presentations

/reports

Readme.md

Metadata.txt

Identifier

Title

Description

Date

PI

Phenodata

../\_p\_project

makeInvestigation.bat

/\_I\_Investigation

makeStudy.bat

/presentations

/reports

Readme.md

Metadata.txt

Identifier  
Title  
Description  
Date  
PI  
Phenodata  
...

/\_S\_Study1

makeAssay.bat

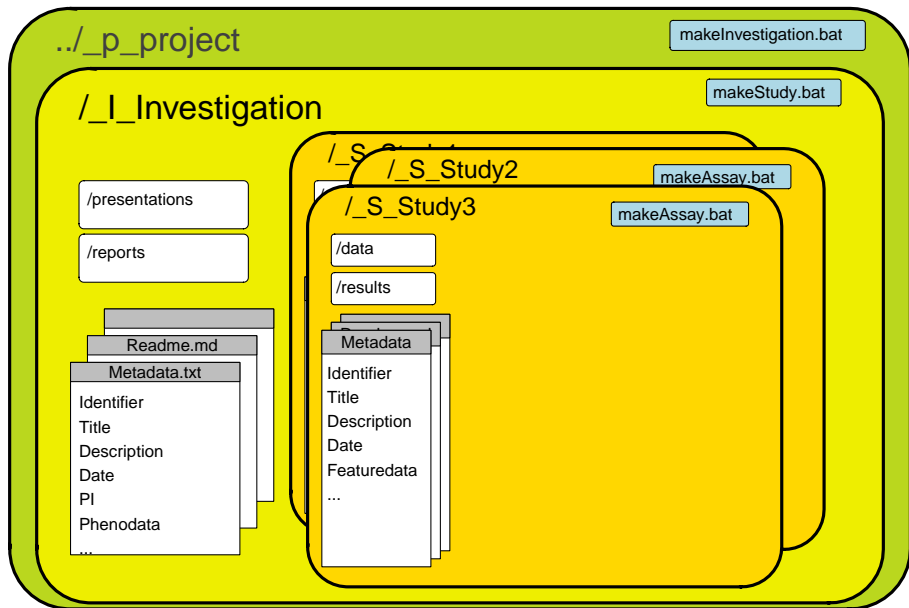
/data

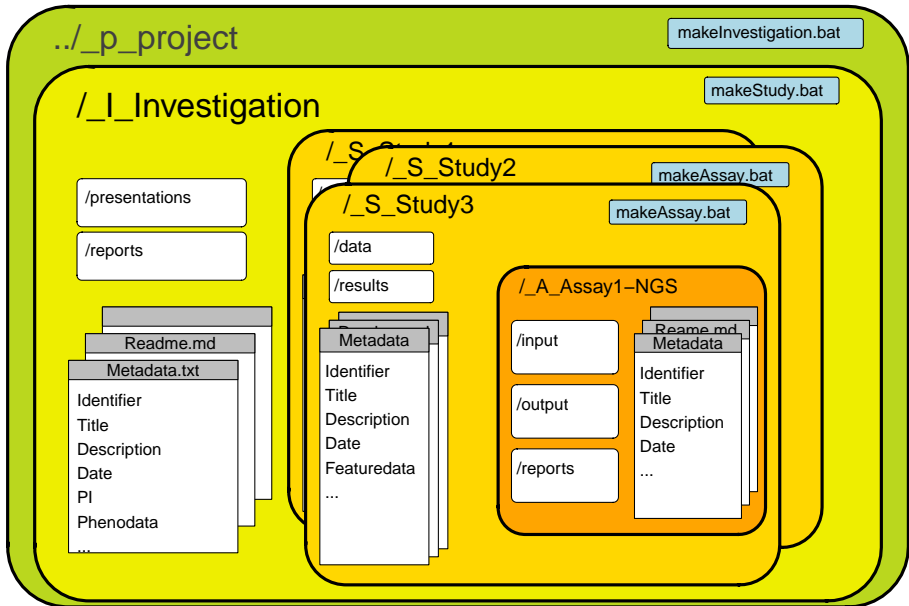
/results

Metadata

Identifier  
Title  
Description  
Date  
Featuredata  
...

# pISA-tree: dodatne Studies





../\_p\_project

makeInvestigation.bat

/\_I\_Investigation

makeStudy.bat

/presentations

/reports

Readme.md

Metadata.txt

Identifier  
Title  
Description  
Date  
PI  
Phenodata  
...

/\_S\_Study2

makeAssay.bat

/\_S\_Study3

makeAssay.bat

/data

/results

Metadata

Identifier  
Title  
Description  
Date  
Featuredata  
...

/\_A\_Assay1-NGS

/\_A\_Assay2-Stat

Reame.md  
Metadata

/input

/results

/R

Identifier  
Title  
Description  
Date  
...

# pISA tree - projekti so zbrani v korenskem direktoriju

File Explorer view showing the pISA tree project structure. The left pane displays a tree view of folders: `_prj2`, `_p_bla`, `_I_xyz`, `_S_stu`, `_A_klm-R`, `_A_nop-RNAisol`, `reports`, `presentations`, `reports`, `presentations`, `reports`, `presentations`, `reports`, `Templates`, `_STAT100`, `_temp`, and `_Y`. The right pane shows a list of files and folders: `_p_bla`, `Templates`, `.gitattributes`, `.gitignore`, `common.ini`, `index.html`, `INSTRUCTIONS-v-6.pdf`, `makeProject.bat`, `meta_p_Template.txt`,  `README.MD`, `showMetadata.bat`, `showTree.bat`, `update.bat`, and `xcheckMetadata.bat`.

```
# pISA-tree: Standard

This set of batch file
Batch files are provid
(**I**nvestigation/**S

Installation:

1. Download (zip file)
SI/pISA/archive/projec
2. Extract files into
3. User instructions a

Additional info:
* Files in `doc` folde
* Files at [http://abl

Links:
* [pISA-tree Web page]
* [ISA Model & Seriali
* [FAIRDOM hub] (https:
```

# pISA tree - makeProject.bat

```
pISA-tree v.3.0
=====
      pISA-tree: make PROJECT
-----
Location: D:\_prj2

Enter project ID: bla

=====

Enter Title [ * ]: Demo project

=====

Enter Description [ * ]: Demonstration of the pISA-tre for projects
```



# pISA tree - makeProject.bat

pISA-tree v.3.0

=====

pISA-tree: make PROJECT

-----

project:	bla
Title:	Demo project
Description:	Demonstration of the pISA-tre for projec
Local pISA-tree organisation	NIB

=====

pISA project creation date

- 1 2019-06-10
- 2 Other

Select [1,2]?

# pISA tree - makeProject.bat

pISA-tree v.3.0

=====

pISA-tree: make PROJECT

-----

project:	bla
Title:	Demo project
Description:	Demonstration of the pISA-tre for projec
Local pISA-tree organisation	NIB
pISA project creation date	2019-06-10

=====

Enter pISA project creator [ \* ]:

# pISA tree - makeProject.bat

pISA-tree v.3.0

```
=====
project METADATA
=====
```

```
project:                _p_bla
Short Name:             bla
Title:                  Demo project
Description:            Demonstration of the pISA-tre for proje
pISA projects path:    D:/_prj2
Local pISA-tree organisation: NIB
pISA project creation date: 2019-06-10
pISA project creator:  AB
Project funding code:  *
Project coordinator:   *
Project partners:      NIB, PTKRF
Project start date:    *
Project end date:      *
Principal investigator: *
License:               CC BY 4.0
Sharing permission:    Private
Upload to FAIRDOMHub:  Yes
```

# pISA tree - direktorij projekta in metapodatki

- \_prj2
  - **\_p\_bla**
    - \_I\_xyz
      - \_S\_stu
        - > \_A\_klm-R
        - > \_A\_nop-RNAisol
          - reports
          - presentations
          - reports
          - presentations
          - reports
        - Templates
      - \_STAT100
      - \_temp
      - \_Y
      - 4tops
      - ablejec
      - AI\_CS2\_IE\_NonRet

- Name
  - \_I\_xyz
  - presentations
  - reports
  - \_PROJECT\_METADATA.TXT**
  - common.ini
  - FST.txt
  - makeInvestigation.bat
  - meta\_I\_Template.txt
  - README.MD
  - showMetadata.bat
  - showTree.bat
  - xcheckMetadata.bat

```
project:      _p_bla
Short Name:  bla
Title:       Demo project
Description:  Demonstration of
pISA projects path:  D:/_prj2
Local pISA-tree organisation:
pISA project creation date:  2019
pISA project creator:  AB
Project funding code:  *
Project coordinator:  *
Project partners:  NIB, PTKRF
Project start date:  2017-04-01
Project end date:
Principal investigator:  *
License:  CC BY 4.0
Sharing permission:  Private
Upload to FAIRDOMHub:  Yes
```

# pISA tree - makeInvestigation.bat

pISA-tree v.3.0

=====

pISA-tree: make INVESTIGATION

-----

Location: D:\\_prj2\\_p\_bla

Enter Investigation ID: xyz

# pISA tree - makeInvestigation.bat

Select pISA-tree v.3.0

=====

pISA-tree: make INVESTIGATION

-----

Investigation: xyz  
project: bla  
Title: Demo investigation  
Description: \*  
pISA Investigation creation date 2019-06-10

=====

Enter pISA Investigation creator [ \* ]: AB

# pISA tree - makeInvestigation.bat

```
ca pISA-tree v.3.0
=====
      Investigation METADATA
=====
Investigation:          _I_xyz
Short Name:            xyz
Title:                 Demo investigation
Description:           *
Phenodata:             ./phenodata_20190610.txt
pISA Investigation creation date: 2019-06-10
pISA Investigation creator: AB
Principal investigator: *
License:               CC BY 4.0
Sharing permission:    Private
Upload to FAIRDOMHub:  Yes












===== pISA ==

Investigation xyz is ready.
Location: D:\_prj2\_p_bla\_I_xyz

=====
```

# pISA tree - direktorij Investigation z metapodatki

- \_prj2
  - \_p\_bla
    - \_I\_xyz**
      - \_S\_stu
        - \_A\_klm-R
        - \_A\_nop-RNAisol
        - reports
        - presentations
        - reports
        - presentations
        - reports
        - Templates
  - \_STAT100
  - \_temp
  - \_Y
  - 4tops
  - ablejec
  - AI\_CS2\_IE\_NonRet

- Name
- \_S\_stu
  - presentations
  - reports
  -  **\_INVESTIGATION\_METADATA**
  -  common.ini
  -  makeStudy.bat
  -  meta\_S\_Template.txt
  -  phenodata\_20190401.txt
  -  phenodata\_20190531.txt
  -  phenodata\_20190610.txt
  -  README.MD
  -  showMetadata.bat
  -  showTree.bat
  -  xcheckMetadata.bat

Investigation: \_I\_xyz  
Short Name: xyz  
Title: Demo investigation  
Description: \*  
Phenodata: ./phenodata\_20190610.  
pISA Investigation creation date:  
pISA Investigation creator: AB  
Principal investigator: \*  
License: CC BY 4.0  
Sharing permission: Private  
Upload to FAIRDOMHub: Yes



# pISA tree - makeStudy.bat

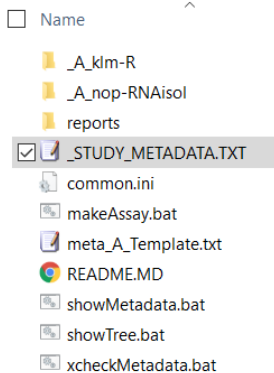
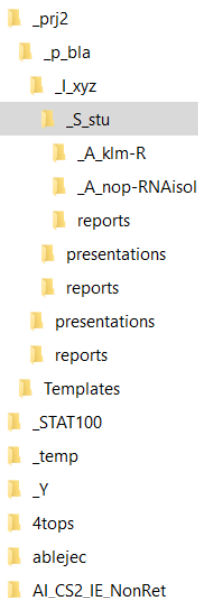
```
ca pISA-tree v.3.0
=====
      Study METADATA
=====
Study:                               _S_stu
Short Name:                           stu
Title:                                 Demo study
Description:                            *
Raw Data:
pISA Study creation date:              2019-06-10
pISA Study creator:                    AB
Principal investigator:                 CD
License:                                CC BY 4.0
Sharing permission:                    Private
Upload to FAIRDOMHub:                  Yes

===== pISA ==

Study stu is ready.
Location: D:\_prj2\_p_bla\_I_xyz\_S_stu

=====
Press any key to continue . . .
```

# pISA tree - direktorij Study z metapodatki



Study: \_S\_stu  
Short Name: stu  
Title: Demo study  
Description: \*  
Raw Data:  
pISA Study creation date: 2019-06-  
pISA Study creator: AB  
Principal investigator: CD  
License: CC BY 4.0  
Sharing permission: Private  
Upload to FAIRDOMHub: Yes

```
pISA-tree v.3.0
=====
      pISA-tree: make ASSAY
-----
Location: D:\_prj2\_p_bla\_I_xyz\_S_stu
=====

Select Assay Class

  1 DRY
  2 WET

Select [1,2]?
```

```
pISA-tree v.3.0
=====
      pISA-tree: make ASSAY
-----
Assay Class:          DRY
Selected: DRY

=====

Select Assay Type

  1 R
  2 Stat
  3 Other

Select [1,2,3]?
```

```
pISA-tree v.3.0
=====
      pISA-tree: make ASSAY
-----
Assay Class:          DRY
Assay Type:           R
Assay ID:             k1m-R
Study:                stu
Title:                Data analysis
Description:          *
pISA Assay creation date      2019-06-10
=====

Enter pISA Assay creator [ * ]:
```

```
ca pISA-tree v.3.0
=====
      Assay METADATA
=====
Assay:                               _A_klm-R
Short Name:                           klm-R
Assay Class:                           DRY
Assay Type:                             R
Title:                                  Data analysis
Description:                             *
pISA Assay creation date:                2019-06-10
pISA Assay creator:                       AB
Analyst:                                  AB
Phenodata:                               None
Featuredata:
Data:
===== pISA ==

Assay klm-R is ready.
Location: D:\_prj2\_p_bla\_I_xyz\_S_stu\_A_klm-R
```

# pISA tree - direktorij za analitični Assay (DRY) z metapodatki

File Explorer view showing a directory structure for an assay. The left pane shows a tree view with folders like `_prj2`, `_p_bla`, `_l_xyz`, `_S_stu`, `_A_klm-R` (selected), `_A_nop-RNAisol`, `reports`, `presentations`, `reports`, `presentations`, `reports`, `Templates`, `_STAT100`, `_temp`, `_Y`, `4tops`, and `ablejec`.

The right pane shows the contents of the selected folder `_A_klm-R`:

- Name
- `input`
- `other`
- `output`
- `reports`
- `scripts`
- `_Assay_METADATA.TXT`
- `README.MD`
- `showMetadata.bat`
- `showTree.bat`
- `xcheckMetadata.bat`

Assay: `_A_klm-R`  
Short Name: `klm-R`  
Assay Class: `DRY`  
Assay Type: `R`  
Title: `Data analysis`  
Description: `*`  
pISA Assay creation date: `2019-06-`  
pISA Assay creator: `AB`  
Analyst: `AB`  
Phenodata: `../../phenodata_20190`  
Featuredata:  
Data:  
|

```
pISA-tree v.3.0
=====
pISA-tree: make ASSAY
-----
Location: D:\_prj2\_p_bla\_I_xyz\_S_stu
=====

Select Assay Class

1 DRY
2 WET

Select [1,2]?
```



```
pISA-tree v.3.0
=====
      pISA-tree: make ASSAY
-----
Assay Class:           WET
Selected: WET

=====

Select Assay Type

 1 Any
 2 DNase
 3 RNAisol
 4 RT
 5 Other

Select [1,2,3,4,5]?
```

```
pISA-tree v.3.0
=====
pISA-tree: make ASSAY
-----
Assay Class:          WET
Assay Type:           RNAisol
Assay ID:             nop-RNAisol
Study:                stu
Title:                Wet class assay
Description:           *
Lab manager           *
=====

Select phenodata file

1 phenodata_20190610.txt
2 phenodata_20190531.txt
3 phenodata_20190401.txt
4 None

Select [1,2,3,4]?
```

```
pISA-tree v.3.0
=====
      pISA-tree: make ASSAY
-----
Assay Class:           WET
Assay Type:            RNAisol
Assay ID:              nop-RNAisol
Study:                 stu
Title:                 Wet class assay
Description:           *
Creation date          2019-06-10
=====

RNA ID

  1 $_RNA
  2 Other

Select [1,2]?
```

```
ca pISA-tree v.3.0
=====
pISA-tree: make ASSAY
-----
Assay Class:          WET
Assay Type:           RNAisol
Assay ID:             nop-RNAisol
Study:                stu
Title:                Wet class assay
Description:          *
Creation date         2019-06-10
RNA ID                $_RNA
=====

Homogenisation protocol

1 fastPrep
2 TissueLyser
3 mortar
4 Other
```

```
ca pISA-tree v.3.0
=====
      Assay METADATA
=====
Assay:                _A_nop-RNAisol
Short Name:           nop-RNAisol
Assay Class:          WET
Assay Type:           RNAisol
Title:                Wet class assay
Description:           *
pISA Assay creation date: 2019-06-10
pISA Assay creator:   AB
Lab manager:          *
Phenodata:            ../../phenodata_20190610.txt
Featuredata:
Creation date:        2019-06-10
RNA ID:               $_RNA
Homogenisation protocol: fastPrep
Date Homogenisation:  2019-06-10
Isolation Protocol:   Rneasy_Plant
Date Isolation:        2019-06-10
Storage RNA:          CU0369
```

# Struktura podatkov

GeneID	Feat1	Feat2	Feat3	Feat4
Gen001	<b>Featuredata</b>  Measurand features and descriptions			
Gen002				
Gen003				
Gen004				
Gen005				
Gen006				
Gen007				
Gen008				
Gen009				
Gen010				
Gen011				
Gen012				

SampleID	Sample1	Sample2	Sample3	Sample4	Sample5	Sample6
Cond1	<b>Phenodata</b>  Sample description and experiment conditions					
Cond2						
Cond3						
Treat1						
Treat2						
Treat3						
Treat3						

	Sample1	Sample2	Sample3	Sample4	Sample5	Sample6
Gen001	<b>Data</b>  Measurements					
Gen002						
Gen003						
Gen004						
Gen005						
Gen006						
Gen007						
Gen008						
Gen009						
Gen010						
Gen011						
Gen012						

# pISA tree - direktorij za laboratorijski Assay (WET) z metapodatki

**Left Pane (Directory Structure):**

- \_prj2
  - \_p\_bla
    - \_l\_xyz
      - \_S\_stu
        - \_A\_klm-R**
        - \_A\_nop-RNAisol**
        - reports
        - presentations
        - reports
        - presentations
        - reports
        - Templates
      - \_STAT100
      - \_temp
      - \_Y
      - 4tops
      - ablejec

**Right Pane (File List):**

- Name
- other
- output
- reports
- \_Assay\_METADATA.TXT
- Analytes.txt
- README.MD
- showMetadata.bat
- showTree.bat
- xcheckMetadata.bat

**Metadata View (Right Side):**

Assay: \_A\_nop-RNAisol  
Short Name: nop-RNAisol  
Assay Class: WET  
Assay Type: RNAisol  
Title: Wet class assay  
Description: \*  
pISA Assay creation date: 2019-06-10  
pISA Assay creator: AB  
Lab manager: \*  
Phenodata: ../../phenodata\_20190610  
Featuredata:  
Creation date: 2019-06-10  
RNA ID: \$\_RNA  
Homogenisation protocol: fastPrep  
Date Homogenisation: 2019-06-10  
Isolation Protocol: Rneasy\_P  
Date Isolation: 2019-06-10  
Storage RNA: CU0369  
Dnase treatment protocol: \*  
Dnase ID: \$\_DNase  
Date DNase\_treatment: 2019-06-10  
Storage\_DNase\_treated: CU0370  
Operator: MJ  
cDNA ID: \$\_cDNA  
DateRT: 2019-04-20  
Notes:  
Data:  
|

# Assay: razredi in tipi

▶ Proceed to features

The screenshot shows a file explorer window with a folder tree on the left and a text editor on the right. The folder tree includes 'Templates', 'DRY', 'WET', and several subfolders. The 'RNAisol' folder is selected. The text editor displays the contents of 'analytes.ini'.

File Explorer Structure:

- Templates
  - DRY
    - R
    - Stat
  - WET
    - Demo
    - DNase
    - RNAisol**
    - RT
  - \_STAT100
  - \_temp
  - \_Y
  - 4tops
  - ablejec
  - AI\_CS2\_IE\_NonRet

Selected File: `analytes.ini`

File Contents:

```
RNA ID      RNA_$
ng/u1 Blank
260/280     Blank
260/230     Blank
Homogenisation protocol fastPrep
Date Homogenisation      %today%
Isolation Protocol      Rneasy_Plant
Date Isolation           %today%
Storage RNA CU0369
Dnase treatment protocol *
Dnase ID      DNase_$
Date DNase_treatment %today%
Storage_DNase_treated CU0370
Operator      *
cDNA ID      cDNA_$
DateRT       %today%
Operator      Anton/Miha Mihav
Notes
Fluidigm_chip chip10/chip11
```

1 item selected 413 bytes



## Posebni metapodatki za Assay

	A	B
1	Item	Value
2	RNA ID	RNA_\$_
3	ng/ul	Blank
4	260/280	Blank
5	260/230	Blank
6	Homogenisation protocol	fastPrep/slowPrep
7	Date Homogenisation	%today%
8	Isolation Protocol	Rneasy_Plant
9	Date Isolation	%today%
10	Storage RNA	CU0369
11	Dnase treatment protocol	*
12	Dnase ID	DNase_\$_
13	Date DNase treatment	%today%

# Vklop posebnih metapodatkov v dodatne tabele vzorcev

	A	B	C	D	E	F	G
1	Sample ID	RNA ID	ng/ul	260/280	260/230	Homogenisation protocol	Date Homogenisation
2	SMPL001	RNA_SMPL001				fastPrep	29.05.2018
3	SMPL002	RNA_SMPL002				fastPrep	29.05.2018
4	SMPL003	RNA_SMPL003				fastPrep	29.05.2018

- `showMetadata.bat`
- `xcheckMetadata.bat`
- `showTree.bat`

# showMetadata.bat

## Vzpodbuja uporabo markdown

```
# Metadata files↓
D: ↓
/_prj ↓
/_p_bla↓
↓
---↓
↓
* **/_PROJECT_METADATA.TXT**↓
---↓
↓
project:→      _p_bla ↓
### PROJECT ↓
Short Name:→   bla ↓
Title:→ Demo project ↓
Description:→   Demonstration of the pISA-tree ↓
```

### Metadata files

---

D:  
/\_prj  
/\_p\_bla

---

*\*/\_PROJECT\_METADATA.TXT*

---

project: \_p\_bla

#### PROJECT

Short Name: bla  
Title: Demo project  
Description: Demonstration of the pISA-tree  
Project Path: D:\OMIKE\pISA\devel\main\_p\_bla  
Investigator: Name Lastname

#### INVESTIGATIONS

# xcheckMetadata.bat

## Prikaz neizpoljenih obveznih meta-vrednosti

D:

/\_prj

/\_p\_bla

---

\* /\_PROJECT\_METADATA.TXT

---

\* /\_I\_xyz/\_INVESTIGATION\_METADATA.TXT

---

?? MISSING: Description: \*

---

\* /\_I\_xyz/\_S\_stu/\_STUDY\_METADATA.TXT

---

?? MISSING: Title: \*

# showTree.bat

## Prikaže datotečno drevo

```
D:\_prj2\_p_bla\_I_xyz\_S_stu\_A_nop-RNAisol
```

```
Folder PATH listing for volume DATA
```

```
Volume serial number is 5859-00FF
```

```
D:.
```

```
| Analytes.txt  
| d.tmp  
| README.MD  
| showMetadata.bat  
| showTree.bat  
| t.tmp  
| xcheckMetadata.bat  
| _Assay_METADATA.TXT  
|
```

```
+---other
```

```
|     README.MD  
|
```

```
+---output
```

```
| | README.MD  
| |
```

```
| \---raw
```

```
|     README.MD  
|
```

```
makeProject bla "Demo project title"  
makeInvestigation xyz  
makeStudy stu  
makeAssay klm DRY R  
makeAssay nop WET RNAisol
```



]

- Sistem z **malo dodatnega dela**.
- **Datoteka z metapodatki** za vsak nivo.
- Različni **Assay razredi** (Wet / Dry / ...).
- Različni **Assay tipi** (RNAisol, RT, Stat, R, ...) .
- Vnos podatkov z izbirami (za **zagotovitev enoličnega vnosa**).
- Upošteva priporočila **FAIRDOM/SEEK okvirja**.
- Možna je razširitev za pripravo standardiziranih **ISA-tab** datotek.
- Možna uporaba v ukazni vrstici.
- Dostopnost: <https://github.com/NIB-SI/pISA>

# pISA-tree in ponovljivost analiz

- R + knitr + (LaTeX ali markdown).
- R paket `pisar` za manipulacijo in uporabo pISA metapodatkov.
- Namesto vkodiranih nizov uporabljamo pare ključ/vrednost iz metapodatkov.
- Relativne poti do datotek, glede na nivo pISA (`/..`) .
- pISA-tree lahko prestavimo na drugi mesto v datotečnem sistemu ali na poljuben zunanji medij.

## Vkodirano ime datoteke

```
file <- "D:/input.txt"  
x <- read.table(file)
```

## Posredno ime datoteke, iz metapodatkov

```
.adesc <- read.table("./ASSAY_METADATA.TXT")  
file <- getMeta(.adesc, "Data")  
x <- read.table(file)
```

## SessionInfo

Windows 10 x64 (build 16299)

- R version 3.3.1 (2016-06-21), x86\_64-w64-mingw32
- Locale: LC\_COLLATE=Slovenian\_Slovenia.1250, LC\_CTYPE=Slovenian\_Slovenia.1250, LC\_MONETARY=Slovenian\_Slovenia.1250, LC\_NUMERIC=C, LC\_TIME=Slovenian\_Slovenia.1250
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, utils
- Other packages: Biobase 2.28.0, BiocGenerics 0.14.0, knitr 1.16, MASS 7.3-45, plotrix 3.6-2, RColorBrewer 1.1-2, rpart 4.1-13, rpart.plot 2.1.2, tree 1.0-37, tsne 0.1-3, xtable 1.8-2
- Loaded via a namespace (and not attached): evaluate 0.10.1, formatR 1.4, magrittr 1.5, stringi 1.1.1, stringr 1.2.0, tools 3.3.1

Project path: [\[link\]](#)

D:/

DEJAVNOSTI/

OMIKE/

pISA-projects/

\_p\_biopharm.si/

\_I\_Task1/

\_S\_doktoratiUM/

\_A\_060-Logistic-Stat/

other/

060-Logistic/

## Bioinformatics group

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Živa Ramšak  
Maja Zagorščak



Hvala za pozornost

../\_p\_project

makeInvestigation.bat

/\_I\_Investigation

makeStudy.bat

/presentations

/reports

Readme.md

Metadata.txt

Identifier  
Title  
Description  
Date  
PI  
Phenodata  
...

/\_S\_Study2

makeAssay.bat

/\_S\_Study3

makeAssay.bat

/data

/results

Metadata

Identifier  
Title  
Description  
Date  
Featuredata  
...

/\_A\_Assay1-NGS

/\_A\_Assay2-Stat

Reame md  
Metadata

/input

/results

/R

Identifier  
Title  
Description  
Date  
...