

One study with 2 sources

- source1
- source2

and 4 samples

- source1_a
- source1_b
- source2_a
- source2_b


and 2 assays

- assay 1 = transcriptomic
- assay 2 = metabolomics


Image 1

STUDY ASSAYS

+ add new assay(s)

 VIEW ✕

transcription profiling
nucleotide sequencing
Illumina
a_mustudyid_transcription...

 VIEW ✕

metabolite profiling
mass spectrometry
TSQ Quantum Ultra (The...
a_mustudyid_metabolite_p...

Image 2

It is not possible to leave 2 rows empty; source name must be duplicated in long format (see image 6)

file	study	view	utilities	options	help
isatab overview					
mustudyID					
s_mustudyID.txt					
a_mustudyid_transcripti					
a_mustudyid_metabolite					
Row No.	Source Name	Characteristics[organism]	Protocol REF	Sample Name	
1	source1	NCBITAXON:Human		source1_a	
2	source2	NCBITAXON:Human		source1_b	
3				source2_a	
4				source2_b	

Image 3

file	study	view	utilities	options	help
isatab overview					
mustudyID					
s_mustudyID.txt					
a_mustudyid_transcripti					
a_mustudyid_metabolite					
Row No.	Sample Name	Protocol REF	Extract Name	Protocol REF	
1	source1_a	nucleic acid extraction	source1_a_extract	library construction	
2	source2_a	nucleic acid extraction	source2_a_extract	library construction	

Image 4

file	study	view	utilities	options	help		
isatab overview							
mustudyID							
s_mustudyID.txt							
a_mustudyid_transcripti							
a_mustudyid_metabolite							
Row No.	Sample Name	Protocol REF	Extract Name	Protocol REF	Labeled Extract Name	Label	
1	source1_b	extraction	source1_b_extract	labeling	source1_b_labeled		ma
2	source2_b	extraction	source1_b_extract	labeling	source2_b_labeled		ma

Image 5

— Errors found in isatab...

— 2 files with fields missing required data

— s_mustudyID.txt has 1 field missing data

— Source Name is missing 2 descriptions

→ Data missing for Source Name at record 2

→ Data missing for Source Name at record 3

+ a_mustudyid_transcription_profiling_nucleotide_sequencing.txt has 1 field missing data

Image 6

Row No.	Source Name	Characteristics[organism]	Protocol REF	Sample Name
1	source1	NCBITAXON:Human		source1_a
2	source1	NCBITAXON:Human		source1_b
3	source2	NCBITAXON:Human		source2_a
4	source2	NCBITAXON:Human		source2_b

Image 7

Not able to see nor select any file from desktop.

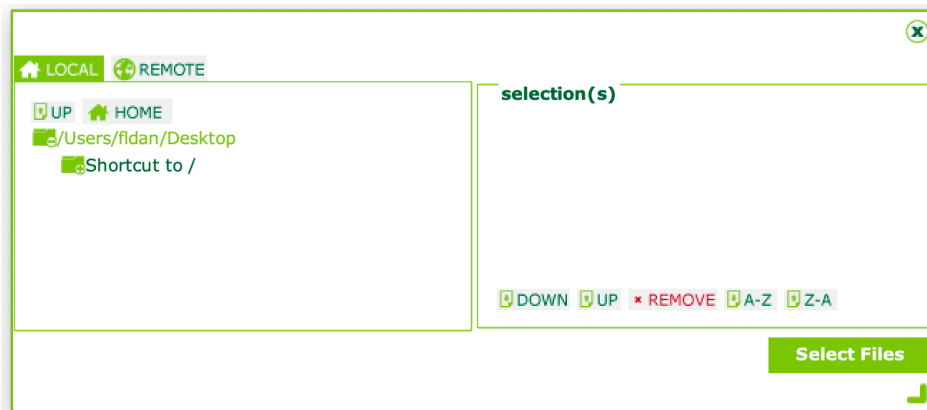


Image 8

Conversion failed with 1 message. Here is why:

error -

The study 'mustudyID' has no SRA Center Name, cannot export to SRA format

Image 9

Row No.	Source Name	Characteristics[organism]	Protocol REF	Sample Name
1	source1	NCBITAXON:Human		source1_a
2	source1	NCBITAXON:Human		source1_b
3	source2	NCBITAXON:Human		source2_a
4	source2	NCBITAXON:Human		source2_b
5	source3	NCBITAXON:Human		source3_a

It is possible to have a source and sample name that is not used in any assay of the study.

Image 10

The screenshot shows the 'isatool' software interface. The top menu bar includes 'file', 'study', 'view', 'utilities', 'options', and 'help'. Below the menu is a toolbar with various icons for file operations and data management. The main window is titled 'overview' and displays a tree view on the left with folders for 'mustudy...', 's_mustudyID.txt', 'a_mustudyid_transcript', and 'a_mustudyid_metabolite'. The central area shows a table with the following data:

Row No.	Source Name	Characteristics[organism]	Protocol REF	Sample Name
1	source1	NCBITAXON:Human		source1_a
2	source1	NCBITAXON:Human		source1_b
3	source2	NCBITAXON:Human		source2_a
4	source2	NCBITAXON:Human		source2_b
5	source3	NCBITAXON:Human		source2_a
6	source4	NCBITAXON:Human		source_2b