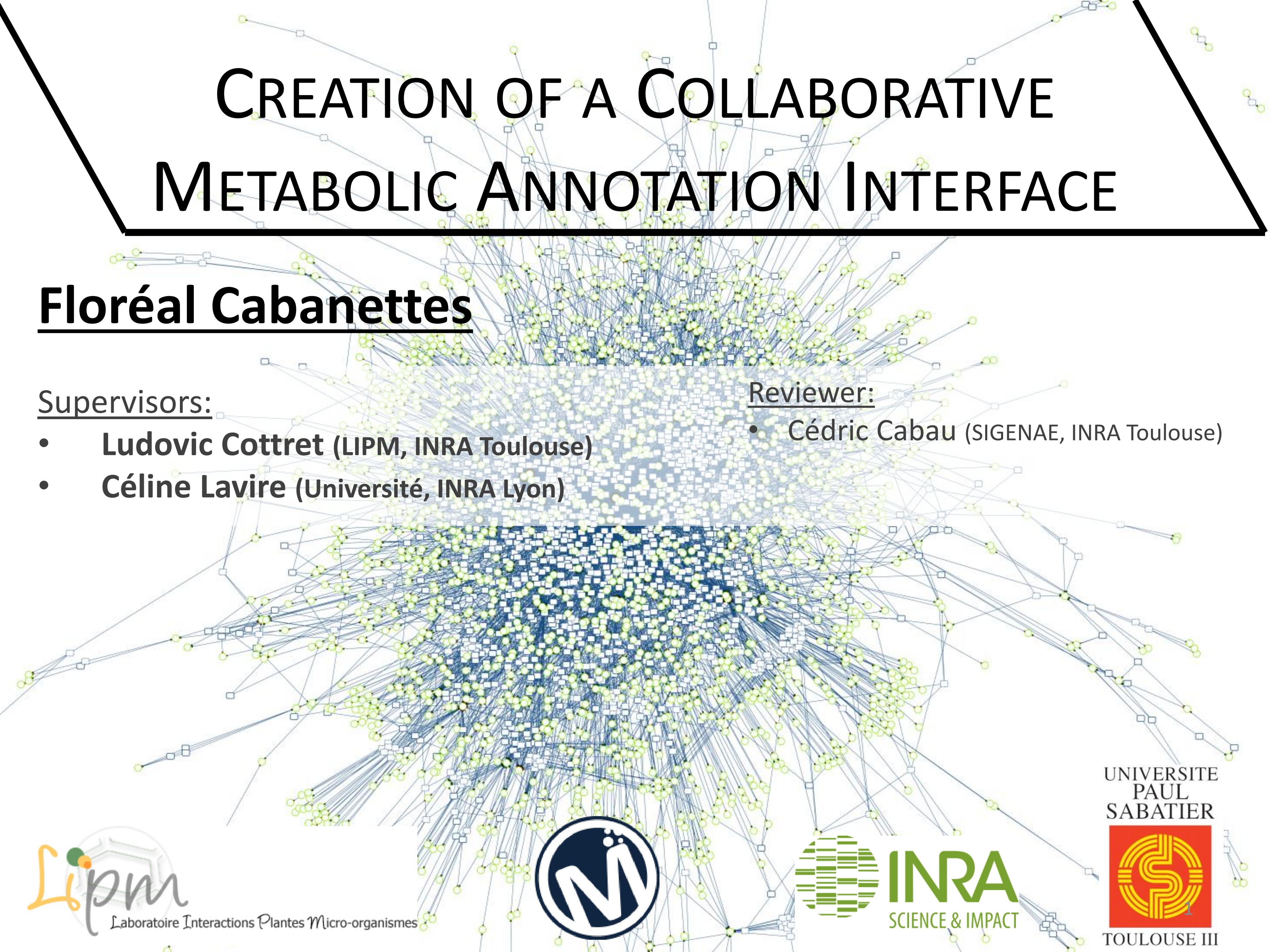
CREATION OF A COLLABORATIVE METABOLIC ANNOTATION INTERFACE



Floréal Cabanettes

Supervisors:
- **Ludovic Cottret (LIPM, INRA Toulouse)**
- **Céline Lavire (Université, INRA Lyon)**

Reviewer:
- Cédric Cabau (SIGENAE, INRA Toulouse)

Laboratoire Interactions Plantes Micro-organismes

INRA
SCIENCE & IMPACT

UNIVERSITE
PAUL
SABATIER
TOULOUSE III

OVERVIEW

1. Introduction
2. Software development strategy
3. Presentation of *MetExplore Annotation*
    - 3.1. Collaborative annotation
    - 3.2. Tools for highlighting mistakes in a metabolic network
    - 3.3. Summarize opinions about the metabolic network
4. Conclusion and future prospects

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1. INTRODUCTION

Why reconstruct a metabolic network?

Phenotype prediction

Omics data mapping

Metabolic network optimization

Gene Essentiality

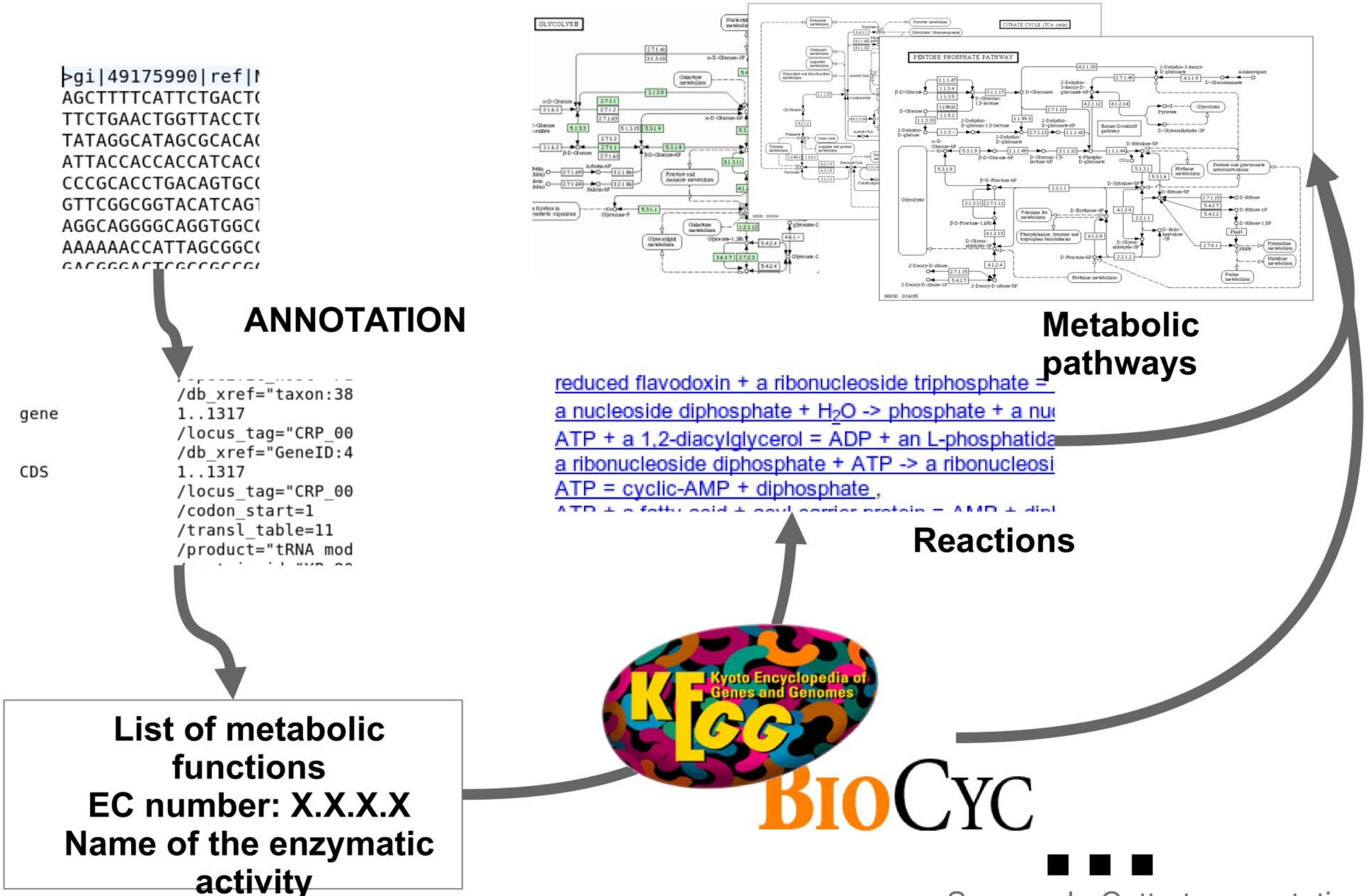
Path prediction

Flux Analysis

…

1. INTRODUCTION

Automatic draft reconstruction



```
>gi|49175990|ref|N
AGCTTTTCATTCTGACT(
TTCTGAACTGGTTACCT(
TATAGGCATAGCGCACA(
ATTACCACCACCATCAC(
CCCGCACCTGACAGTGC(
GTTCGGCGGTACATCAGT
AGGCAGGGGCAGGTGGC(
AAAAAACCATTAGCGGC(
```

ANNOTATION

```
                   /db_xref="taxon:38
gene               1..1317
                   /locus_tag="CRP_00
                   /db_xref="GeneID:4
CDS                1..1317
                   /locus_tag="CRP_00
                   /codon_start=1
                   /transl_table=11
                   /product="tRNA mod
```

List of metabolic functions
EC number: X.X.X.X
Name of the enzymatic activity

Metabolic pathways

reduced flavodoxin + a ribonucleoside triphosphate =
a nucleoside diphosphate + H_2O -> phosphate + a nu(
ATP + a 1,2-diacylglycerol = ADP + an L-phosphatida
a ribonucleoside diphosphate + ATP -> a ribonucleosi
ATP = cyclic-AMP + diphosphate ,

Reactions

Source : L. Cottret presentation

1. INTRODUCTION

So… Is the work finished?

1. INTRODUCTION

Automatic draft reconstruction

- x A lot of errors
- x No reversibility of reactions
- x No compartmentalization
- x Bad enzyme specificity
- x Generic compounds/reactions
- x …

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Curation:

→ Correction of errors
→ Add missing information
… using specific organism literature and DB

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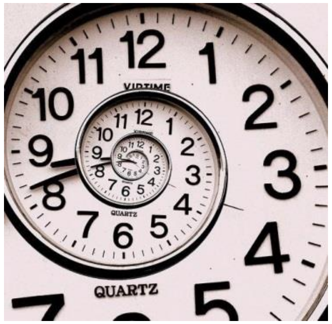
6 months to Several years



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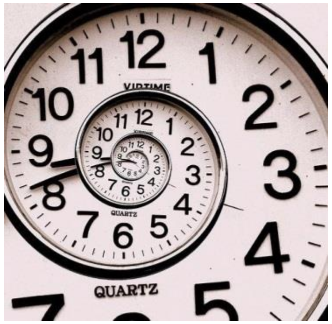

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Curated reconstruction

- ✓ More precise
- ✓ Reversibility of reactions
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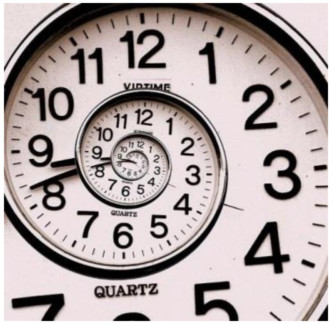

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Curated reconstruction

✓ More precise
✓ Reversibility of reactions
✓ Compartmentalization
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✓ …

1. INTRODUCTION

Agromics project:

To study several species of the genre *Agrobacterium* localized in very different environments, and visualize the impact of these environments on the metabolic network.

→ The reconstruction of an *A. tumefaciens* network, as a reference, then using it to propagate the reconstruction to other species of the genre.

- → From existing automatic reconstructions
- → Tools to facilitate the job :
  - → Annotation of several reconstructions

→ The collaboration of a lot of scientists with different skills

- → Tools that promotes collaborative annotation

1. INTRODUCTION

	MetExplore + M. Annotation	Pathway tools	rBioNet	GEMSiRV	Raven Toolbox	Sublim. Toolbox
Automatic reconstruction	🟥	🟩	🟥	🟩	🟩	🟥
Manual curation	🟧	🟩	🟩	🟩	🟩	🟩
SBML Import/Export	🟩	🟥	🟩	🟩/🟥	🟩	🟩
Excel Import/Export	🟥	🟥	🟩	🟩/🟥	🟩	🟥
Direct import from KEGG	🟩	🟥	🟥	🟥	🟥	🟩
Direct import from BioCyc	🟥	🟥	🟥	🟥	🟥	🟩
Collaborative annotation**	🟥	🟩	🟥	🟥	🟥	🟥
Projects management	🟥	🟥	🟥	🟥	🟥	🟥
Simulations on networks	🟩	🟥	🟥	🟩	🟩	🟥
Evaluation tools***	🟥	🟥	🟥	🟥	🟥	🟥
Network visualization	🟩	🟩	🟩	🟩	🟩	🟥
Mapping on networks	🟩	🟩	🟥	🟥	🟥	🟥
Cytoscape export	🟩	🟥	🟥	🟥	🟩	🟥

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Simulations on networks	🟩	🟥	🟥	🟩	🟩	🟥
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Mapping on networks	🟩	🟩	🟥	🟥	🟥	🟥
Cytoscape export	🟩	🟥	🟥	🟥	🟩	🟥

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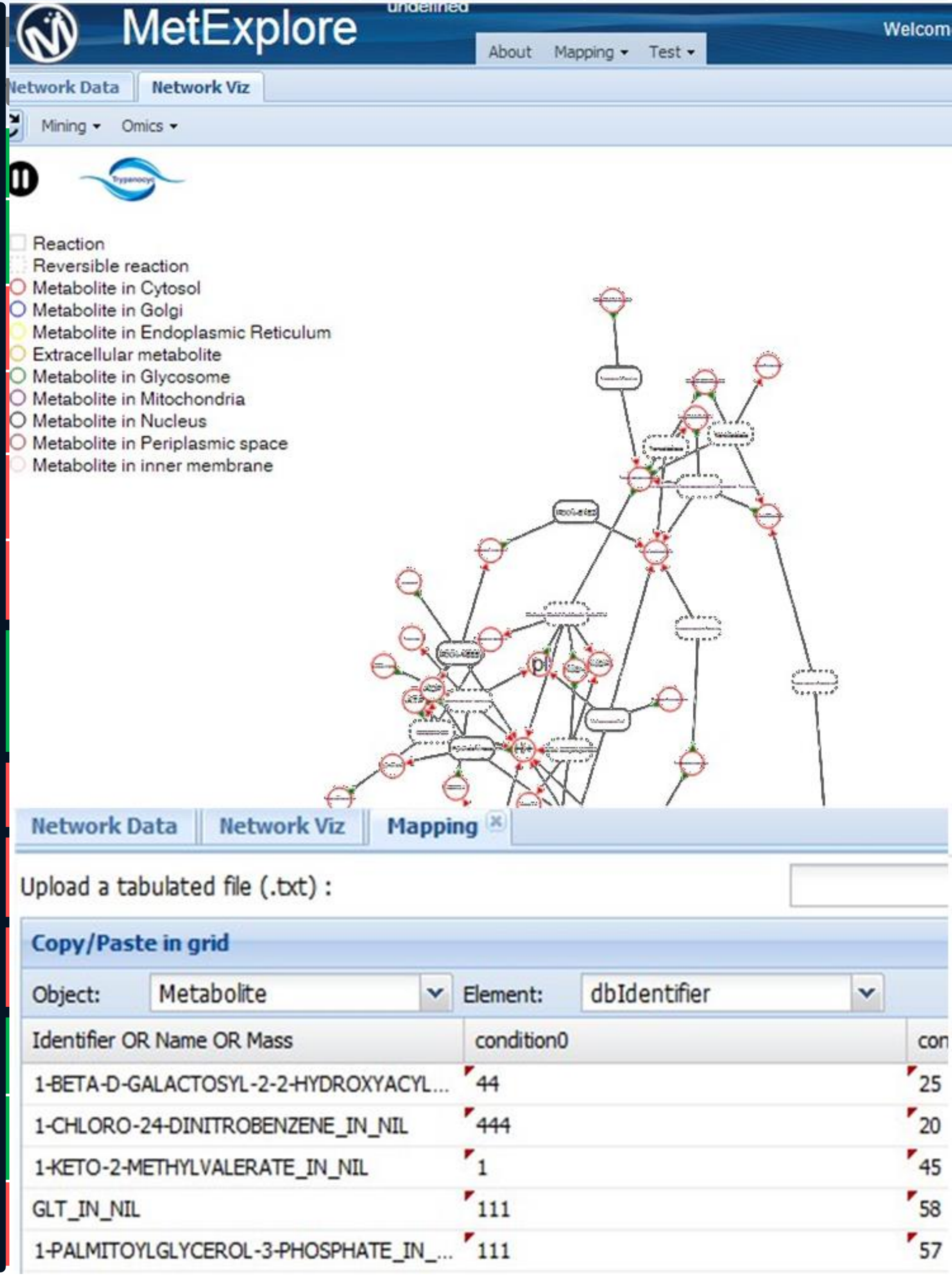


Upload a tabulated file (.txt) :

Copy/Paste in grid

Object: Metabolite
Element: dbIdentifier

Identifier OR Name OR Mass	condition0	con
1-BETA-D-GALACTOSYL-2-2-HYDROXYACYL...	44	25
1-CHLORO-24-DINITROBENZENE_IN_NIL	444	20
1-KETO-2-METHYLVALERATE_IN_NIL	1	45
GLT_IN_NIL	111	58
1-PALMITOYLGLYCEROL-3-PHOSPHATE_IN_...	111	57

1. Introduction

→ Jamboree 16 & 17 June

Biologists

Metabolism specialists

Chemists

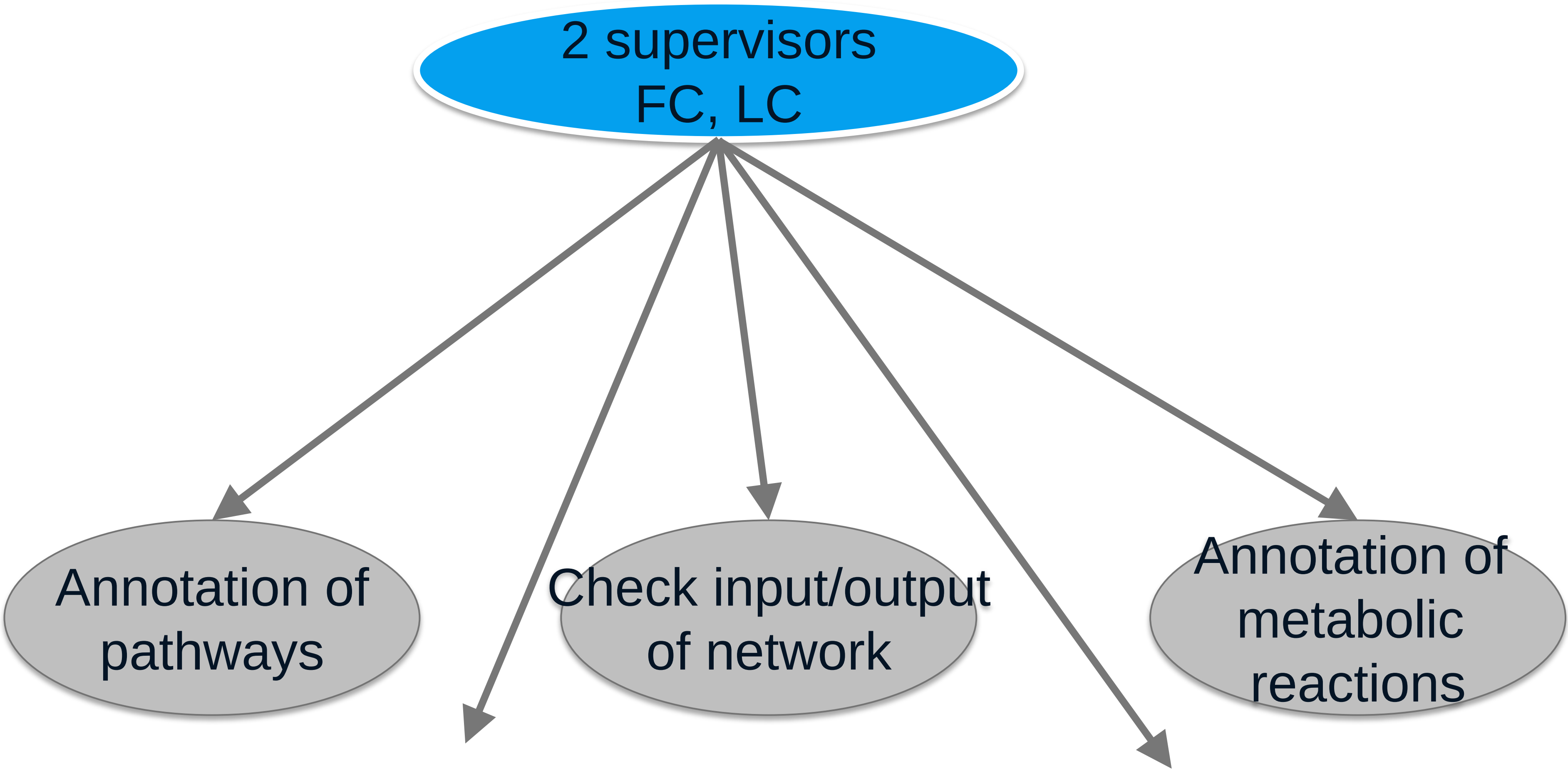
GPR association specialists

Bioinformaticians

MetExplore Annotation

1. Introduction

→ Jamboree 16 & 17 June



2 supervisors
FC, LC

Annotation of pathways

Check input/output of network

Annotation of metabolic reactions

Working Groups

OVERVIEW

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2. **Software development strategy**
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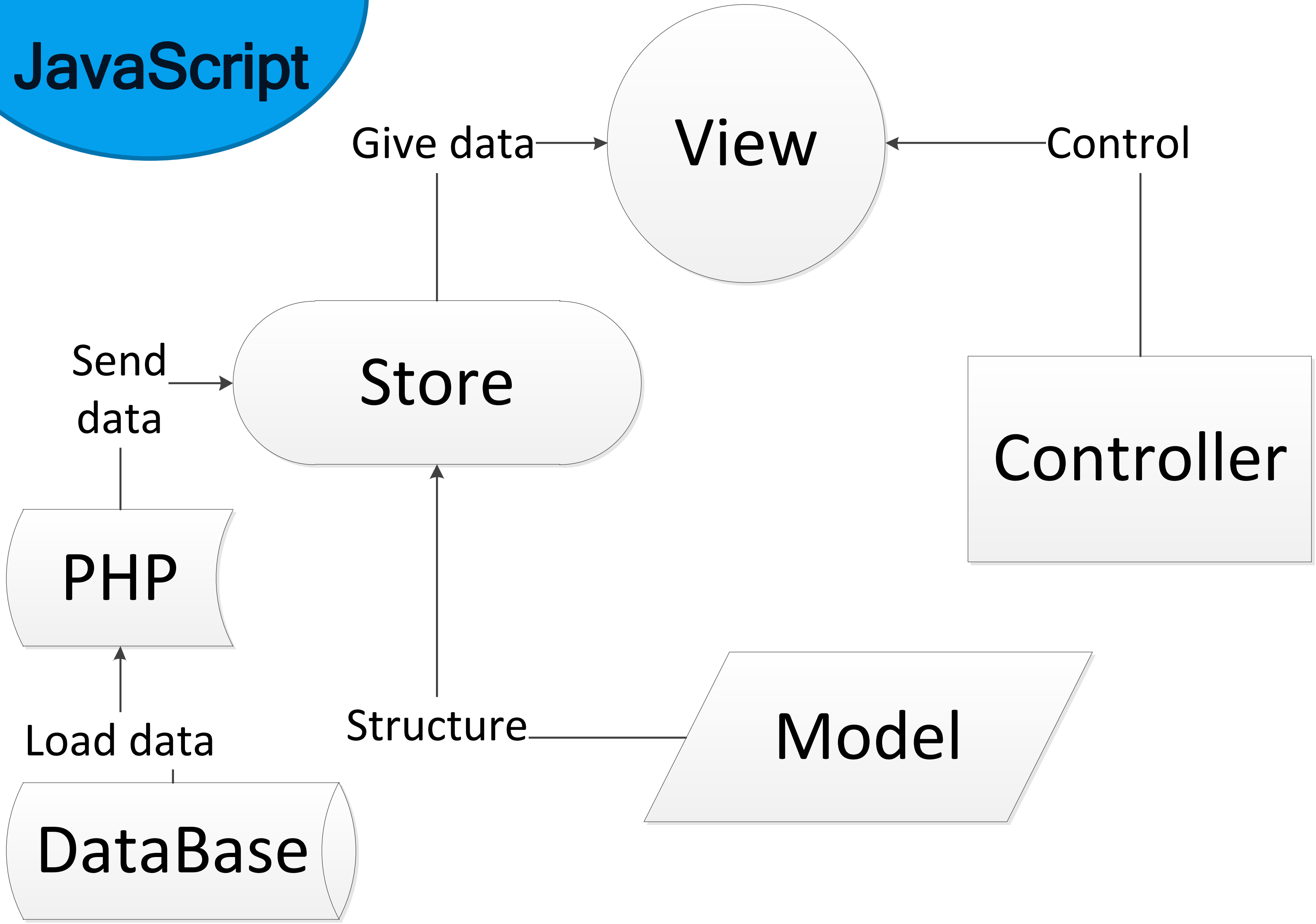
2. SOFTWARE DEVELOPMENT STRATEGY

- ExtJS → Rich Web Applications

JavaScript



Give data

View

Control

Store

Send data

Controller

PHP

Load data

Structure

Model

DataBase

2. SOFTWARE DEVELOPMENT STRATEGY

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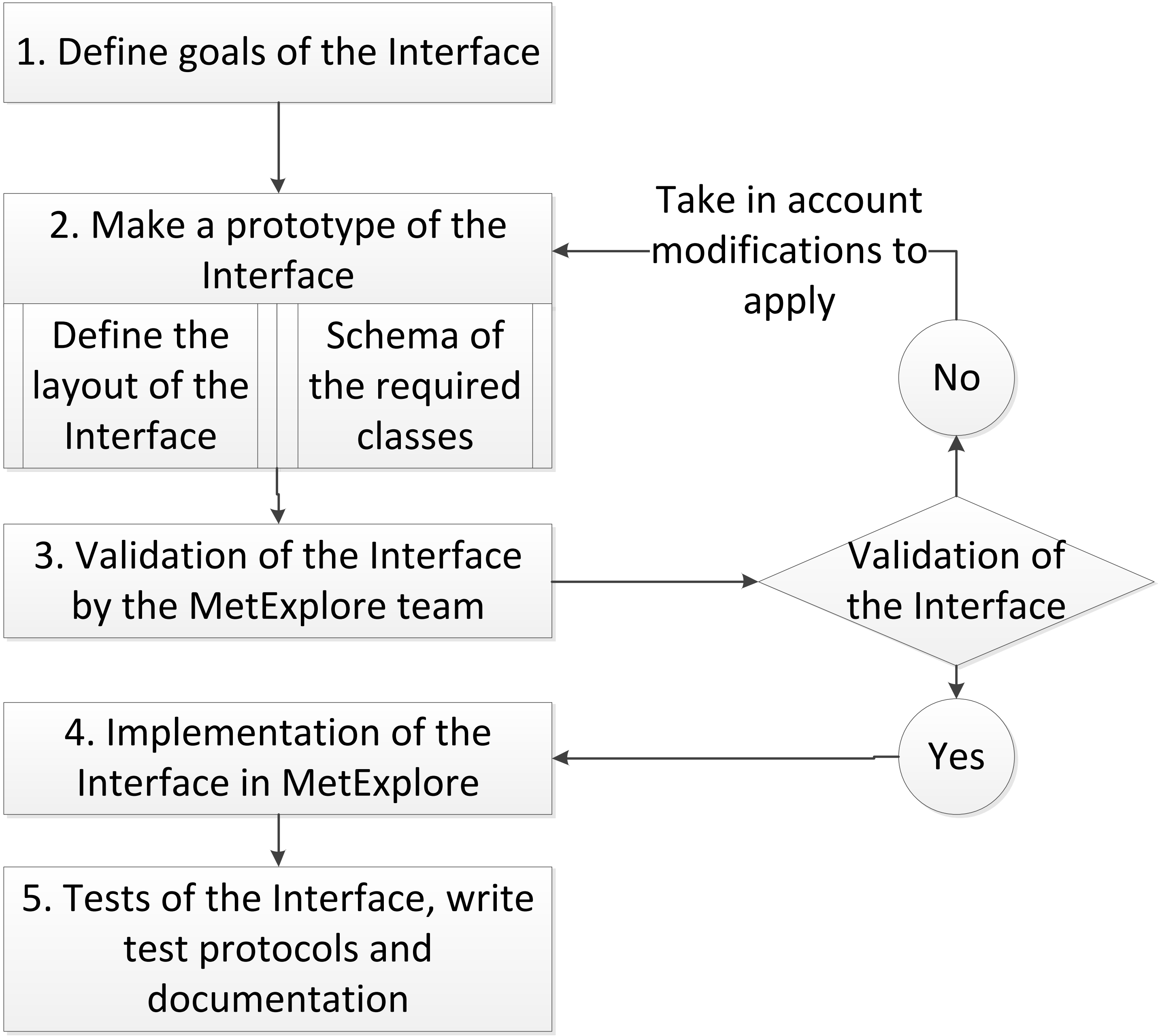
→ Work in a team
→ Respect standards
→ Interaction!

2. SOFTWARE DEVELOPMENT STRATEGY



1. Define goals of the Interface

2. Make a prototype of the Interface

Define the layout of the Interface

Schema of the required classes

3. Validation of the Interface by the MetExplore team

Validation of the Interface

No

Take in account modifications to apply

Yes

4. Implementation of the Interface in MetExplore

5. Tests of the Interface, write test protocols and documentation

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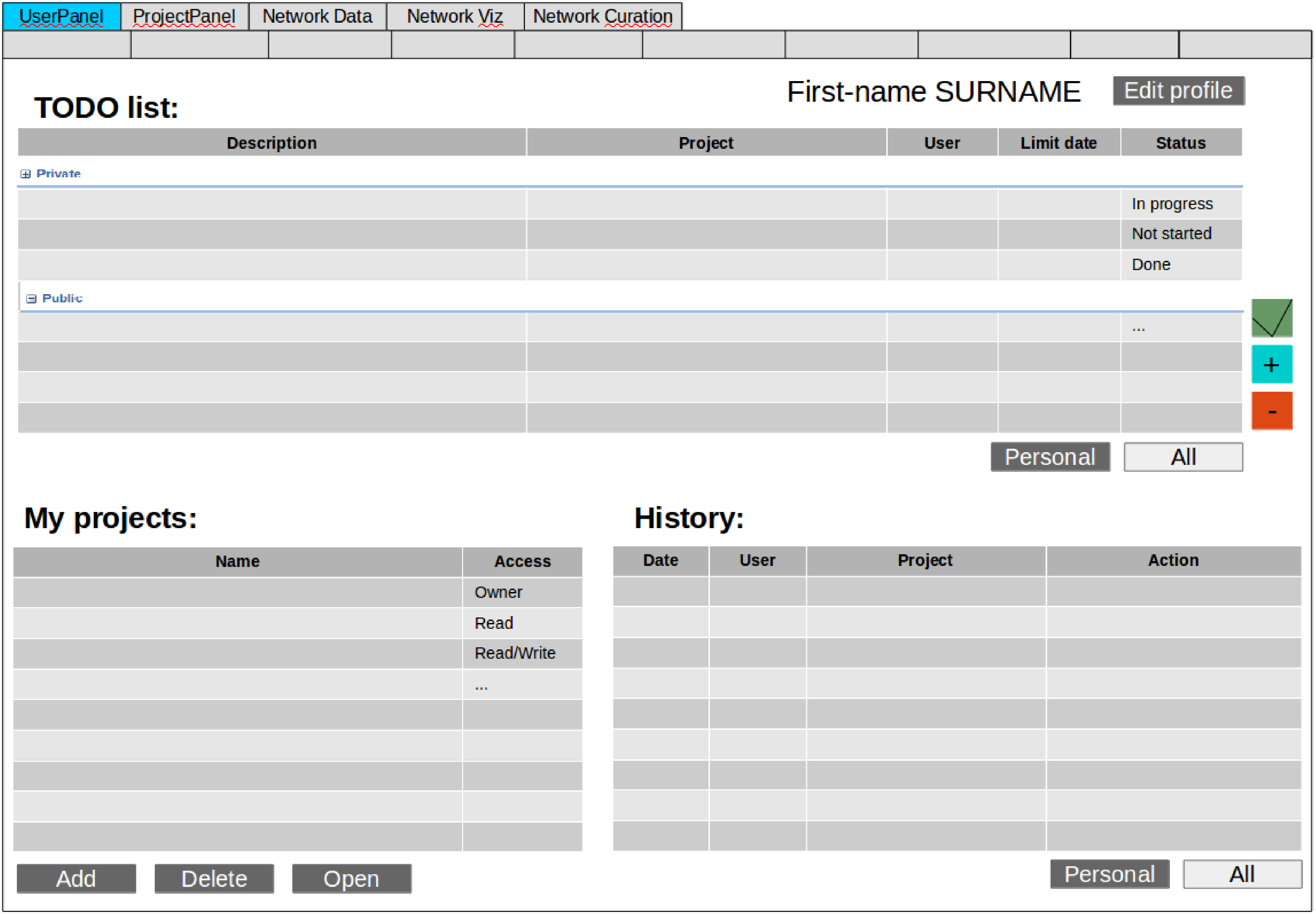


First-name SURNAME

TODO list:

Description	Project	User	Limit date	Status
⊞ Private				
				In progress
				Not started
				Done
⊟ Public				
				...

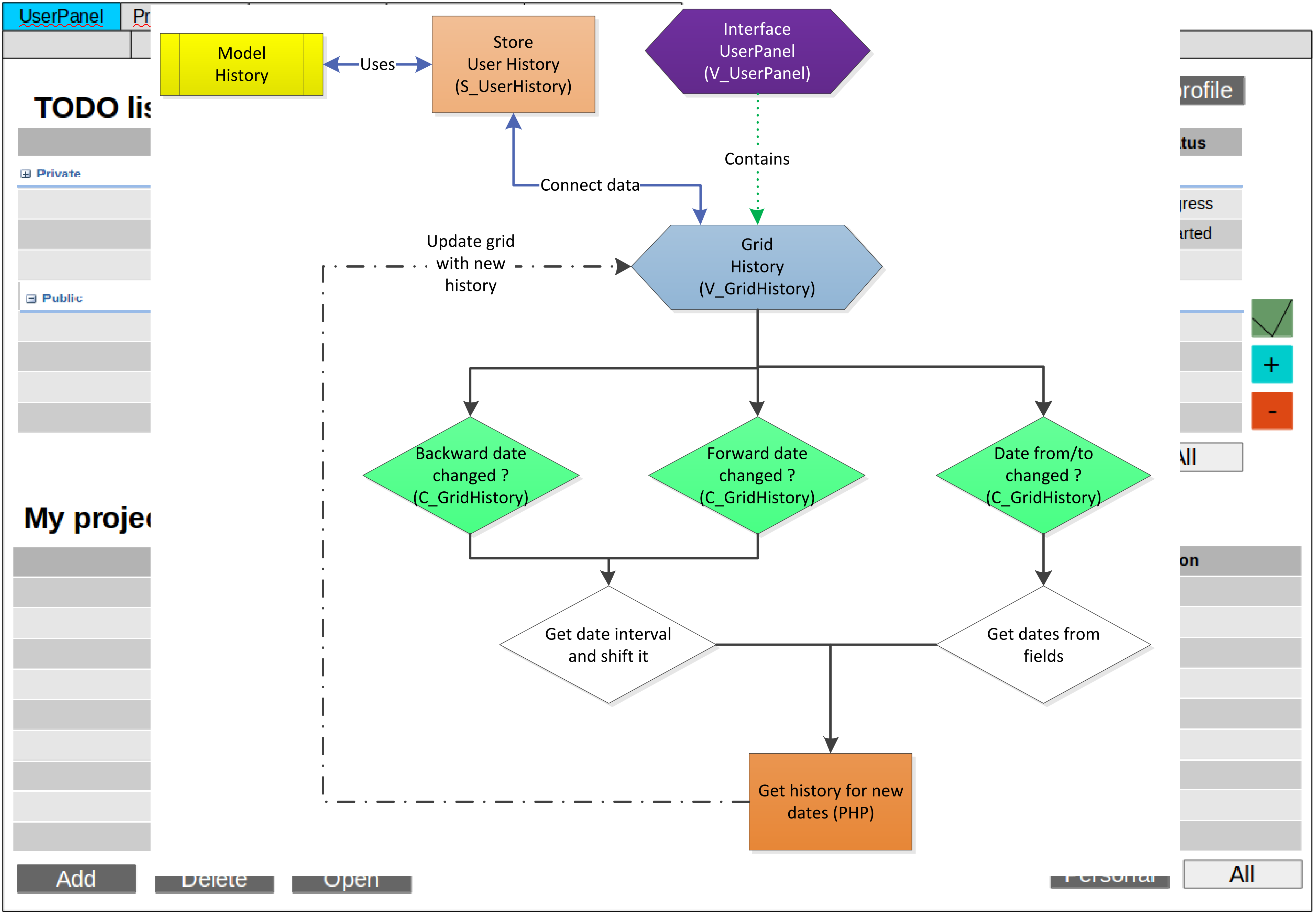
My projects:

Name	Access
	Owner
	Read
	Read/Write
	...

History:

Date	User	Project	Action

2. SOFTWARE DEVELOPMENT STRATEGY



Model History

Store User History (S_UserHistory)

Interface UserPanel (V_UserPanel)

Grid History (V_GridHistory)

Backward date changed ? (C_GridHistory)

Forward date changed ? (C_GridHistory)

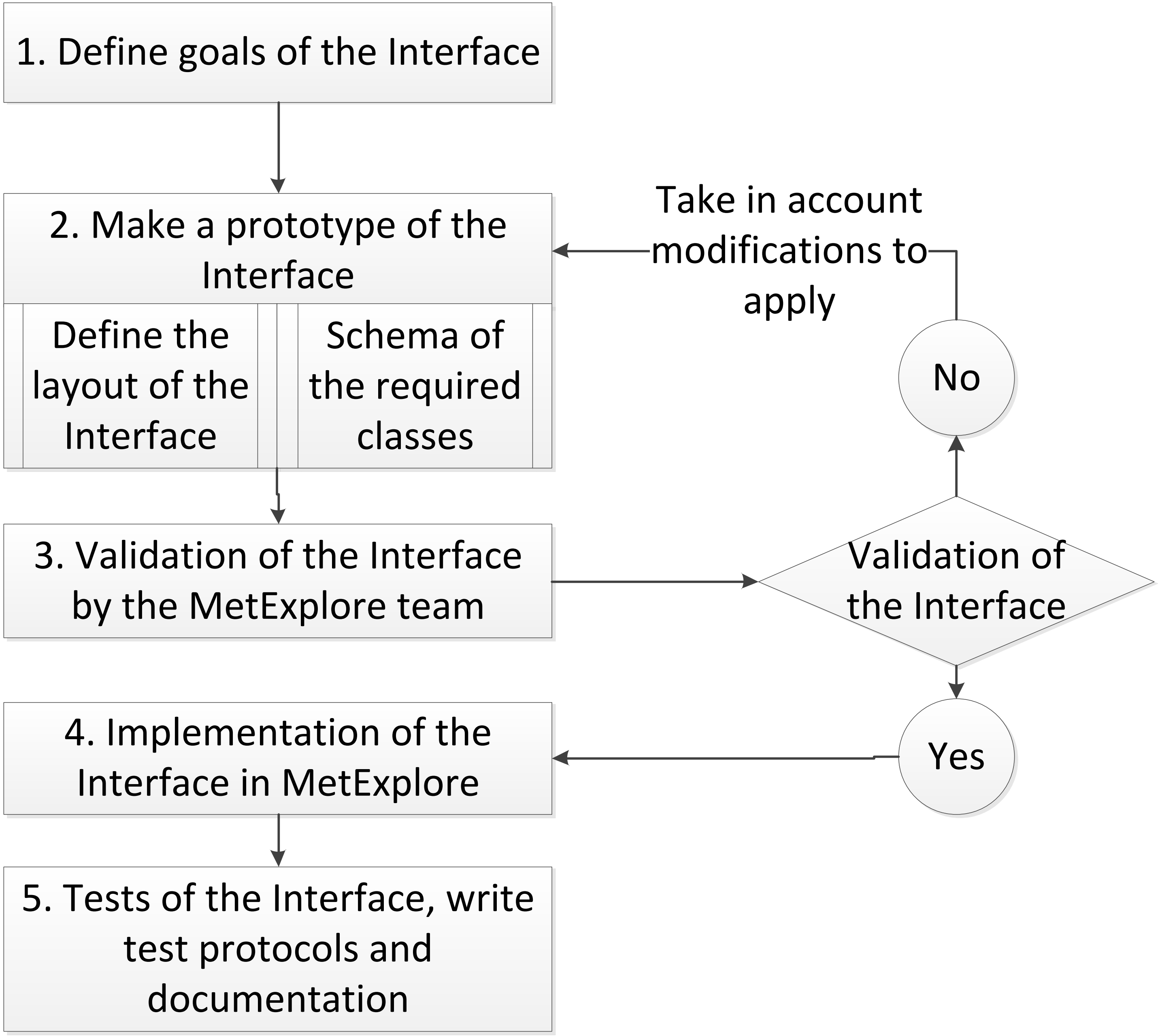
Date from/to changed ? (C_GridHistory)

Get date interval and shift it

Get dates from fields

Get history for new dates (PHP)

2. SOFTWARE DEVELOPMENT STRATEGY



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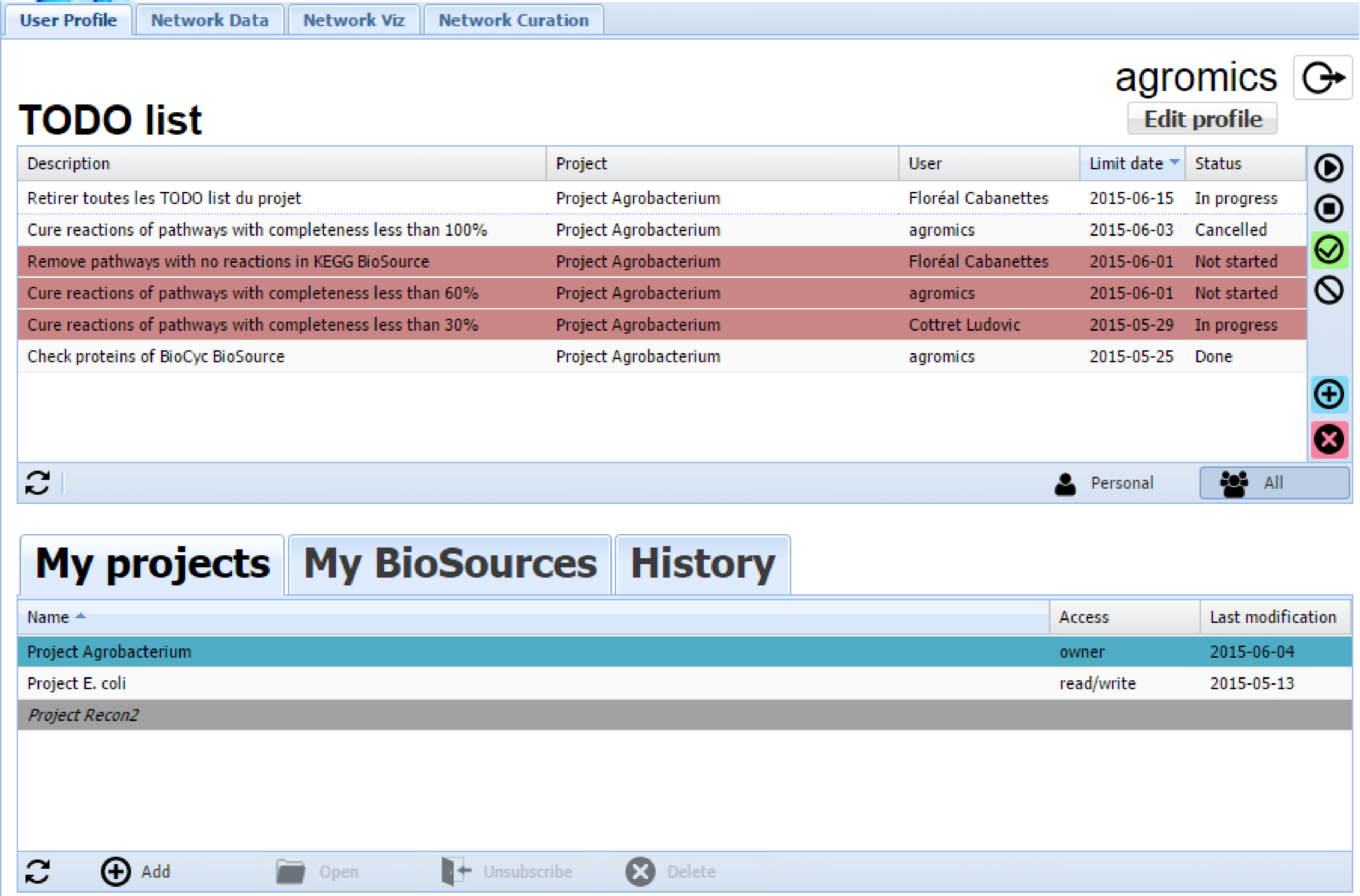
3.1 Collaborative Annotation



TODO list

Description	Project	User	Limit date	Status
Retirer toutes les TODO list du projet	Project Agrobacterium	Floréal Cabanettes	2015-06-15	In progress
Cure reactions of pathways with completeness less than 100%	Project Agrobacterium	agromics	2015-06-03	Cancelled
Remove pathways with no reactions in KEGG BioSource	Project Agrobacterium	Floréal Cabanettes	2015-06-01	Not started
Cure reactions of pathways with completeness less than 60%	Project Agrobacterium	agromics	2015-06-01	Not started
Cure reactions of pathways with completeness less than 30%	Project Agrobacterium	Cottret Ludovic	2015-05-29	In progress
Check proteins of BioCyc BioSource	Project Agrobacterium	agromics	2015-05-25	Done

My projects | My BioSources | History

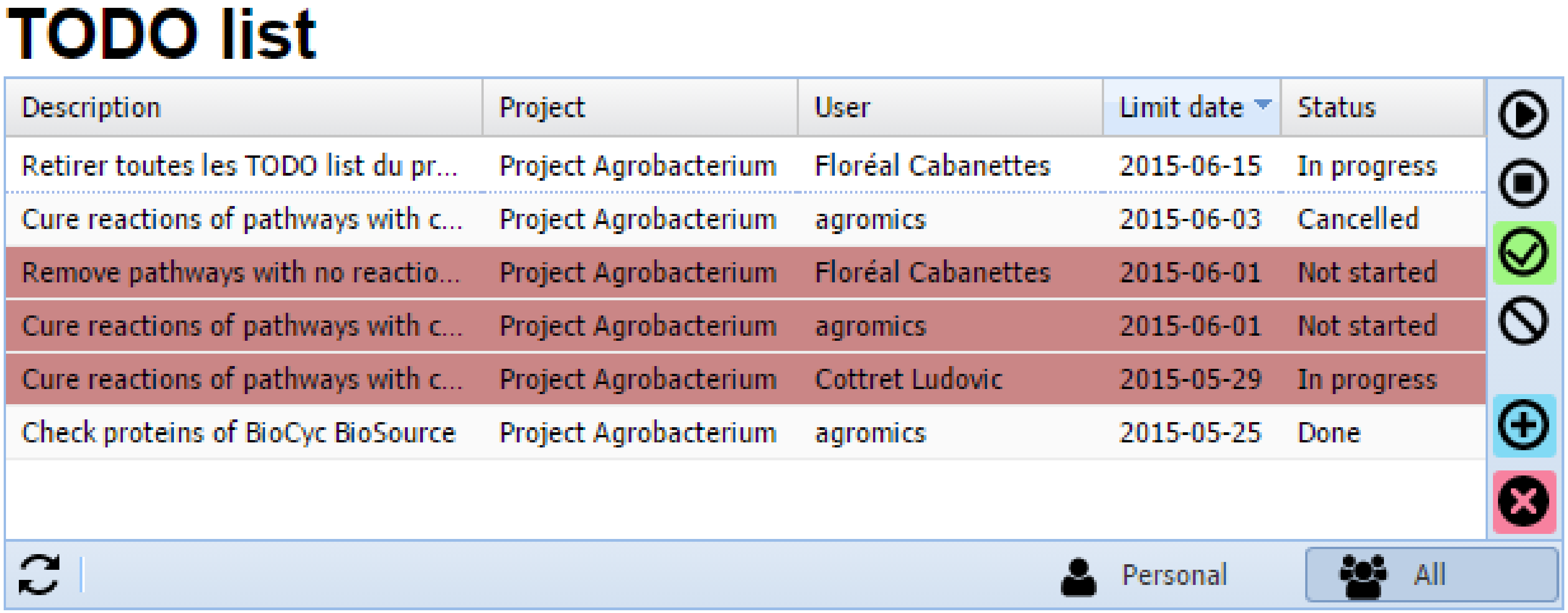
Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

3.1 COLLABORATIVE ANNOTATION

3.1.1 THE TODO LIST

Goal:

Summarize all to do or done tasks in a list



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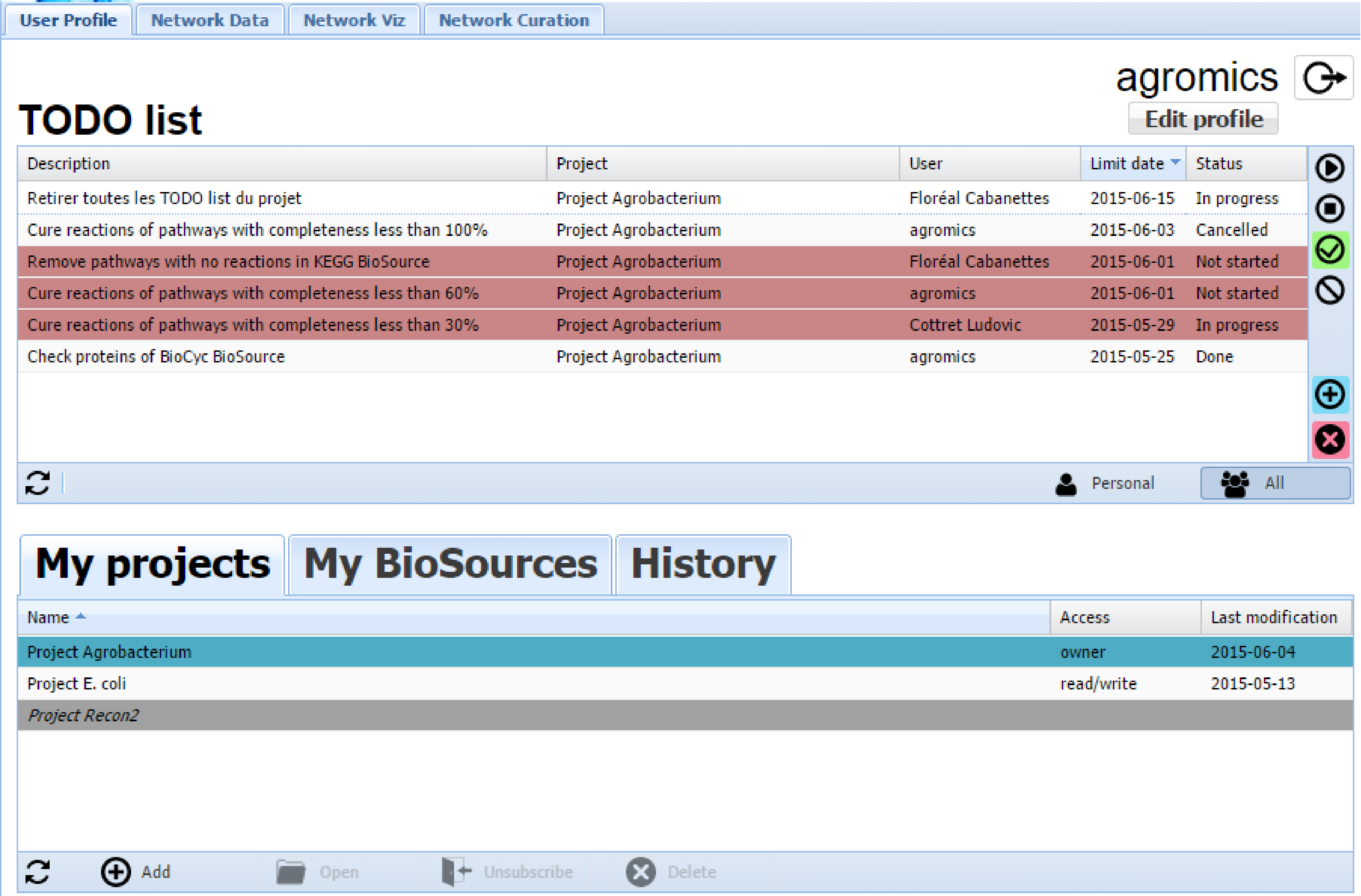
→ Organize and plan tasks

3.1 Collaborative Annotation



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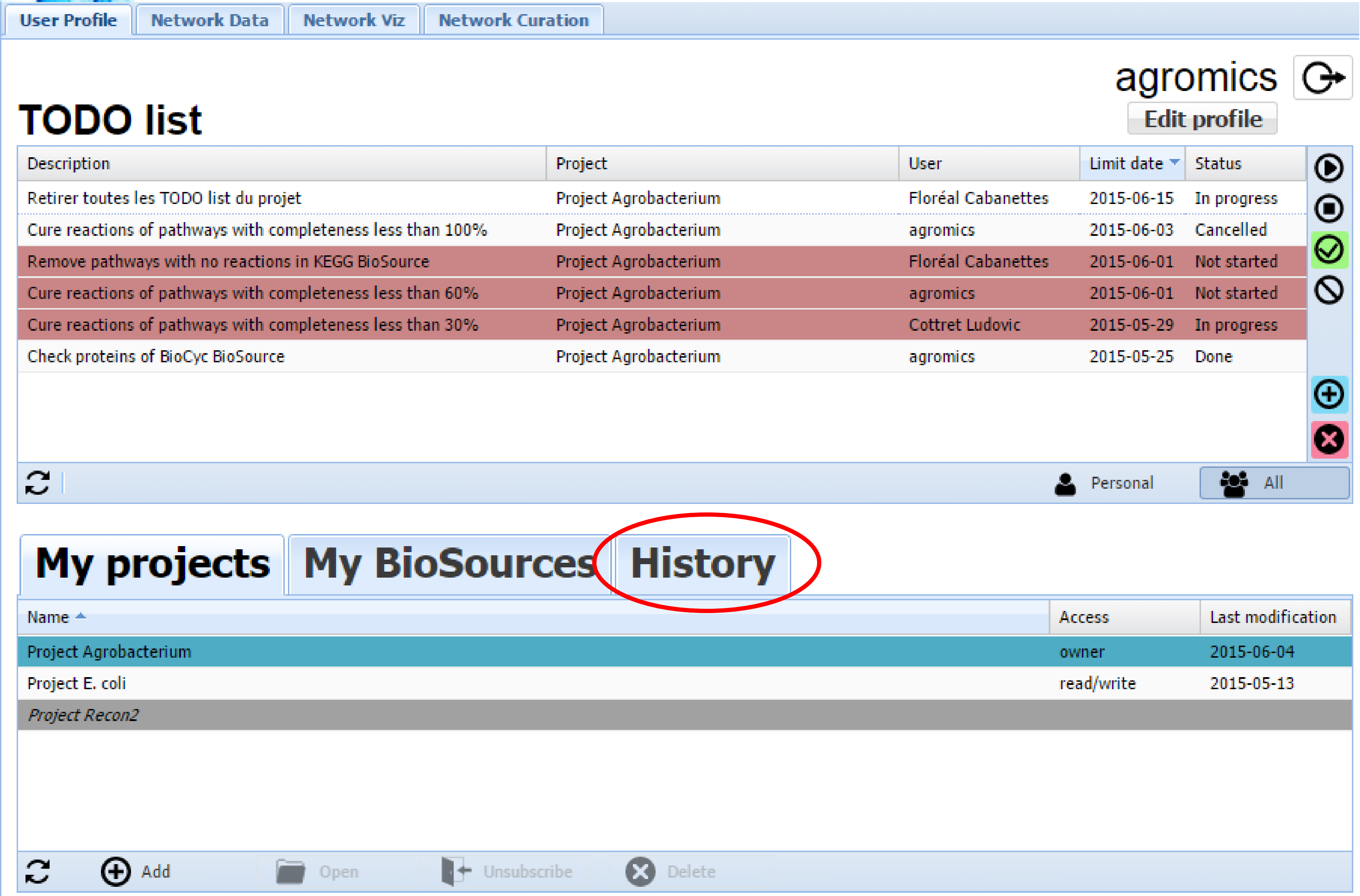

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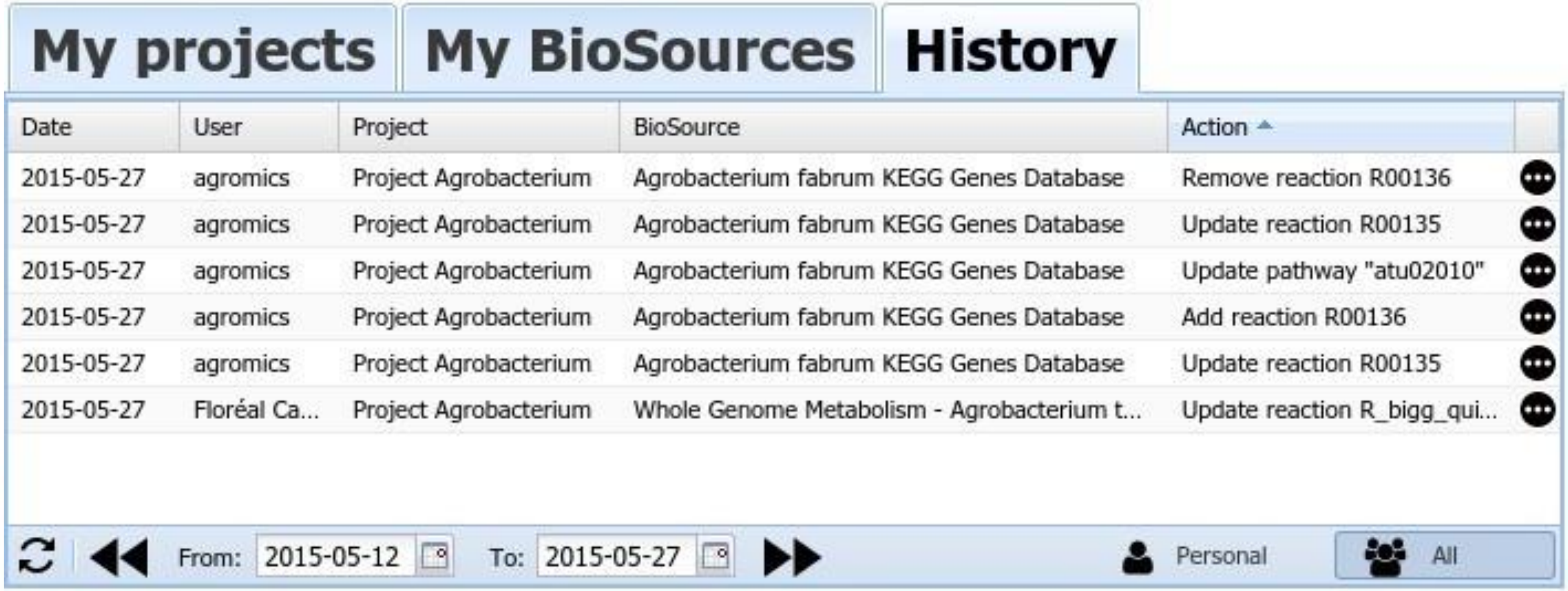
Project Recon2		

3.1 Collaborative Annotation

3.1.2 The History

Goal:

Keep track of all the modifications in all networks of our projects



Date	User	Project	BioSource	Action
2015-05-27	agromics	Project Agrobacterium	Agrobacterium fabrum KEGG Genes Database	Remove reaction R00136
2015-05-27	agromics	Project Agrobacterium	Agrobacterium fabrum KEGG Genes Database	Update reaction R00135
2015-05-27	agromics	Project Agrobacterium	Agrobacterium fabrum KEGG Genes Database	Update pathway "atu02010"
2015-05-27	agromics	Project Agrobacterium	Agrobacterium fabrum KEGG Genes Database	Add reaction R00136
2015-05-27	agromics	Project Agrobacterium	Agrobacterium fabrum KEGG Genes Database	Update reaction R00135
2015-05-27	Floréal Ca...	Project Agrobacterium	Whole Genome Metabolism - Agrobacterium t...	Update reaction R_bigg_qui...

From: 2015-05-12 To: 2015-05-27

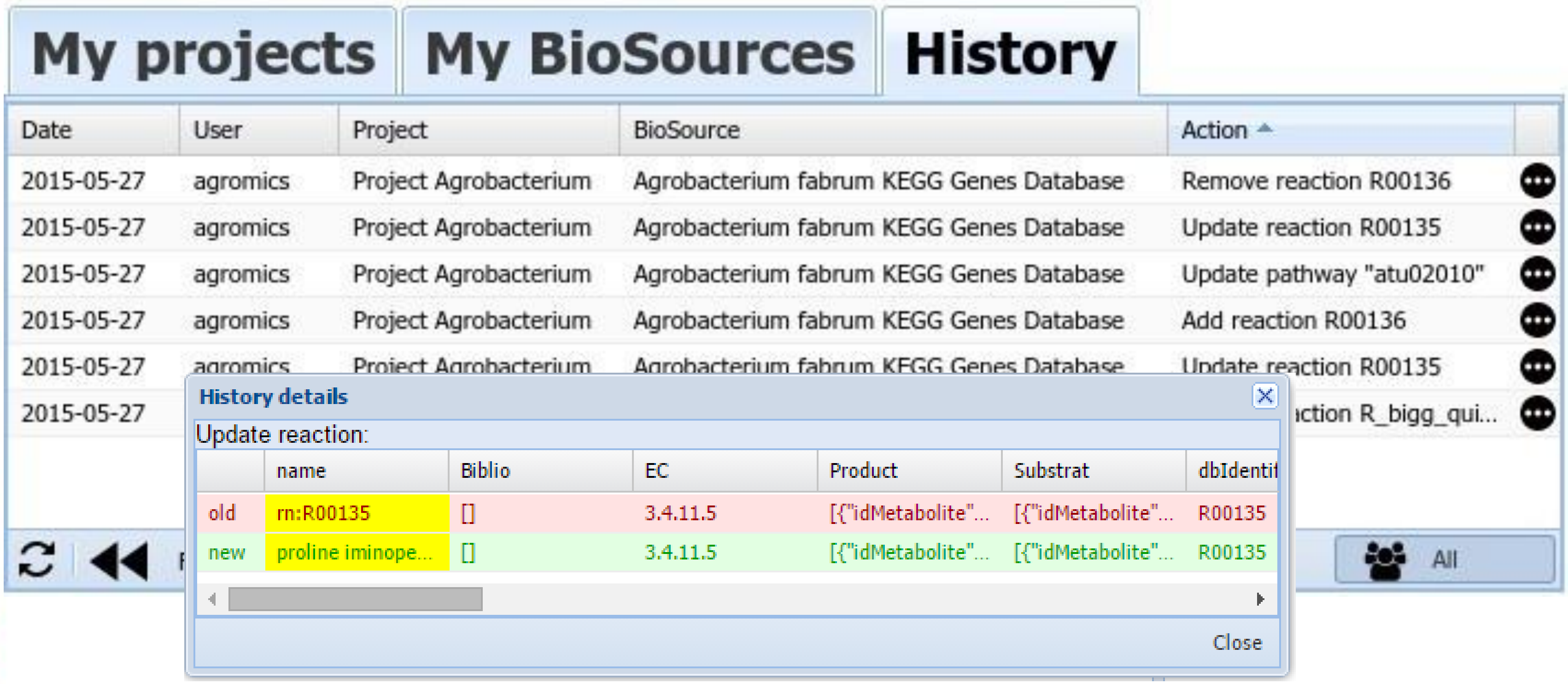
→ **Facilitate the work when publishing the Network on papers**
→ **Help to retrieve bad changes done on Network**

3.1 COLLABORATIVE ANNOTATION

3.1.2 THE HISTORY

Goal:

Keep track of all the modifications in all networks of our projects



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2015-05-27	agromics	Project Agrobacterium	Agrobacterium fabrum KEGG Genes Database	Update reaction R00135
2015-05-27				ction R_bigg_qui...

History details

Update reaction:

	name	Biblio	EC	Product	Substrat	dbIdentif
old	rn:R00135	[]	3.4.11.5	[{"idMetabolite"...	[{"idMetabolite"...	R00135
new	proline iminope...	[]	3.4.11.5	[{"idMetabolite"...	[{"idMetabolite"...	R00135

→ Facilitate the work when publishing the Network on papers
→ Help to retrieve bad changes done on Network

3.1 Collaborative Annotation

3.1.3 Projects

Goal:

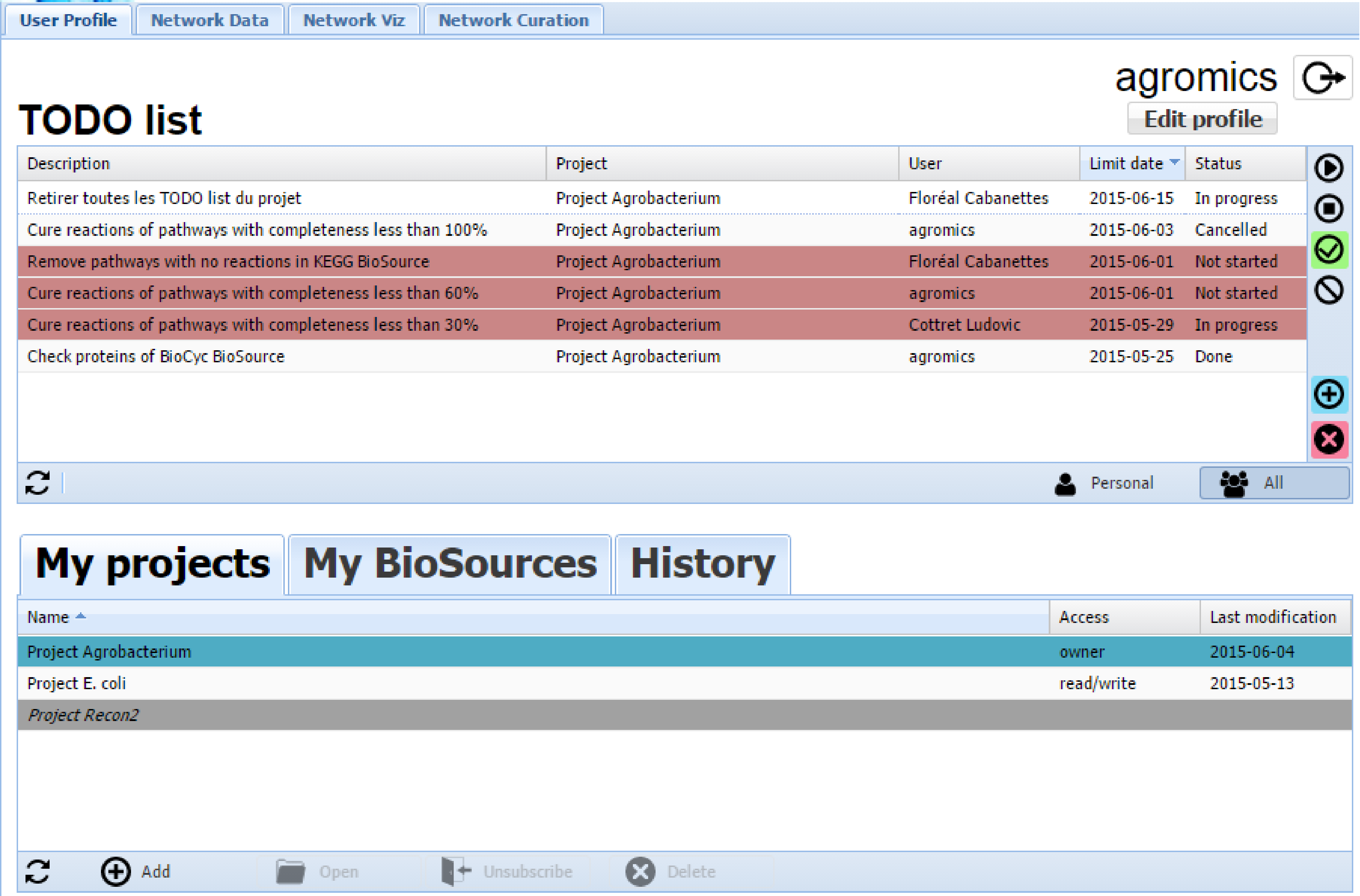
To group a list of metabolic networks for a list of users.
Associate access for each to the role they have in the project

Access Level	Description
Owner	Can manage *Projects* and their *Users*.
Read/Write	Can edit the Network.
Annotator	Can comment and give their opinion about the Network.
Read only	Can view all components of the Network.
Access denied	Has no access to the Network.

→ **Every user has the same access level for all networks in a Project**

3.1 Collaborative Annotation

3.1.3 Projects



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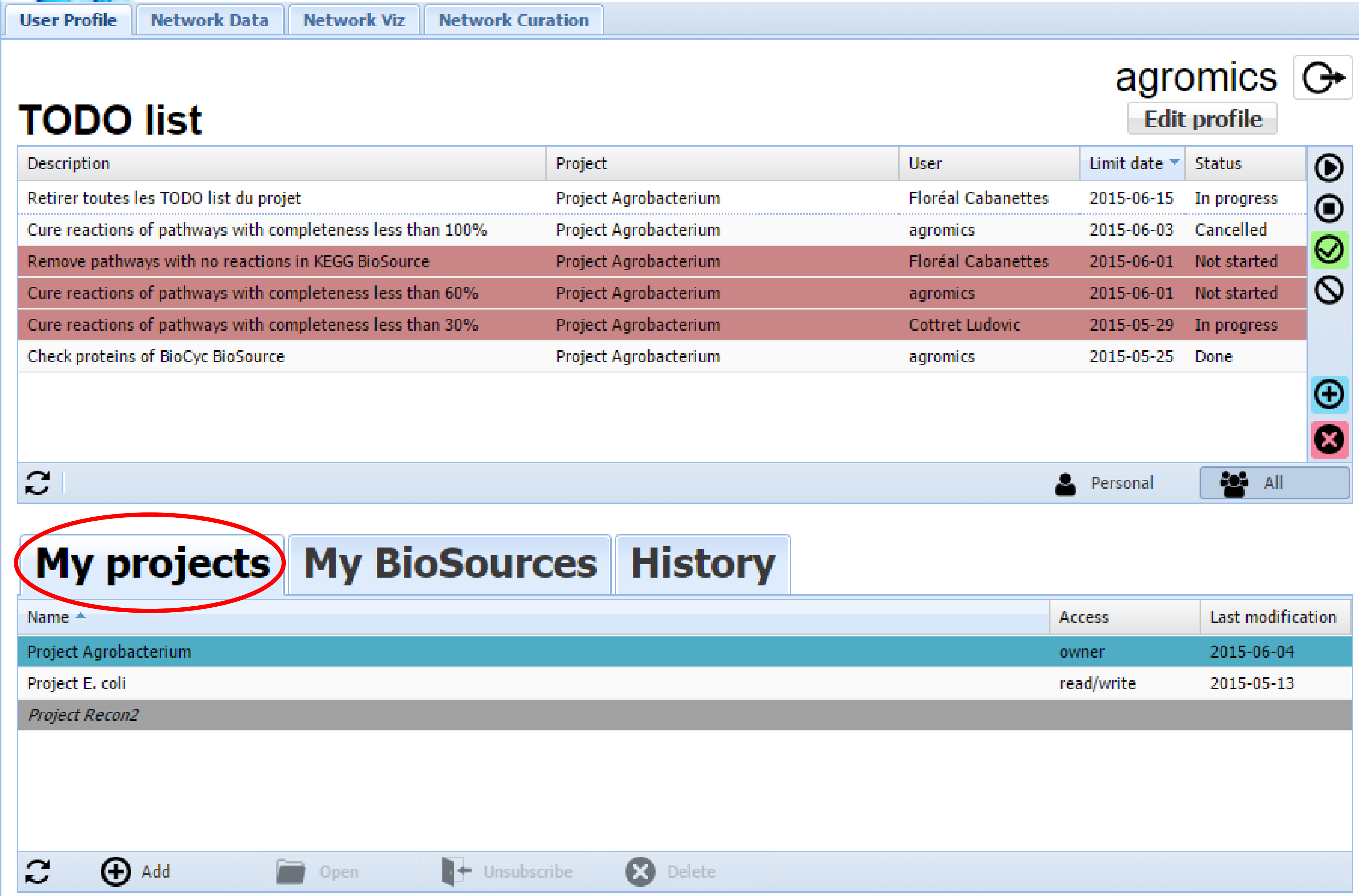
Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

3.1 Collaborative Annotation

3.1.3 Projects



TODO list

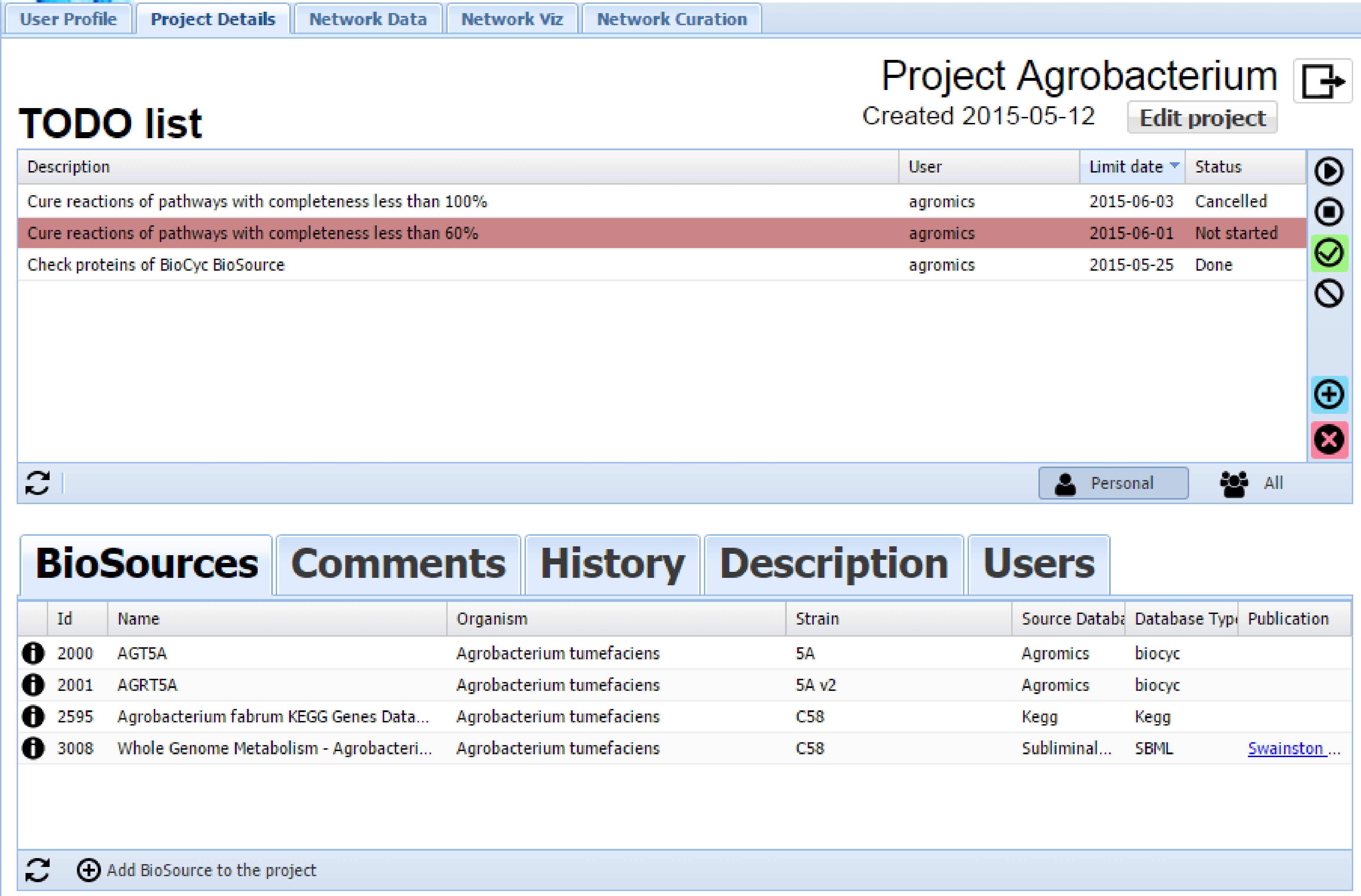
Description	Project	User	Limit date	Status
Retirer toutes les TODO list du projet	Project Agrobacterium	Floréal Cabanettes	2015-06-15	In progress
Cure reactions of pathways with completeness less than 100%	Project Agrobacterium	agromics	2015-06-03	Cancelled
Remove pathways with no reactions in KEGG BioSource	Project Agrobacterium	Floréal Cabanettes	2015-06-01	Not started
Cure reactions of pathways with completeness less than 60%	Project Agrobacterium	agromics	2015-06-01	Not started
Cure reactions of pathways with completeness less than 30%	Project Agrobacterium	Cottret Ludovic	2015-05-29	In progress
Check proteins of BioCyc BioSource	Project Agrobacterium	agromics	2015-05-25	Done

My projects | My BioSources | History

Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

3.1 COLLABORATIVE ANNOTATION

3.1.3 PROJECTS



Project Agrobacterium

Created 2015-05-12

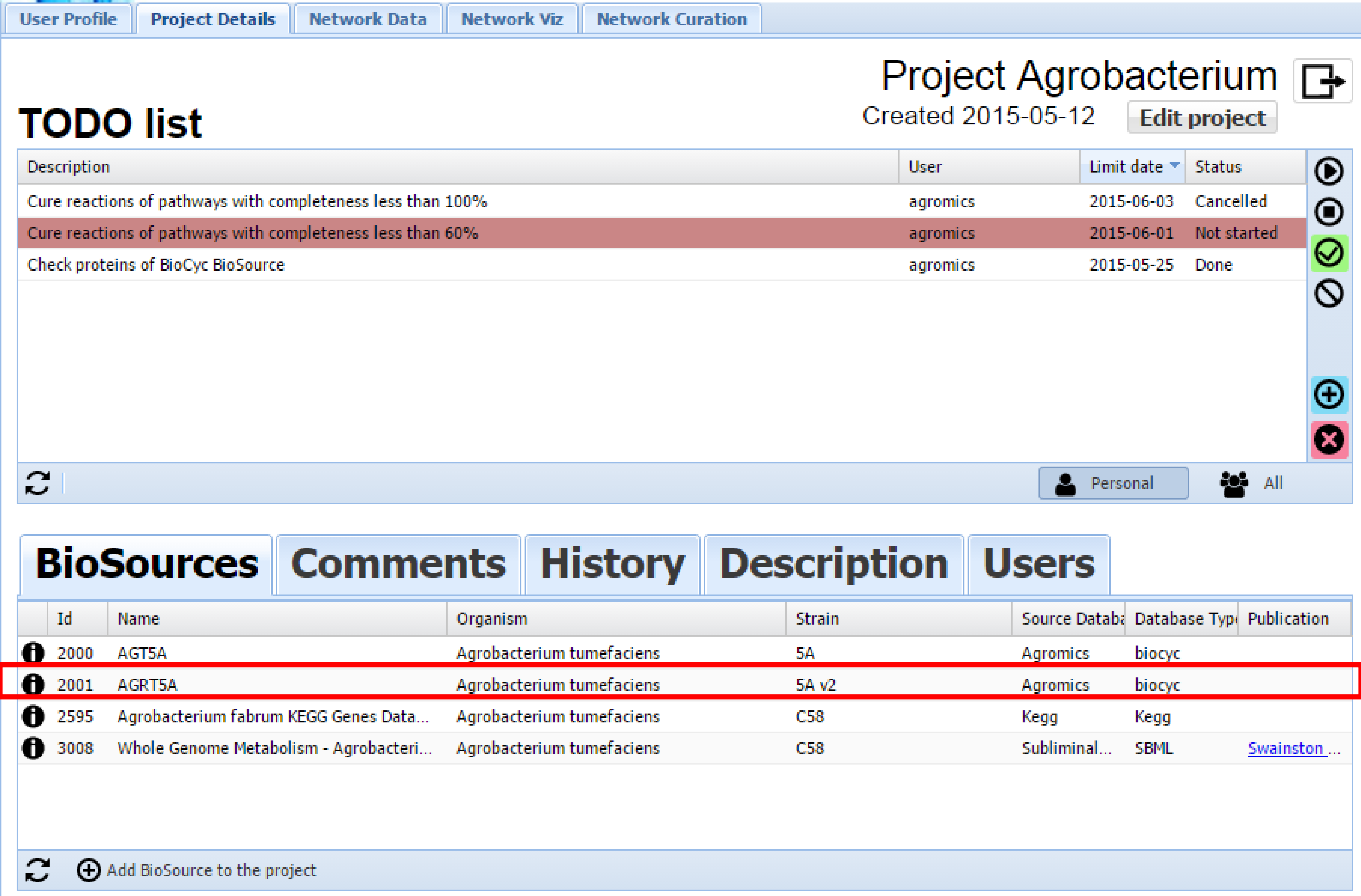
TODO list

Description	User	Limit date	Status
Cure reactions of pathways with completeness less than 100%	agromics	2015-06-03	Cancelled
Cure reactions of pathways with completeness less than 60%	agromics	2015-06-01	Not started
Check proteins of BioCyc BioSource	agromics	2015-05-25	Done

Id	Name	Organism	Strain	Source Databa	Database Typ	Publication
2000	AGT5A	Agrobacterium tumefaciens	5A	Agromics	biocyc	
2001	AGRT5A	Agrobacterium tumefaciens	5A v2	Agromics	biocyc	
2595	Agrobacterium fabrum KEGG Genes Data...	Agrobacterium tumefaciens	C58	Kegg	Kegg	
3008	Whole Genome Metabolism - Agrobacteri...	Agrobacterium tumefaciens	C58	Subliminal...	SBML	Swainston ...

3.1 COLLABORATIVE ANNOTATION

3.1.3 PROJECTS



Project Agrobacterium

Created 2015-05-12

TODO list

Description	User	Limit date	Status
Cure reactions of pathways with completeness less than 100%	agromics	2015-06-03	Cancelled
Cure reactions of pathways with completeness less than 60%	agromics	2015-06-01	Not started
Check proteins of BioCyc BioSource	agromics	2015-05-25	Done

Id	Name	Organism	Strain	Source Databa	Database Typ	Publication
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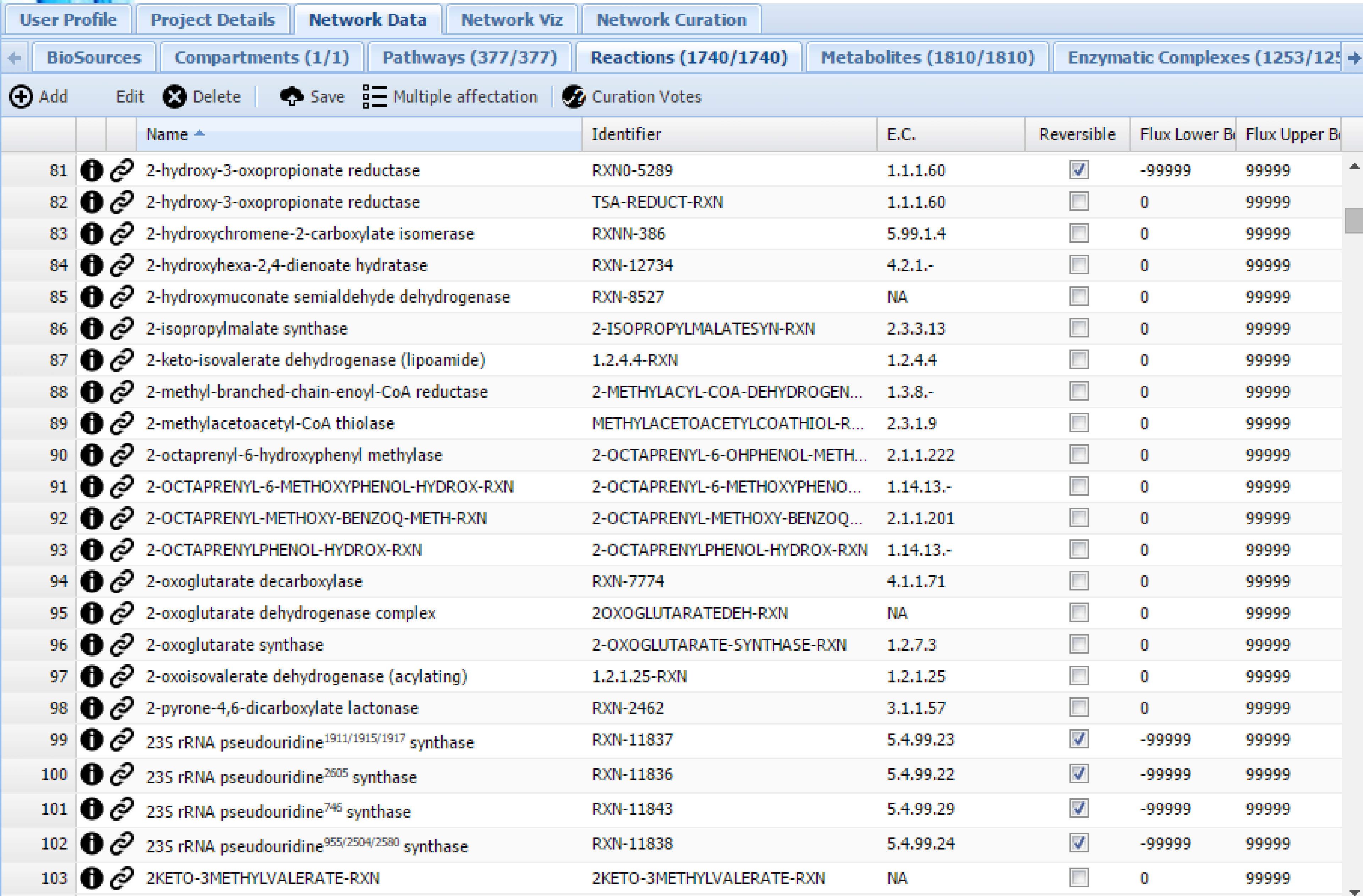
2595	Agrobacterium fabrum KEGG Genes Data...	Agrobacterium tumefaciens	C58	Kegg	Kegg	
3008	Whole Genome Metabolism - Agrobacteri...	Agrobacterium tumefaciens	C58	Subliminal...	SBML	Swainston ...

3. Presentation of *MetExplore* Annotation

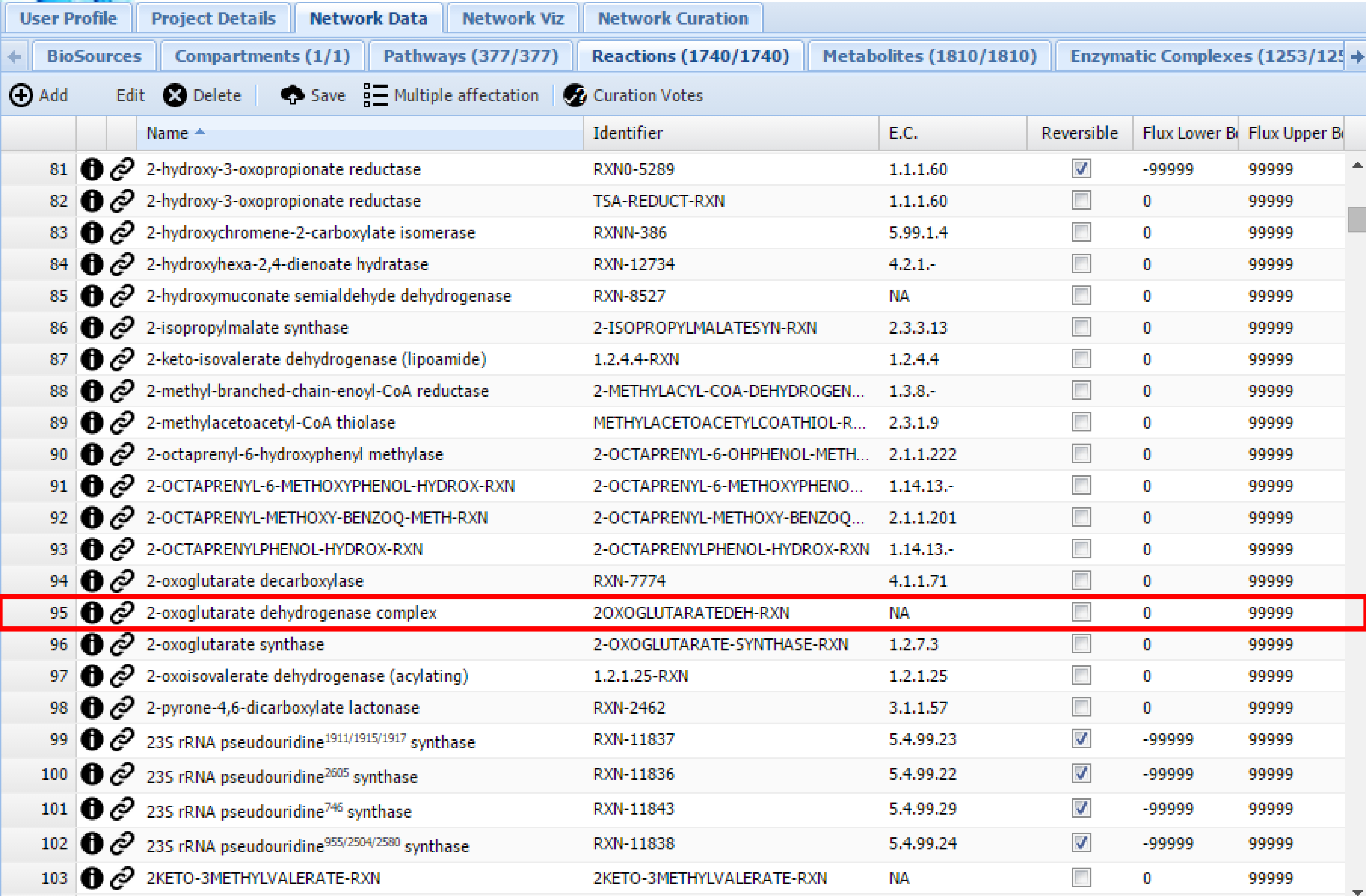


			Name ▲	Identifier	E.C.	Reversible	Flux Lower B	Flux Upper B
81	ℹ	🔗	2-hydroxy-3-oxopropionate reductase	RXN0-5289	1.1.1.60	☑	-99999	99999
82	ℹ	🔗	2-hydroxy-3-oxopropionate reductase	TSA-REDUCT-RXN	1.1.1.60	☐	0	99999
83	ℹ	🔗	2-hydroxychromene-2-carboxylate isomerase	RXNN-386	5.99.1.4	☐	0	99999
84	ℹ	🔗	2-hydroxyhexa-2,4-dienoate hydratase	RXN-12734	4.2.1.-	☐	0	99999
85	ℹ	🔗	2-hydroxymuconate semialdehyde dehydrogenase	RXN-8527	NA	☐	0	99999
86	ℹ	🔗	2-isopropylmalate synthase	2-ISOPROPYLMALATESYN-RXN	2.3.3.13	☐	0	99999
87	ℹ	🔗	2-keto-isovalerate dehydrogenase (lipoamide)	1.2.4.4-RXN	1.2.4.4	☐	0	99999
88	ℹ	🔗	2-methyl-branched-chain-enoyl-CoA reductase	2-METHYLACYL-COA-DEHYDROGEN...	1.3.8.-	☐	0	99999
89	ℹ	🔗	2-methylacetoacetyl-CoA thiolase	METHYLACETOACETYLCOATHIOL-R...	2.3.1.9	☐	0	99999
90	ℹ	🔗	2-octaprenyl-6-hydroxyphenyl methylase	2-OCTAPRENYL-6-OHPHENOL-METH...	2.1.1.222	☐	0	99999
91	ℹ	🔗	2-OCTAPRENYL-6-METHOXYPHENOL-HYDROX-RXN	2-OCTAPRENYL-6-METHOXYPHENO...	1.14.13.-	☐	0	99999
92	ℹ	🔗	2-OCTAPRENYL-METHOXY-BENZOQ-METH-RXN	2-OCTAPRENYL-METHOXY-BENZOQ...	2.1.1.201	☐	0	99999
93	ℹ	🔗	2-OCTAPRENYLPHENOL-HYDROX-RXN	2-OCTAPRENYLPHENOL-HYDROX-RXN	1.14.13.-	☐	0	99999
94	ℹ	🔗	2-oxoglutarate decarboxylase	RXN-7774	4.1.1.71	☐	0	99999
95	ℹ	🔗	2-oxoglutarate dehydrogenase complex	2OXOGLUTARATEDEH-RXN	NA	☐	0	99999
96	ℹ	🔗	2-oxoglutarate synthase	2-OXOGLUTARATE-SYNTHASE-RXN	1.2.7.3	☐	0	99999
97	ℹ	🔗	2-oxoisovalerate dehydrogenase (acylating)	1.2.1.25-RXN	1.2.1.25	☐	0	99999
98	ℹ	🔗	2-pyrone-4,6-dicarboxylate lactonase	RXN-2462	3.1.1.57	☐	0	99999
99	ℹ	🔗	23S rRNA pseudouridine$^{1911/1915/1917}$ synthase	RXN-11837	5.4.99.23	☑	-99999	99999
100	ℹ	🔗	23S rRNA pseudouridine^{2605} synthase	RXN-11836	5.4.99.22	☑	-99999	99999
101	ℹ	🔗	23S rRNA pseudouridine^{746} synthase	RXN-11843	5.4.99.29	☑	-99999	99999
102	ℹ	🔗	23S rRNA pseudouridine$^{955/2504/2580}$ synthase	RXN-11838	5.4.99.24	☑	-99999	99999
103	ℹ	🔗	2KETO-3METHYLVALERATE-RXN	2KETO-3METHYLVALERATE-RXN	NA	☐	0	99999

OVERVIEW

1. Introduction
2. Software development strategy
3. **Presentation of *MetExplore Annotation***
    - 3.1. Collaborative annotation
    - **3.2. Tools for highlighting mistakes in a metabolic network**
    - 3.3. Summarize opinions about the metabolic network
4. Conclusion and future prospects

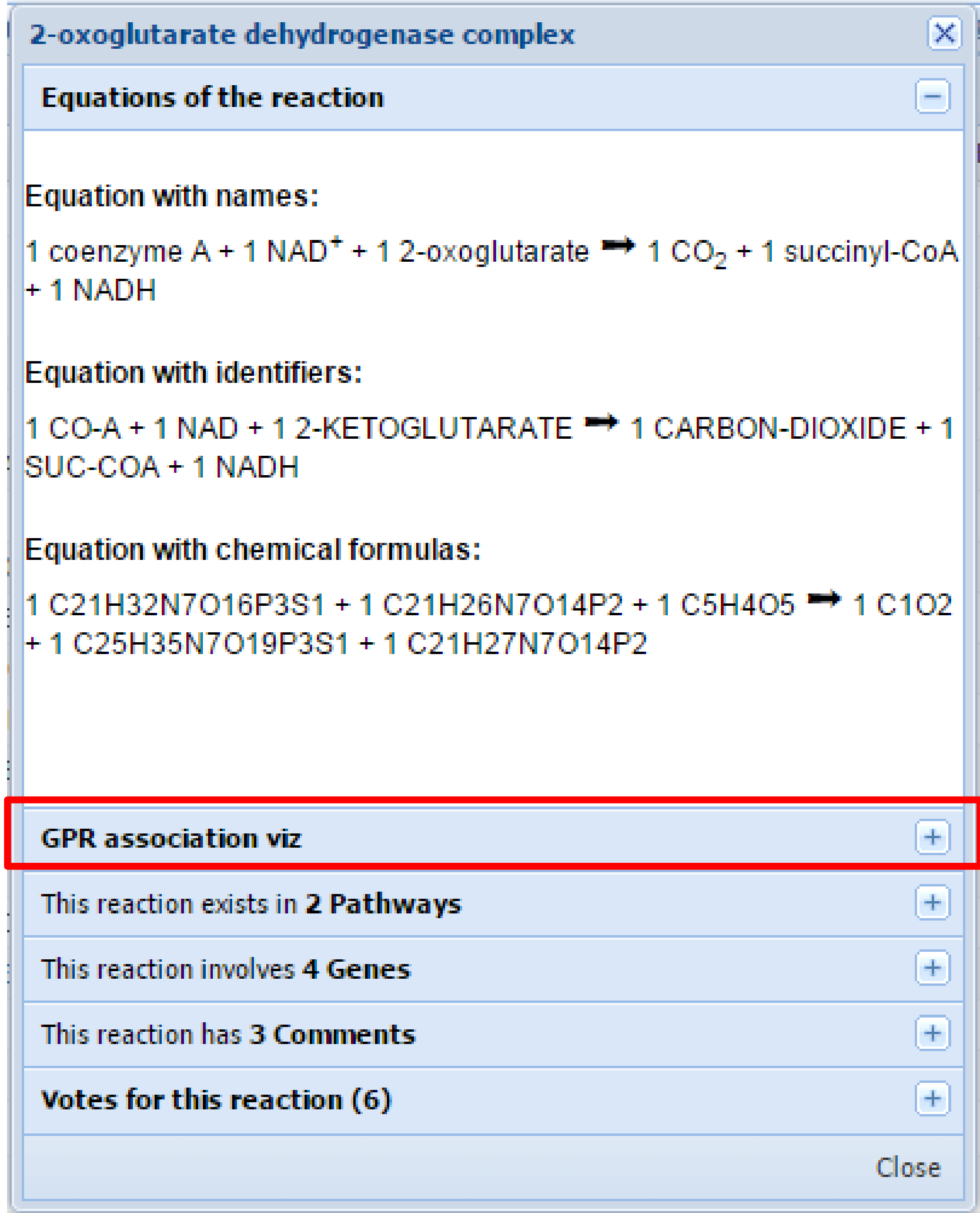
3.2. TOOLS FOR HIGHLIGHTING MISTAKES IN A METABOLIC NETWORK



	Name	Identifier	E.C.	Reversible	Flux Lower B	Flux Upper B
81	2-hydroxy-3-oxopropionate reductase	RXN0-5289	1.1.1.60	☑	-99999	99999
82	2-hydroxy-3-oxopropionate reductase	TSA-REDUCT-RXN	1.1.1.60	☐	0	99999
83	2-hydroxychromene-2-carboxylate isomerase	RXNN-386	5.99.1.4	☐	0	99999
84	2-hydroxyhexa-2,4-dienoate hydratase	RXN-12734	4.2.1.-	☐	0	99999
85	2-hydroxymuconate semialdehyde dehydrogenase	RXN-8527	NA	☐	0	99999
86	2-isopropylmalate synthase	2-ISOPROPYLMALATESYN-RXN	2.3.3.13	☐	0	99999
87	2-keto-isovalerate dehydrogenase (lipoamide)	1.2.4.4-RXN	1.2.4.4	☐	0	99999
88	2-methyl-branched-chain-enoyl-CoA reductase	2-METHYLACYL-COA-DEHYDROGEN...	1.3.8.-	☐	0	99999
89	2-methylacetoacetyl-CoA thiolase	METHYLACETOACETYLCOATHIOL-R...	2.3.1.9	☐	0	99999
90	2-octaprenyl-6-hydroxyphenyl methylase	2-OCTAPRENYL-6-OHPHENOL-METH...	2.1.1.222	☐	0	99999
91	2-OCTAPRENYL-6-METHOXYPHENOL-HYDROX-RXN	2-OCTAPRENYL-6-METHOXYPHENO...	1.14.13.-	☐	0	99999
92	2-OCTAPRENYL-METHOXY-BENZOQ-METH-RXN	2-OCTAPRENYL-METHOXY-BENZOQ...	2.1.1.201	☐	0	99999
93	2-OCTAPRENYLPHENOL-HYDROX-RXN	2-OCTAPRENYLPHENOL-HYDROX-RXN	1.14.13.-	☐	0	99999
94	2-oxoglutarate decarboxylase	RXN-7774	4.1.1.71	☐	0	99999
95	2-oxoglutarate dehydrogenase complex	2OXOGLUTARATEDEH-RXN	NA	☐	0	99999
96	2-oxoglutarate synthase	2-OXOGLUTARATE-SYNTHASE-RXN	1.2.7.3	☐	0	99999
97	2-oxoisovalerate dehydrogenase (acylating)	1.2.1.25-RXN	1.2.1.25	☐	0	99999
98	2-pyrone-4,6-dicarboxylate lactonase	RXN-2462	3.1.1.57	☐	0	99999
99	23S rRNA pseudouridine$^{1911/1915/1917}$ synthase	RXN-11837	5.4.99.23	☑	-99999	99999
100	23S rRNA pseudouridine^{2605} synthase	RXN-11836	5.4.99.22	☑	-99999	99999
101	23S rRNA pseudouridine^{746} synthase	RXN-11843	5.4.99.29	☑	-99999	99999
102	23S rRNA pseudouridine$^{955/2504/2580}$ synthase	RXN-11838	5.4.99.24	☑	-99999	99999
103	2KETO-3METHYLVALERATE-RXN	2KETO-3METHYLVALERATE-RXN	NA	☐	0	99999

3.2. TOOLS FOR HIGHLIGHTING MISTAKES IN A METABOLIC NETWORK

3.2.1 GPR ASSOCIATION VISUALIZATION



2-oxoglutarate dehydrogenase complex

Equations of the reaction

Equation with names:

1 coenzyme A + 1 NAD^+ + 1 2-oxoglutarate → 1 CO_2 + 1 succinyl-CoA + 1 NADH

Equation with identifiers:

1 CO-A + 1 NAD + 1 2-KETOGLUTARATE → 1 CARBON-DIOXIDE + 1 SUC-COA + 1 NADH

Equation with chemical formulas:

1 C21H32N7O16P3S1 + 1 C21H26N7O14P2 + 1 C5H4O5 → 1 C1O2 + 1 C25H35N7O19P3S1 + 1 C21H27N7O14P2

GPR association viz

This reaction exists in **2 Pathways**

This reaction involves **4 Genes**

This reaction has **3 Comments**

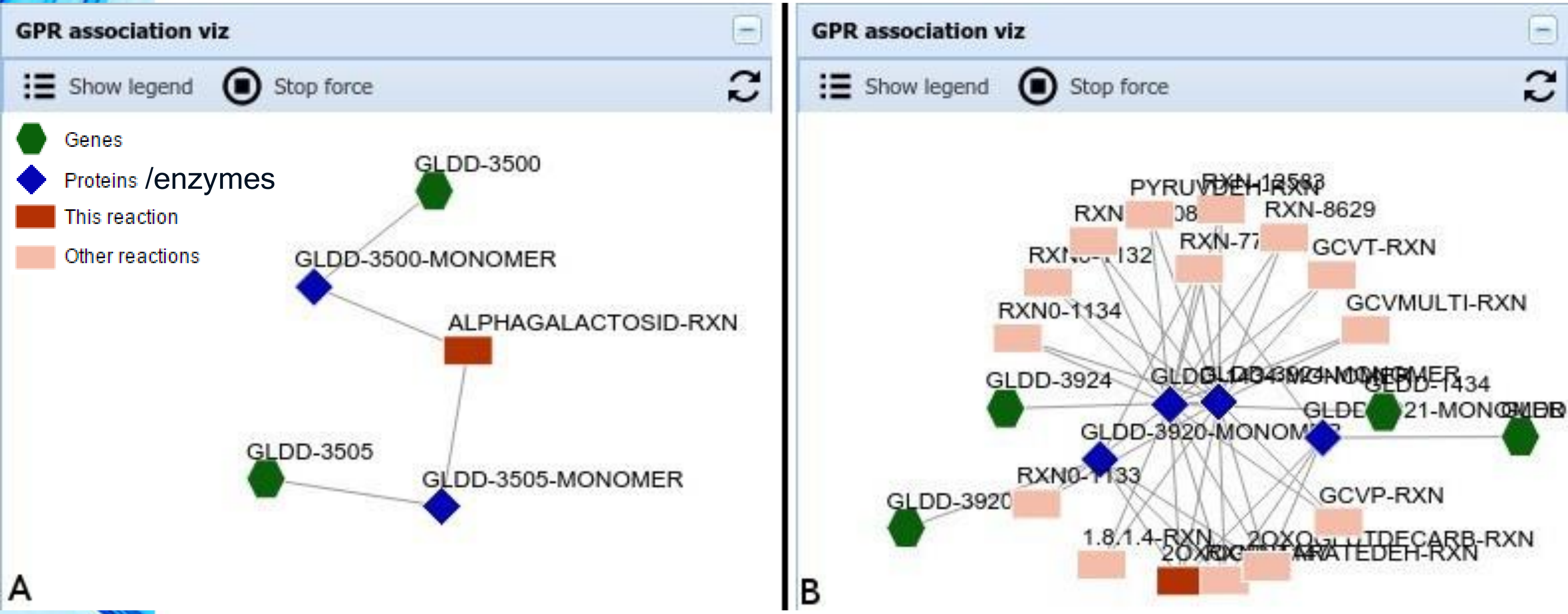
Votes for this reaction (6)

3.2. TOOLS FOR HIGHLIGHTING MISTAKES IN A METABOLIC NETWORK

3.2.1 GPR ASSOCIATION VISUALIZATION

Goal:

To visualize links between Genes, Proteins and Reactions, and highlight potentially badly annotated reactions



A : Expected GPR association

B : A group of enzymes catalyzes a lot of reactions !

3.2. TOOLS FOR HIGHLIGHTING MISTAKES IN A METABOLIC NETWORK

3.2.2 COMPLETENESS OF PATHWAYS

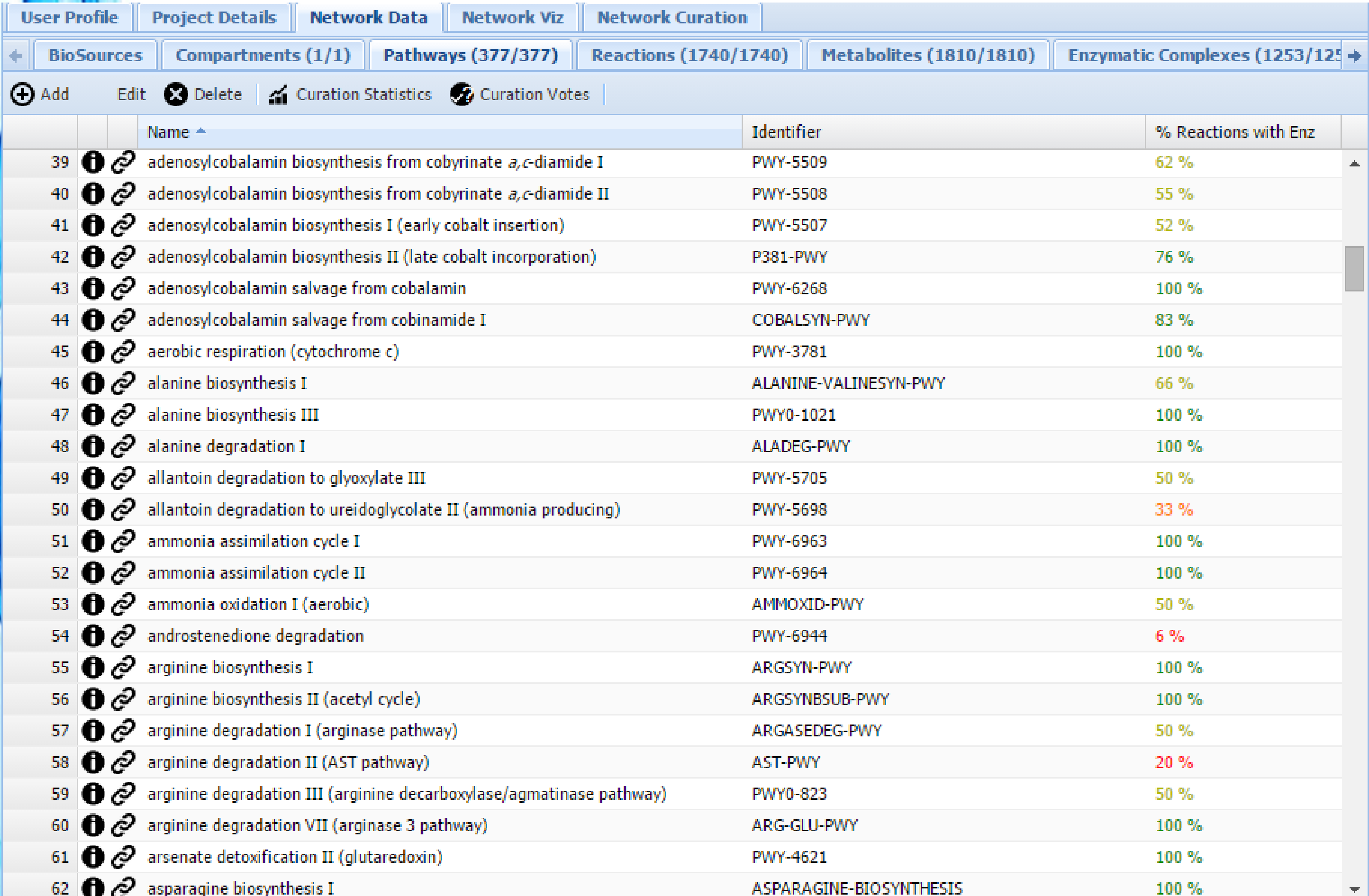
The problem:

- *Automatic reconstruction adds pathways if enough of their reactions are present*
- *Some pathways may be false positives*

→ **Create tools to detect them!**

3.2. TOOLS FOR HIGHLIGHTING MISTAKES IN A METABOLIC NETWORK

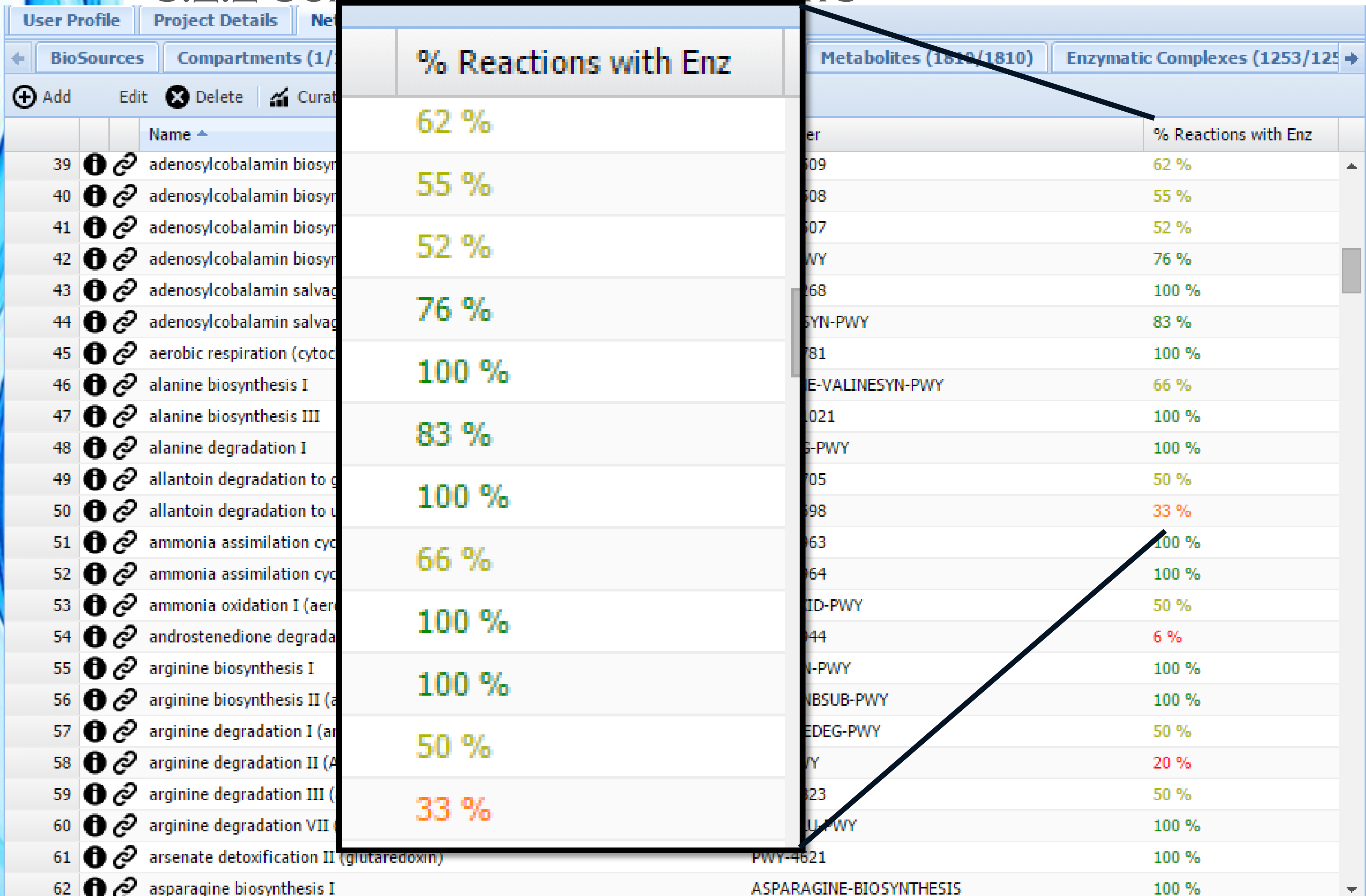
3.2.2 COMPLETENESS OF PATHWAYS



			Name ▲	Identifier	% Reactions with Enz
39	ℹ	🔗	adenosylcobalamin biosynthesis from cobyrinate *a*,*c*-diamide I	PWY-5509	62 %
40	ℹ	🔗	adenosylcobalamin biosynthesis from cobyrinate *a*,*c*-diamide II	PWY-5508	55 %
41	ℹ	🔗	adenosylcobalamin biosynthesis I (early cobalt insertion)	PWY-5507	52 %
42	ℹ	🔗	adenosylcobalamin biosynthesis II (late cobalt incorporation)	P381-PWY	76 %
43	ℹ	🔗	adenosylcobalamin salvage from cobalamin	PWY-6268	100 %
44	ℹ	🔗	adenosylcobalamin salvage from cobinamide I	COBALSYN-PWY	83 %
45	ℹ	🔗	aerobic respiration (cytochrome c)	PWY-3781	100 %
46	ℹ	🔗	alanine biosynthesis I	ALANINE-VALINESYN-PWY	66 %
47	ℹ	🔗	alanine biosynthesis III	PWY0-1021	100 %
48	ℹ	🔗	alanine degradation I	ALADEG-PWY	100 %
49	ℹ	🔗	allantoin degradation to glyoxylate III	PWY-5705	50 %
50	ℹ	🔗	allantoin degradation to ureidoglycolate II (ammonia producing)	PWY-5698	33 %
51	ℹ	🔗	ammonia assimilation cycle I	PWY-6963	100 %
52	ℹ	🔗	ammonia assimilation cycle II	PWY-6964	100 %
53	ℹ	🔗	ammonia oxidation I (aerobic)	AMMOXID-PWY	50 %
54	ℹ	🔗	androstenedione degradation	PWY-6944	6 %
55	ℹ	🔗	arginine biosynthesis I	ARGSYN-PWY	100 %
56	ℹ	🔗	arginine biosynthesis II (acetyl cycle)	ARGSYNBSUB-PWY	100 %
57	ℹ	🔗	arginine degradation I (arginase pathway)	ARGASEDEG-PWY	50 %
58	ℹ	🔗	arginine degradation II (AST pathway)	AST-PWY	20 %
59	ℹ	🔗	arginine degradation III (arginine decarboxylase/agmatinase pathway)	PWY0-823	50 %
60	ℹ	🔗	arginine degradation VII (arginase 3 pathway)	ARG-GLU-PWY	100 %
61	ℹ	🔗	arsenate detoxification II (glutaredoxin)	PWY-4621	100 %
62	ℹ	🔗	asparagine biosynthesis I	ASPARAGINE-BIOSYNTHESIS	100 %

3.2. Tools for highlighting mistakes in a metabolic network

3.2.2 Completeness of pathways



	Name	er	% Reactions with Enz
39	adenosylcobalamin biosyn	09	62 %
40	adenosylcobalamin biosyn	08	55 %
41	adenosylcobalamin biosyn	07	52 %
42	adenosylcobalamin biosyn	WY	76 %
43	adenosylcobalamin salvag	68	100 %
44	adenosylcobalamin salvag	SYN-PWY	83 %
45	aerobic respiration (cytoc	81	100 %
46	alanine biosynthesis I	E-VALINESYN-PWY	66 %
47	alanine biosynthesis III	1021	100 %
48	alanine degradation I	G-PWY	100 %
49	allantoin degradation to g	05	50 %
50	allantoin degradation to u	98	33 %
51	ammonia assimilation cyc	63	100 %
52	ammonia assimilation cyc	64	100 %
53	ammonia oxidation I (aer	ID-PWY	50 %
54	androstenedione degrada	44	6 %
55	arginine biosynthesis I	N-PWY	100 %
56	arginine biosynthesis II (a	NBSUB-PWY	100 %
57	arginine degradation I (ar	EDEG-PWY	50 %
58	arginine degradation II (A	Y	20 %
59	arginine degradation III (	23	50 %
60	arginine degradation VII (	U-PWY	100 %
61	arsenate detoxification II (glutaredoxin)	PWY-4621	100 %
62	asparagine biosynthesis I	ASPARAGINE-BIOSYNTHESIS	100 %

% Reactions with Enz
62 %
55 %
52 %
76 %
100 %
83 %
100 %
66 %
100 %
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50 %
33 %

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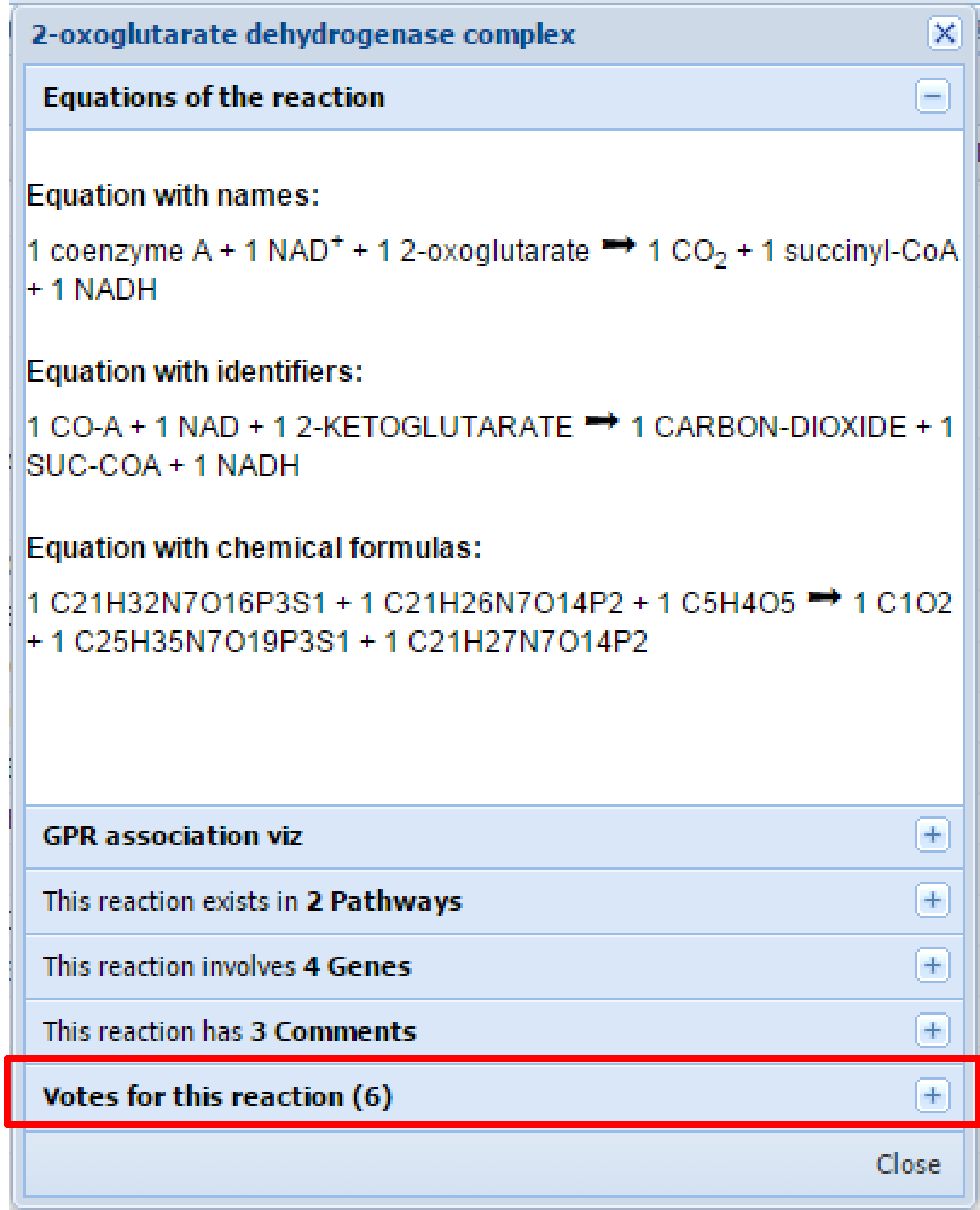
3.3. RESUME OPINIONS ABOUT THE METABOLIC NETWORK

3.3.1 VOTES FOR AN OBJECT OF THE METABOLIC NETWORK

Goal:

To combine and summarize the opinions of all the specialists in an interface



2-oxoglutarate dehydrogenase complex

Equations of the reaction

Equation with names:

1 coenzyme A + 1 NAD^+ + 1 2-oxoglutarate ➡ 1 CO_2 + 1 succinyl-CoA + 1 NADH

Equation with identifiers:

1 CO-A + 1 NAD + 1 2-KETOGLUTARATE ➡ 1 CARBON-DIOXIDE + 1 SUC-COA + 1 NADH

Equation with chemical formulas:

1 $C_{21}H_{32}N_7O_{16}P_3S_1$ + 1 $C_{21}H_{26}N_7O_{14}P_2$ + 1 $C_5H_4O_5$ ➡ 1 C_1O_2 + 1 $C_{25}H_{35}N_7O_{19}P_3S_1$ + 1 $C_{21}H_{27}N_7O_{14}P_2$

GPR association viz

This reaction exists in **2 Pathways**

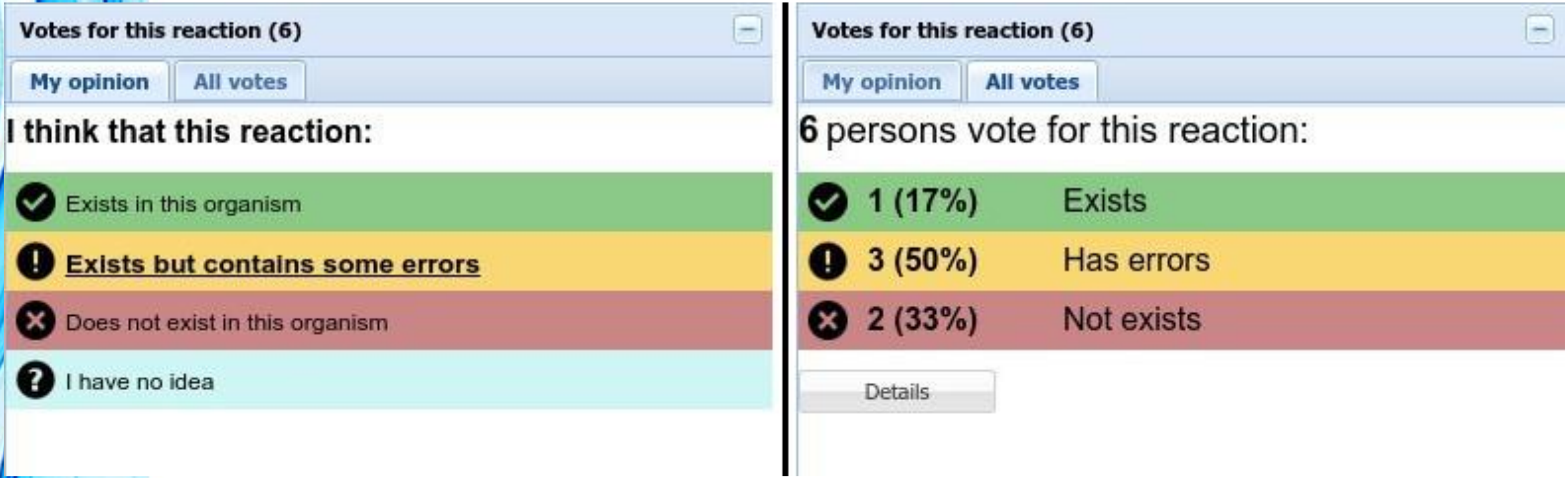
This reaction involves **4 Genes**

This reaction has **3 Comments**

Votes for this reaction (6)

3.3. Resume opinions about the metabolic network

3.3.1 Votes for an object of the metabolic network



Votes for this reaction (6)

I think that this reaction:

✓ Exists in this organism

! **Exists but contains some errors**

✕ Does not exist in this organism

? I have no idea

Votes for this reaction (6)

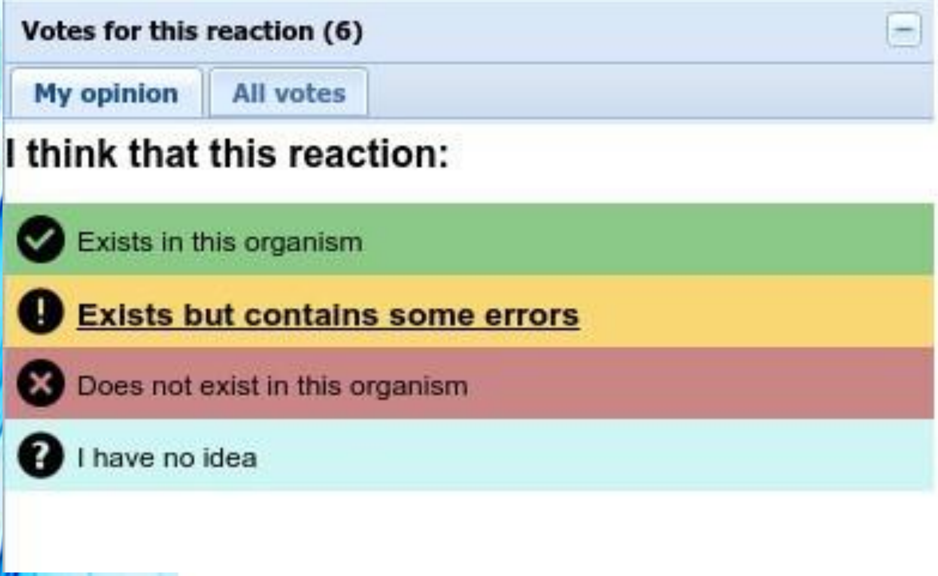
6 persons vote for this reaction:

✓	1 (17%)	Exists
!	3 (50%)	Has errors
✕	2 (33%)	Not exists

→ Organizers view a summary of all votes and change objects in consequence in the Database

3.3. Resume opinions about the metabolic network

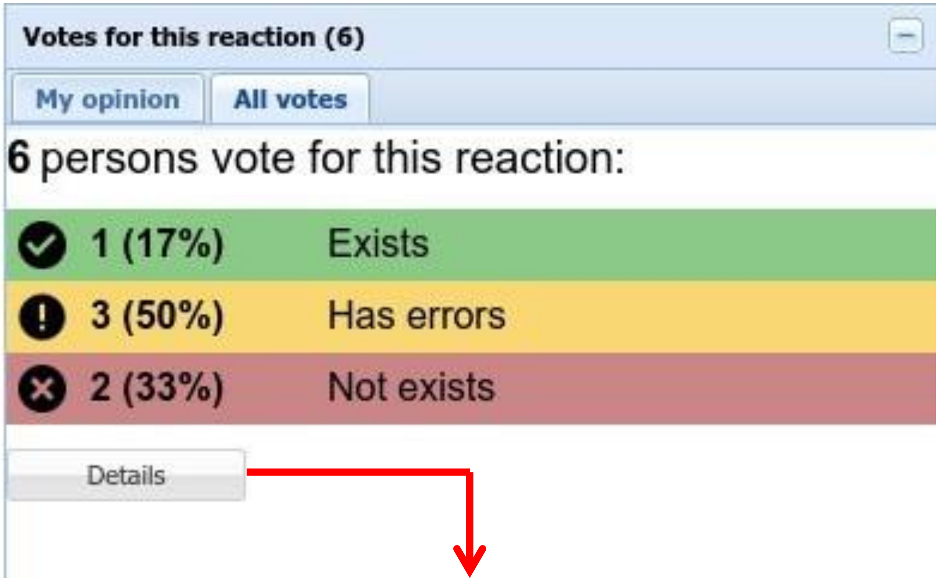
3.3.1 Votes for an object of the metabolic network



Votes for this reaction (6)

I think that this reaction:

- ✓ Exists in this organism
- ! **Exists but contains some errors**
- ✗ Does not exist in this organism
- ? I have no idea



Votes for this reaction (6)

6 persons vote for this reaction:

✓	1 (17%)	Exists
!	3 (50%)	Has errors
✗	2 (33%)	Not exists

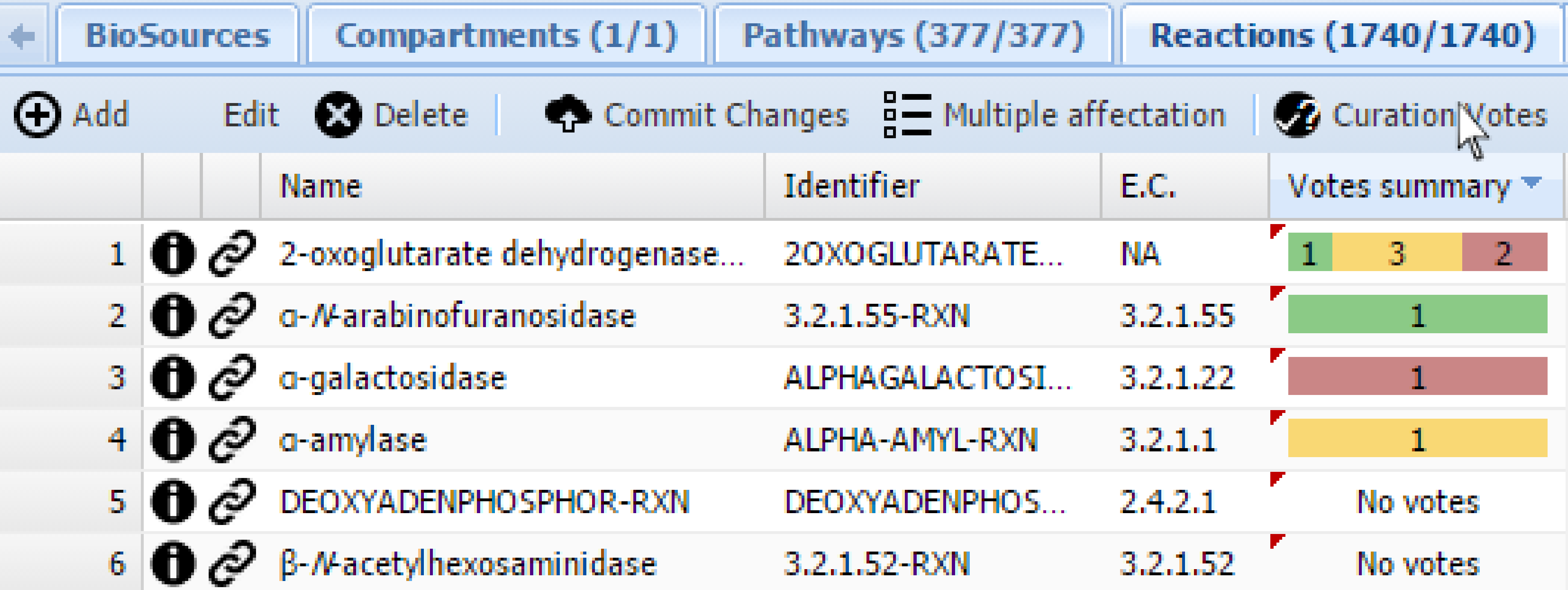
Details of voters

	Vote	Name of the voter
✓	Exists	Floréal Cabanettes
!	Has errors	agromics
!	Has errors	Cottret Ludovic
!	Has errors	Fabien
✗	Not exists	Nathalie Poupin
✗	Not exists	Merlet Benjamin

→ Organizers view a summary of all votes and change objects in consequence in the Database

3.3. RESUME OPINIONS ABOUT THE METABOLIC NETWORK

3.3.1 VOTES FOR AN OBJECT OF THE METABOLIC NETWORK



			Name	Identifier	E.C.	Votes summary
1	ℹ	🔗	2-oxoglutarate dehydrogenase...	2OXOGLUTARATE...	NA	🟩 1 🟨 3 🟥 2
2	ℹ	🔗	α-*N*-arabinofuranosidase	3.2.1.55-RXN	3.2.1.55	🟩 1
3	ℹ	🔗	α-galactosidase	ALPHAGALACTOSI...	3.2.1.22	🟥 1
4	ℹ	🔗	α-amylase	ALPHA-AMYL-RXN	3.2.1.1	🟨 1
5	ℹ	🔗	DEOXYADENPHOSPHOR-RXN	DEOXYADENPHOS...	2.4.2.1	No votes
6	ℹ	🔗	β-*N*-acetylhexosaminidase	3.2.1.52-RXN	3.2.1.52	No votes

→ Organizers have easy access to objects that have votes, with a summary for each

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3. CONCLUSION

I have improved *MetExplore Annotation* with new crucial features:

- Creation of a **collaborative** interface
- **Access level** system → manage access to a *Project*
- Tools to **evaluate** metabolic networks
- **Give** and **summarize** opinions
- Make an **intuitive** tool → good human-computer interaction

3. CONCLUSION

	MetExplore + M. Annotation	Pathway tools	rBioNet	GEMSiRV	Raven Toolbox	Sublim. Toolbox
Automatic reconstruction	🟥	🟩	🟥	🟩	🟩	🟥
Manual curation	🟩	🟩	🟩	🟩	🟩	🟩
SBML Import/Export	🟩	🟥	🟩	🟩 / 🟥	🟩	🟩
Excel Import/Export	🟨 / 🟩	🟥	🟩	🟩 / 🟥	🟩	🟥
Direct import from KEGG	🟩	🟥	🟥	🟥	🟥	🟩
Direct import from BioCyc	🟥	🟥	🟥	🟥	🟥	🟩
Collaborative annotation**	🟩	🟩	🟥	🟥	🟥	🟥
Projects management	🟩	🟥	🟥	🟥	🟥	🟥
Simulations on networks	🟩	🟥	🟥	🟩	🟩	🟥
Evaluation tools***	🟩	🟥	🟥	🟥	🟥	🟥
Network visualization	🟩	🟩	🟩	🟩	🟩	🟥
Mapping on networks	🟩	🟩	🟥	🟥	🟥	🟥
Cytoscape export	🟩	🟥	🟥	🟥	🟩	🟥

3. FUTURE PROSPECTS

Add new tools for facilitating Metabolic Network Curation:

- Gap Filling ➔ detection / curation tools
- Tools to compare several networks
- Tools to propagate network to related species
- Be able to undo any changes on networks
- …

→ **Better accuracy when reconstructing networks**

→ **Have a better network in less time**

→ Jamboree 16 & 17 June

THANKS TO…

My supervisors, **Ludovic Cottret** and **Céline Lavire** for allowing me to work on such an exciting and instructive subject!

Ludovic Cottret for all the advice he has given me.

All the MetExplore team, I have learned a lot from you :
Ludovic Cottret, **Benjamin Merlet**, **Florence Vinson**, **Fabien Jourdan**, **Maxime Chazalviel**, **Nathalie Poupin**, **Clément Frainay**, **Yoann Gloaguen**, **Sanu Shameer**, …

And all the Bioinformatic team of the LIPM (**Jérôme Gouzy** *et al*) for welcoming me!

Some questions?

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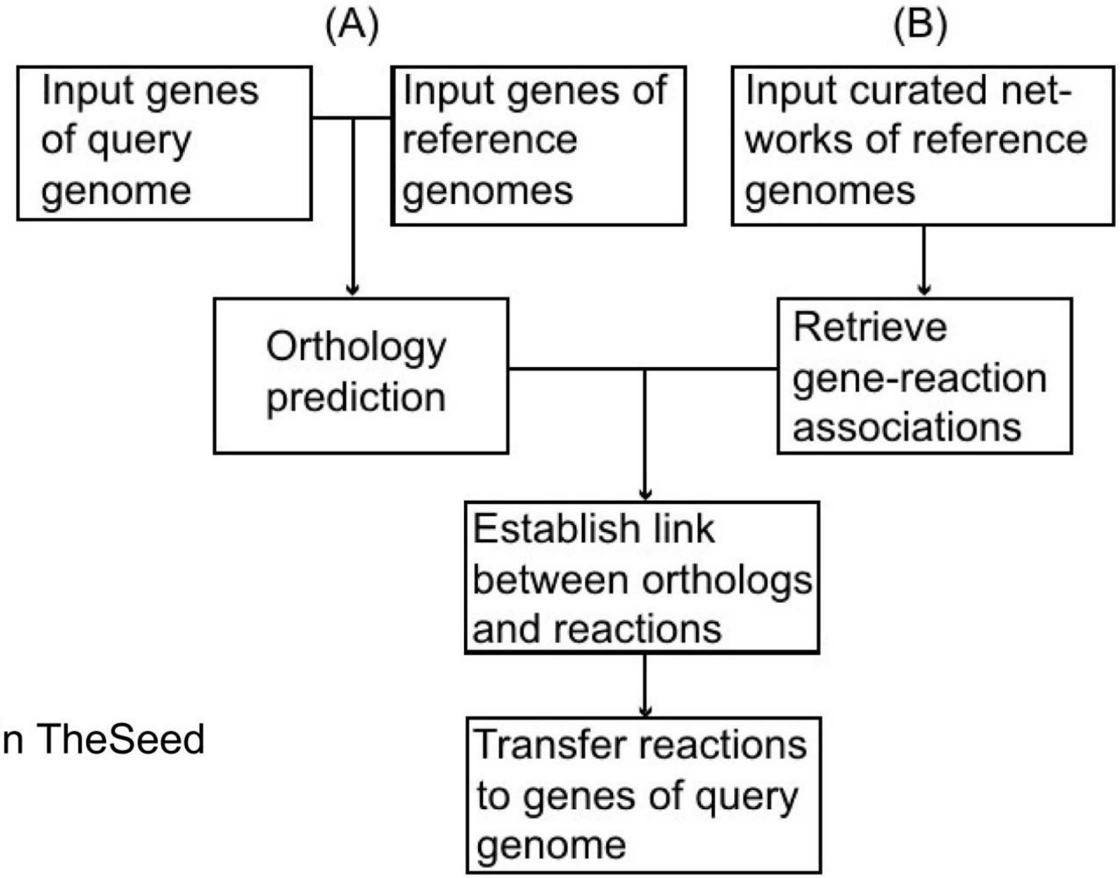
PROPAGATION FROM CURATED METABOLIC MODELS



Integrated in TheSeed

Accelerating the reconstruction of genome-scale metabolic networks. Notebaart et al. 2006.

Source : L. Cottret presentation

Figure 2. Organisation des données sous ***MetExplore***. *En gris, les relations secondaires.*

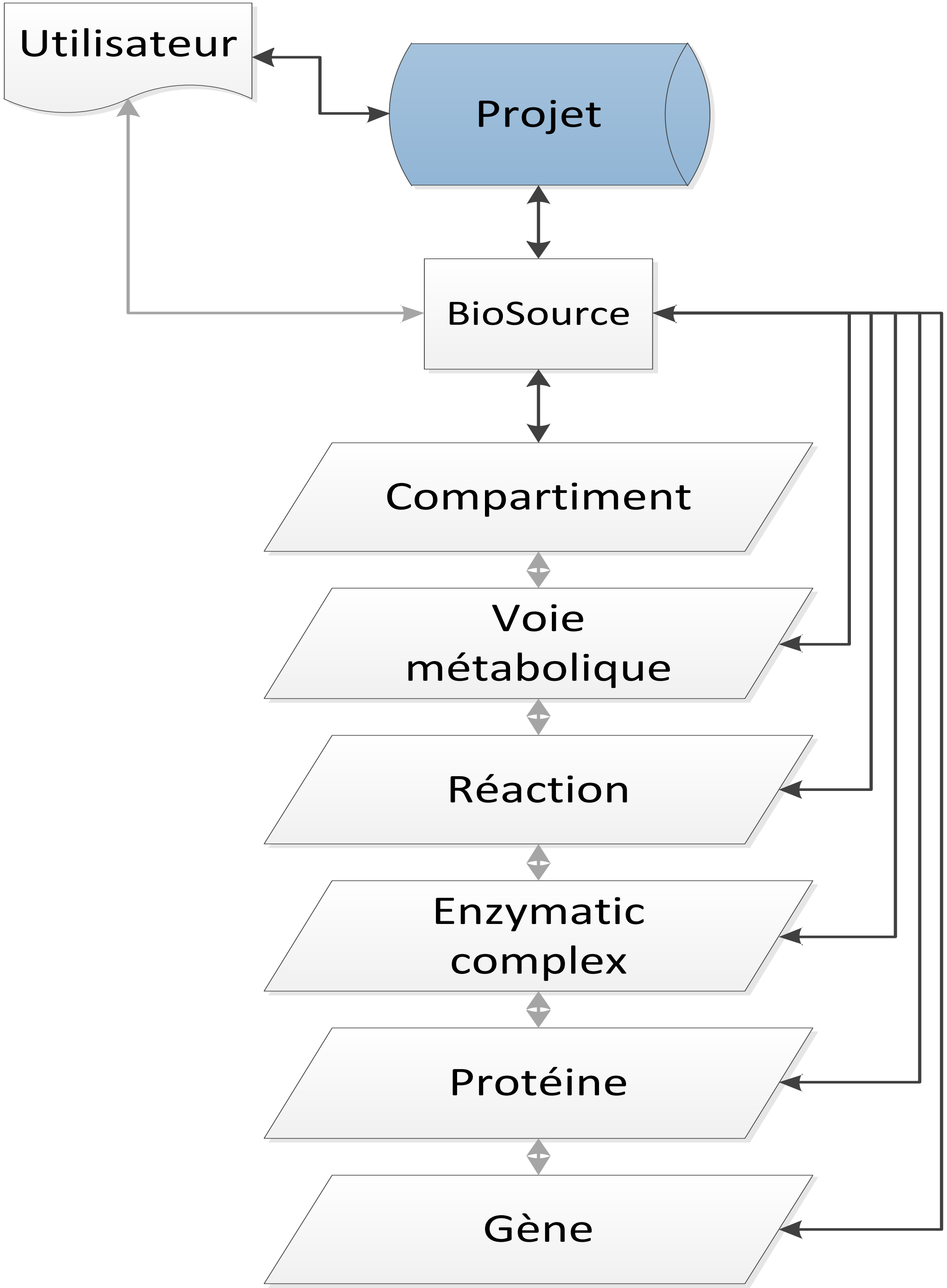
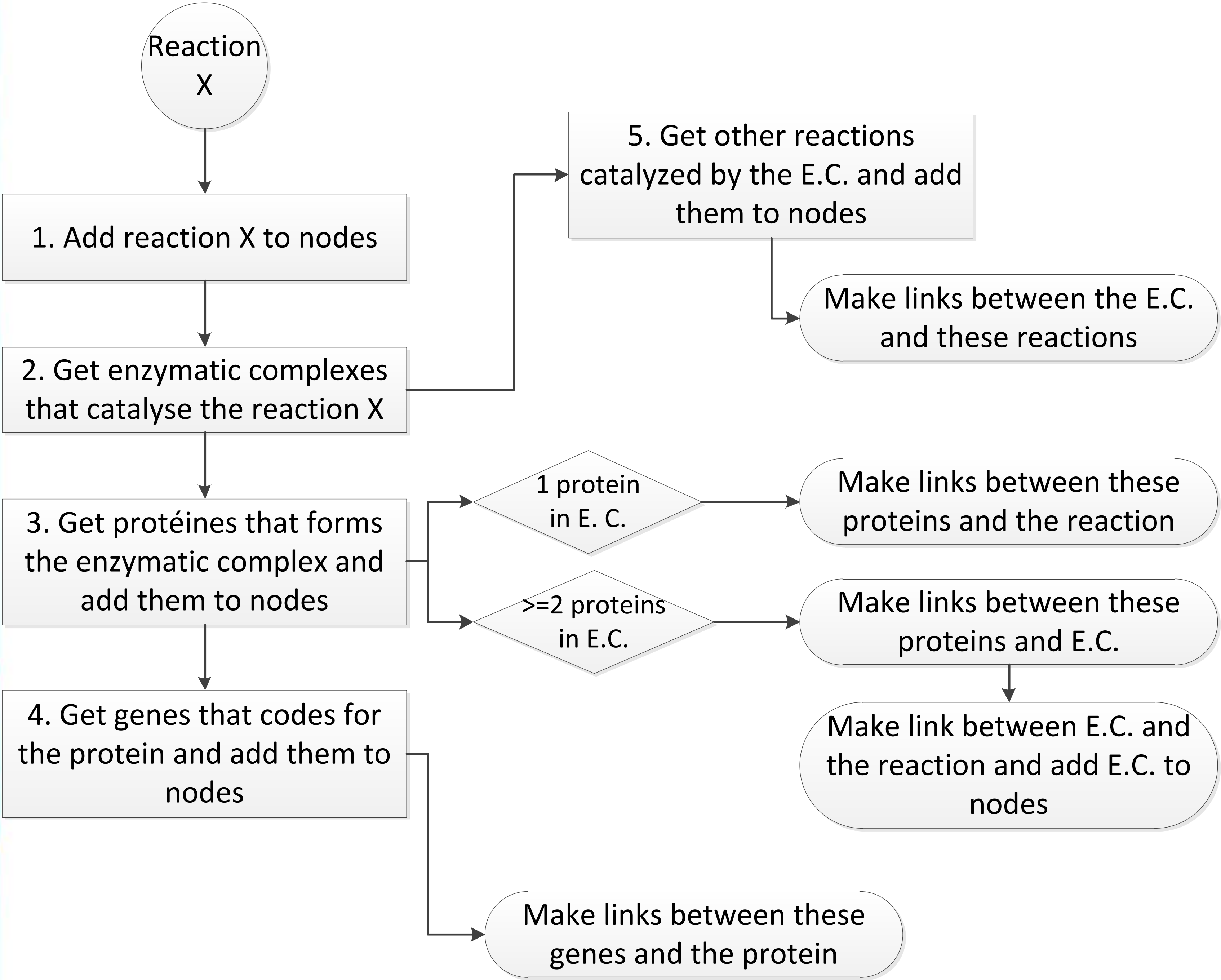


Figure 5. Chargement des données de l’association GPR. *E.C. : enzymatic complex.*



Reaction X

1. Add reaction X to nodes

2. Get enzymatic complexes that catalyse the reaction X

3. Get protéines that forms the enzymatic complex and add them to nodes

4. Get genes that codes for the protein and add them to nodes

5. Get other reactions catalyzed by the E.C. and add them to nodes

Make links between the E.C. and these reactions

1 protein in E. C.

Make links between these proteins and the reaction

>=2 proteins in E.C.

Make links between these proteins and E.C.

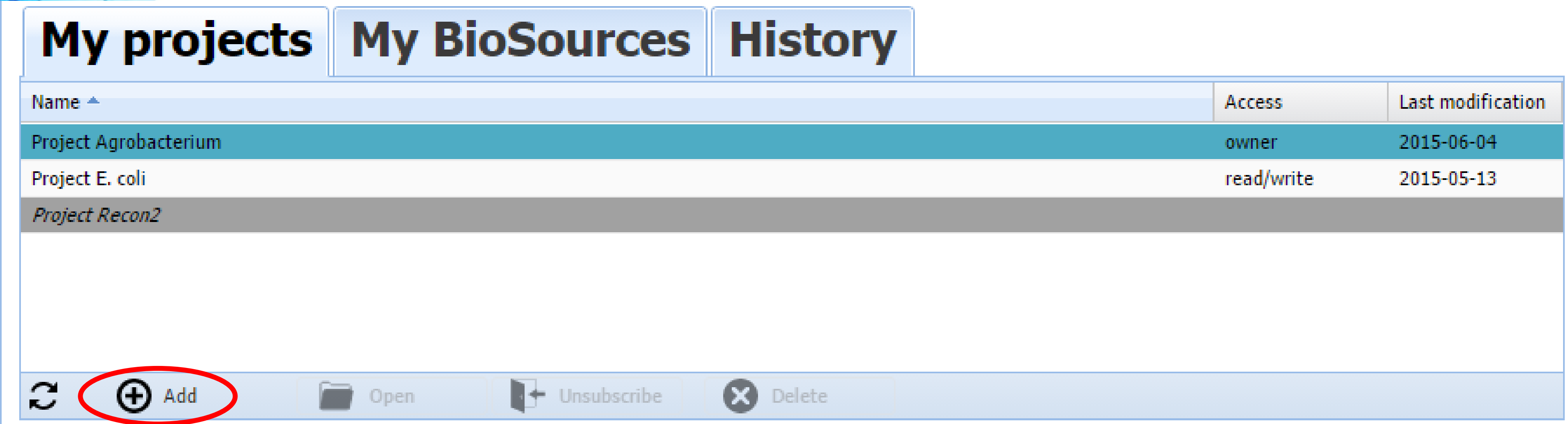
Make link between E.C. and the reaction and add E.C. to nodes

Make links between these genes and the protein

3.1 COLLABORATIVE ANNOTATION

3.1.3 PROJECTS

→ Add a *Project*

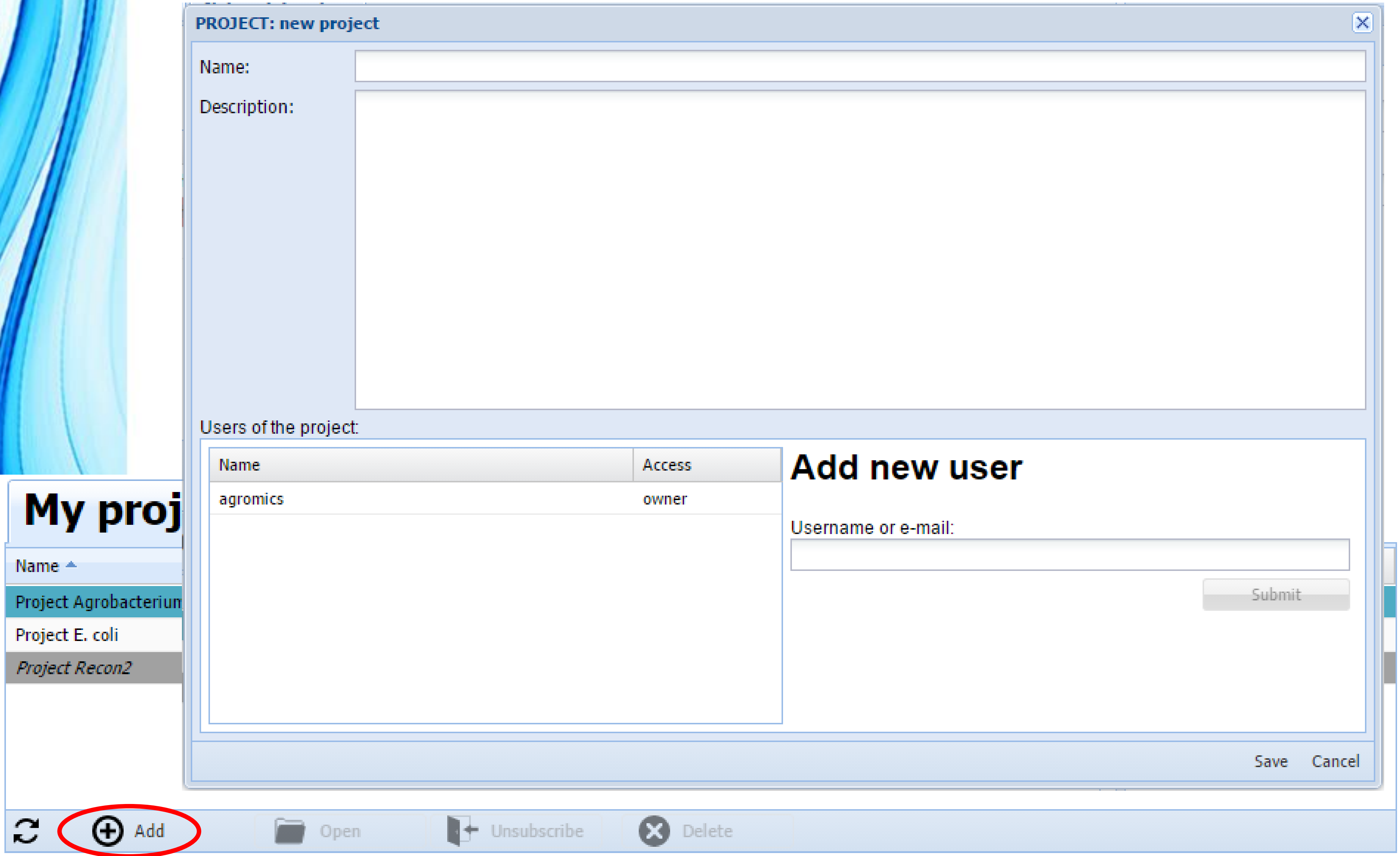


Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

3.1 COLLABORATIVE ANNOTATION

3.1.3 PROJECTS

→ Add a *Project*



PROJECT: new project

Name:

Description:

Users of the project:

Name	Access
agromics	owner

Add new user

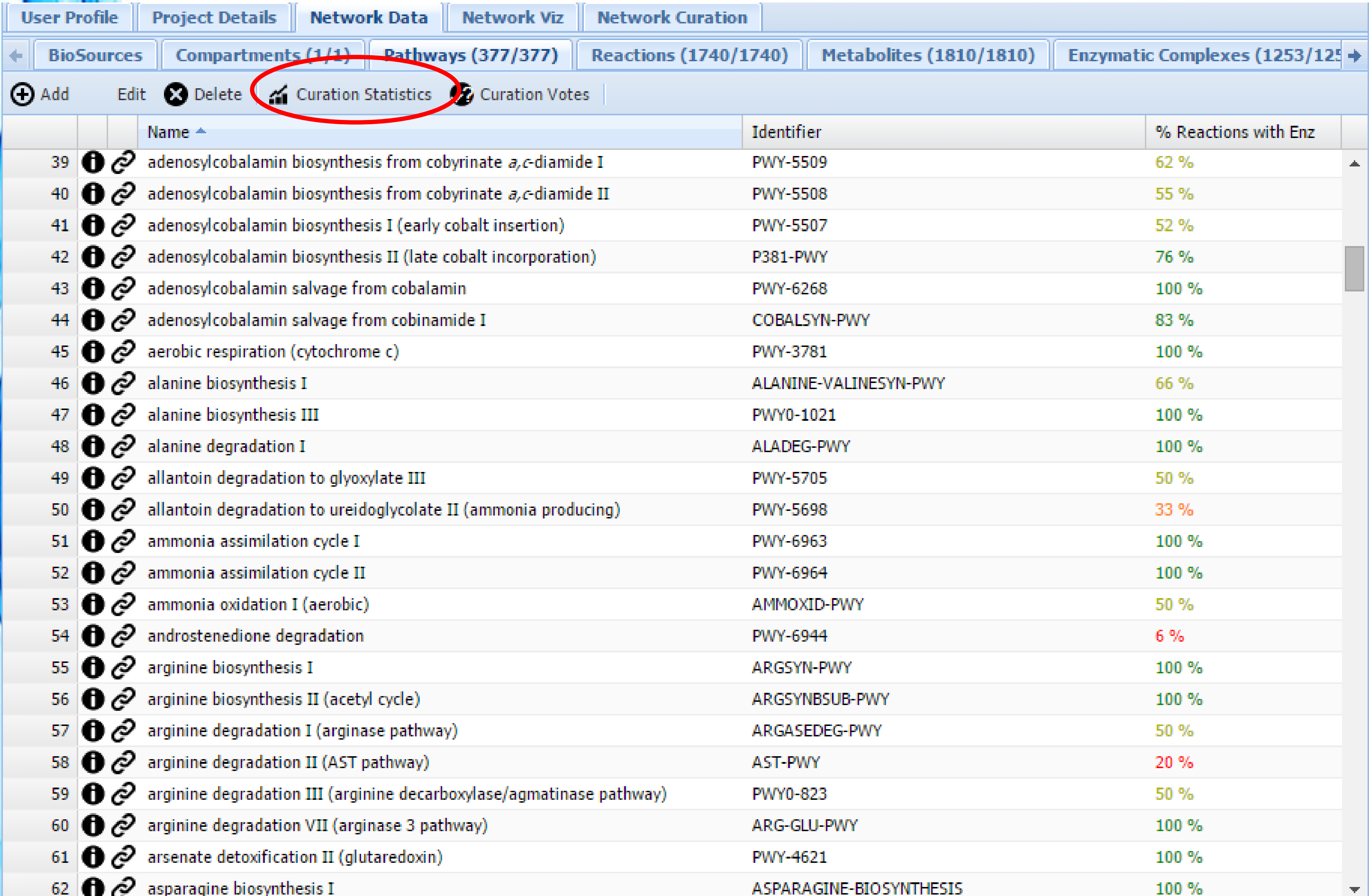
Username or e-mail:

My proj

Name ▲
Project Agrobacteriun
Project E. coli
Project Recon2

3.2. TOOLS FOR HIGHLIGHTING ANOMALIES IN A METABOLIC NETWORK

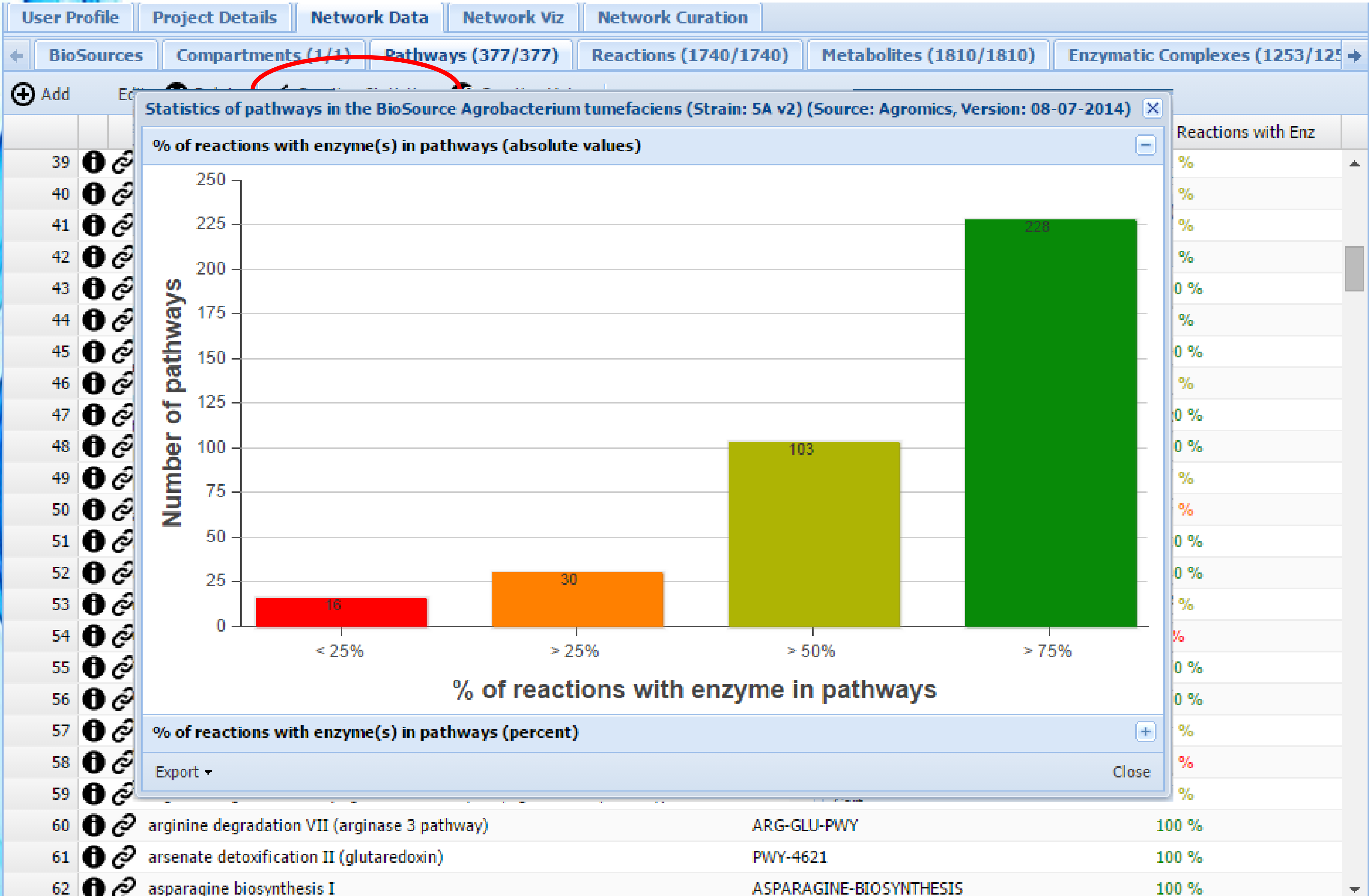
3.2.2 COMPLETENESS OF PATHWAYS



			Name ▲	Identifier	% Reactions with Enz
39	ℹ	🔗	adenosylcobalamin biosynthesis from cobyrinate *a,c*-diamide I	PWY-5509	62 %
40	ℹ	🔗	adenosylcobalamin biosynthesis from cobyrinate *a,c*-diamide II	PWY-5508	55 %
41	ℹ	🔗	adenosylcobalamin biosynthesis I (early cobalt insertion)	PWY-5507	52 %
42	ℹ	🔗	adenosylcobalamin biosynthesis II (late cobalt incorporation)	P381-PWY	76 %
43	ℹ	🔗	adenosylcobalamin salvage from cobalamin	PWY-6268	100 %
44	ℹ	🔗	adenosylcobalamin salvage from cobinamide I	COBALSYN-PWY	83 %
45	ℹ	🔗	aerobic respiration (cytochrome c)	PWY-3781	100 %
46	ℹ	🔗	alanine biosynthesis I	ALANINE-VALINESYN-PWY	66 %
47	ℹ	🔗	alanine biosynthesis III	PWY0-1021	100 %
48	ℹ	🔗	alanine degradation I	ALADEG-PWY	100 %
49	ℹ	🔗	allantoin degradation to glyoxylate III	PWY-5705	50 %
50	ℹ	🔗	allantoin degradation to ureidoglycolate II (ammonia producing)	PWY-5698	33 %
51	ℹ	🔗	ammonia assimilation cycle I	PWY-6963	100 %
52	ℹ	🔗	ammonia assimilation cycle II	PWY-6964	100 %
53	ℹ	🔗	ammonia oxidation I (aerobic)	AMMOXID-PWY	50 %
54	ℹ	🔗	androstenedione degradation	PWY-6944	6 %
55	ℹ	🔗	arginine biosynthesis I	ARGSYN-PWY	100 %
56	ℹ	🔗	arginine biosynthesis II (acetyl cycle)	ARGSYNBSUB-PWY	100 %
57	ℹ	🔗	arginine degradation I (arginase pathway)	ARGASEDEG-PWY	50 %
58	ℹ	🔗	arginine degradation II (AST pathway)	AST-PWY	20 %
59	ℹ	🔗	arginine degradation III (arginine decarboxylase/agmatinase pathway)	PWY0-823	50 %
60	ℹ	🔗	arginine degradation VII (arginase 3 pathway)	ARG-GLU-PWY	100 %
61	ℹ	🔗	arsenate detoxification II (glutaredoxin)	PWY-4621	100 %
62	ℹ	🔗	asparagine biosynthesis I	ASPARAGINE-BIOSYNTHESIS	100 %

3.2. TOOLS FOR HIGHLIGHTING ANOMALIES IN A METABOLIC NETWORK

3.2.2 COMPLETENESS OF PATHWAYS



Statistics of pathways in the BioSource Agrobacterium tumefaciens (Strain: 5A v2) (Source: Agromics, Version: 08-07-2014)

% of reactions with enzyme(s) in pathways (absolute values)

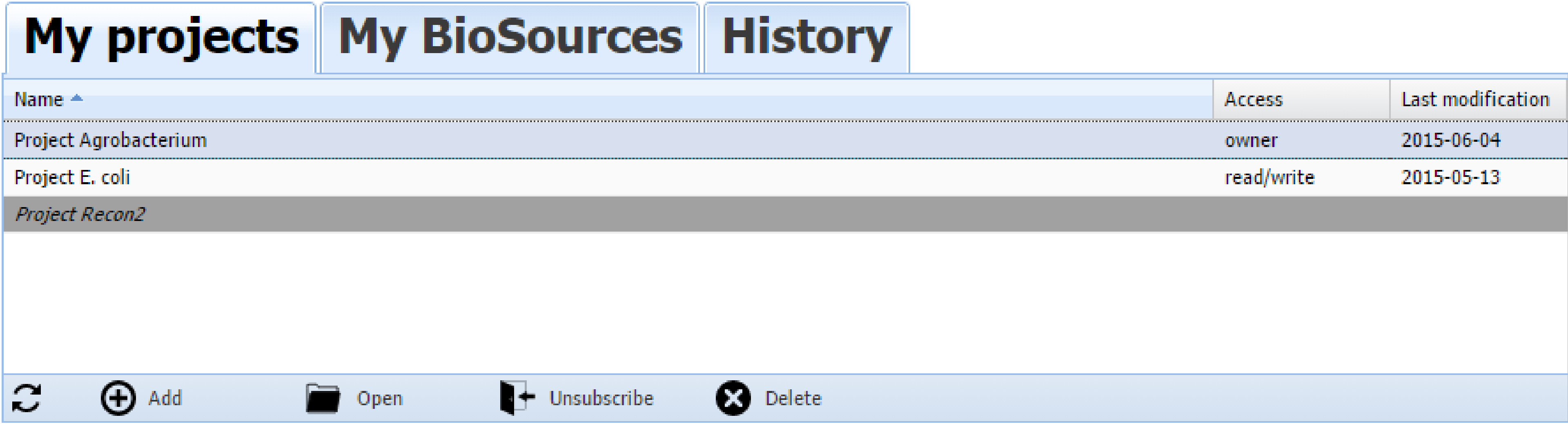
% of reactions with enzyme(s) in pathways (percent)

60	arginine degradation VII (arginase 3 pathway)	ARG-GLU-PWY	100 %
61	arsenate detoxification II (glutaredoxin)	PWY-4621	100 %
62	asparagine biosynthesis I	ASPARAGINE-BIOSYNTHESIS	100 %

3.1 COLLABORATIVE ANNOTATION

3.1.3 PROJECTS

→ Add a *Project*



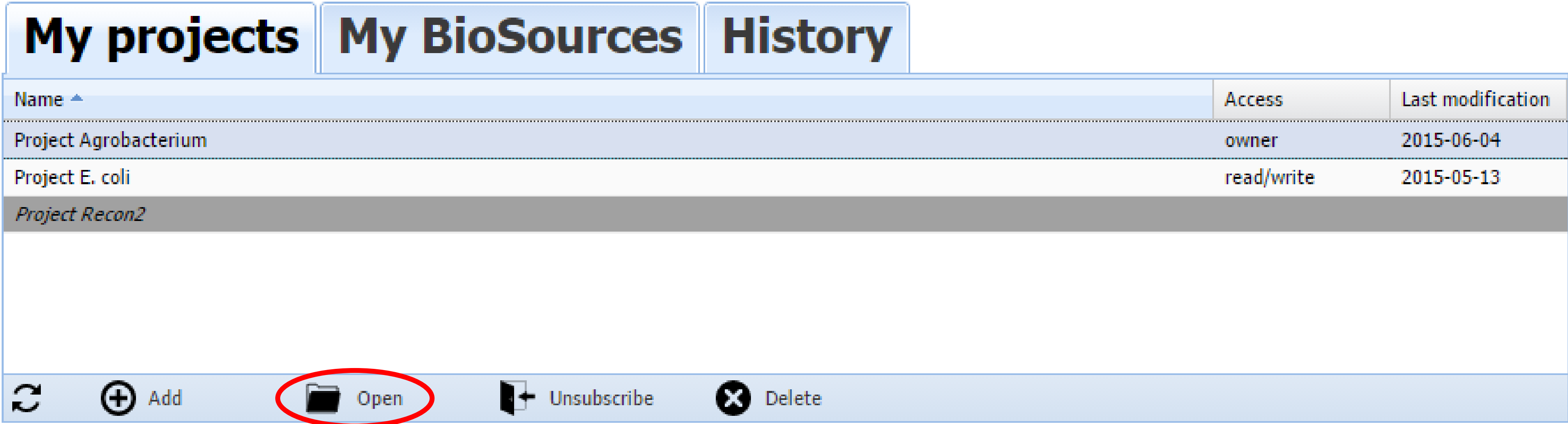
Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

3.1 COLLABORATIVE ANNOTATION

3.1.3 PROJECTS

→ Add a *Project*

→ Open an existing *Project*

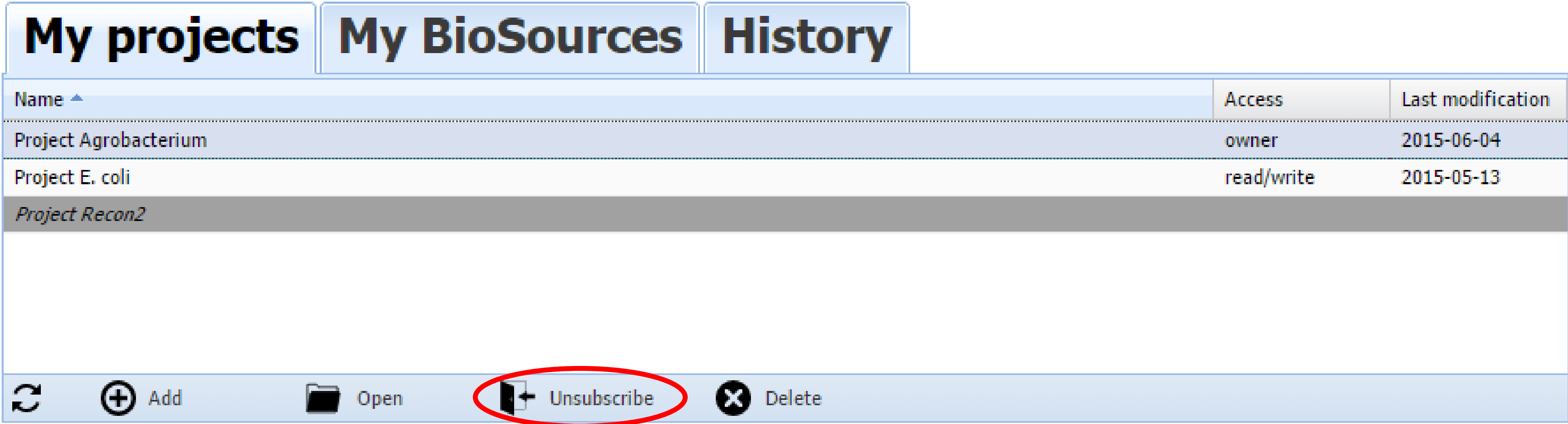


Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

3.1 COLLABORATIVE ANNOTATION

3.1.3 PROJECTS

- → Add a *Project*
- → Open an existing *Project*
- → Unsubscribe to a *Project*



Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

3.1 COLLABORATIVE ANNOTATION

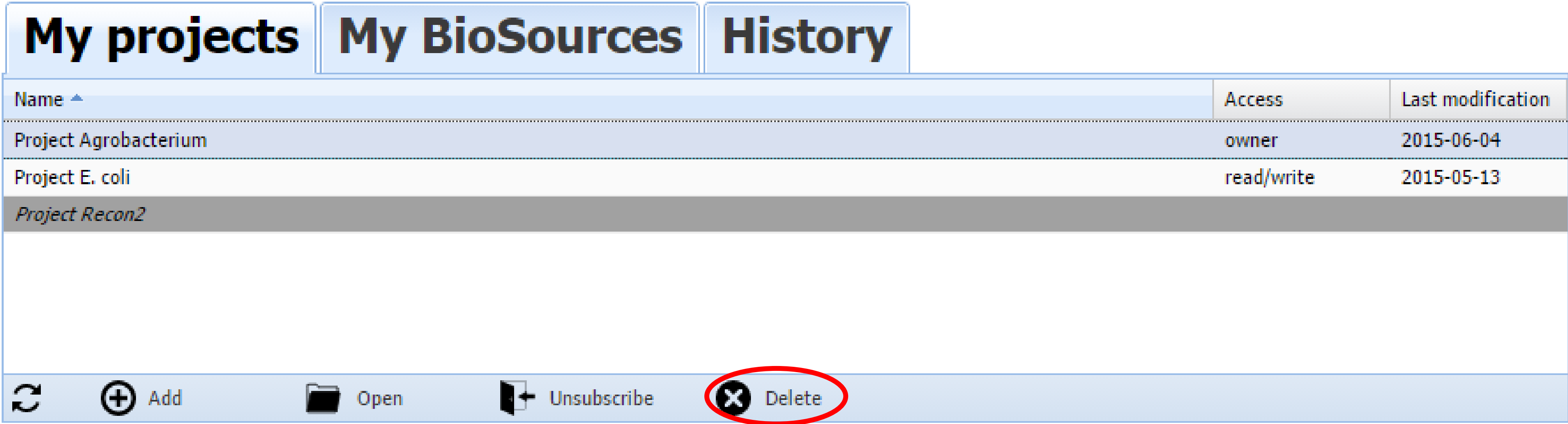
3.1.3 PROJECTS

→ Add a *Project*

→ Open an existing *Project*

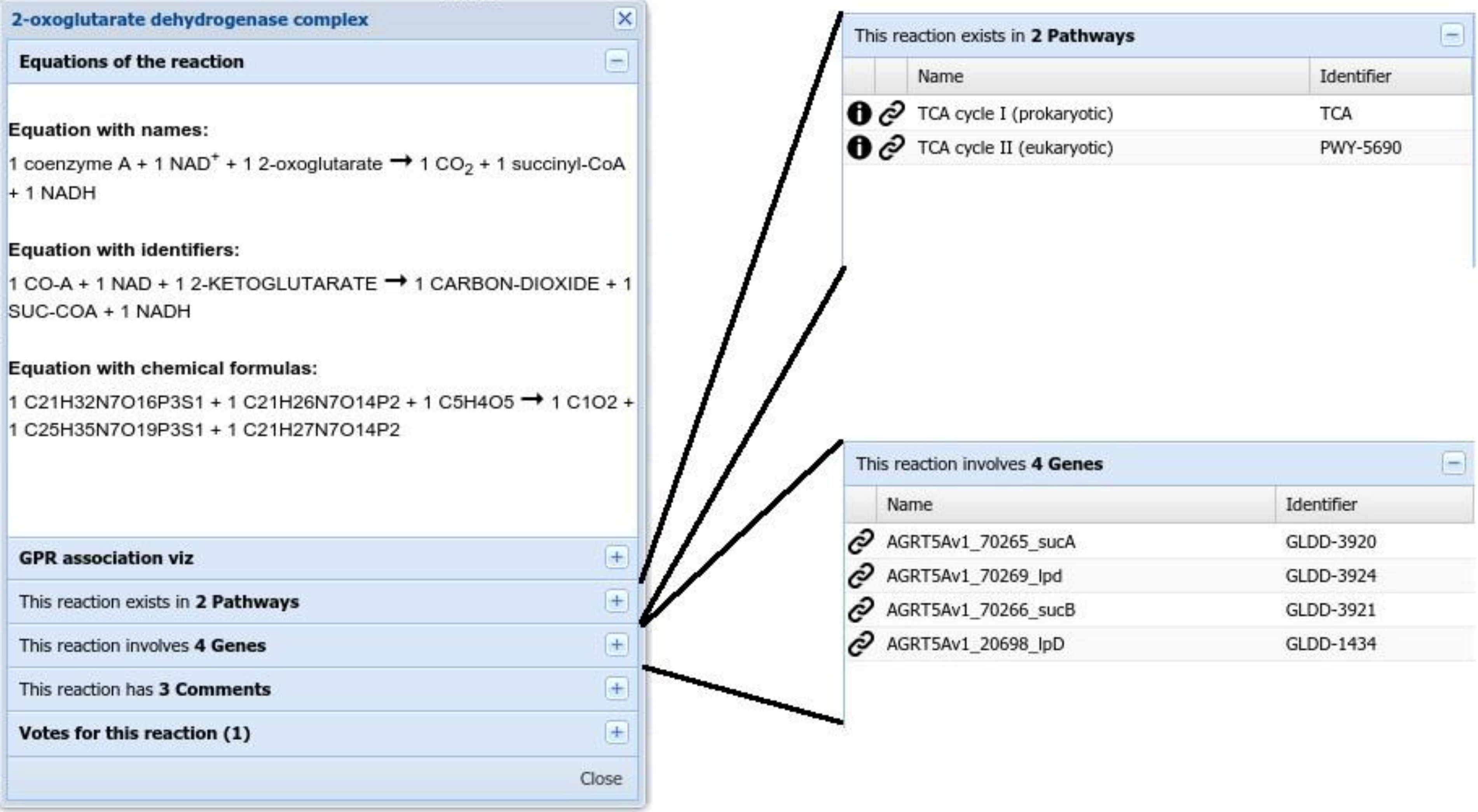
→ Unsubscribe to a *Project*

→ Delete a *Project*



Name	Access	Last modification
Project Agrobacterium	owner	2015-06-04
Project E. coli	read/write	2015-05-13
Project Recon2		

Fiche Reaction



2-oxoglutarate dehydrogenase complex

Equations of the reaction

Equation with names:

1 coenzyme A + 1 NAD^+ + 1 2-oxoglutarate → 1 CO_2 + 1 succinyl-CoA + 1 NADH

Equation with identifiers:

1 CO-A + 1 NAD + 1 2-KETOGLUTARATE → 1 CARBON-DIOXIDE + 1 SUC-COA + 1 NADH

Equation with chemical formulas:

1 C21H32N7O16P3S1 + 1 C21H26N7O14P2 + 1 C5H4O5 → 1 C1O2 + 1 C25H35N7O19P3S1 + 1 C21H27N7O14P2

GPR association viz

This reaction exists in **2 Pathways**

This reaction involves **4 Genes**

This reaction has **3 Comments**

Votes for this reaction (1)

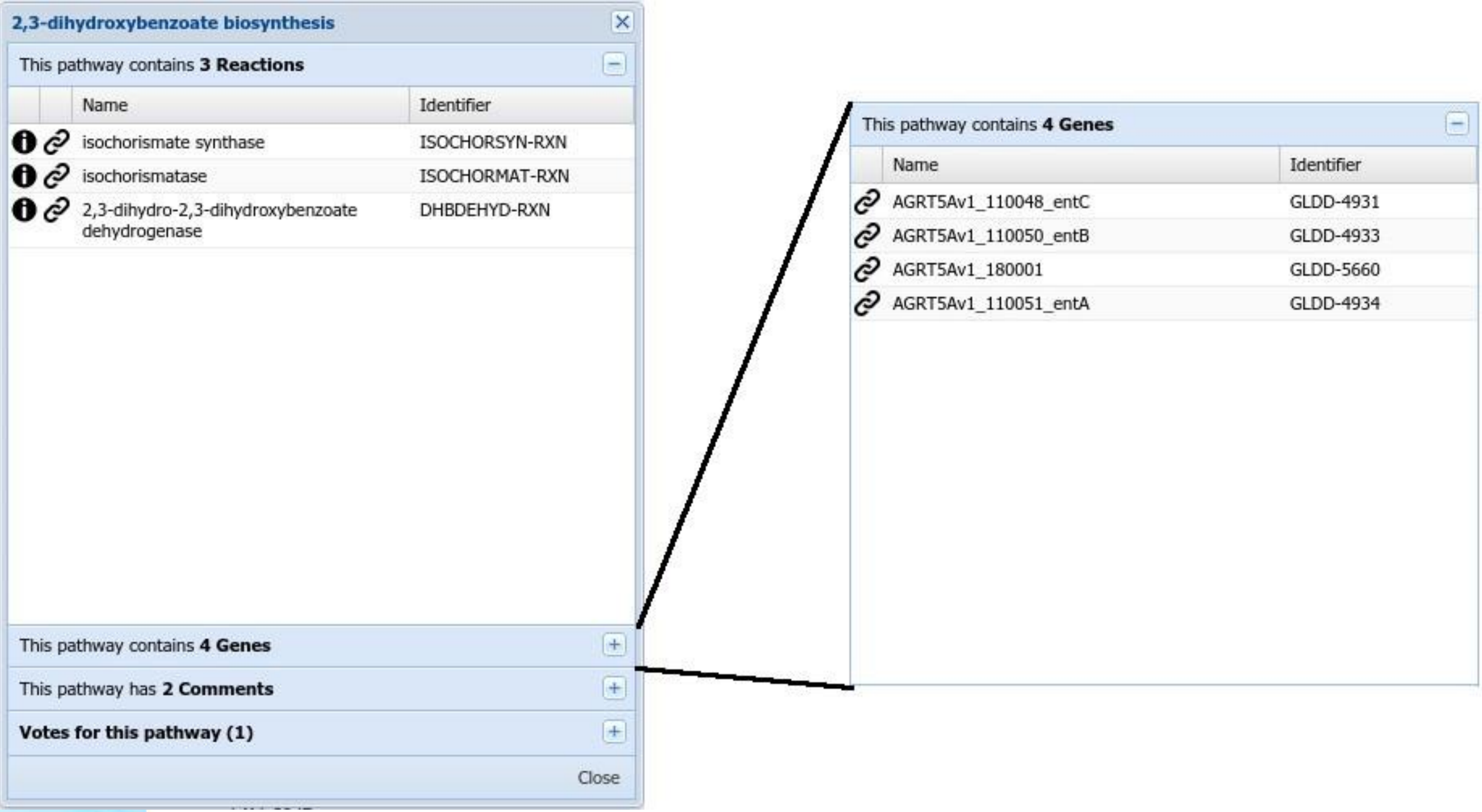
This reaction exists in **2 Pathways**

		Name	Identifier
ℹ	🔗	TCA cycle I (prokaryotic)	TCA
ℹ	🔗	TCA cycle II (eukaryotic)	PWY-5690

This reaction involves **4 Genes**

	Name	Identifier
🔗	AGRT5Av1_70265_sucA	GLDD-3920
🔗	AGRT5Av1_70269_lpd	GLDD-3924
🔗	AGRT5Av1_70266_sucB	GLDD-3921
🔗	AGRT5Av1_20698_lpD	GLDD-1434

Fiche Pathway



2,3-dihydroxybenzoate biosynthesis

This pathway contains **3 Reactions**

		Name	Identifier
ℹ	🔗	isochorismate synthase	ISOCHORSYN-RXN
ℹ	🔗	isochorismatase	ISOCHORMAT-RXN
ℹ	🔗	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	DHBDEHYD-RXN

This pathway contains **4 Genes**

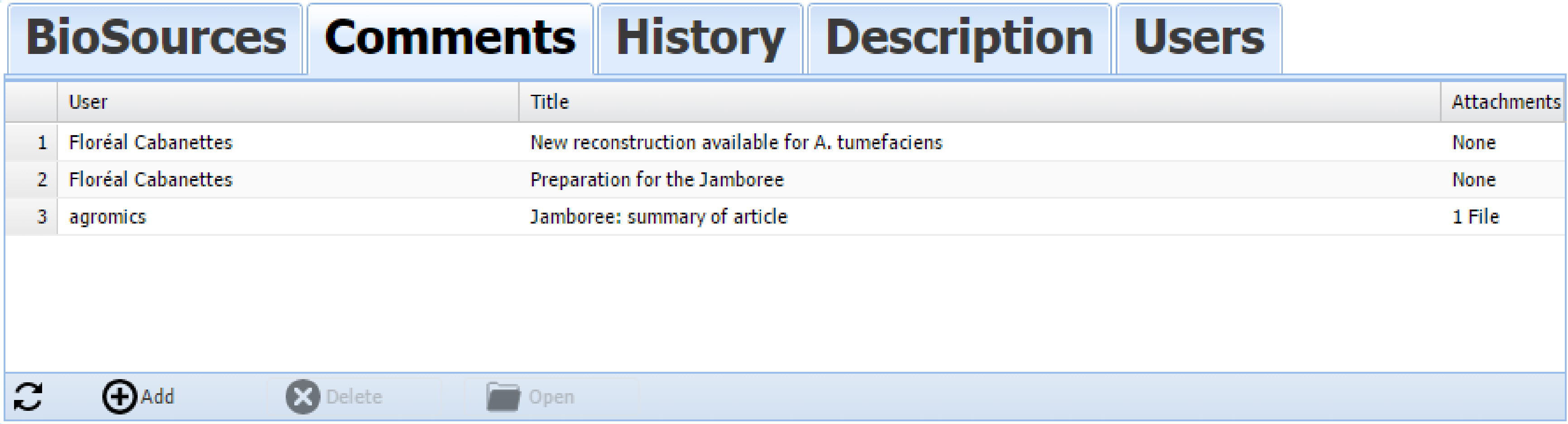
This pathway has **2 Comments**

Votes for this pathway (1)

This pathway contains **4 Genes**

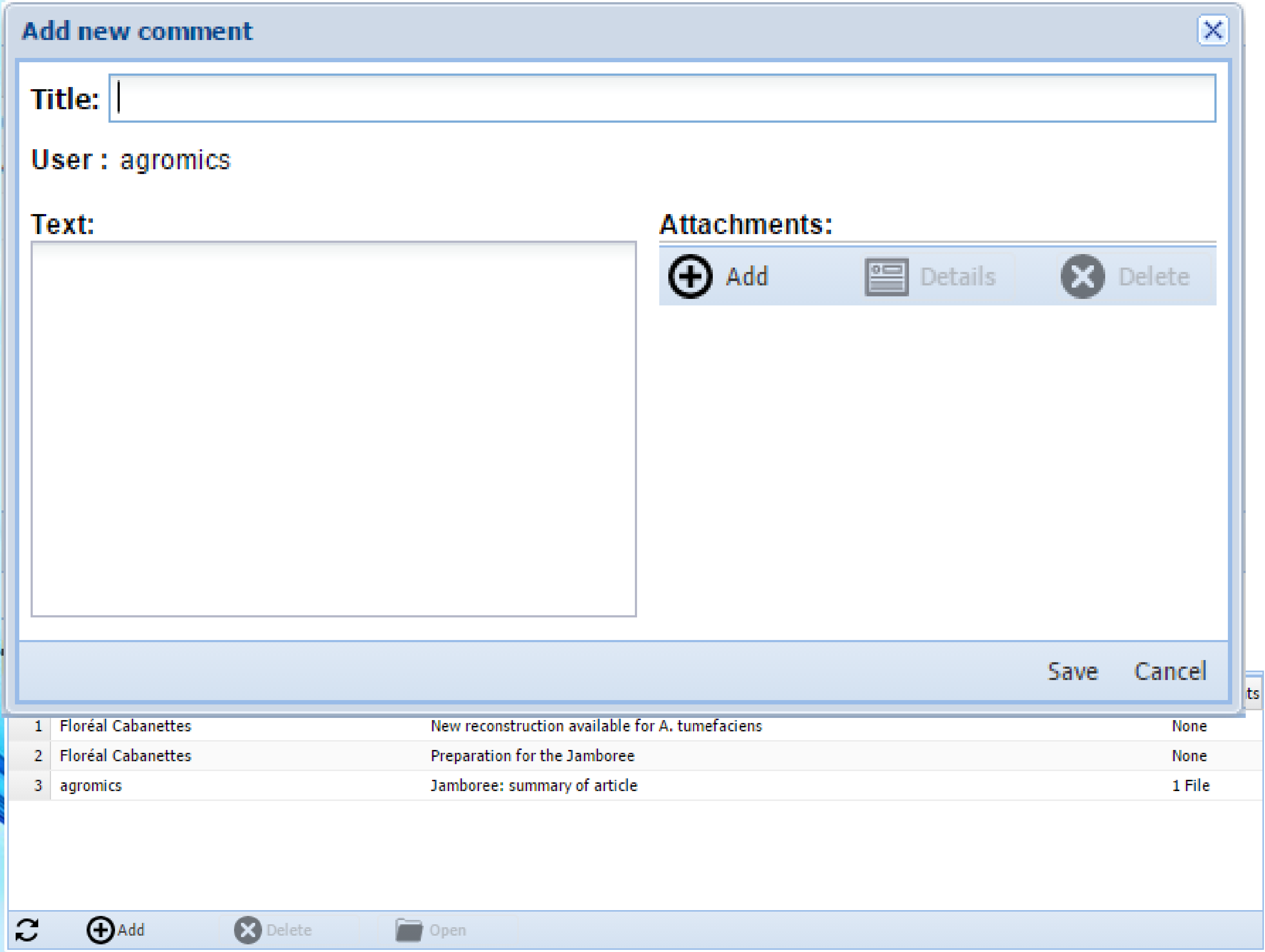
	Name	Identifier
🔗	AGRT5Av1_110048_entC	GLDD-4931
🔗	AGRT5Av1_110050_entB	GLDD-4933
🔗	AGRT5Av1_180001	GLDD-5660
🔗	AGRT5Av1_110051_entA	GLDD-4934

COMMENTS



	User	Title	Attachments
1	Floréal Cabanettes	New reconstruction available for A. tumefaciens	None
2	Floréal Cabanettes	Preparation for the Jamboree	None
3	agromics	Jamboree: summary of article	1 File

Comments



Add new comment

Title:

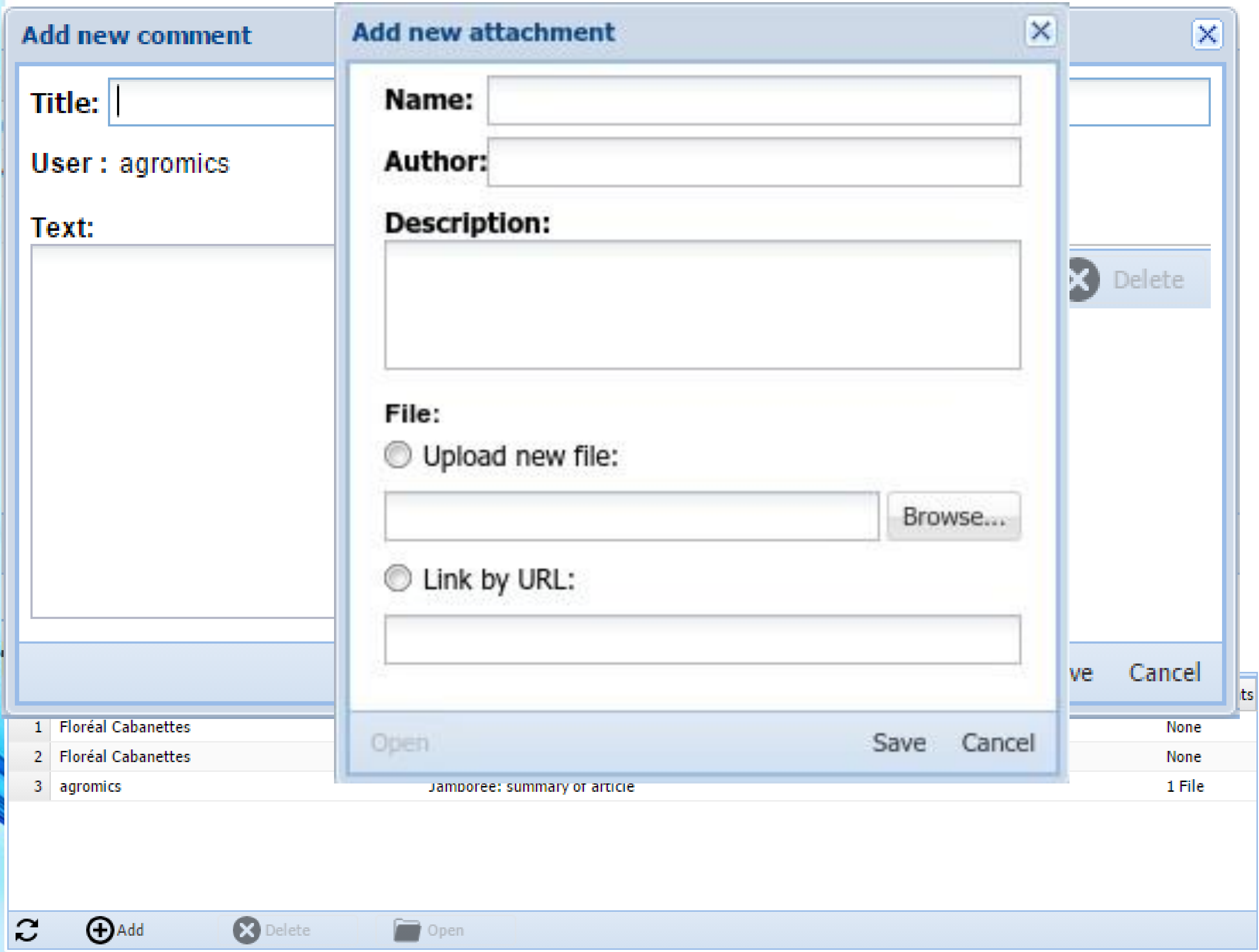
User : agromics

Text:

Attachments:

1	Floréal Cabanettes	New reconstruction available for A. tumefaciens	None
2	Floréal Cabanettes	Preparation for the Jamboree	None
3	agromics	Jamboree: summary of article	1 File

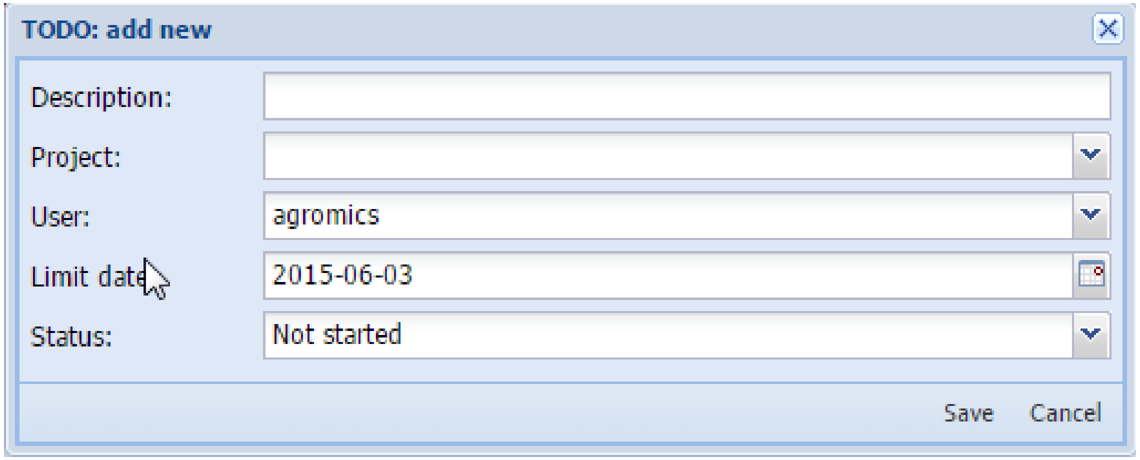
Comments



User : agromics

1	Floréal Cabanettes		None
2	Floréal Cabanettes		None
3	agromics	Jamboree: summary of article	1 File

ADD NEW ACTION IN TODO LIST



Description:

Project:

User: agromics

Limit date: 2015-06-03

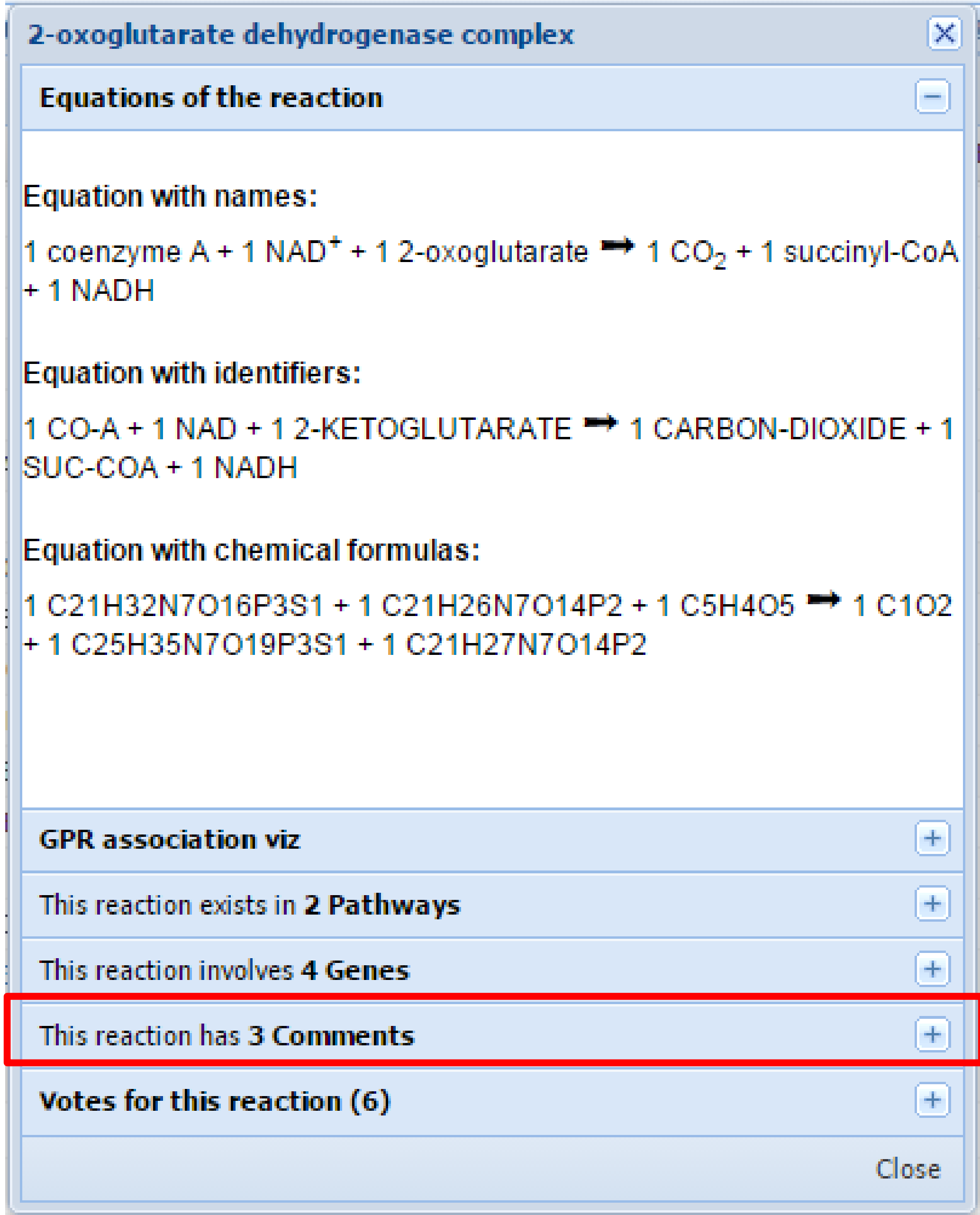
Status: Not started

3.3. RESUME OPINIONS ABOUT THE METABOLIC NETWORK

3.3.2 ADD COMMENTS TO AN OBJECT OF THE NETWORK

<u>Goal:</u>

To provide more information to organizers to help facilitate decision-making.



2-oxoglutarate dehydrogenase complex

Equations of the reaction

Equation with names:

1 coenzyme A + 1 NAD^+ + 1 2-oxoglutarate ➡ 1 CO_2 + 1 succinyl-CoA + 1 NADH

Equation with identifiers:

1 CO-A + 1 NAD + 1 2-KETOGLUTARATE ➡ 1 CARBON-DIOXIDE + 1 SUC-COA + 1 NADH

Equation with chemical formulas:

1 C21H32N7O16P3S1 + 1 C21H26N7O14P2 + 1 C5H4O5 ➡ 1 C1O2 + 1 C25H35N7O19P3S1 + 1 C21H27N7O14P2

GPR association viz

This reaction exists in **2 Pathways**

This reaction involves **4 Genes**

This reaction has **3 Comments**

Votes for this reaction (6)

SCHEMAS CLASSES

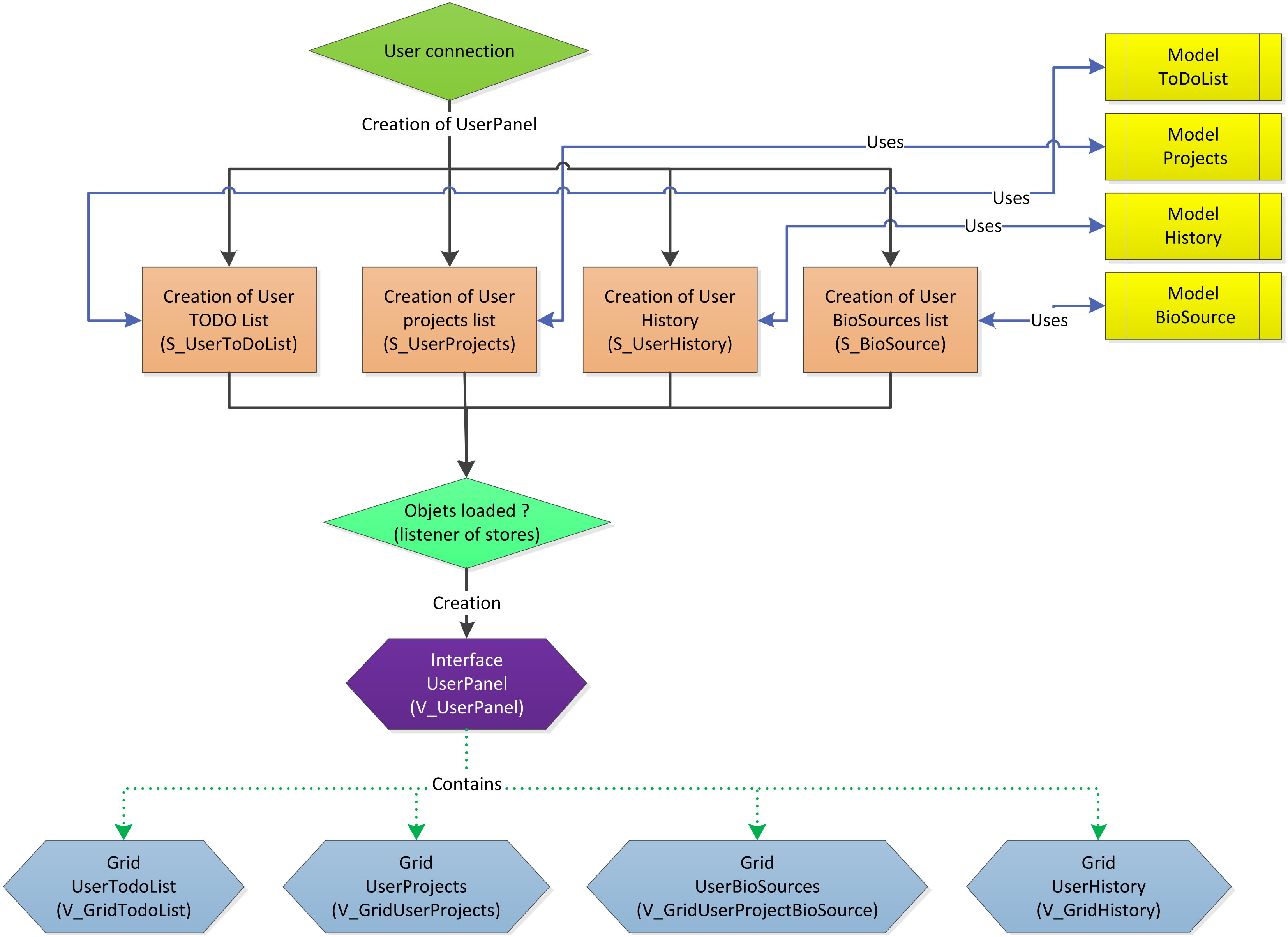


Figure S1. Connection d'un utilisateur à MetExplore : initialisation du panneau Utilisateur. Entre parenthèse est indiquée la Classe ExtJS concernée. En violet les super-vues contenant d'autres vues, en bleu les vues, en vert les contrôleurs et en marron les stores. Les Stores sont remplis depuis la base de donnée du serveur via des scripts PHP.

SCHEMAS CLASSES

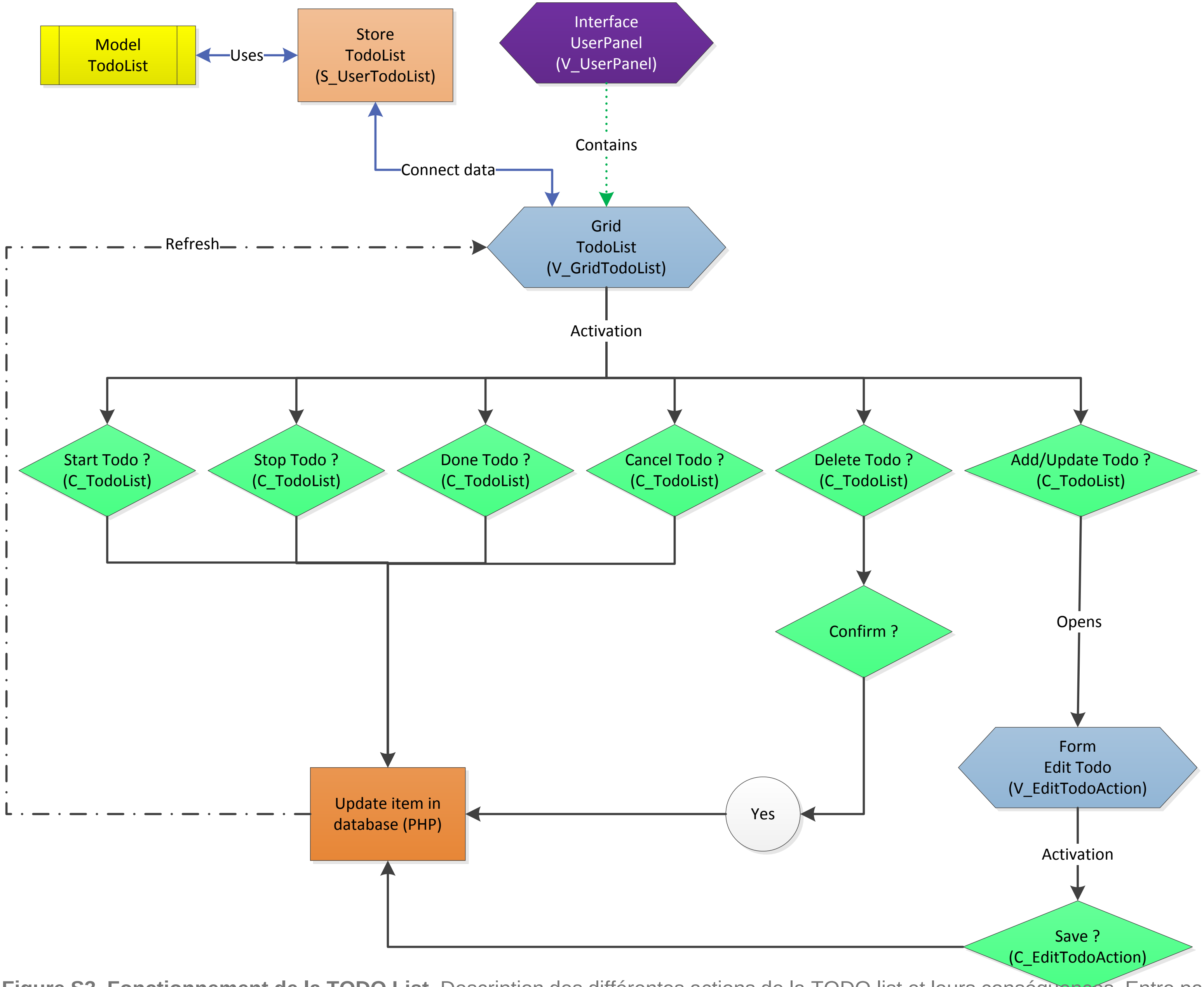


Figure S3. Fonctionnement de la TODO List. Description des différentes actions de la TODO list et leurs conséquences. Entre parenthèse est indiquée la Classe ExtJS concernée. En violet les super-vues contenant d'autres vues, en bleu les vues, en vert les contrôleurs et en violet les scripts PHP. En traits pointillés les actions asynchrones, réalisées une fois la réponse PHP reçue.

SCHEMAS CLASSES

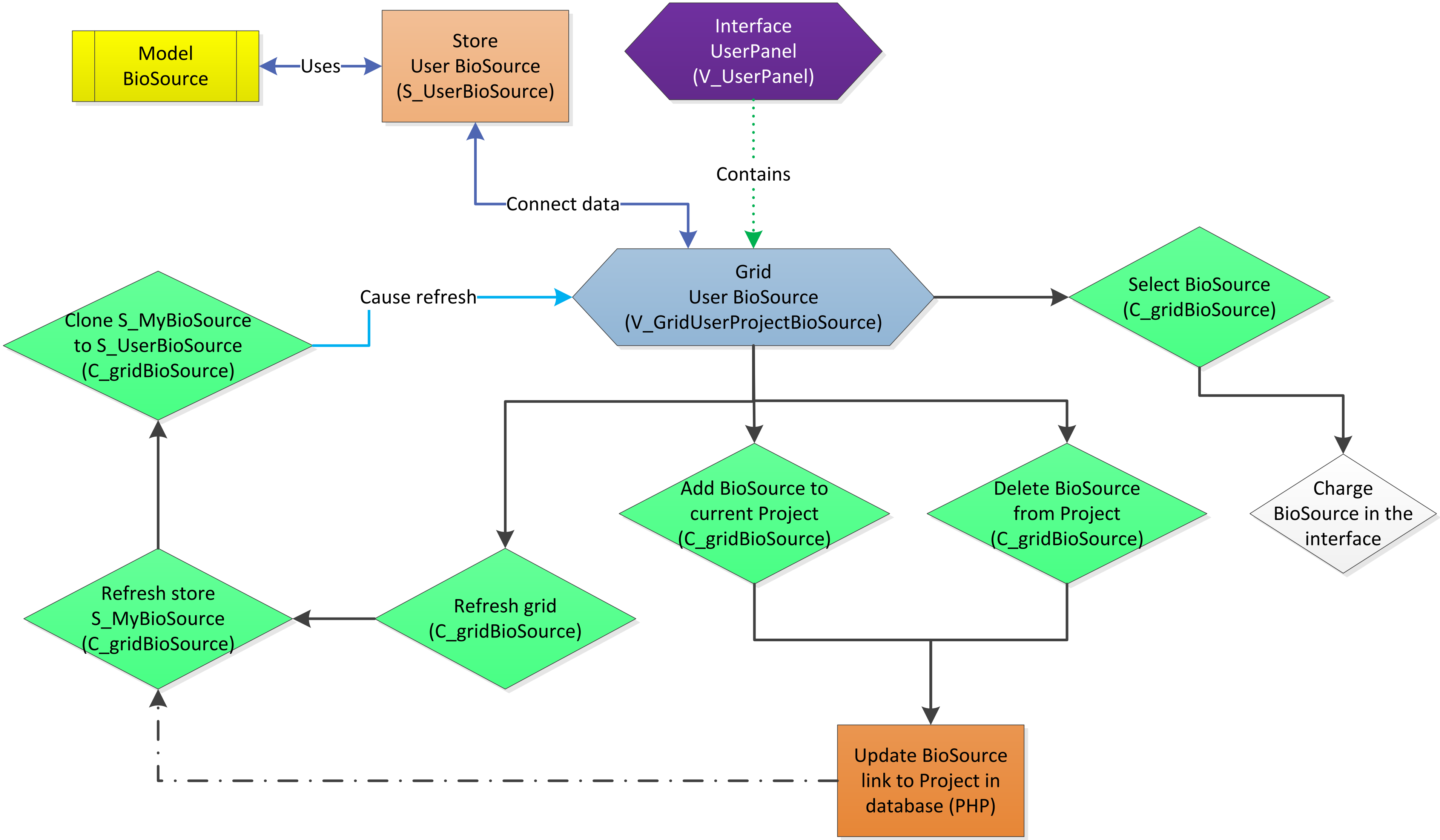


Figure S4. Fonctionnement de la grille *BioSource* Utilisateur. *Description des différentes actions sur la grille et leur conséquences. Entre parenthèse est indiquée la Classe ExtJS concernée. En violet les super-vues contenant d'autres vues, en bleu les vues, en vert les contrôleurs et en violet les scripts PHP. En traits pointillés les actions asynchrones, réalisées une fois la réponse PHP reçue. Les losanges correspondent aux actions réalisées côté client.*

SCHEMAS CLASSES

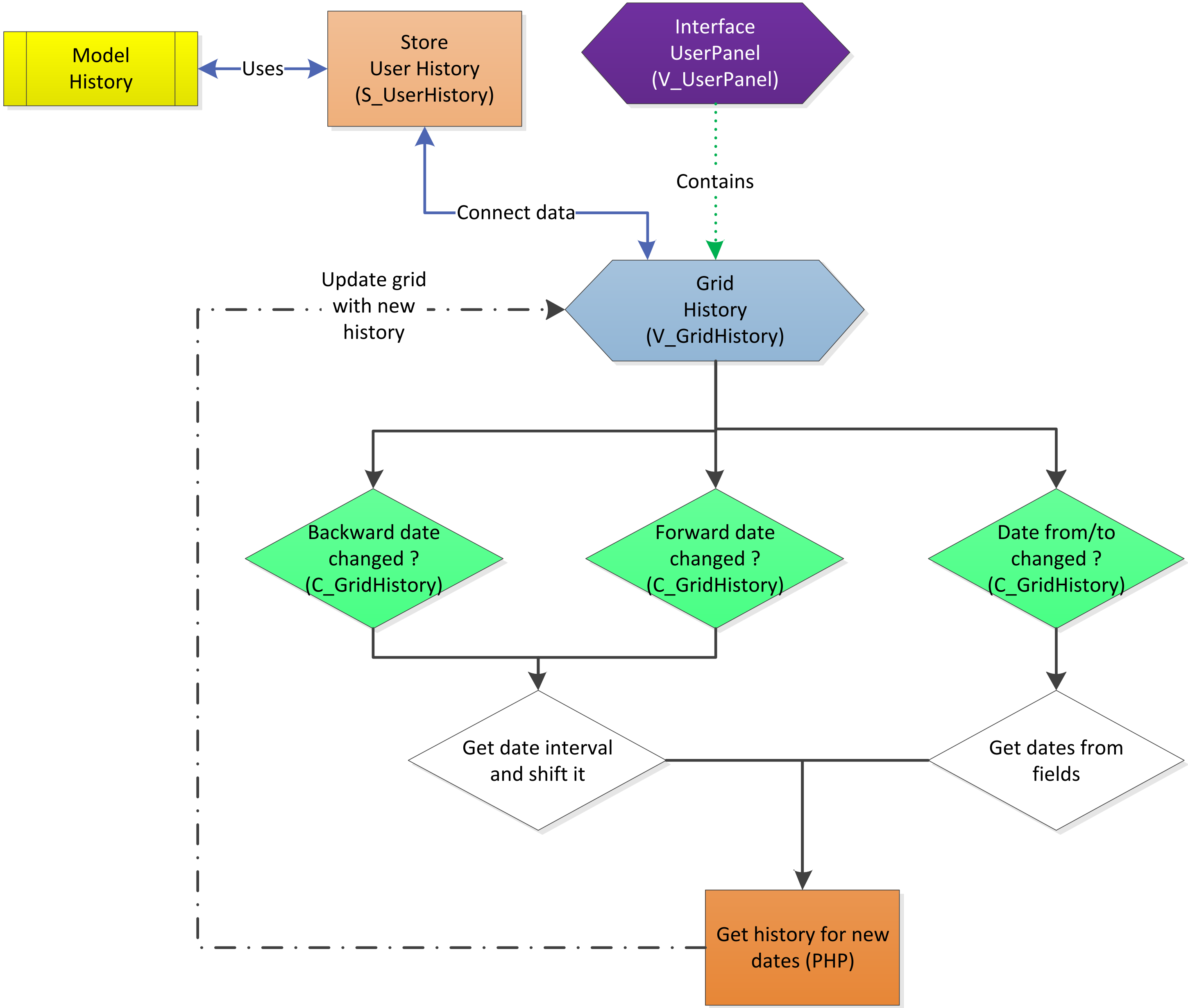


Figure S5. Fonctionnement de la grille Historique. *Description des différentes actions sur la grille et leurs conséquences. Entre parenthèse est indiquée la Classe ExtJS concernée. En violet les super-vues contenenant d'autres vues, en bleu les vues, en vert les contrôleurs et en violet les scripts PHP. En traits pointillés les actions asynchrones, réalisées une fois la réponse PHP reçue. Les losanges correspondent aux actions réalisées côté client.*

SCHEMAS CLASSES

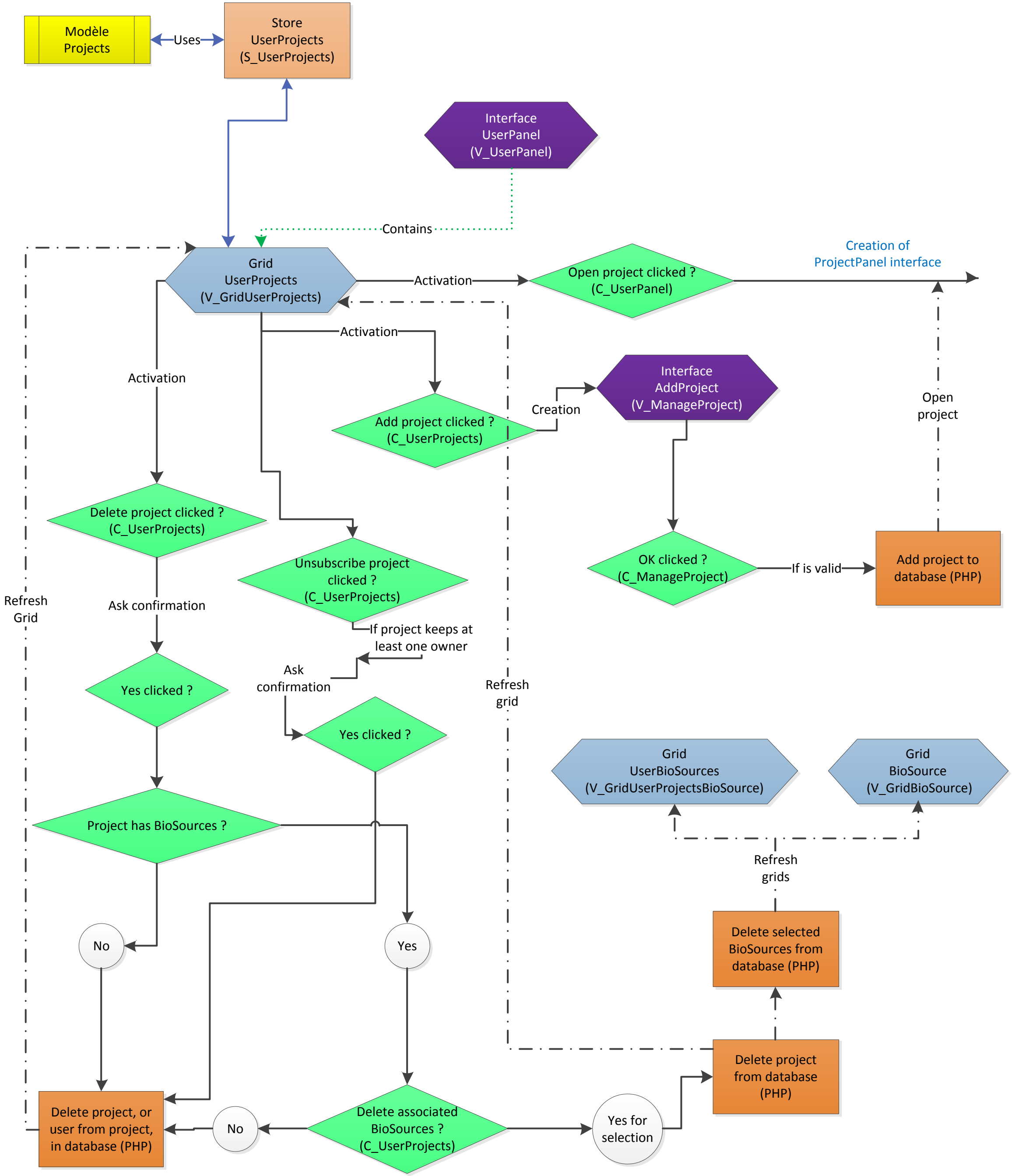
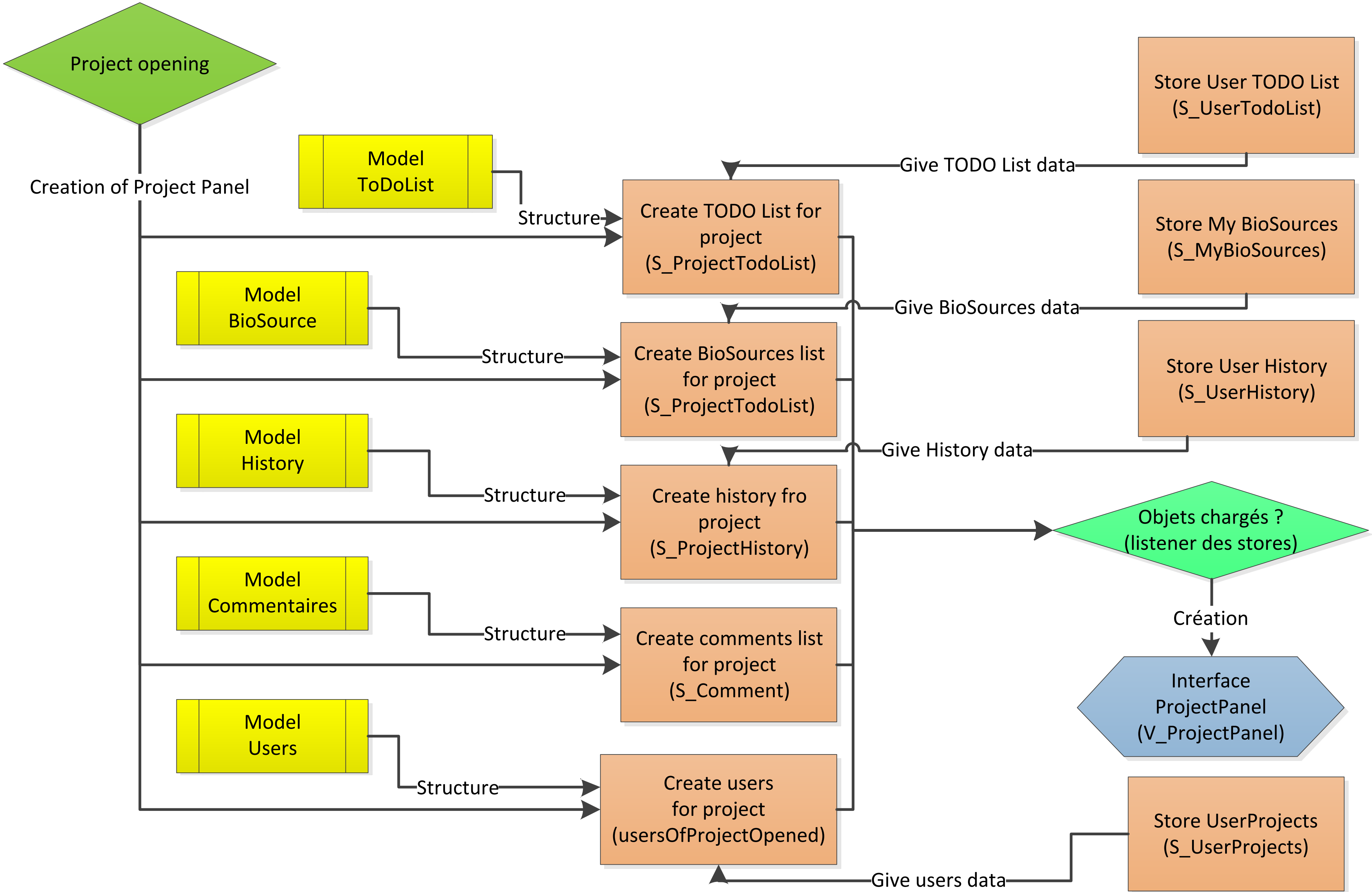


Figure S6 Fonctionnement de la grille Liste des *Projets*. *Description des différentes actions sur la grille et leurs conséquences. Entre parenthèse est indiquée la Classe ExtJS concernée. En violet les super-vues contenenant d'autres vues, en bleu les vues, en vert les contrôleurs et en violet les scripts PHP. En traits pointillés les actions asynchrones, réalisées une fois la réponse PHP reçue. Les losanges correspondent aux actions réalisées côté client.*

SCHEMAS CLASSES



Project opening

Creation of Project Panel

Model ToDoList

Structure

Create TODO List for project (S_ProjectTodoList)

Store User TODO List (S_UserTodoList)

Give TODO List data

Model BioSource

Structure

Create BioSources list for project (S_ProjectTodoList)

Store My BioSources (S_MyBioSources)

Give BioSources data

Model History

Structure

Create history fro project (S_ProjectHistory)

Store User History (S_UserHistory)

Give History data

Model Commentaires

Structure

Create comments list for project (S_Comment)

Model Users

Structure

Create users for project (usersOfProjectOpened)

Store UserProjects (S_UserProjects)

Give users data

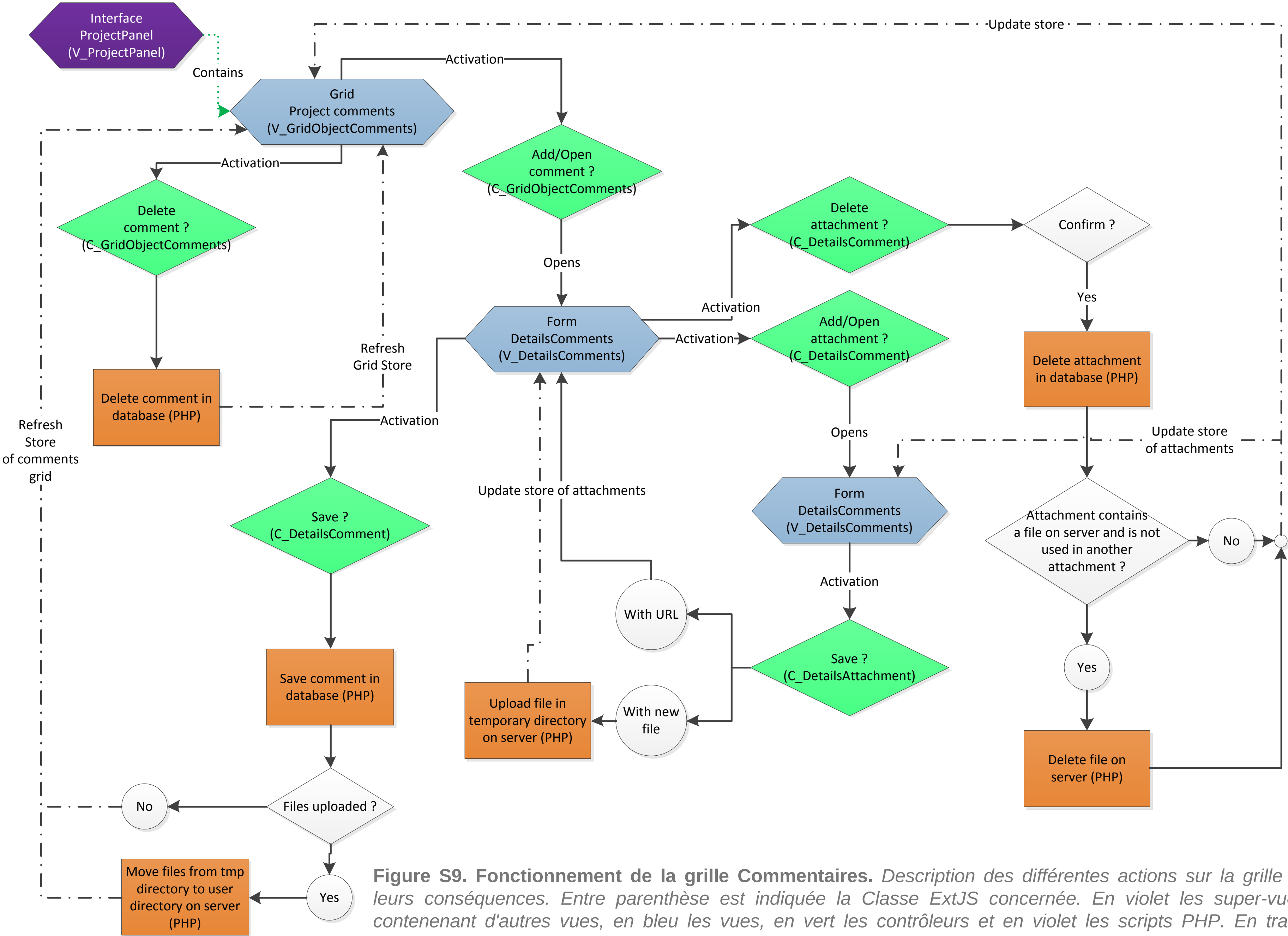
Objets chargés ? (listener des stores)

Création

Interface ProjectPanel (V_ProjectPanel)

Figure S7. Ouverture d’un *Projet* : initialisation du panneau *Projet*. Entre parenthèse est indiquée la Classe ExtJS concernée. En violet les super-vues contenant d'autres vues, en bleu les vues, en vert les contrôleurs et en marron les stores. Le Store S_Comment est rempli depuis la base de données du serveur via un script PHP. Les autres Stores du panneau sont remplis depuis d’autres Stores déjà chargés, mentionnés sur la figure.

Schemas classes



Interface ProjectPanel (V_ProjectPanel)

Contains

Grid Project comments (V_GridObjectComments)

Update store

Activation

Add/Open comment ? (C_GridObjectComments)

Opens

Form DetailsComments (V_DetailsComments)

Activation

Delete comment ? (C_GridObjectComments)

Delete comment in database (PHP)

Refresh Grid Store

Refresh Store of comments grid

Activation

Save ? (C_DetailsComment)

Save comment in database (PHP)

Files uploaded ?

No

Yes

Move files from tmp directory to user directory on server (PHP)

Update store of attachments

Upload file in temporary directory on server (PHP)

With URL

With new file

Activation

Delete attachment ? (C_DetailsComment)

Confirm ?

Yes

Delete attachment in database (PHP)

Activation

Add/Open attachment ? (C_DetailsComment)

Opens

Form DetailsComments (V_DetailsComments)

Activation

Save ? (C_DetailsAttachment)

Update store of attachments

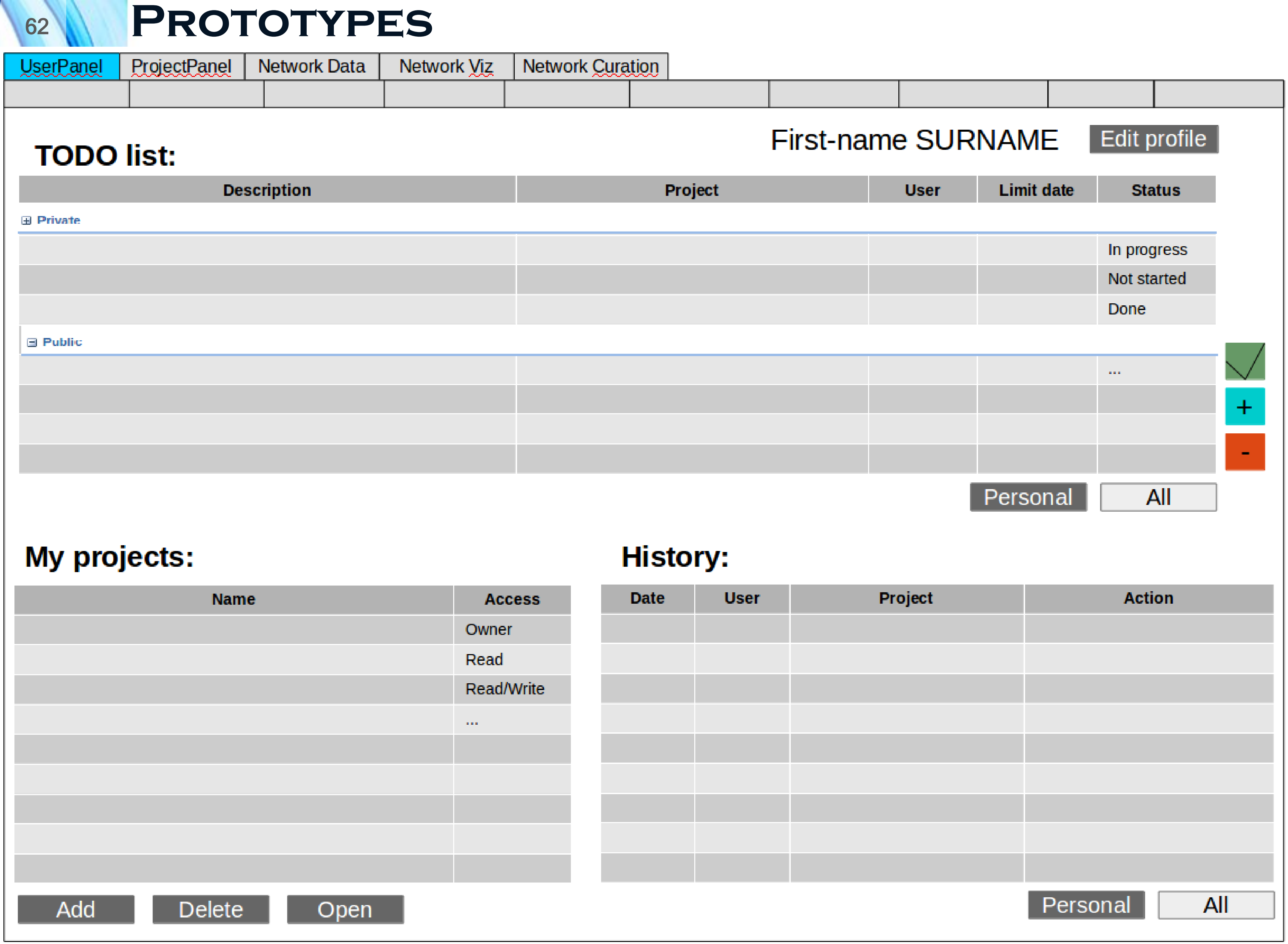
Attachment contains a file on server and is not used in another attachment ?

No

Yes

Delete file on server (PHP)

Figure S9. Fonctionnement de la grille Commentaires. *Description des différentes actions sur la grille et leurs conséquences. Entre parenthèse est indiquée la Classe ExtJS concernée. En violet les super-vues contenenant d'autres vues, en bleu les vues, en vert les contrôleurs et en violet les scripts PHP. En traits pointillés les actions asynchrones, réalisées une fois la réponse PHP reçue.*



TODO list:

Description	Project	User	Limit date	Status
⊞ Private				
				In progress
				Not started
				Done
⊟ Public				
				...

My projects:

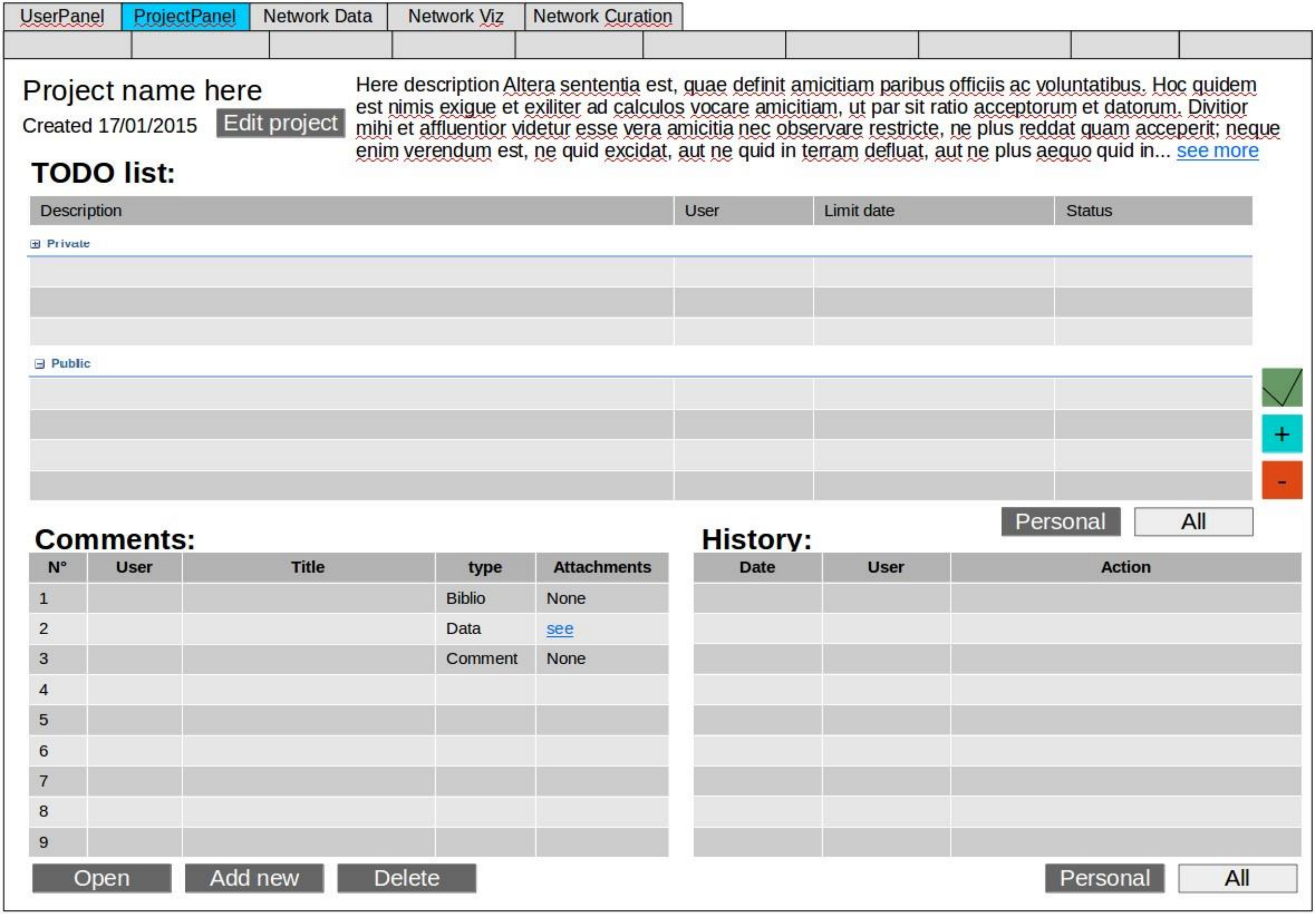
Name	Access
	Owner
	Read
	Read/Write
	...

History:

Date	User	Project	Action

Figure S2. Schéma du Panneau Utilisateur prévue avant l'implémentation concrète dans *MetExplore*

PROTOTYPES



Project name here

Created 17/01/2015

Here description Altera sententia est, quae definit amicitiam paribus officiis ac voluntatibus. Hoc quidem est nimis exigue et exiliter ad calculos vocare amicitiam, ut par sit ratio acceptorum et datorum. Divitior mihi et affluentior videtur esse vera amicitia nec observare restricte, ne plus reddat quam acceperit; neque enim verendum est, ne quid excidat, aut ne quid in terram defluat, aut ne plus aequo quid in... see more

TODO list:

Description	User	Limit date	Status
⊞ Private			
⊟ Public			

Comments:

N°	User	Title	type	Attachments
1			Biblio	None
2			Data	see
3			Comment	None
4				
5				
6				
7				
8				
9				

History:

Date	User	Action

Figure S8. Schéma du Panneau *Projet* prévue avant l'implémentation concrète dans *MetExplore*.