

AskOmics: Integration and Interrogation of Genomic and PostGenomic Regulation Networks

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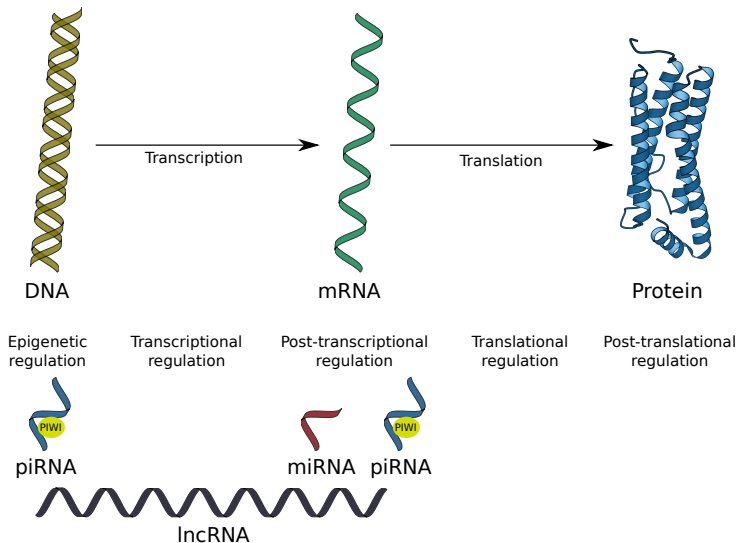
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Pea aphid phenotypic plasticity

MiRNAAdapt ANR Project

- Identify gene functions involved in the pea aphid phenotypic plasticity
 - ▶ Sexual reproduction
 - ▶ Asexual reproduction
- PhD work (Valentin Wucher)
 - ▶ Post-transcriptional regulation network between microRNAs and mRNAs
 - ▶ Kinetic expressions change depending on the embryogenesis
- Regulation network enrichment
 - ▶ piRNAs
 - ▶ lncRNAs
 - ▶ additional informations

RNA Regulation



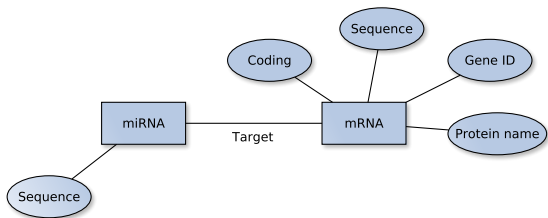
Data inventory

- 36939 coding transcripts (mRNAs)
- 2172 long non coding transcripts (lncRNAs)
- 6059 overlaps between the coding transcripts and the lncRNAs
- 802 micro RNAs (miRNAs)
- 4998271 pairings between the transcripts and the miRNAs
- 77811 piRNAs clusters
- 99382 overlaps between the transcripts and the piRNAs
- 10062 coding transcripts are annotated by 41030 Gene Ontology terms
- Difference of expression between sexual and asexual Aphid pea embryogenesis for:
 - ▶ 4996 coding transcripts
 - ▶ 370 long non coding transcripts
 - ▶ 15 micro RNAs
 - ▶ 408 piRNAs clusters

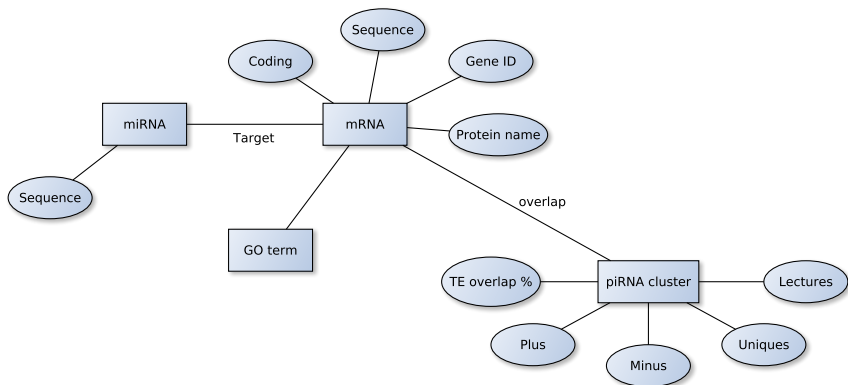
Linked data



Linked data



Linked data



Biologists files

correspondance_mirdeep2_mirbaseNom_seq5p3p.csv

	A	B
1	TGAGATCATATAACTTTAC	api-mir-novel1a-5p
2	AAAGTGTTGTTTTGATCTCATT	api-mir-novel1a-3p
3	TGAGATCATATAAACTTTAT	api-mir-novel1b-5p
4	AAAGTGTTATTTTGATCTTCAT	api-mir-novel1b-3p
5	TGAGATCATATAACTTTAT	api-mir-novel1c-1-5p
6	AAAGTGTTATTTTGATCTTCTT	api-mir-novel1c-1-3p
7	TGAGATCATATAACTTTAT	api-mir-novel1c-2-5p
8	AAAGTGTTATTTTGATCTTCTT	api-mir-novel1c-2-3p
9	TGAGATCATATAACTTTAT	api-mir-novel1c-3-5p
10	AAAGTGTTATTTTGATCTTCTT	api-mir-novel1c-3-3p
11	TGAGATCATATAACTTTAT	api-mir-novel1d-5p
12	AAAATGTTATTTTGATCTTCTT	api-mir-novel1d-3p
799	TACCCTGTAGATCCGAATTTGT	api-mir-10-5p
800	CAAATTCGGTCTAGAGAGGTTT	api-mir-10-3p
801	AAGAGAGCTATCCGTCGACAGT	api-mir-281-5p
802	TGTCATGGAGTTGCTCTCTTTA	api-mir-281-3p

Biologists files

microRNA_disc_Ti_vs_Tj_edgeR_distance_profilesDiff.csv

	A	B	C	D
1	nom	sexué	asexué	règle
2	aagagagctatccgtcgacagt	1,0,0	0,0,0	diminution
3	aatggcactgaaagaattcacggg	1,0,0	0,0,0	diminution
4	aaltaattggagagtcagtagc	1,0,0	0,0,0	diminution
5	acggcgaaggtttc atcaatc	0,1,1	0,0,1	diminution
6	agcgaagatgaggcaagctgt	1,1,0	1,0,0	diminution
7	atattgtcctgtcacagcag	1,0,0	0,0,0	diminution
8	caatgccttagaaatcccatg	1,1,0	1,0,0	diminution
9	gtgagcaagtttcaggtgtgc	1,0,0	0,0,0	diminution
10	taggccggcggaaactactagc	1,1,0	1,0,1	retard
11	tcagctttttctctcctat	1,1,0	1,0,0	diminution
12	tcggcgtaacatgatgtgtgcg	1,0,0	0,0,0	diminution
13	tggaatgtaagaagatggag	1,1,0	0,0,1	nulle
14	tggcagtgtaggactggtgtg	0,0,0	0,0,1	augmentation
15	tgtcttttccgcttctgctcgcg	0,0,0	0,0,1	augmentation
16	ttttctgtcgggtgtgtg	-1,0,0	0,0,0	augmentation

correspondance_mirdeep2_mirbaseNom_seq5p3p.csv

	A	B
1	TGAGATCATATAATACTTTAC	api-mir-novel1a-5p
2	AAAGTGTGTTTTGATCTCATT	api-mir-novel1a-3p
3	TGAGATCATATAAACTTTAT	api-mir-novel1b-5p
4	AAAGTGTATTTTGATCTTCAT	api-mir-novel1b-3p
5	TGAGATCATATAATACTTTAT	api-mir-novel1c-1-5p
6	AAAGTGTATTTTGATCTTCTT	api-mir-novel1c-1-3p
7	TGAGATCATATAATACTTTAT	api-mir-novel1c-2-5p
8	AAAGTGTATTTTGATCTTCTT	api-mir-novel1c-2-3p
9	TGAGATCATATAATACTTTAT	api-mir-novel1c-3-5p
10	AAAGTGTATTTTGATCTTCTT	api-mir-novel1c-3-3p
11	TGAGATCATATAATACTTTAT	api-mir-novel1d-5p
12	AAAGTGTATTTTGATCTTCTT	api-mir-novel1d-3p
799	TACCCTGTAGATCCGAATTTGT	api-mir-10-5p
800	CAAATTCGGTTCTAGAGAGGTTT	api-mir-10-3p
801	AAGAGAGCTATCCGTCGACAGT	api-mir-281-5p
802	TGTCATGGAGTTGCTCTCTTTA	api-mir-281-3p

Linking data using triples



Linking data using triples



Subject Predicate Object

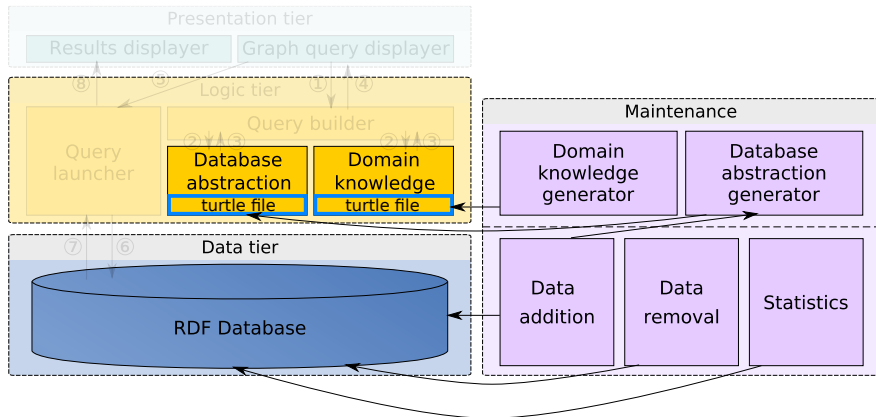
Resource Description Framework

- RDF allow to store the information in the form of triples
- Several syntaxes for this purpose
 - ▶ RDF/XML
 - ▶ Turtle
 - ▶ N-Triples
 - ▶ N3
 - ▶ ...

Integration work

Parse all the data describing our RNA regulation network in order to build an RDF database

AskOmics: Integration



Source files RDF conversion

- Numerous solutions for automatic conversion:
 - ▶ RDF123¹
 - ▶ XLWrap¹
 - ▶ csv2rdf4lod¹
 - ▶ Tarql¹
 - ▶ Datalift²
- Difficult in case of heterogeneous files
- Custom scripts dedicated to each source file
- New generic import script for standardized source files (and guidelines for biologists)

¹ <http://www.w3.org/wiki/ConverterToRdf>

² <http://mondeca.com/index.php/en/>

Generating additional RDF while source files conversion

- Database abstraction
 - ▶ Description of all classes, data properties and object properties
 - ▶ Useful for the interrogation part of AskOmics
 - ▶ Generated on the fly during data conversion
- Domain knowledge
 - ▶ Customizable additional information facilitating interrogation process:
 - ★ Startpoints definition
 - ★ Shortcuts definition
 - ★ Define hidden classes to the user

Use case #1

We want to obtain the messengerRNA cis-regulated by a lncRNA and being also the target of a microRNA. We want each of these RNA to have a differential trend of expression comparing sexual and asexual Aphid peas, this trend being “increase” for the microRNA.

PREFIX : <<http://www.irisa.fr/dyliss/base/>>

SELECT DISTINCT ?messengerRNA1 ?lncRNA1 ?microRNA1

WHERE { ?messengerRNA1 a :messengerRNA .

?lncRNA1 a :lncRNA .

?lncRNA1 :cis_regulates ?messengerRNA1 .

?microRNA1 a :microRNA .

?microRNA1 :has_target ?messengerRNA1 .

?messengerRNA1 :studied_in/:has_results/:trend ?trend1 .

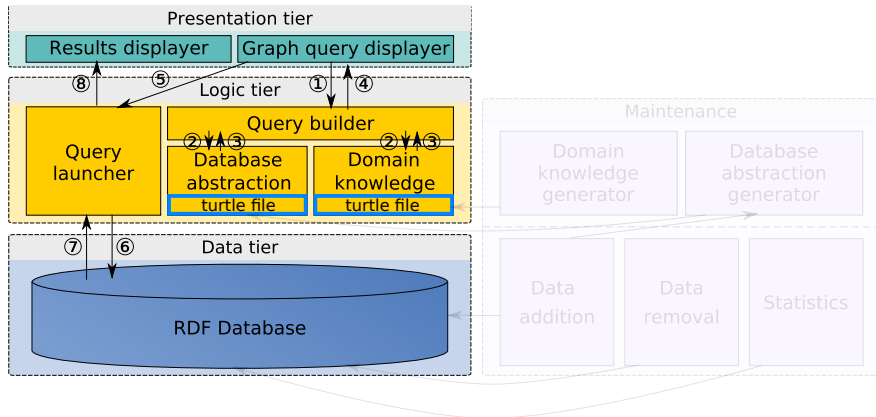
?lncRNA1 :studied_in/:has_results/:trend ?trend2 .

?microRNA1 :studied_in/:has_results/:trend ?trend3 .

FILTER (regex(str(?trend3), "increase", "i")) .

}

AskOmics: Interrogation



Simple use case with AskOmics

All microRNA targeting a lncRNA, altogether having a differential trend between sexual and asexual Aphid peas.

Simple use case with AskOmics

Use case #1 with AskOmics

We want to obtain the messengerRNA cis-regulated by a lncRNA and being also the target of a microRNA. We want each of these RNA to have a differential trend of expression comparing sexual and asexual Aphid peas, this trend being “increase” for the microRNA.

Try it!

- Which piRNA having a trend "increase" overlap with messengerRNA having a trend "decrease"?
- Which microRNA having a trend "increase" target messengerRNA having a trend "decrease"?
- Which piRNA having a trend "increase" overlap with messengerRNA having a trend "decrease" and being the target of a microRNA having a trend "increase"?
- Which target of the microRNA "api-mir-2c-5p" have a trend "decrease" and are also cis-regulated?
- Which messengerRNA targeted by a microRNA are also overlapping a piRNA and are cis-regulated by a lncRNA, these last three RNA having a differential trend?

Conclusion

