A short overview of a developed state of things

I. My background

II. Data-bases vs Knowledge-bases in a nutshell

III. Current work-flow for Mycoplasma:

1. Schematically
2. Sequentially
3. Visually

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2016, Mar: contract with **CRG**

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cellular phenotype

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Cellular phenotype is the conglomerate of multiple **cellular** processes involving gene and protein expression that result in the elaboration of a **cell's** particular morphology and function. May 5, 2009

Transcriptome transfer produces a predictable cellular phenotype
www.pnas.org/content/106/18/7624.full

About this result • Feedback

Cellular Phenotype Database - European Bioinformatics Institute
www.ebi.ac.uk/fg/sym
The **Cellular Phenotype** database provides easy access to phenotypic data derived from high-throughput screening, facilitating data sharing and integration.

Cellular Phenotype Ontology < EMBL-EBI
www.ebi.ac.uk/cmpo/
The **Cellular** Microscopy **Phenotype** Ontology (CMPO) provides a species-neutral controlled vocabulary for describing **phenotypic** qualities relating to the whole ...

Phenotype - Wikipedia, the free encyclopedia
https://en.wikipedia.org/wiki/**Phenotype**
A **phenotype** is the composite of an organism's observable characteristics or traits, such as its ... (living) organism in itself, meaning that the lowest level of biological organization compatible with the **phenotype** concept is at the **cellular** level.
Genotype-phenotype distinction · Endophenotype · Genotype · Phenology

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cellular phenotype

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Cellular Phenotype Database - European Bioinformatics Institute
www.ebi.ac.uk/fg/sym
The **Cellular Phenotype** database provides easy access to phenotypic data derived from high-throughput screening, facilitating data sharing and integration.

Cellular Phenotype Ontology < EMBL-EBI
www.ebi.ac.uk/cmpo/
The **Cellular** Microscopy **Phenotype** Ontology (CMPO) provides a species-neutral controlled vocabulary for describing **phenotypic** qualities relating to the whole ...

Phenotype - Wikipedia, the free encyclopedia
https://en.wikipedia.org/wiki/**Phenotype**
A **phenotype** is the composite of an organism's observable characteristics or traits, such as its ... (living) organism in itself, meaning that the lowest level of biological organization compatible with the **phenotype** concept is at the **cellular** level.
Genotype-phenotype distinction · Endophenotype · Genotype · Phenology

Genes to Phenotypes Heat-maps

8 genes found: **export search results**

Gene	Internal ID	Cell death	Enhanced secretion	Grape	Intracellular retent...	Intracellular retent...	Large	Mitotic delay	Polylobed
	Screen:	M1	E1	M1	B1	B1	M1	M1	M1
1. DHX15	• AMBN10032577		1			0.5			
	• AMBN10032589							0.6	
2. DNM1P34	• AMBN10036793		1						
	• AMBN10044542					1	0.6	0.6	
	• AMBN10044554						0.6		
3. EDDM3A	• AMBN10023464		1						
	• AMBN10023465							0.5	
4. MST4	• AMBN10001057		1					0.6	
	• AMBN10001059				0.5				
5. PRR14L	• AMBN10023595				0.5				
	• AMBN10023596		1		0.5				
	• AMBN10035846						0.5	0.5	0.5
6. PRSS55	• AMBN10004579		1						
	• AMBN10004580				0.5	0.5			
	• AMBN10004581	0.6						0.6	
7. RAD23A	• AMBN10027133	1		1				1	1
	• AMBN10027134		1						
8. SV2B	• AMBN10032015		1						
	• AMBN10032025							0.5	

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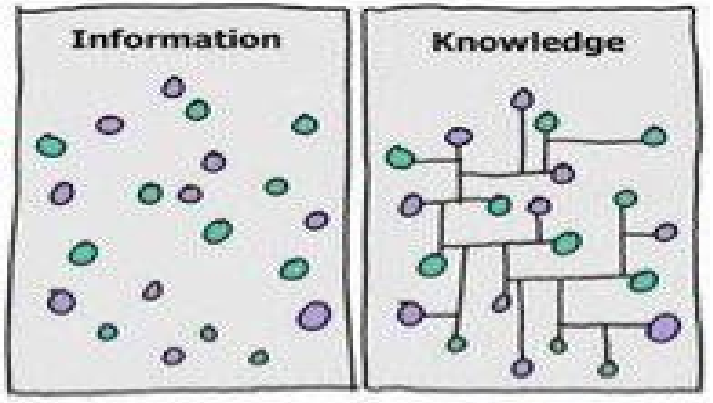

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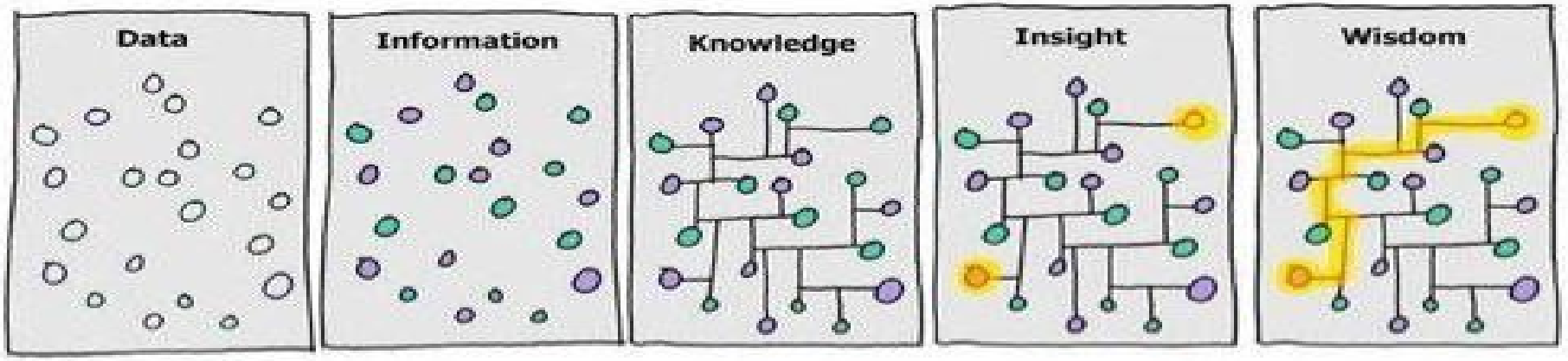

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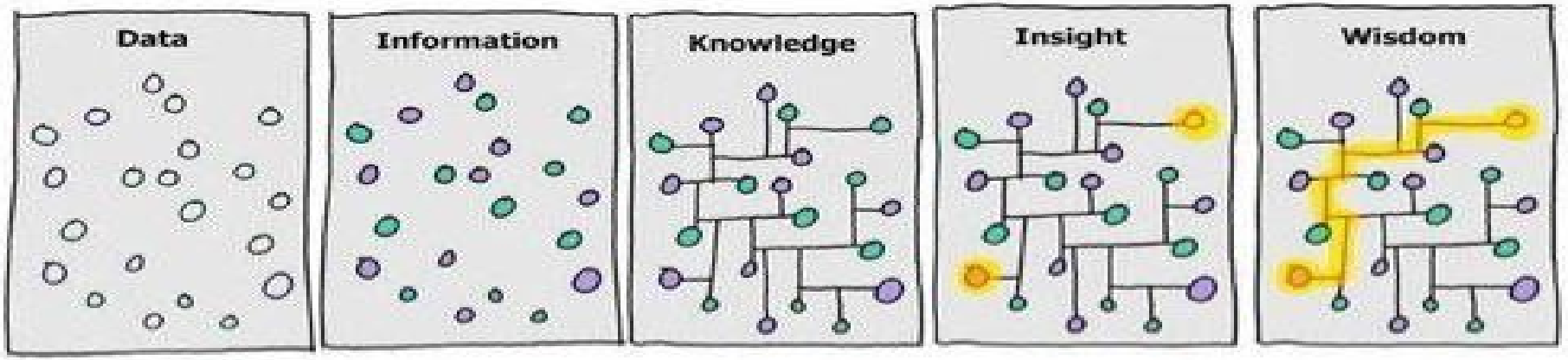

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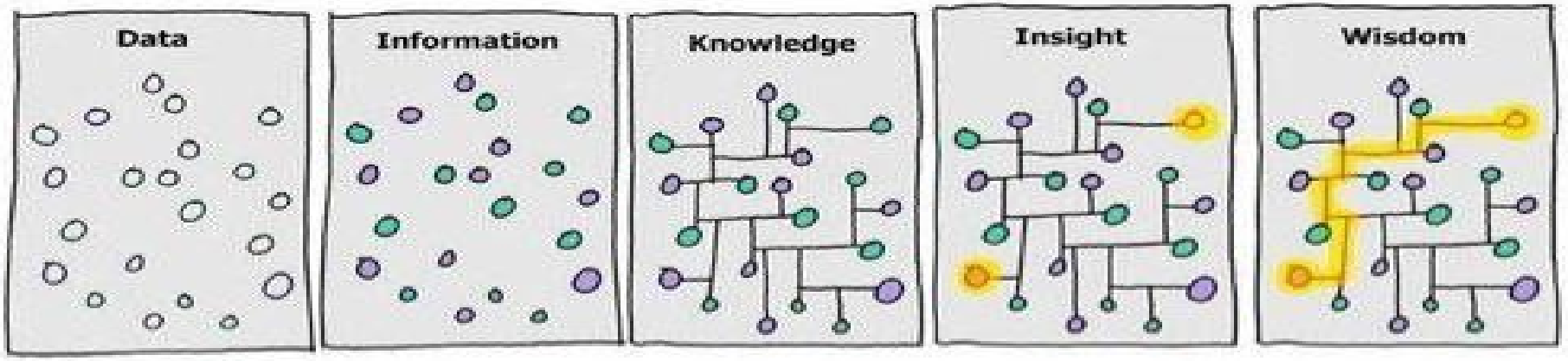

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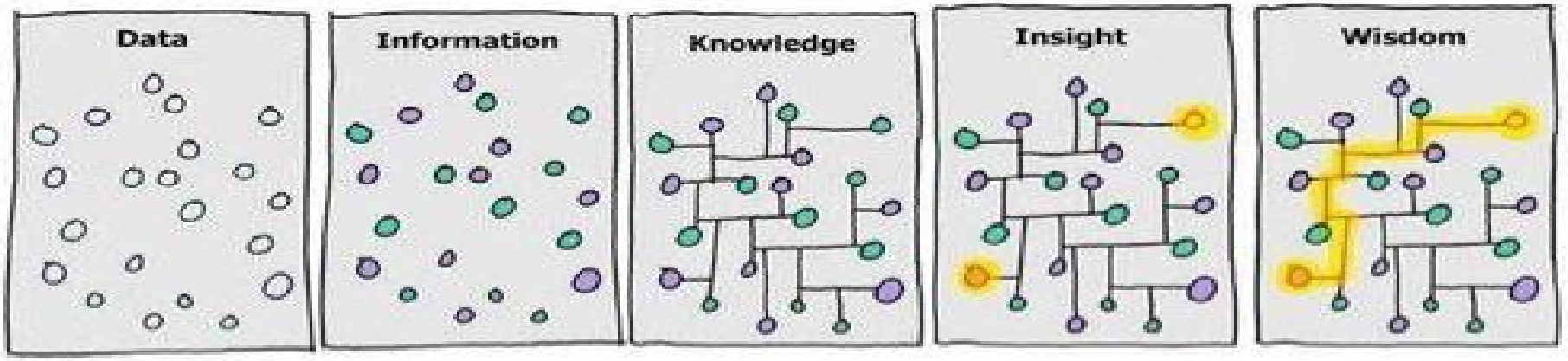

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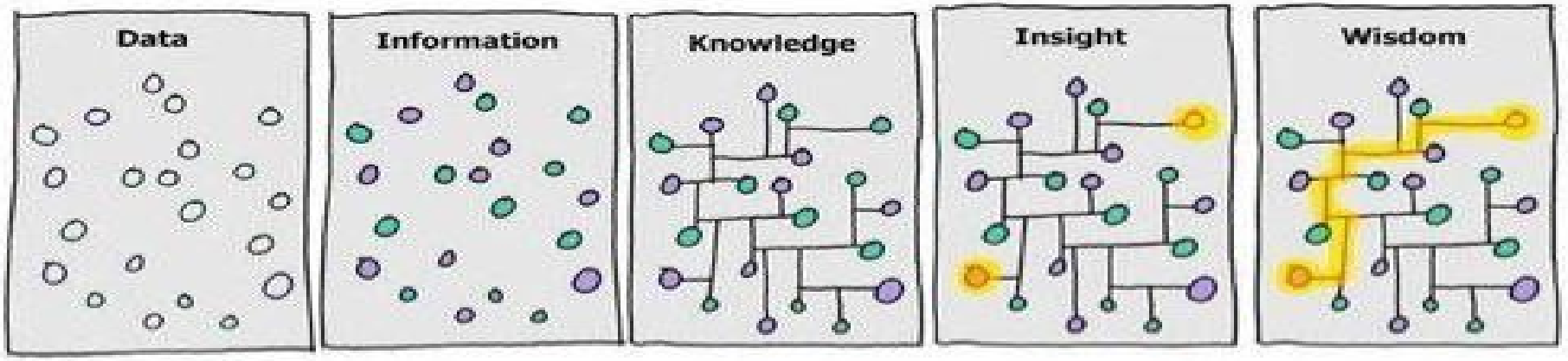

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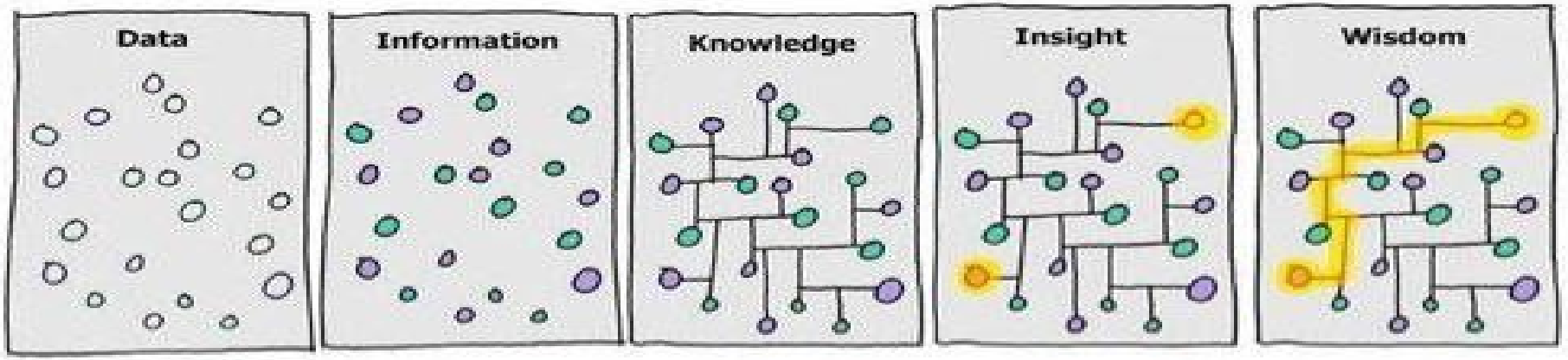

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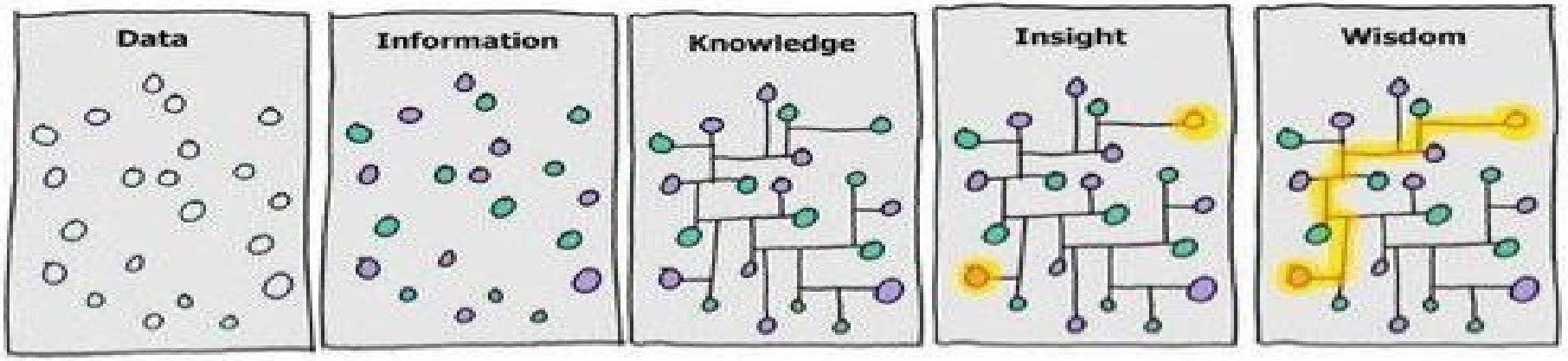

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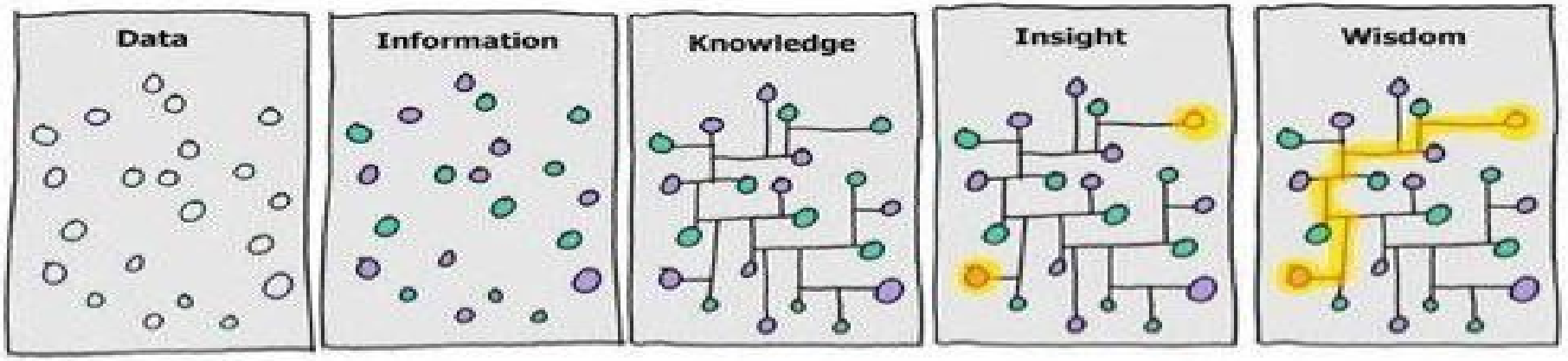

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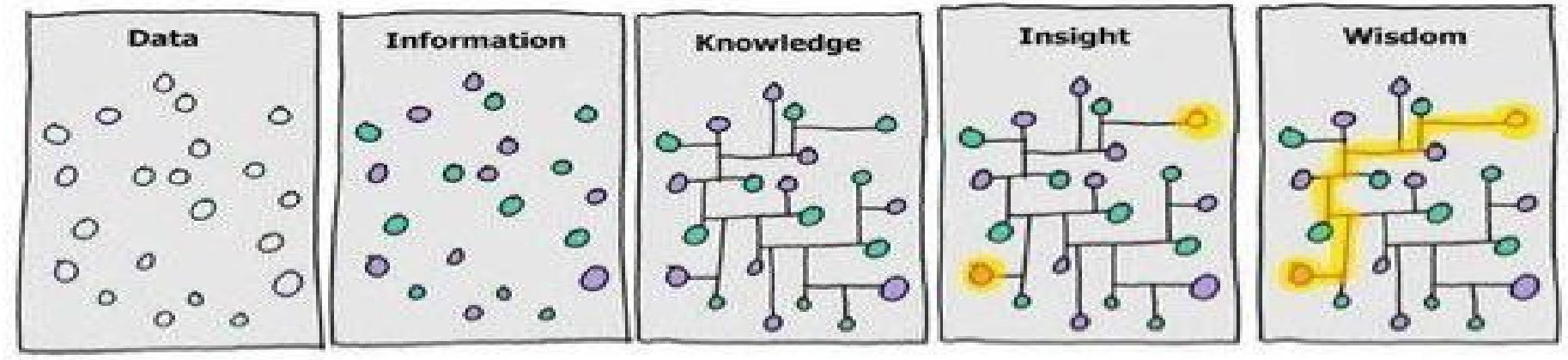

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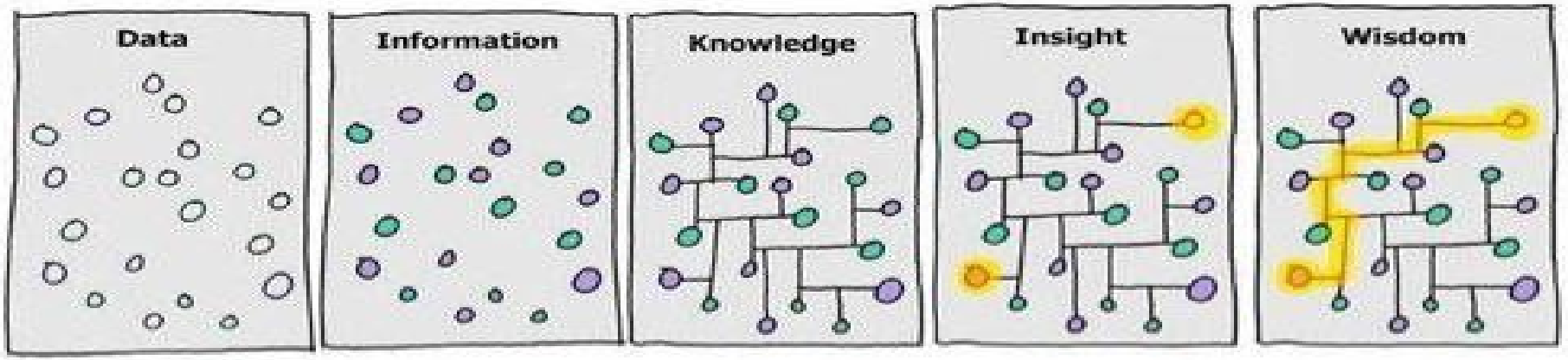

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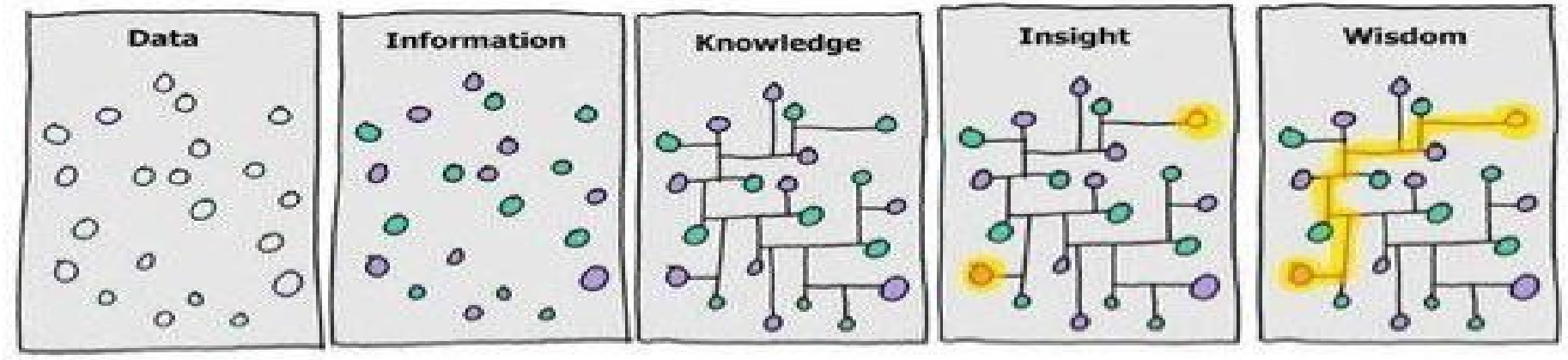

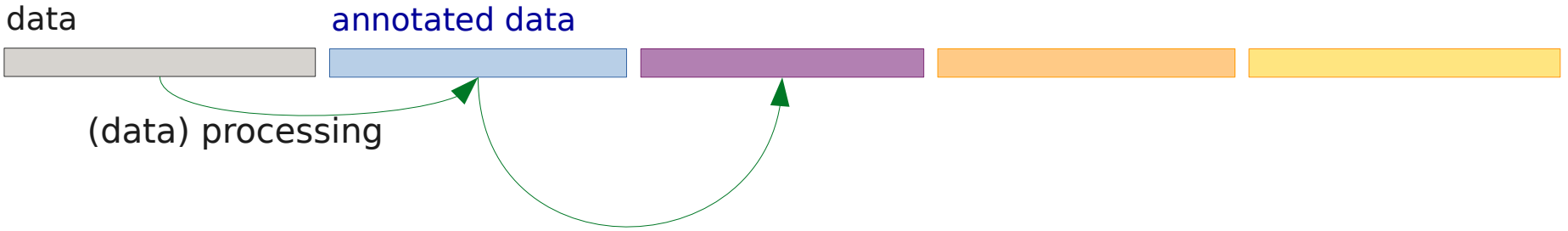

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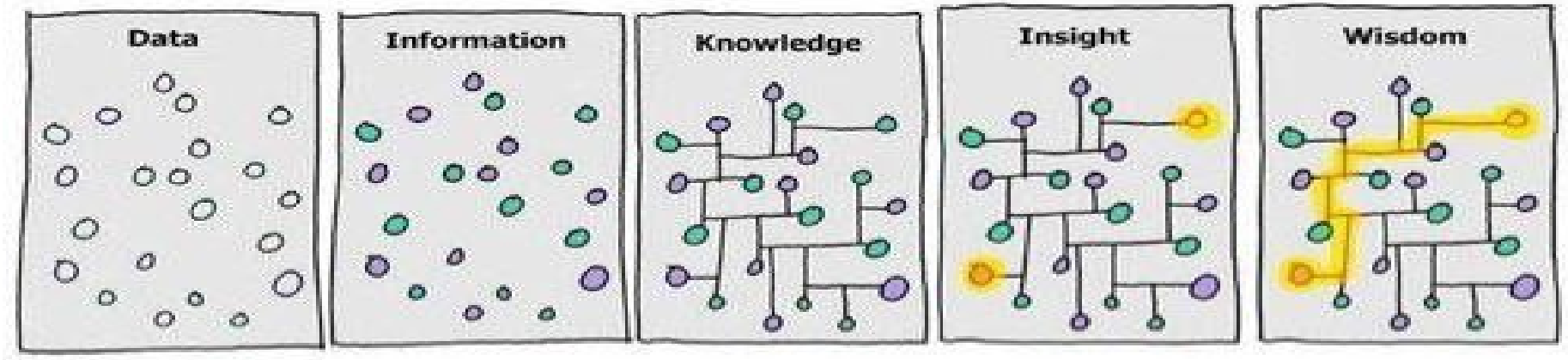

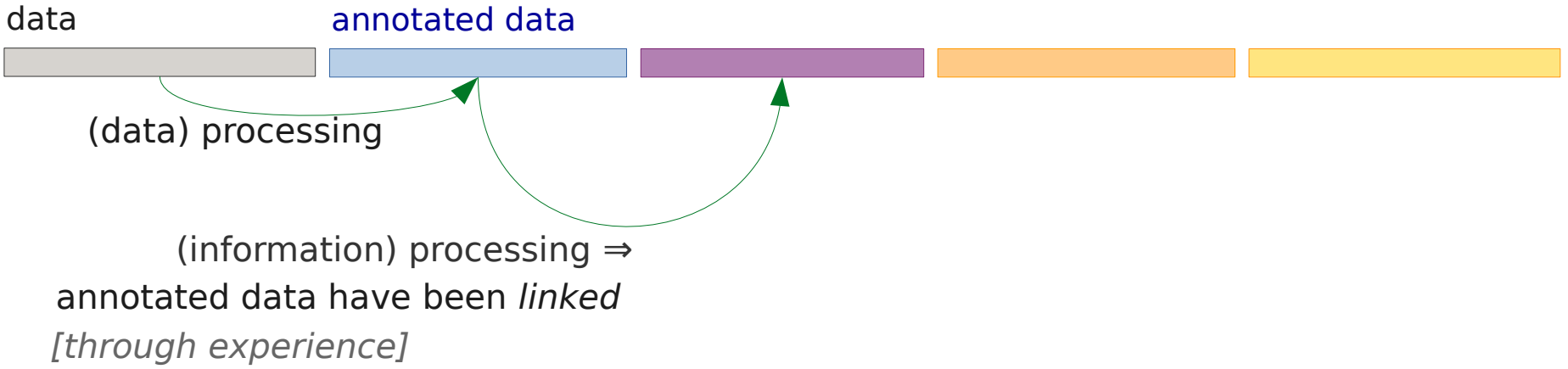

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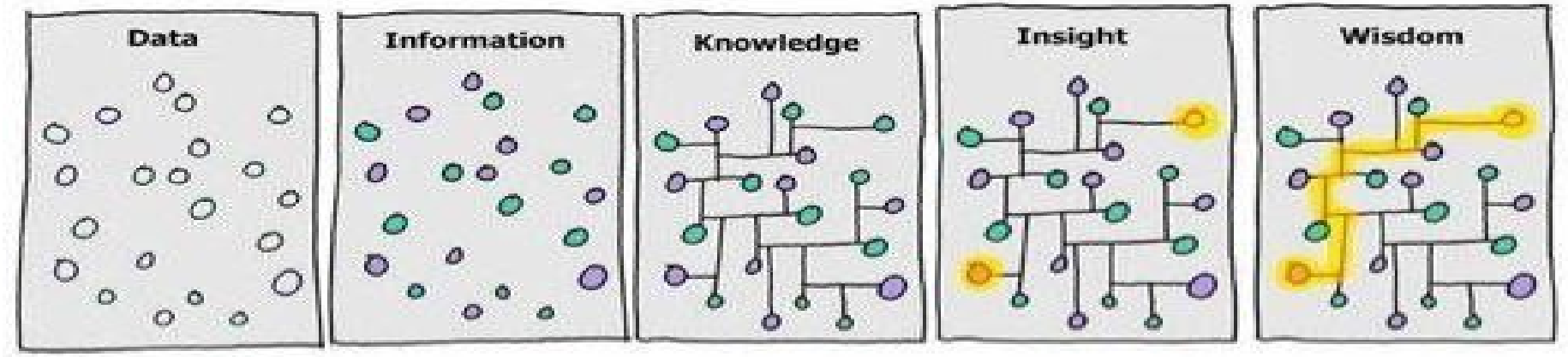

linked

data

annotated data

(data) processing

(information) processing ⇒
annotated data have been *linked*
[through experience]

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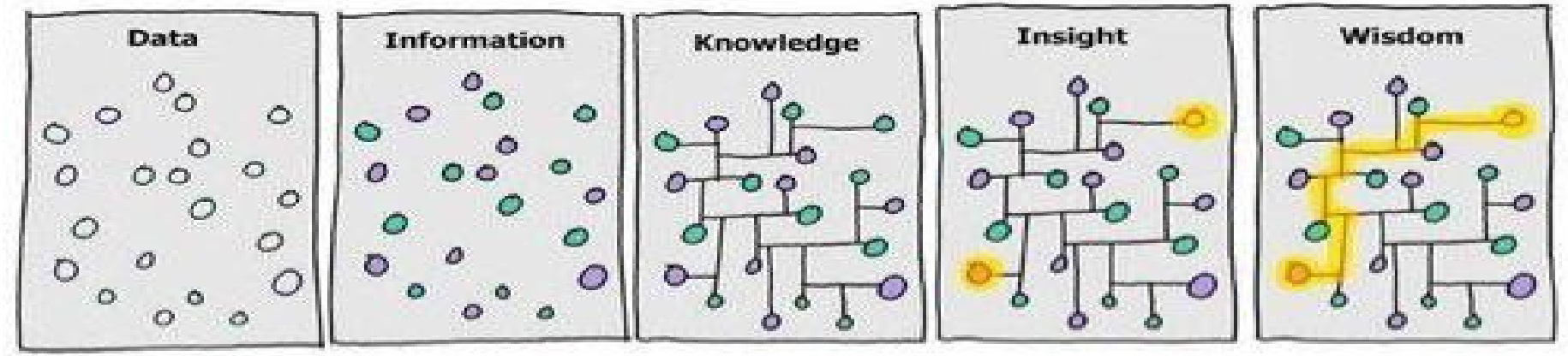

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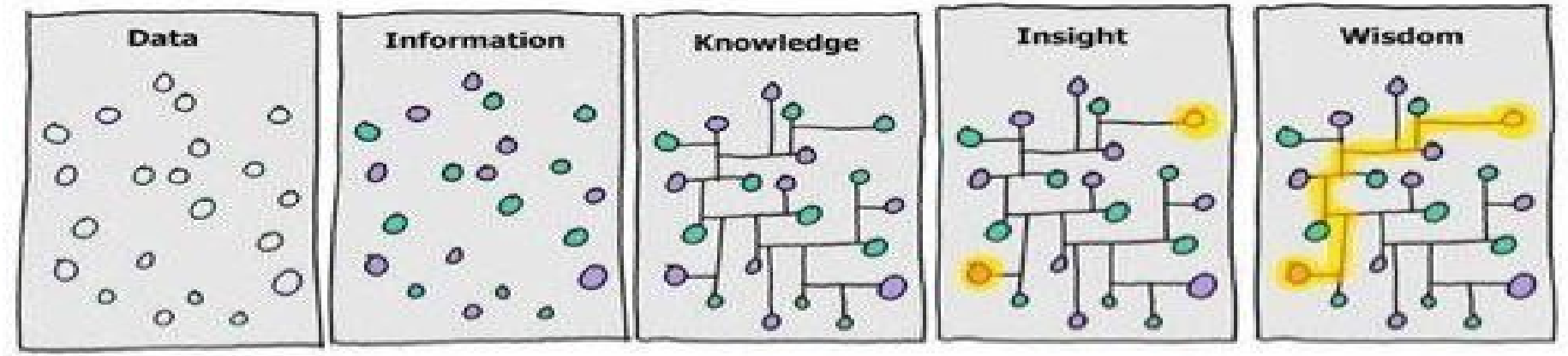

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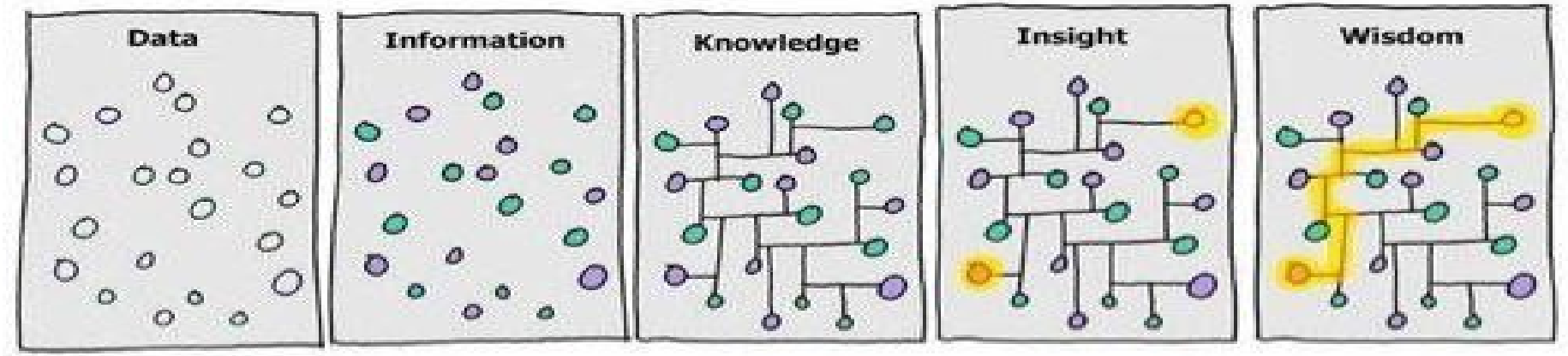

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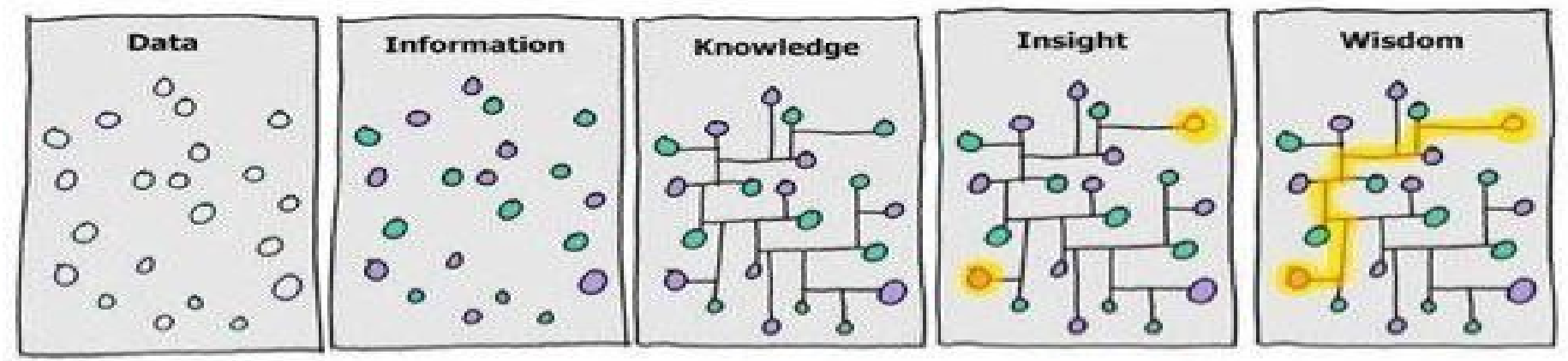

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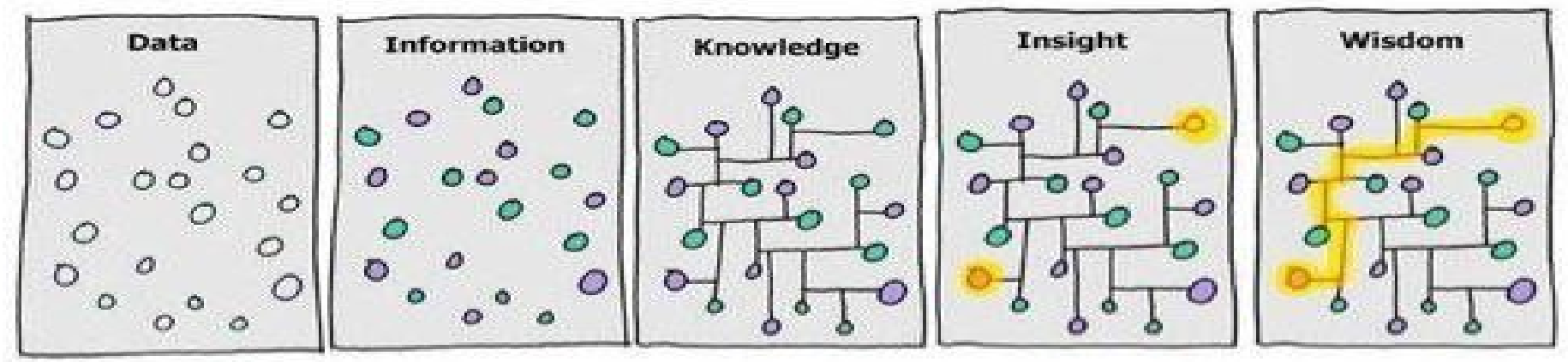

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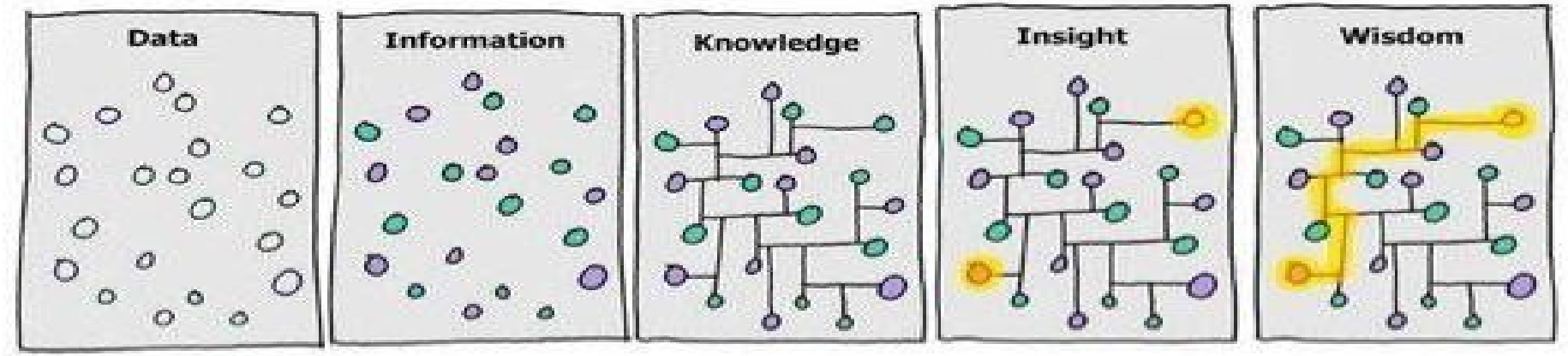

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pathways/how-to trial/finding

knowledge/*experience* processing

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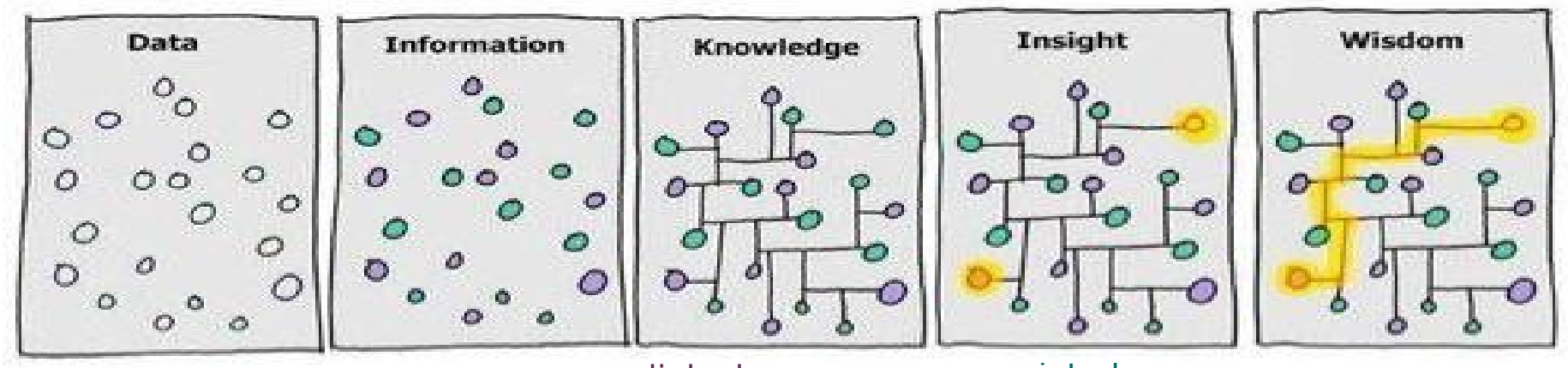

data

annotated data

linked information

associated knowledge

lore/skills

(data) processing

(information) processing ⇒
annotated data have been *linked*
[through experience]

associations processing ⇒
pathways/how-to trial/finding

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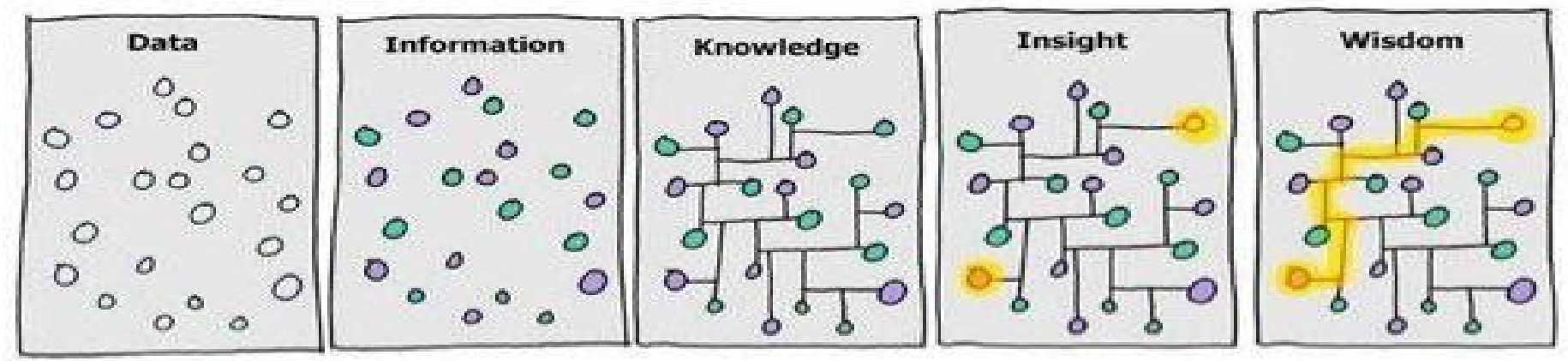

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⇓

Model Verification

knowledge/*experience* processing

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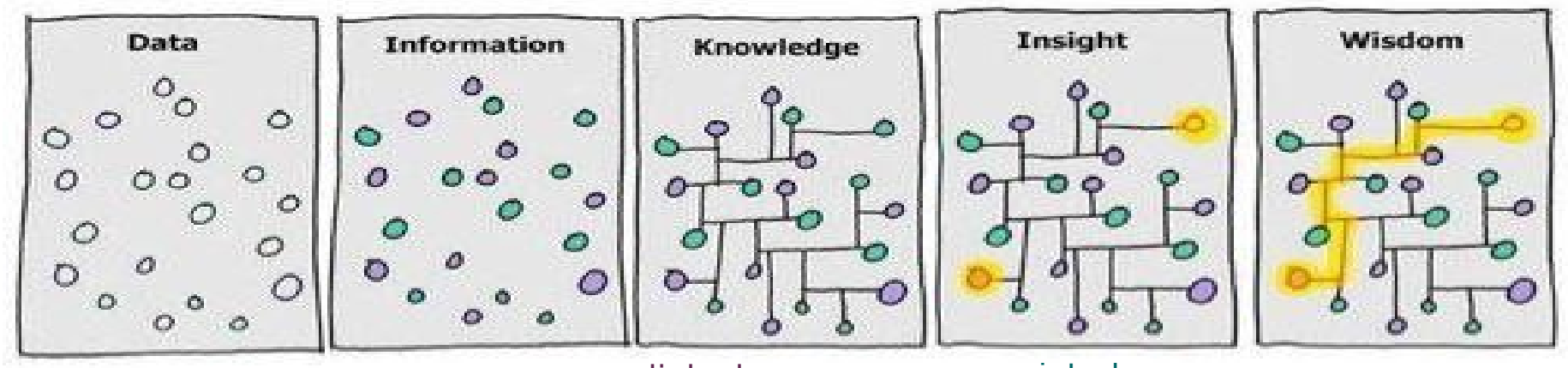

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Model Verification
Or

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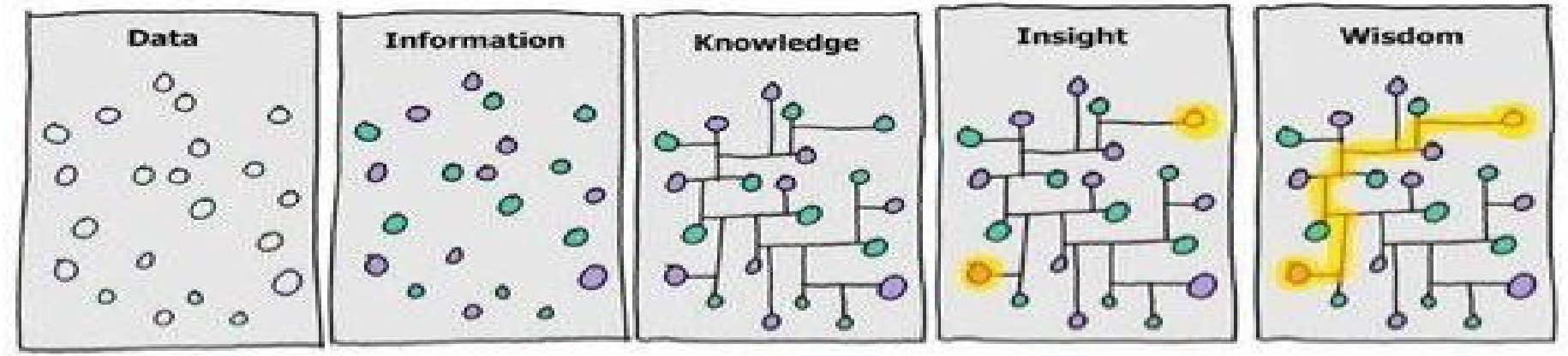

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pathways/how-to trial/finding

⇓

Model Verification
Or
Paradigm Change

I. My background

II. Data-bases vs Knowledge-bases in a nutshell

III. Current work-flow for Mycoplasma:

1. Schematically

2. Sequentially

3. Visually

IV. Q & A

Current work-flow for Mycoplasma

Scheme

Legend:

processed data:

data sources:

released job's results:

data

job

data flow

DB with annotated/scored [ORFs]

Current work-flow for Mycoplasma

Scheme

Legend:

processed data:

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data

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data flow

DB with annotated/scored [ORFs]

Full genome seqs

Annotated seq data

MetaData for RNAseq

PILE files with read counts per base

Sample

Parametrized MS data with study MetaData

MS mzXML file

MS RAW data

Current work-flow for Mycoplasma

Scheme

Legend:

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data sources:

released job's results:

data

job

data flow

DB with annotated/scored [ORFs]

ORFs search [getorf]

Full genome seqs

Conservation search [blast: diamond]

Annotated seq data

Annotation with MS data

Sample

Parametrized MS data with study MetaData

MS Stuy

Annotation with proteome data [blast: diamond]

MetaData for RNAseq

MzXML file processing

PILE files with read counts per base

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MS RAW data

Annotation with MetaData

data converting

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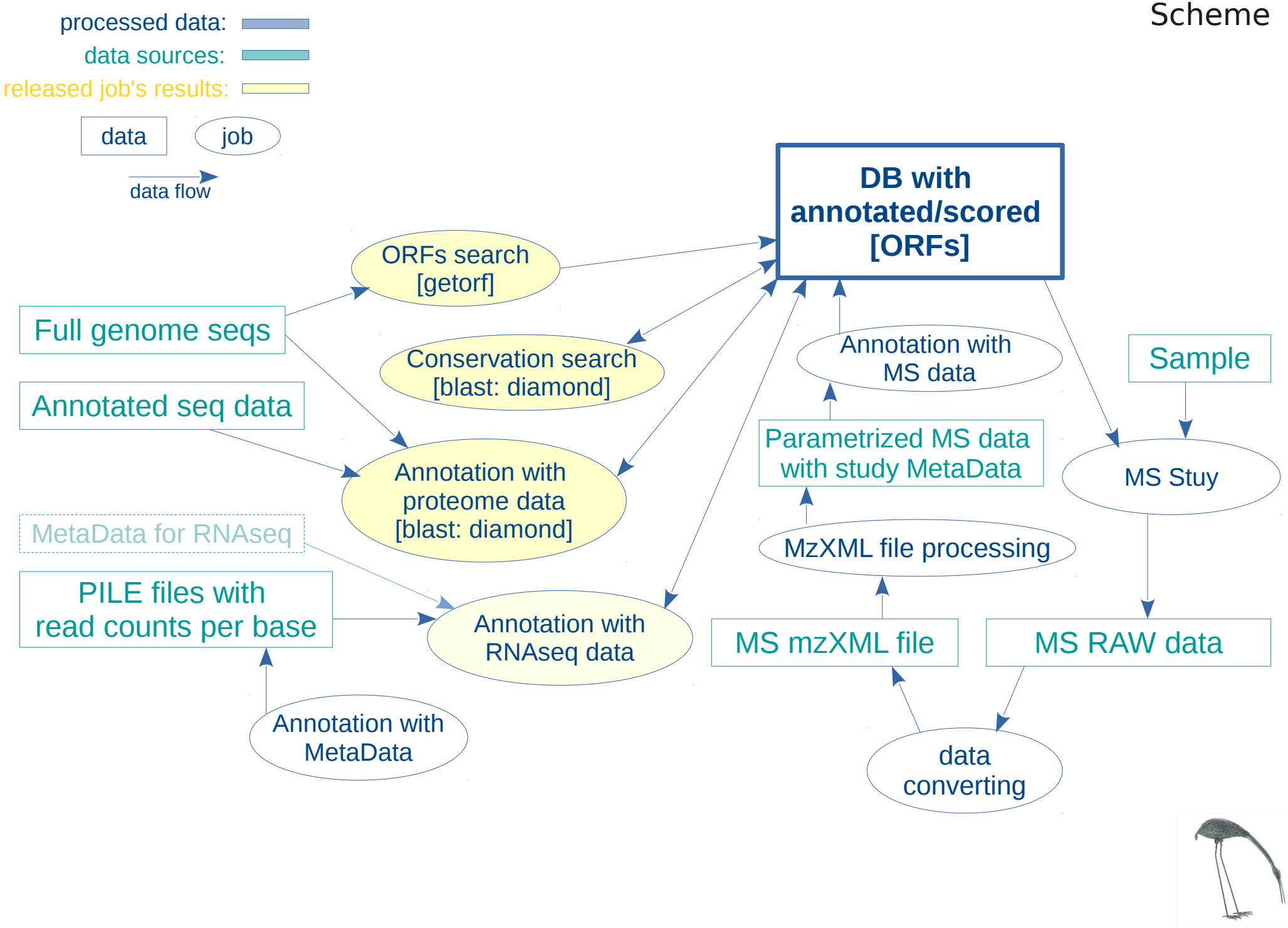
Current work-flow for Mycoplasma

Scheme



Current work-flow for Mycoplasma

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Legend:

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data sources:

released job's results:

data

job

data flow

Scoring

DB with annotated/scored [ORFs]

ORFs search [getorf]

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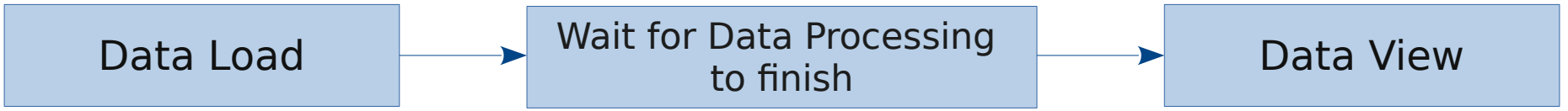
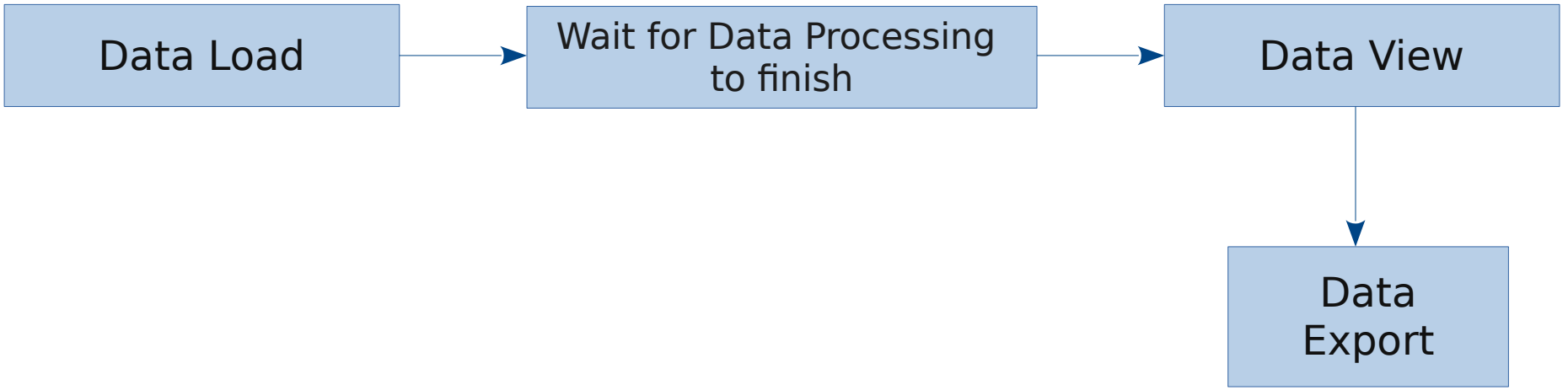
Current work-flow for Mycoplasma

Sequential steps for users



Current work-flow for Mycoplasma

Sequential steps for users



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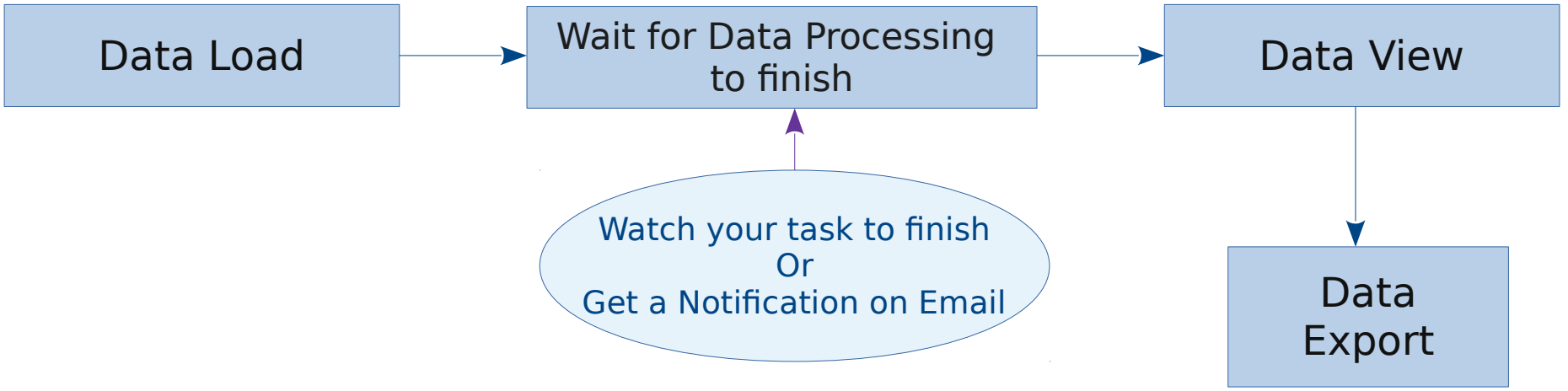
Sequential steps for users



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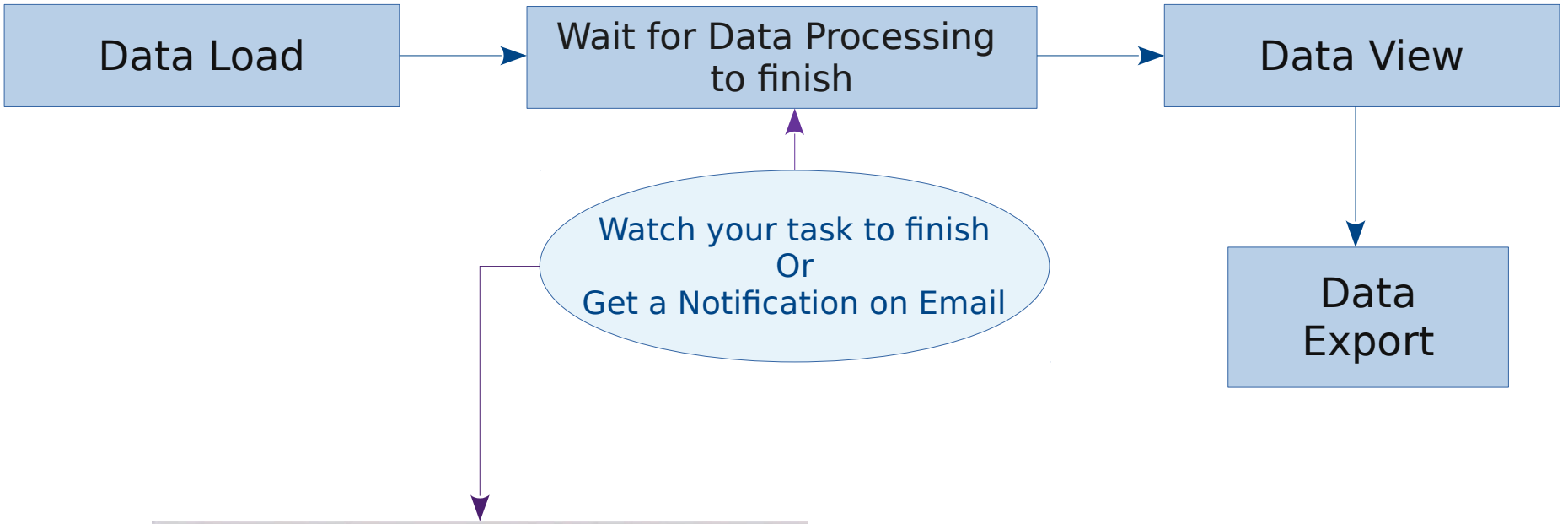

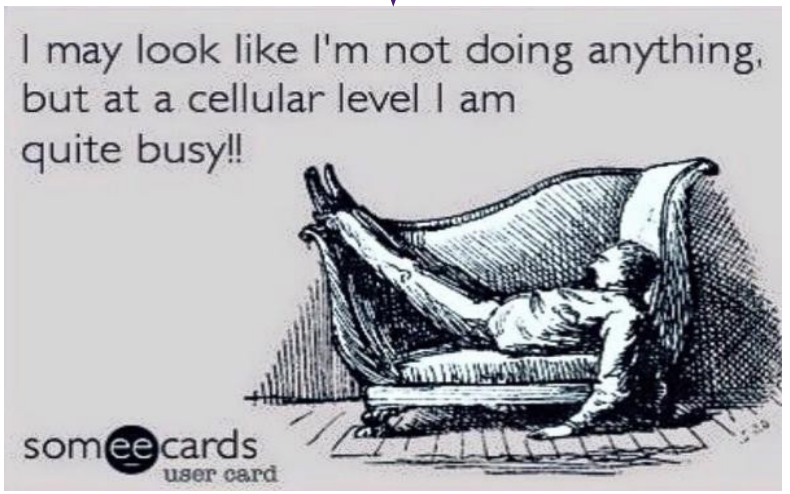

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Current work-flow for Mycoplasma GUI

Data Load → Wait for Data Processing to finish → Data View

M Home | Tools | Studies | Pipelines | Data | Search | Submit | Login | System

Genome Annotation → ORFs search | Conservation search | RNAseq validation | MS validation

RNAseq data mapping

ORFs data to attach RNAseq data	PILE file	Experiment metadata

Showing 1 to 4 of 4 entries **Search:**

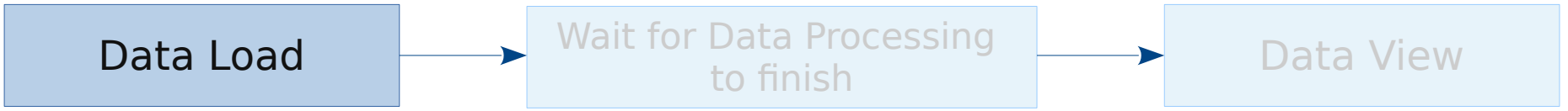
Species, strain
Mycoplasma Pneumoniae, M129
Mycoplasma Genitalium, G37
Mycoplasma Gallisepticum, S6
Mycoplasma Conjunctivae, HRC/581T

Browse …

Specification is to be provided!

Submit

Current work-flow for Mycoplasma GUI



M Home Tools Studies Pipelines Data Search Submit Login System

This file is already in the system and the task is NOT launched!

RNAseq data mapping

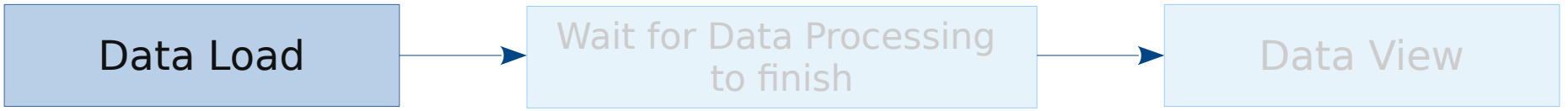
As soon as your task is finished the information will be posted to your email (if you are signed in).
Also, you can watch task page for the updates on time when the task is finished.

Species name to attach RNAseq data of ORFs:
Mycoplasma Pneumoniae, M129

Your PILE file name:
Tn223_gly_2_11013_GTGAAA_read.pile

Your PILE file md5sum:
0d298a39e1529c7faedbe6bbca7f5a82

Current work-flow for Mycoplasma GUI



M Home Tools Studies Pipelines Data Search Submit Login System

Your task is launched, process's pid is: **24377**

RNAseq data mapping

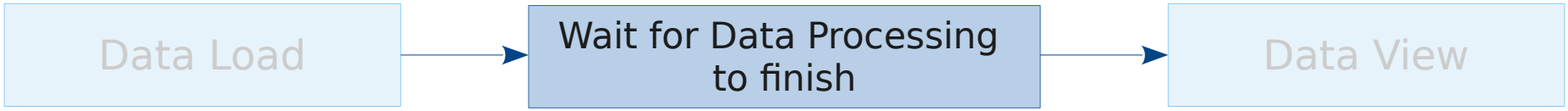
As soon as your task is finished the information will be posted to your email (if you are signed in).
Also, you can watch task page for the updates on time when the task is finished.

Species name to attach RNAseq data of ORFs:
Mycoplasma Pneumoniae, M129

Your PILE file name:
TF433_6h_1_11032_TTAGGC_read.pile

Your PILE file md5sum:
e5998991224633fc3ad981a34a1991ed

Current work-flow for Mycoplasma GUI



M Home | Tools | Studies | Pipelines | Data | Search | Submit | Login | System

System → About / Browse tasks / Help

System tasks

Showing 1 to 7 of 7 entries

Search:

	Task name	Pid	Started	Finished	Status	
1	ORFs search	16158	2016-07-07 19:02:10.321000	2016-07-07 19:02:24.139000	delivered	admin
2	ORFs search	17278	2016-07-07 19:03:23.339000	2016-07-07 19:03:36.105000	delivered	admin
3	ORFs search	18876	2016-07-07 19:05:08.276000	2016-07-07 19:05:25.602000	delivered	admin
4	Conservation search	27159	2016-07-18 15:00:47.793000	2016-07-18 15:02:45.558000	delivered	admin
5	MS data processing	29872	2016-07-18 16:08:47.800000	2016-07-18 16:08:50.133000	delivered	admin
6	RNAseq maps	20138	2016-07-19 10:44:11.646000	2016-07-19 10:49:28.118000	delivered	admin
7	RNAseq maps	28301	2016-07-19 11:19:10.298000	2016-07-19 11:24:26.395000	delivered	admin

Show 50 entries

First | Previous | 1 | Next | Last

Current work-flow for Mycoplasma GUI

Data Load → Wait for Data Processing to finish → **Data View**

M Home | Tools | Studies | Pipelines | Data | Search | Submit | Login | System

Data → ORFs / Conservation / RNAseq / MS data

RNAseq for Mycoplasma Pneumoniae, strain M12

Overlaping: if you are looking at annotated or putative ORFs … ORFs in an overlap bunch.
For all ORFs in an overlap bunch please click show all ORFs.

show annotated ORFs only
show putative ORFs only
show all ORFs

Showing 101 to 150 of 13,041 entries

Search:

orf_id	J_id	start	end	strand	length	FPKM data	exprScore	FPKM data	exprScore	locus tag	# found ORFs [consrv]	overlaps
100	id00227	14992	15762	+	257	0.75	7.95	0.75	7.19	MPN013	0	100
101	id00235	15794	15859	+	22	0.12	1.34	0.18	1.81		0	101
102	id00236	15829	15888	+	20	0.13	1.42	0.2	2.0		0	101
103	id00240	16090	16149	+	20	0.34	3.61	0.17	1.66		0	101
104	id00237	15867	16502	+	212	0.34	3.63	0.24	2.32	daE	1	101
105	id00243	16573	16656	+	28	0.36	3.81	0.28	2.72		1	105
106	NF	16696	16749	+	18	0.35	3.72	0.34	3.28		0	106
107	NF	16743	16796	+	18	0.32	3.46	0.33	3.24		0	106
108	id00245	16790	16873	+	28	0.34	3.61	0.32	3.1		0	106
109	id00247	16923	17033	+	37	0.29	3.14	0.24	2.37		0	109

Current work-flow for Mycoplasma GUI

Data Load → Wait for Data Processing to finish → Data View

M Home | Tools | Studies | Pipelines | Data | Search | Submit | Login | System

Data → ORFs / Conservation / RNAseq / MS data

ORFs for Mycoplasma Pneumoniae, strain M129 (only putative orfs)

show annotated ORFs only
show putative ORFs only
show all ORFs

Showing 1 to 7 of 7 entries (filtered from 12,346 total entries)

Search: AAAAAAAAA

orf_id	J_id	start	end	strand	length	nucleotides seq	peptides seq
1387	NF	199622	199675	+	18	TTGGTTTTAAAAGTAATTTCAAAAAAAAATAATAACACACTGAGTAGAACCATT	MVLKVISKKNNNTLSRTI
4726	id09746	641127	641216	+	30	TTGAACCAGAGTCAAACCATACTTCCAAGGTATCAGTTTCCTTTTTATATTCAACTCCT GGCTGTATTTTCTTTGGGTTTAAAAAAAAAT	MNQSQTILPRYQFPFYIQLLAVF SLGLKKN
6310	id12361	811915	811787	-	43	ATGGGATTCCCCTGCGCGCTGGGATTGCTCGCTTTCCTGGTGATAAAGGGAAGGGTGAG GATAAGAAAACTACTAAAAAAAAATCAGAAATCAAGCAAGCGAGTAGTGCCACAACAGT TTTACAACCGT	MGFPCALGLLAFLVIKGRVRIRK LLKKNQKSSKRVVPQQFYNR
6656	id11658	763377	763156	-	74	GTGGTTTCTATATTACCGTCACTTTTAATGTGAATTACGCGTGAATTGAAATCAGTTGA CCAAGGCGATCAAAAGTTAAAGCCGTCAGCAAAGGCTGAAAACATTAAAAAAAAACAAA AGACAATGAGCAAAACAACGAACACTGTCGATCGTTTTTTAGCGAAGGAATTATCTTTC AGATCCATTAGACCACTAATAGTTCTTTTTCTTTTTGTTTTTGAA	MVSILPSLLMWITRELKSVDQGD QKLKPSAKAENIKKKQKTMSKTT NTVDRFLAKELSFRSIRPLIVLF LFVFE
7156	id10543	690791	690606	-	62	TTGTCGATAAGAGTTTTGATCAAGCTAAAAACCTGTTGAAGCTACACCTTTCCATTAGT GTGCCTAAACTTAGTCAAAAAAAAATTATTATTGGCCGTAATGCCCAAATGGTGAAAAA GATCGGGATGCAAATGCGTCAAAAACTACTGGAGTACTATGACTGCAATGTCTTTGTGG AATTGTTTG	MSIRVLIKLKTCWSYTFPLVCLN LVKKKLLLAVMPKWWKRSGCKCV KNYWSTMTAMSLWNCL
7677	NF	622654	622601	-	18	TTGCAGTTTCTTTCACCAACCCGTTTTGAGTTCAAACTAAAAAAAAAAAAAAC	MQFLSPTRFEFKLKKKKN
7749	id09334	614065	613883	-	61	ATGATTGAAAATTTCAGTTTTTTAATTAATGTTCAAACCGAAATTTCAATTAGCTTTCC GTTTTTAAAGTTGCTTTTCCAAAAAAAAACAAAATTAAAGAGTTATTTTTACTGTTGAT GCGCAAAAAGAGATTGTTGTCAAGGATTTCCTTTAGTTCTCTATTTTTATTATGTGGAA CAGTTT	MIENFSFLINVQTEISISFPFLK LLFQKKTKLKSYFYCWCAKRDCC QGFPLVLYFYYVEQF
orf_id	J_id	start	end	strand	length	nucleotides_seq	peptides_seq

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IV. Q & A

Questions and Answers

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Would it be possible to chose columns for data view or export?

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— yes

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Could you implement that?

— yes

Other questions please?

Thanks to:

Maria

Samuel

Javier

Eva

Veronica

Eduard

Luis

&

BioCore Unit