Mapping protein file with PPI

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Steps

Clean the input files

- In order to have only the necessary information and eliminate duplicated interactions.
- Files: all_interactions.csv; proteins1.csv; proteins2.csv

Run Python codes

- So we can proceed with the mapping.
- Files: map_proteins1.py; map_proteins2.py

Obtain output files

• Files: mapping1.csv; mapping2.csv

Why two "all_interactions.csv" files?

Notice that in the previous slide we have as input :

proteins1.csv; proteins2.csv

- In the files "proteinsX.csv", we have two interacting proteins with their ensembl codes (so they can be identified).
- For the mapping, first we'll search for ENST similarities for the column C, with the file "'proteins1.csv" and code "map_proteins1.py". And we obtain the file "mapping1.csv".
- Then we do the same process but searching similarities with the file "proteins2.csv" and code "map_proteins2.py". And we obtain the file "mapping2.csv".
- The ENST is a unique ID for each human transcript and contains an 11 digit number. In the protein file this ENST is related with protein it encodes.
- With this methodology we'll obtain a large amount of duplicates as in many cases the ENST is available in both columns and linked to the same interacting protein we found before.
- Notice that proteins are coded with their respectives uniprotkb codes.

Input files

For the "proteins.csv" file some modifications were made. There were a large amount of duplicated interactions.
Some data treatment is done and then these duplicated interactions are deleted.

ld molecule A				Species molecule A		Publication Identifier	Interaction Type		Confidence Value	Exp Role mole
X6RM59	Q9UHD9	X6RM59 [+]	Q9UHD9 [+]	Homo sapiens (9606)	Homo sapiens (<u>9606</u>)	doi:10.1101/605451	· ^	two hybrid prey pooling approach two hybrid array validated two hybrid	hyr:51482 lpr/51482 pp:1	
X6RM59	Q6ICB0	X6RM59 [+]	Q6ICB0 [+]	Homo sapiens (9606)	Homo sapiens (<u>9606</u>)	doi:10.1101/605451	A	two in brid prev pooling epproach two hybrid array validated two hybrid	hpr:51482 lpr:51482 np:1	

Figure 1. There are duplicates in the file because the interaction was detected by more than one method.

• This interacting proteins are distributed in two columns (A, B). And their respective ensembl codes ENST, ENSP and ENSG are in C/D/E for protein 1 and in F/G/H for protein 2. Maybe an specific protein is only available as protein 2 but we have found interesting information about how it can interact, that's why I fliped columns and created "proteins2.csv", where protein 2 takes the role of protein 1 and viceversa.

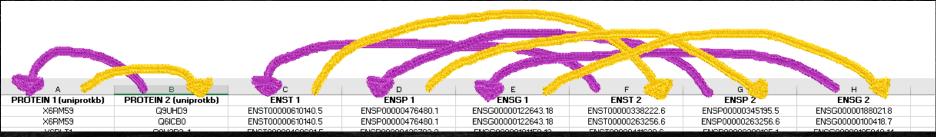


Figure 2. Flip data in file in order to have protein 2 as protein 1 and viceversa.

Input files

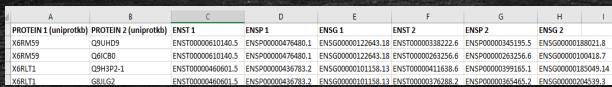


Figure 3. Screenshot of the file "proteins1.csv". For each row we have the two interacting proteins and the respective ensemblid. ENST/ENSP/ENSG 1 are from PROTEIN 1 and ENST/ENSP/ENSG 2 are from PROTEIN 2.

A B		С	D	E	F	G	Н	
PROTEIN 1 (uniprotkb)	PROTEIN 2 (uniprotkb)	ENST 1	ENSP 1	ENSG 1	ENST 2	ENSP 2	ENSG 2	
X6RM59	Q9UHD9	ENST00000610140.5	ENSP00000476480.1	ENSG00000122643.18	ENST00000338222.6	ENSP00000345195.5	ENSG00000188021.8	
X6RM59	Q6ICB0	ENST00000610140.5	ENSP00000476480.1	ENSG00000122643.18	ENST00000263256.6	ENSP00000263256.6	ENSG00000100418.7	
X6RLT1	Q9H3P2-1	ENST00000460601.5	ENSP00000436783.2	ENSG00000101158.13	ENST00000411638.6	ENSP00000399165.1	ENSG00000185049.14	

Figure 4. Screenshot of the file "proteins2.csv". Here protein 1 is protein 2 from the original file and viceversa.

4	А	В	С	D	E	
1	ENST 1	INTERACTING DOMAIN	DOMAIN	LINEAR MOTIF	INTERACTION TYPE	
2	ENST00000428680.6	zf-RING_4	UQ_con		DDI	
3	ENST00000428680.6	RRM_1	2OG-FeII_Oxy_2		DDI	
4	ENST00000428680.6	RRM_1	Bud13		DDI	
5	ENST00000428680.6	RRM_1	CPSF_A		DDI	

Figure 3. Screenshot of the file "all_interactions.csv". Is the output from the mapping with ELM/3DID databases, we can see the domains/ linear motifs interacting for each ENST. Here the ENST has been named ENST 1, so we can search similarities with column ENST 1 in file "proteinsX.csv".

The original file "all_interactions" was obtained in the previous mapping of HuRI with ELM and 3DID databases.

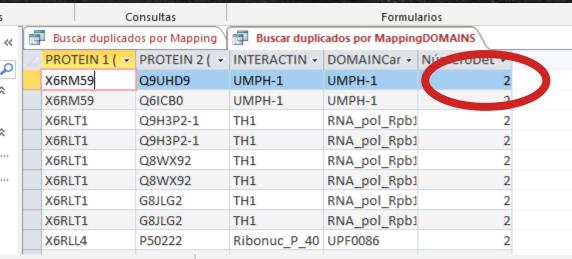
Some information was deleted as there were too many details for each entry. This way we can obtain a precise output with just the information we need.

Our goal is to obtain a file with the two interacting proteins and which interactions are likely to happen.

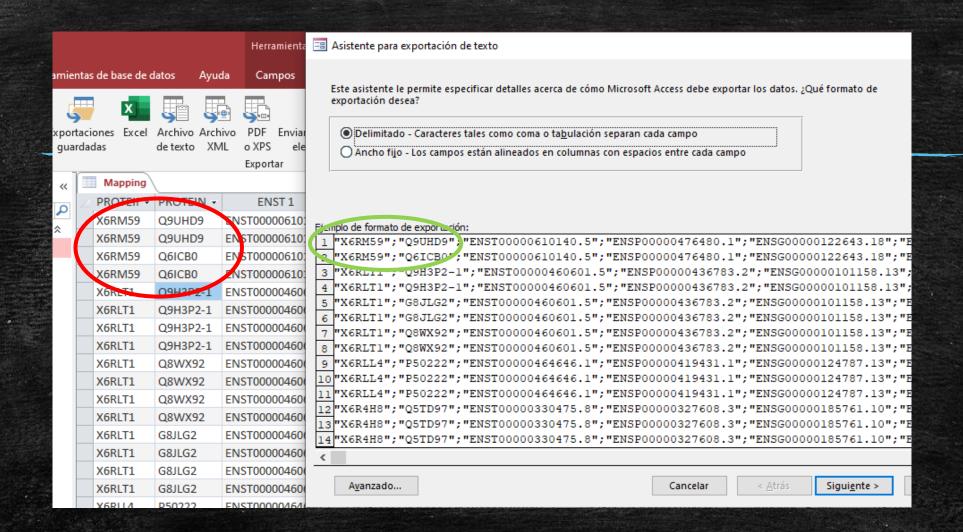
Output files

- Once we have run the codes we obtain two output files. We convert these two files in a single one that has all the information.
- For each pair of interacting proteins we have displayed all the likely interaction types detailed with Domain/Domain or Domain/Linear-Motif.

Output files



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«	Mapping														
0	PROTEIN	- NOTEIN Y	ENST 1 🔻	ENSP: •	ENSG 🕶		ENST 2	v	ENS ▼		ENSG 2	*	INTERACTIN	▼	LINE
	X6RM59	Q9UHD9	ENST00000610140.5	ENSP000	ENSG000	ENST	Г00000338222.6		ENSP0	ENSG	00000188021.	8	UMPH-1	UMPH-1	
	X6RM59	Q9UHD9	ENST00000610140.5	ENSP000	ENSG000	ENST	Г00000338222.6		ENSP0	ENSG	00000188021.	8	UMPH-1	UMPH-1	
	X6RM59	Cion.	ENST00000610140.5	ENSP000	ENSG000	ENST	Г00000263256.6		ENSP0	ENSG	00000100418.	7	UMPH-1	HARM	
	X6RM59	Q6ICB0	ENST00000610140.5	ENSP000	ENSGUUL	ENS	00000203230.0		ENSPU	ENSG	00000100418.	7	UMPH-1	UMPH-1	
	X6RLT1	Q9H3P2-1	ENST00000460601.5	ENSP000	ENSG000	ENST	Г00000411638.6		ENSP0	ENSG	00000185049.	14	TH1	RNA_pol_Rpb1_4	
	X6RLT1	Q9H3P2-1	ENST00000460601.5	ENSP000	ENSG000	ENST	Г00000411638.6		ENSP0	ENSG	00000185049.	14	TH1	RNA_pol_Rpb1_5	
	X6RLT1	Q9H3P2-1	ENST00000460601.5	ENSP000	ENSG000	ENST	Г00000411638.6		ENSP0	ENSG	00000185049.	14	TH1	RNA_pol_Rpb1_4	
	X6RLT1	Q9H3P2-1	ENST00000460601.5	ENSP000	ENSG000	ENST	Г00000411638.6		ENSP0	ENSG	00000185049.	14	TH1	RNA_pol_Rpb1_5	
8	X6RLT1	Q8WX92	ENST00000460601.5	ENSP000	ENSG000	ENST	Г00000634710.2		ENSP0	ENSG	00000188986.	5	TH1	RNA_pol_Rpb1_4	
# "							X6R4H8	Q5	TD97	T	SP_1	TED	_complem	2	
							X6R4H8	Q5	TD97	Т	SP_1	TSP	_1	2	
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When I was exporting the data from Access to .txt in order to delete the duplicates... it just imported the value once!!! It didn't import the duplicates!!

Next tasks

- Obtain a unique output file.
- Eliminate duplicates.
- Proceed with the Statistical Analysis.
- PPI network with Cytoscape.