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SFI Centre for Research Training in **GENOMICS DATA SCIENCE**

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Computational approaches for the therapeutic target discovery to ameliorate muscle wasting during aging and disease

Msc Karen Guerrero Vazquez

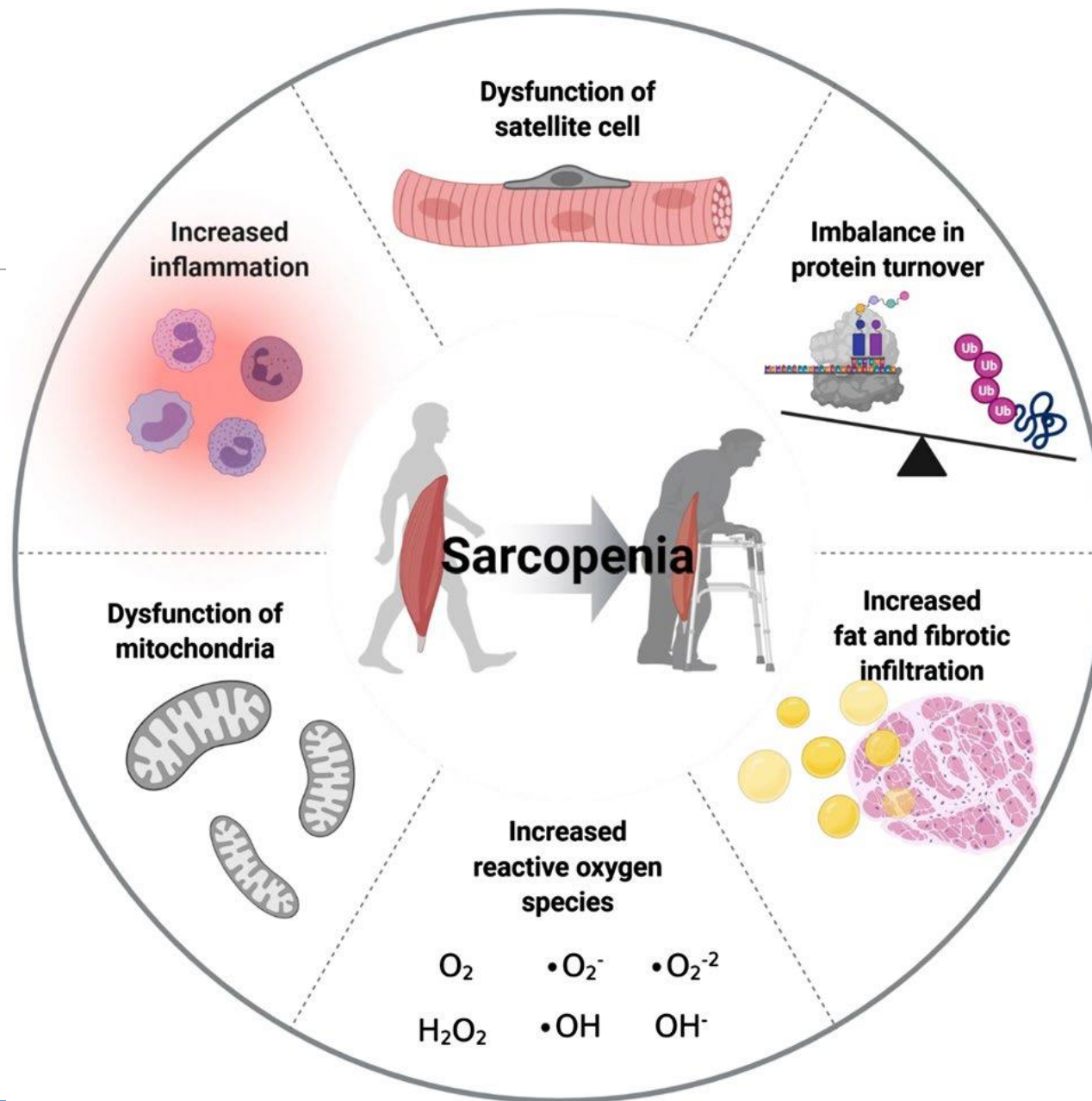
Dr. Katarzyna Whysall

Dr. Pilib O Broin



~3 – 8 %

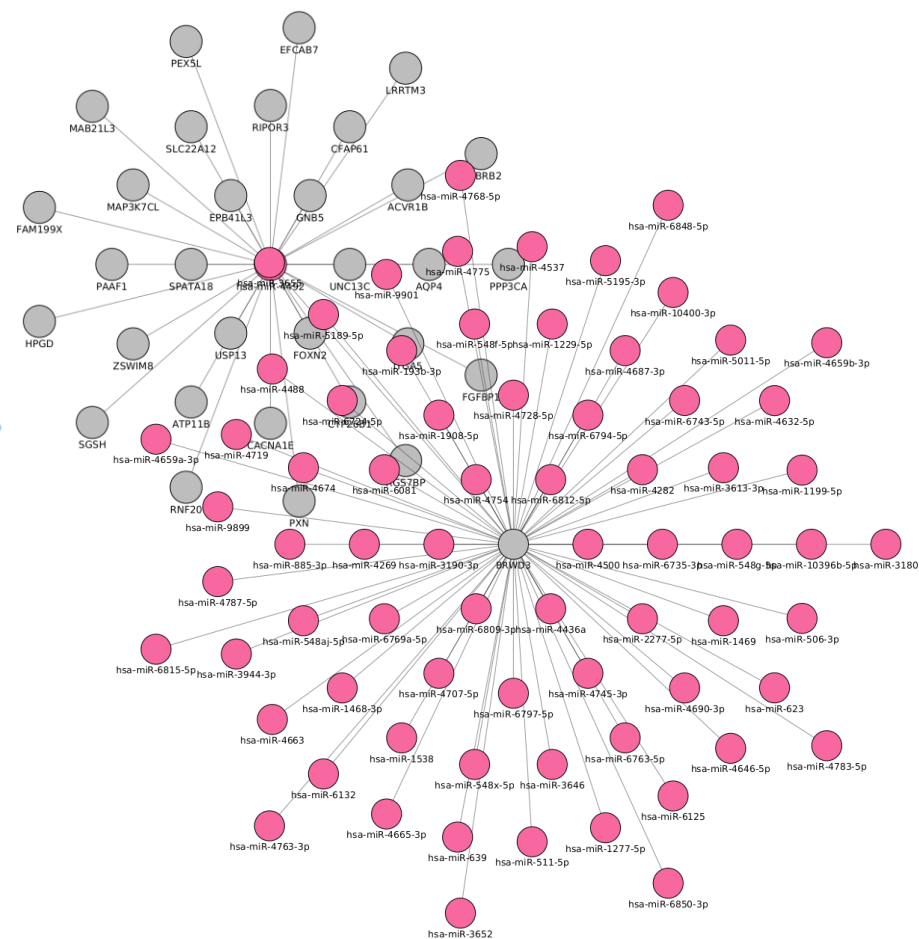
**Loss of muscle mass
per decade**



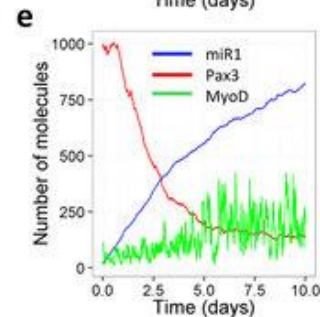
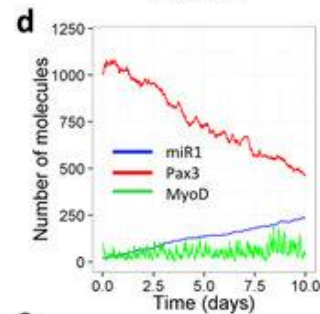
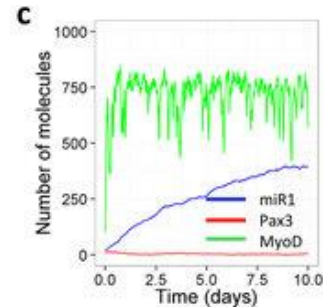
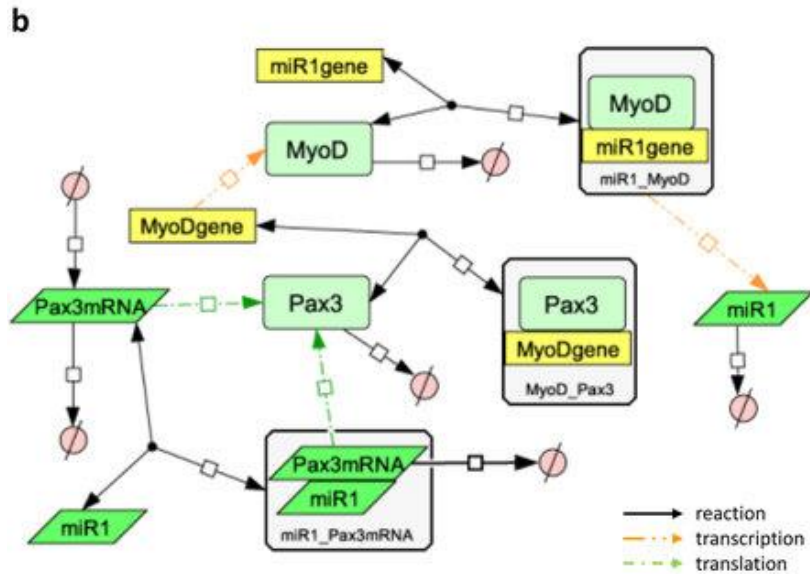
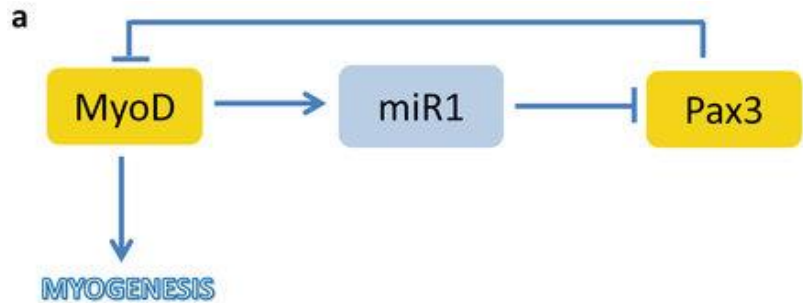
MicroRNA (miRNAs)



The diagram illustrates the relationship between the brain, a neuron, and a virus. On the left, a cross-section of the brain shows internal structures like the ventricles and surrounding tissue. In the center, a single neuron is depicted with its cell body (soma) containing a nucleus, and branching out into dendrites and an axon. On the right, a spherical virus particle is shown, composed of a dark outer shell (capsid) and a lighter inner core (nucleocapsid), representing the viral component of the disease.



Objective



- Create independent models and a common model of miR:target interactions in muscle loss during aging and critical illness based on differentially expressed (DE) miRs and genes
- Identification or shortlisted microRNAs as candidates for therapeutics targets against sarcopenia.

Carole J. Proctor & Katarzyna Goljanek-Whysall, 2017, Using computer simulation models to investigate the most promising microRNAs to improve muscle regeneration during ageing

Tools to analyze miRNAs



Tools to analyze miRNAs



Tools to analyze miRNAs



miRDB

miR^{tar}Base

miTED

Tools to analyze miRNA



miRWalk 2.0

miRDB

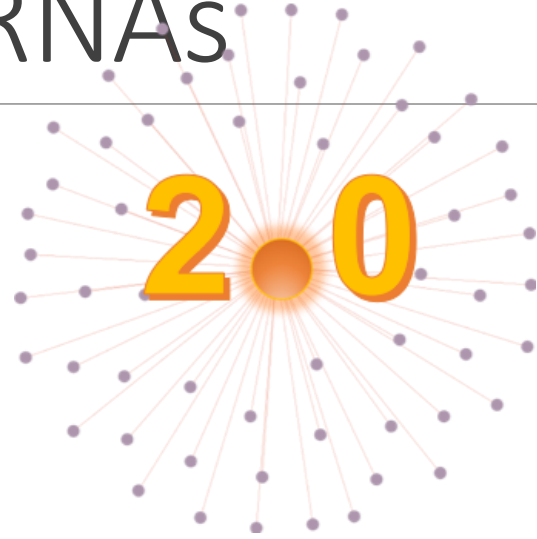
miRstarBase

miTED

Tools to analyze miRNAs



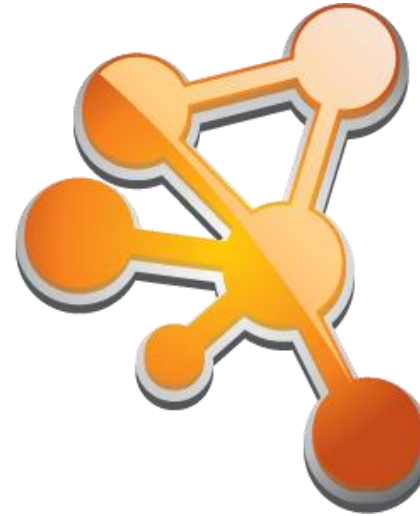
Tools to analyze miRNAs

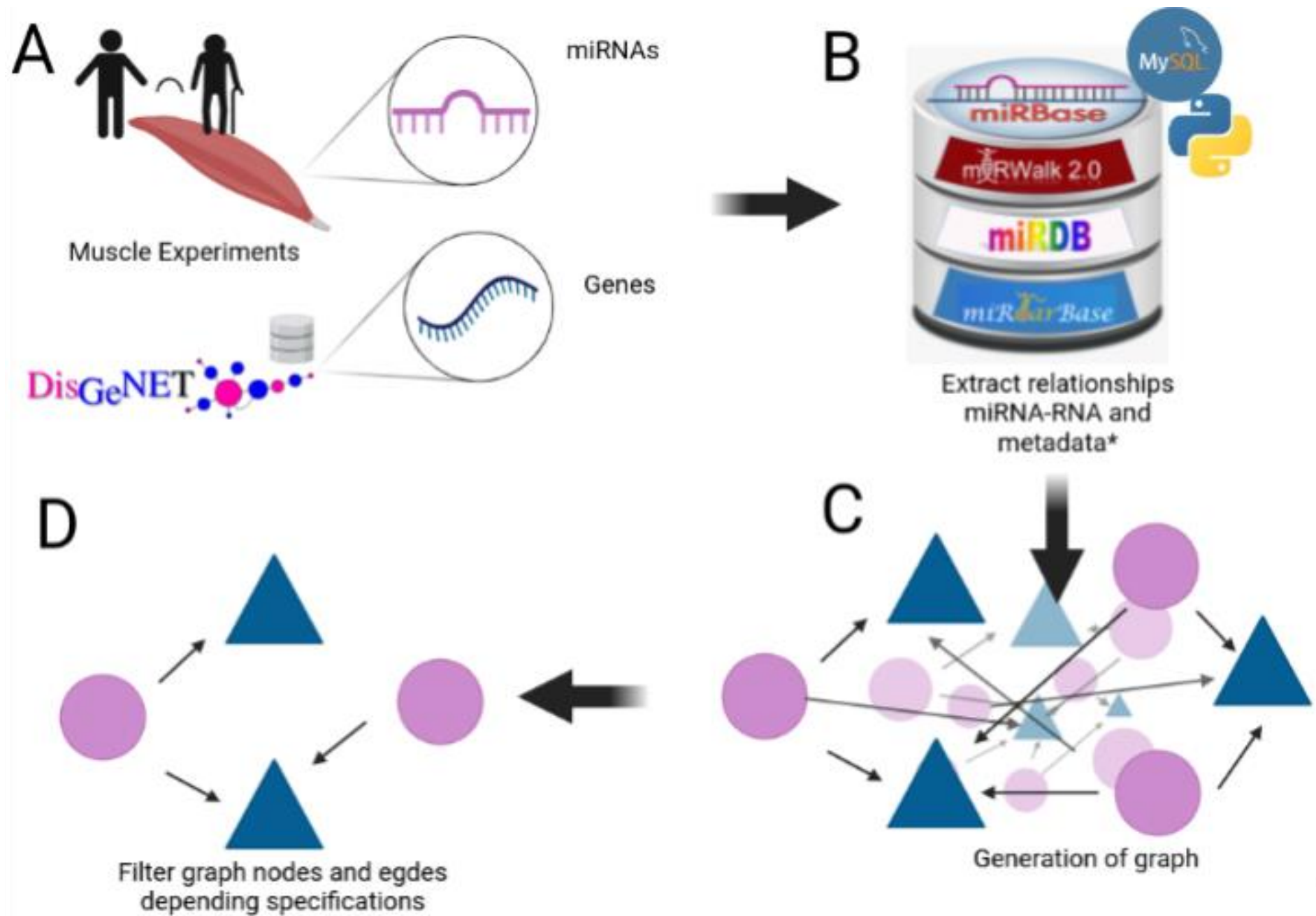


Tools to analyze miRNAs

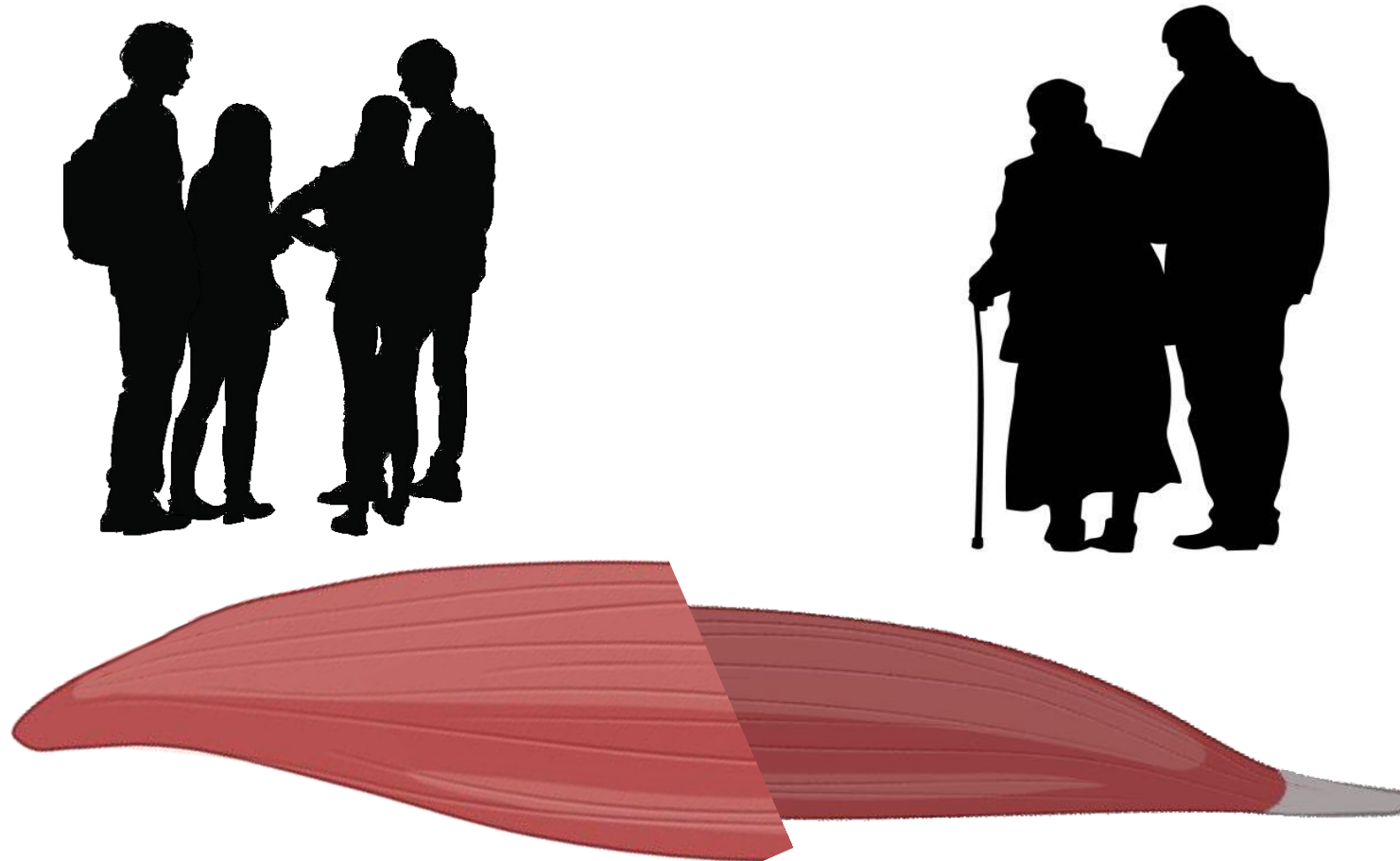


Tools to analyze miRNAs





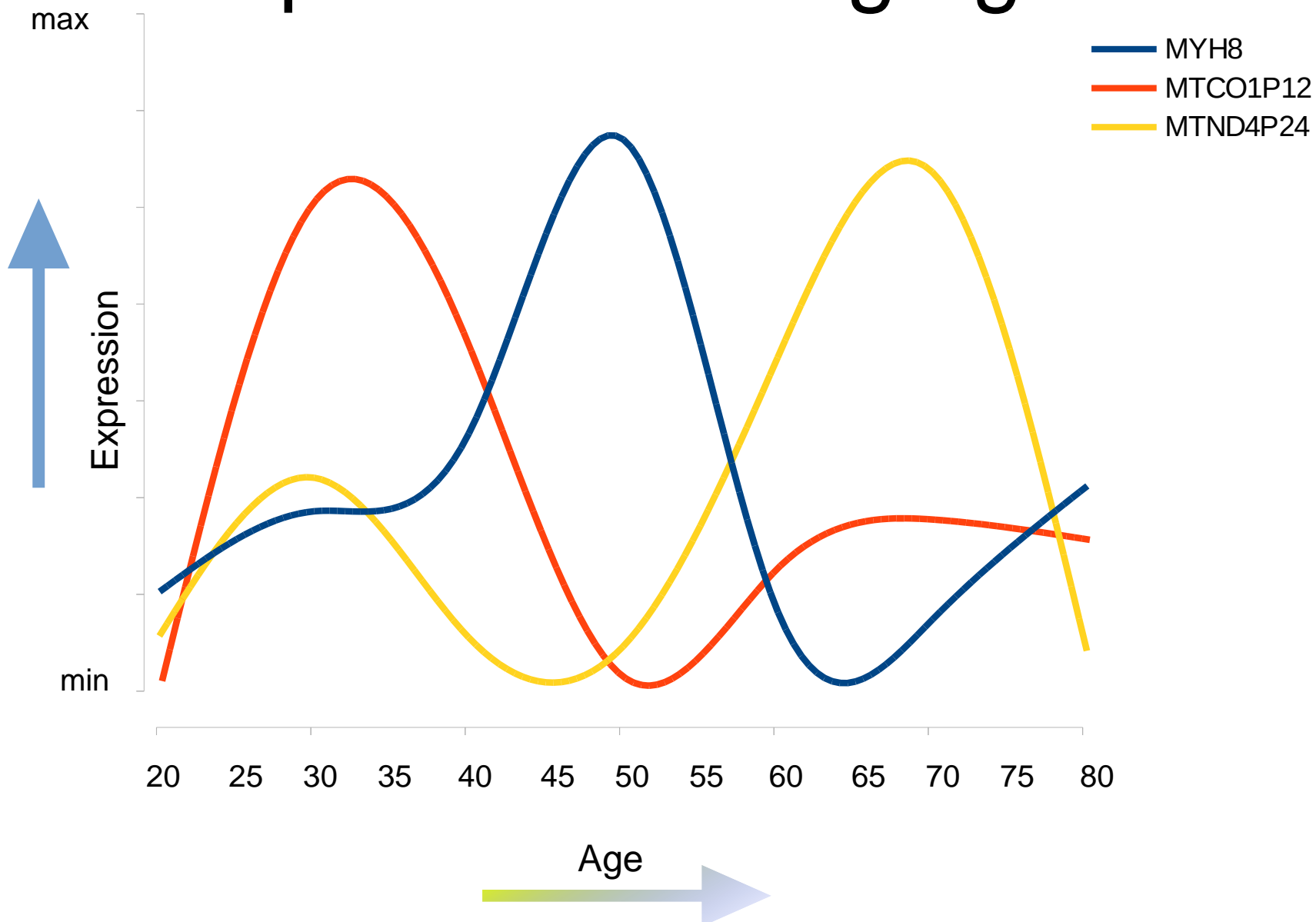
How to start



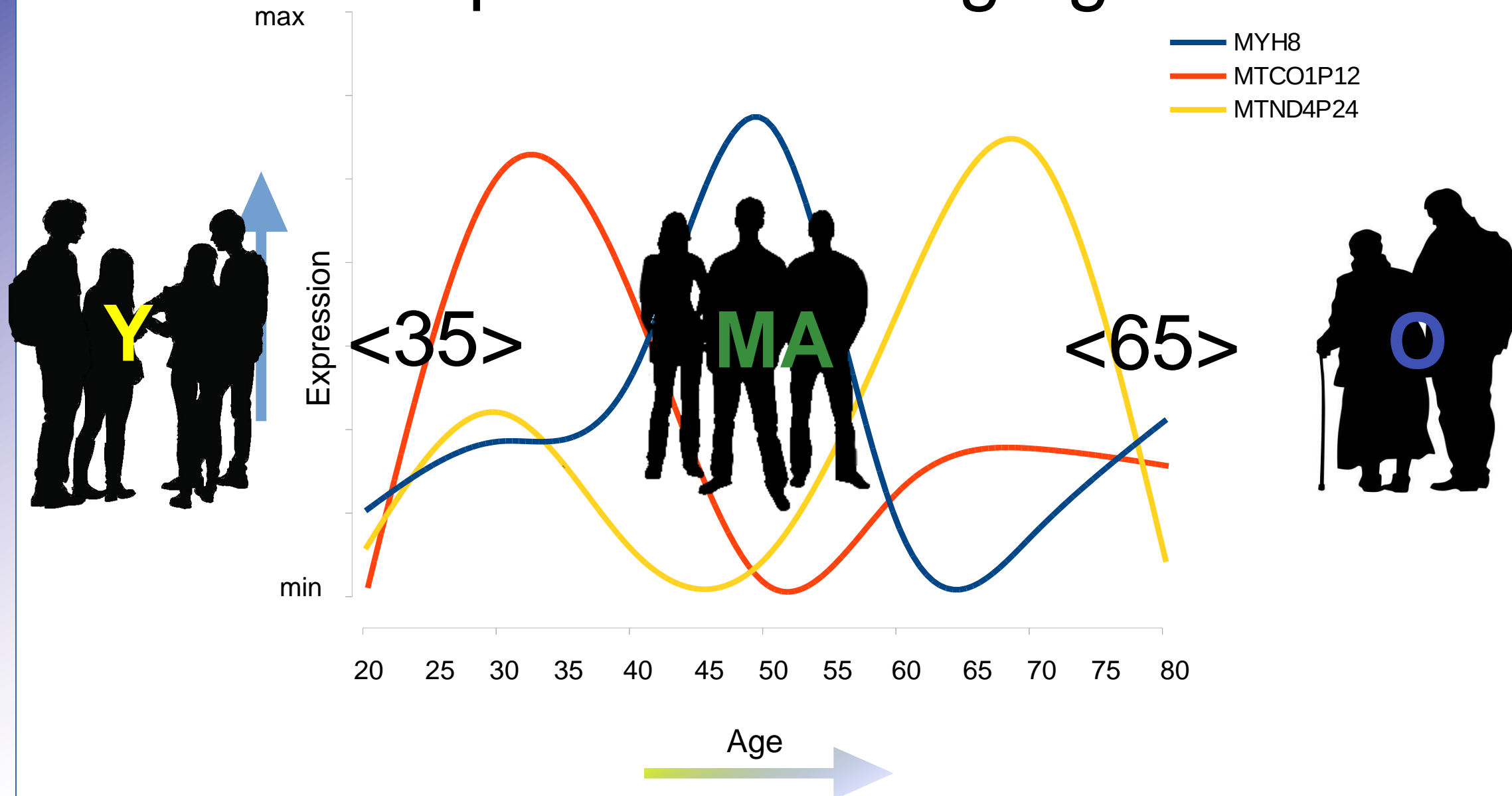
My Experiments

Target	Type	N. Experiments	Healthy	Non healthy
mRNA	RNAseq	3	3	0
	Microarray	4	2	2
miRNA	Microarray	2	2	0
	miRSeq	1	0	1

Expression during age

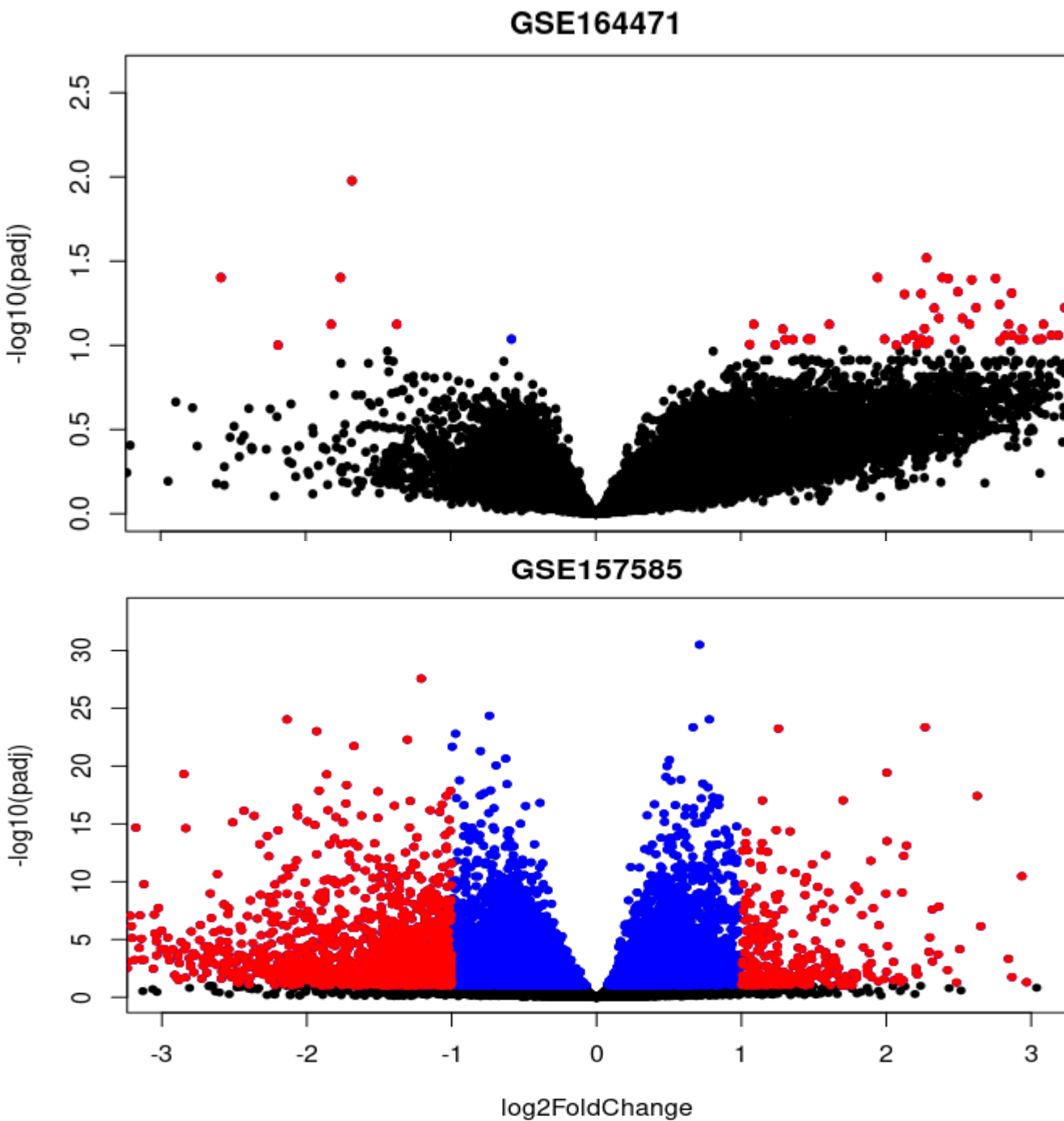


Expression during age



Experiments

GEO number	Samples	Min Age	Max Age	Reference
GSE152558	5	41	85	Tharakan, R., Ubaida-Mohien, C., Piao, Y., Gorospe, M., & Ferrucci, L. (2021).
GSE164471	53	34	80	Tumasian III, R. A., Harish, A., Kundu, G., Yang, J. H., Ubaida-Mohien, C., Gonzalez-Freire, M., ... & Ferrucci, L. (2021).
GSE157585	136	19	>65	Kulkarni, A. S., Peck, B. D., Walton, R. G., Kern, P. A., Mar, J. C., Windham, S. T., ... & Peterson, C. A. (2020).
GSE87105	16	30	78	Mercken, E. M., Capri, M., Carboneau, B. A., Conte, M., Heidler, J., Santoro, A., ... & de Cabo, R. (2017)..
GSE23527	36	29	76	Drummond, M. J., McCarthy, J. J., Sinha, M., Spratt, H. M., Volpi, E., Esser, K. A., & Rasmussen, B. B. (2011)



1)GSE152558

2)GSE164471

3)GSE157585

4)GSE87105

5)GSE23527

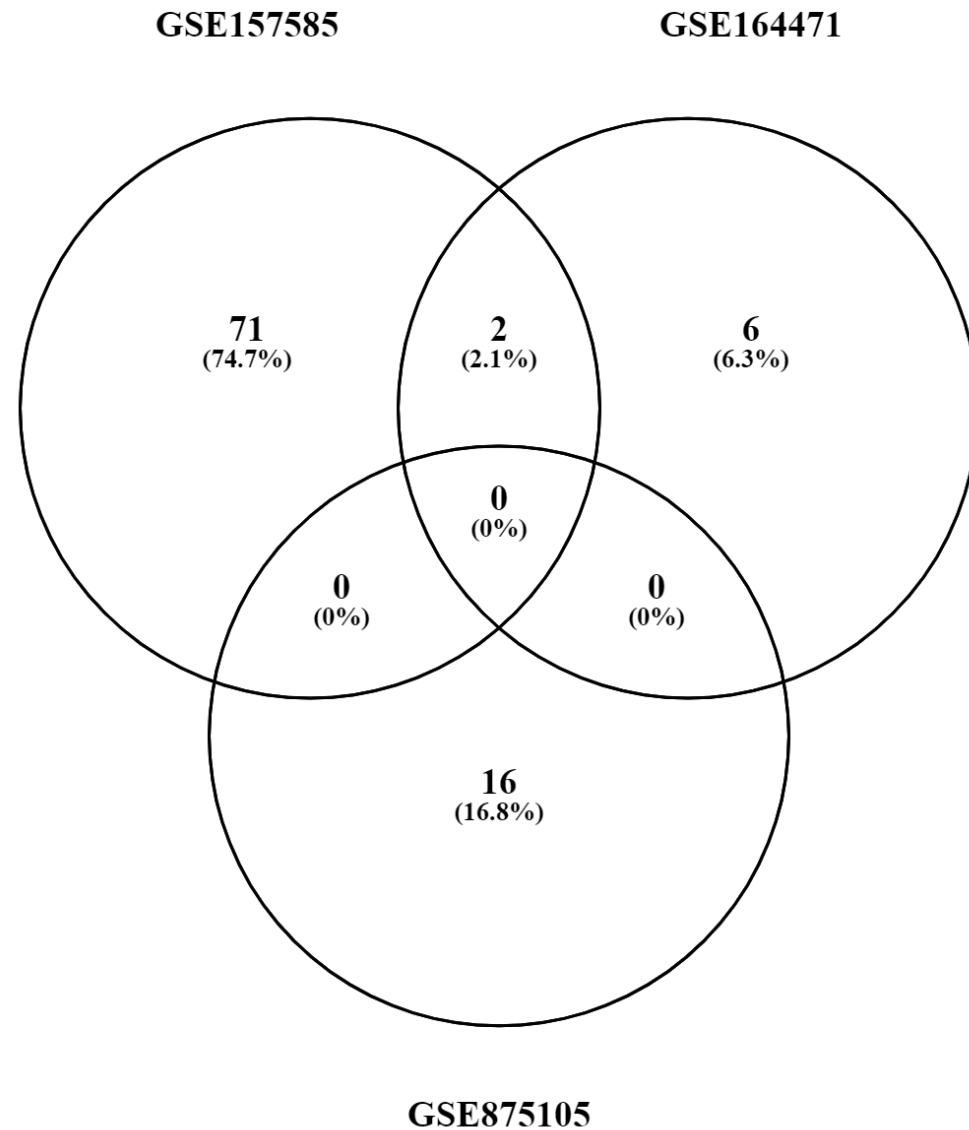


Differentially Expressed Genes

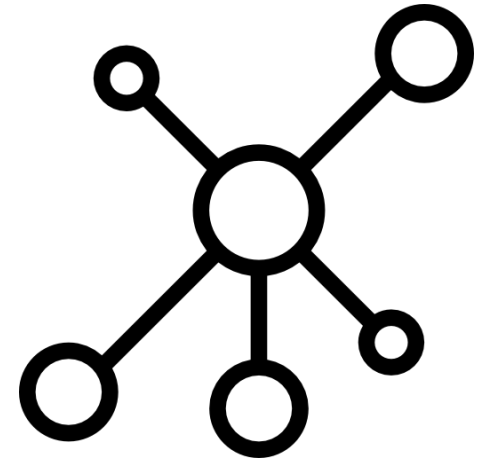
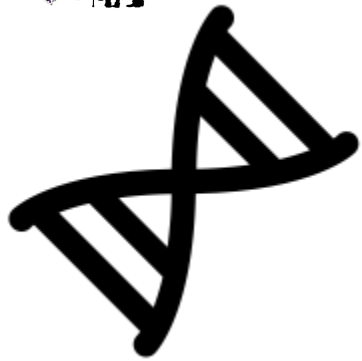
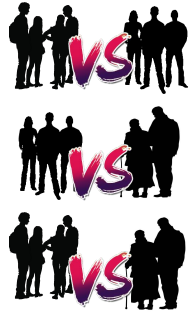
Experiment	Evaluation	Regulation	Genes
GSE152558	MO	UP	8
GSE152558	MO	Down	9
GSE157585	YO	UP	9
GSE157585	YO	Down	73
GSE164471	YO	UP	5
GSE164471	YM	UP	2
GSE164471	MO	UP	6
GSE164471	YO	Down	8
GSE164471	YM	Down	2
GSE164471	MO	Down	11
GSE23527	YO	Up	1
GSE23527	YO	Down	5
GSE875105	OY	Down	88
GSE875105	MO	Up	6
GSE875105	OY	Up	18

Old vs Young (up or down)

- MYH8
- HCN1

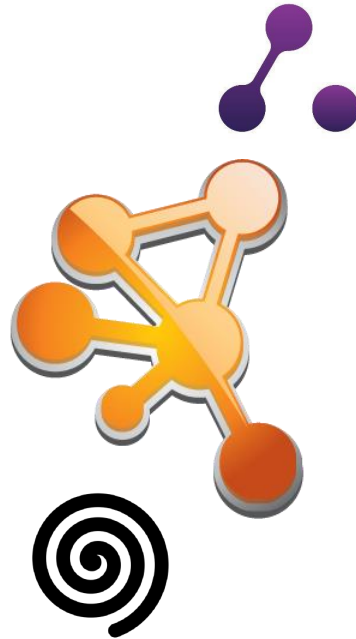








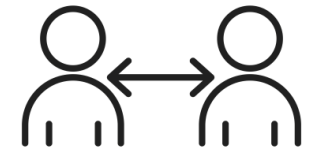
20 genes



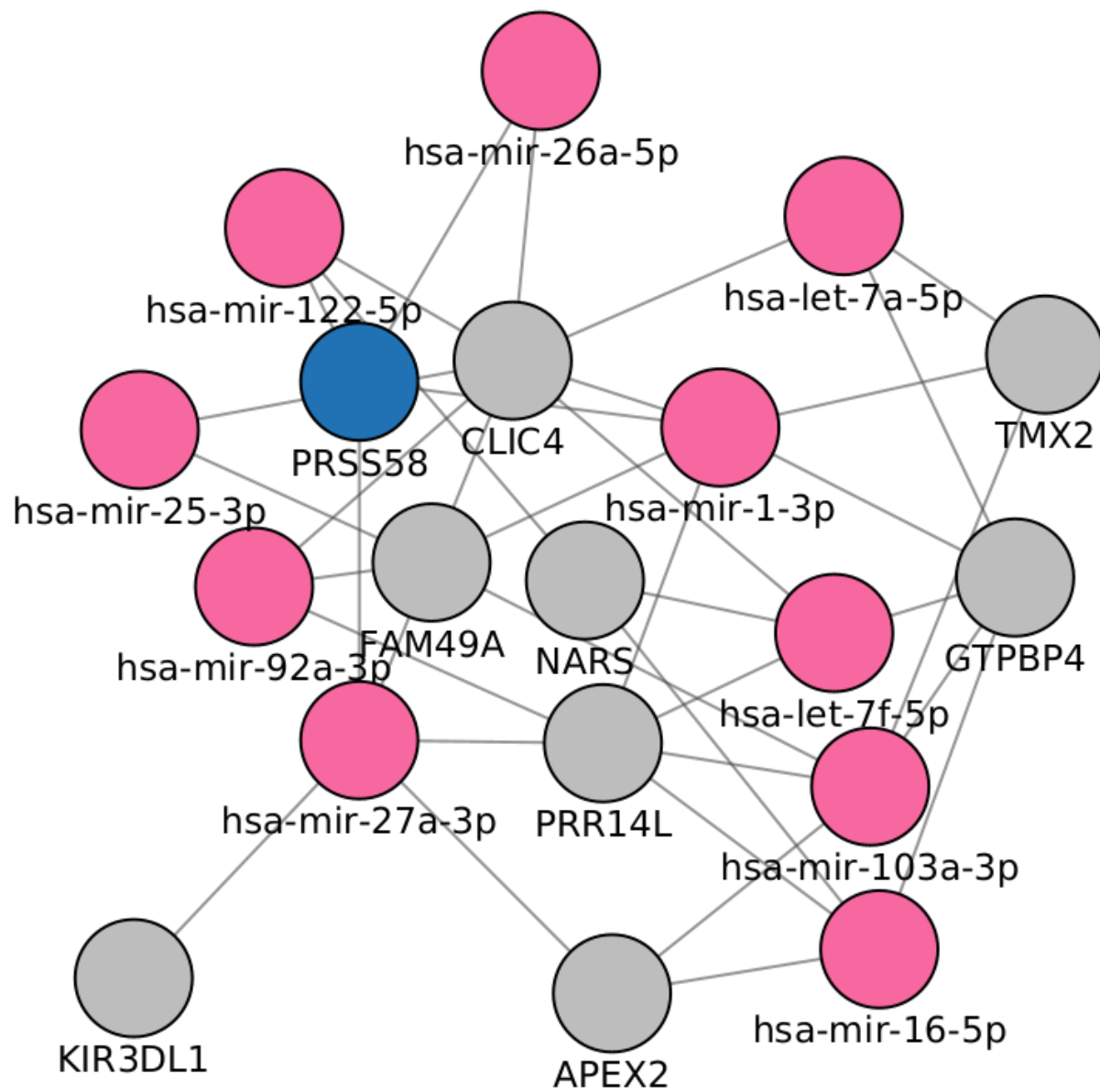
446 genes
1.2k edges

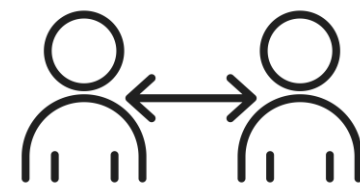
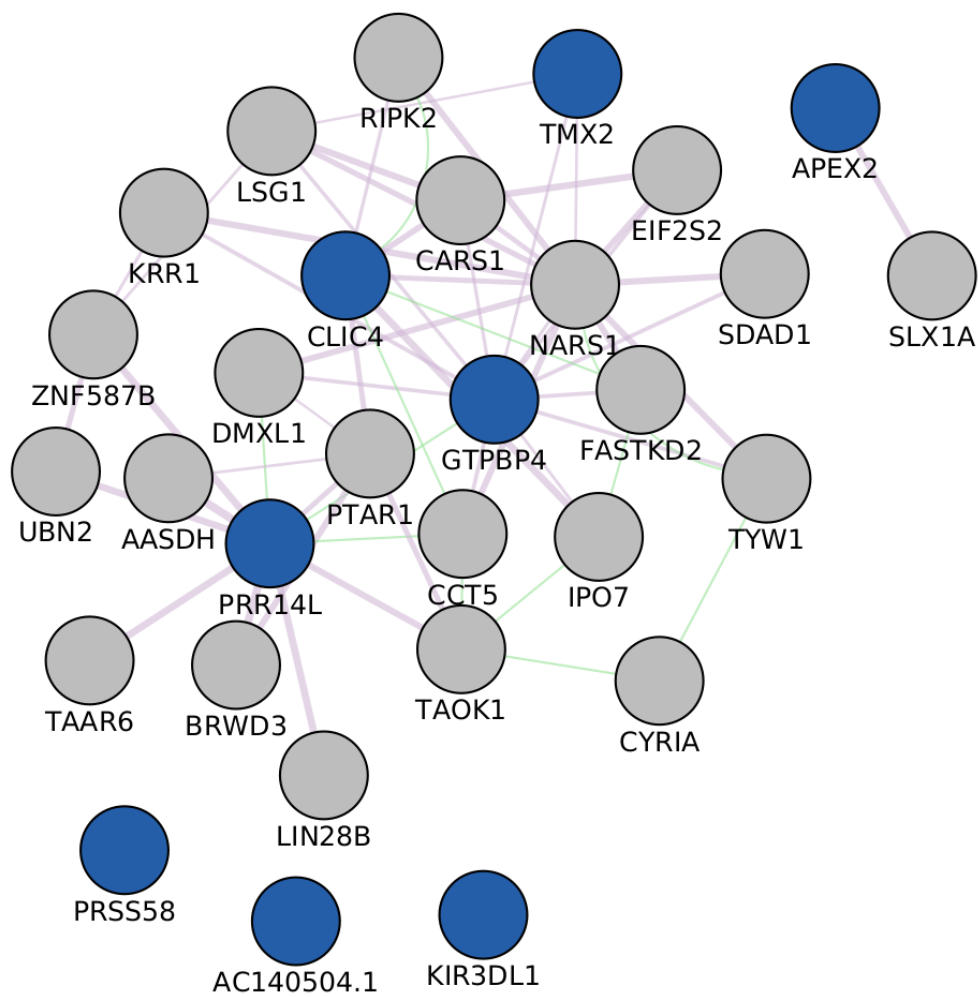


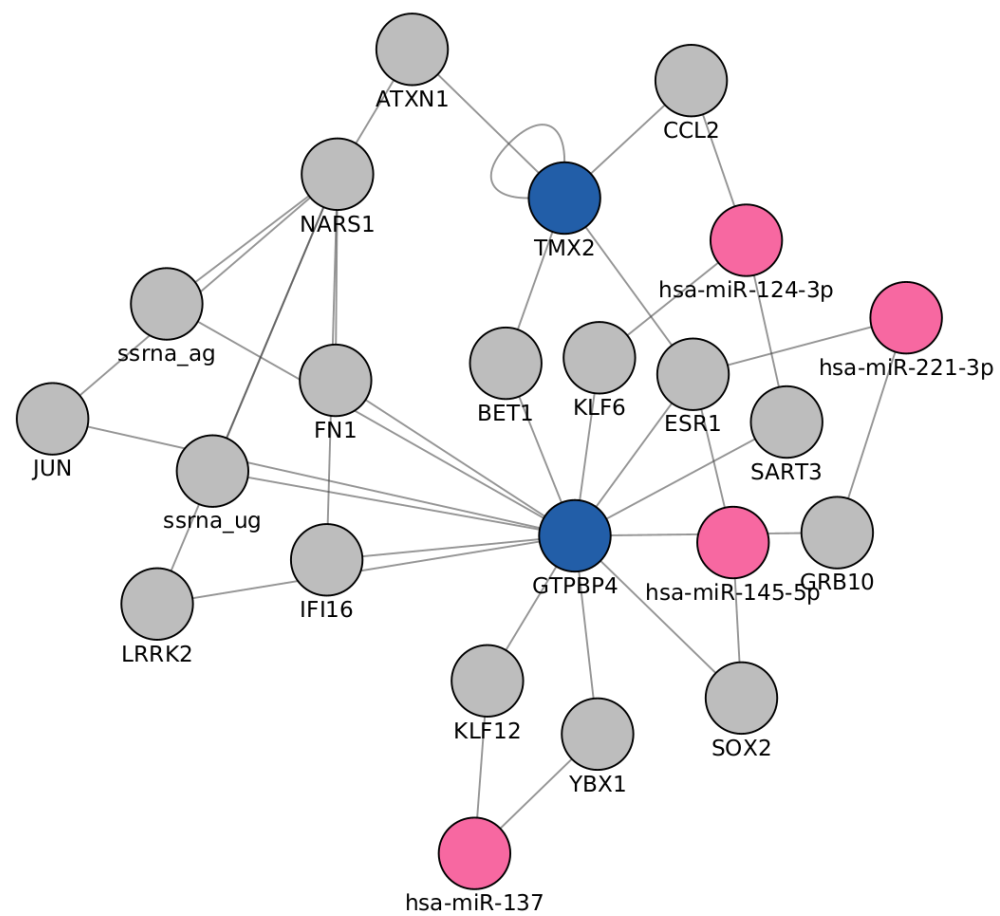
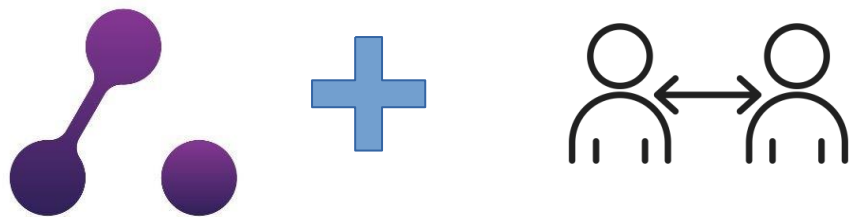
446 genes
2k miRNAs
3.5 edges

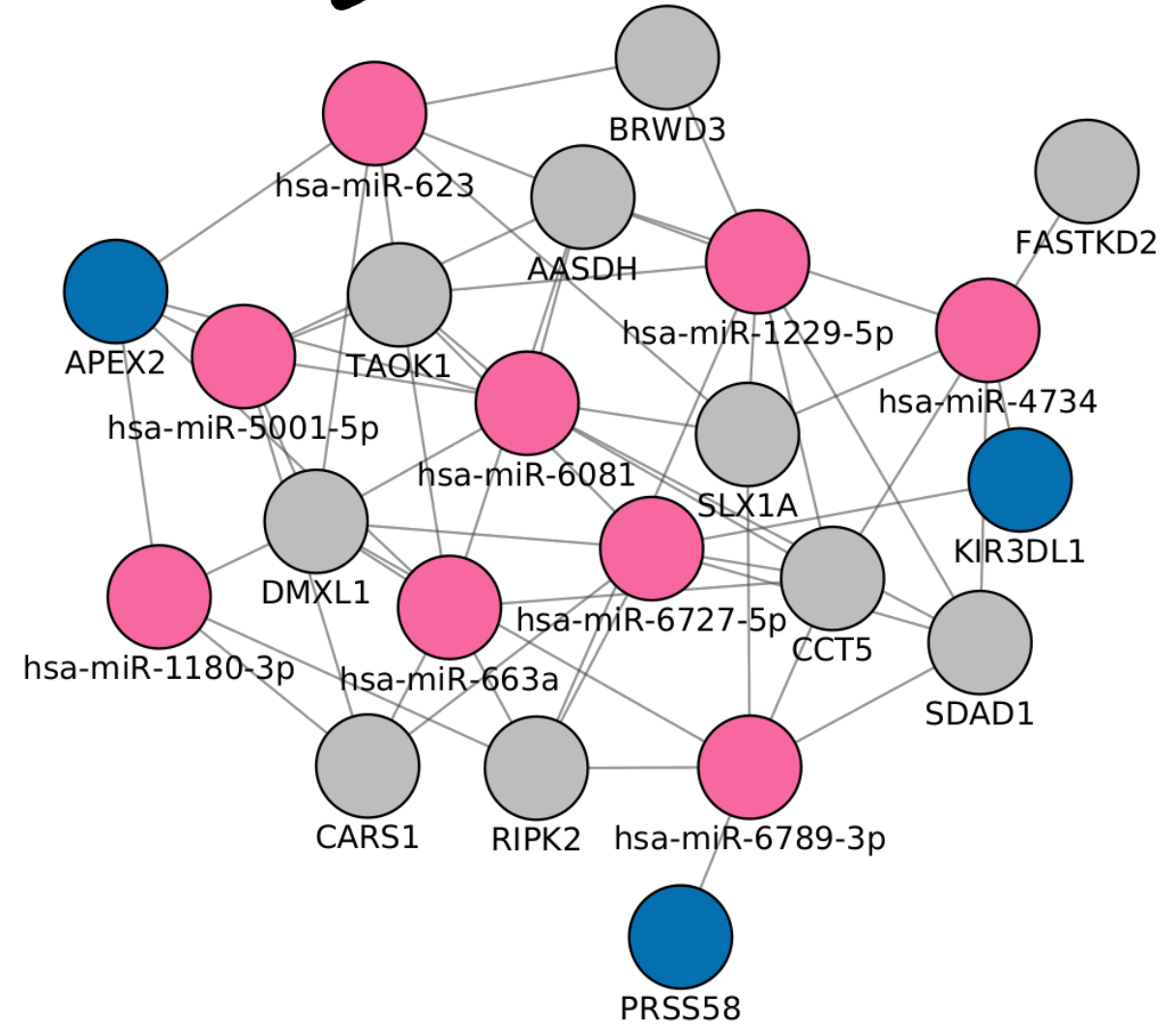


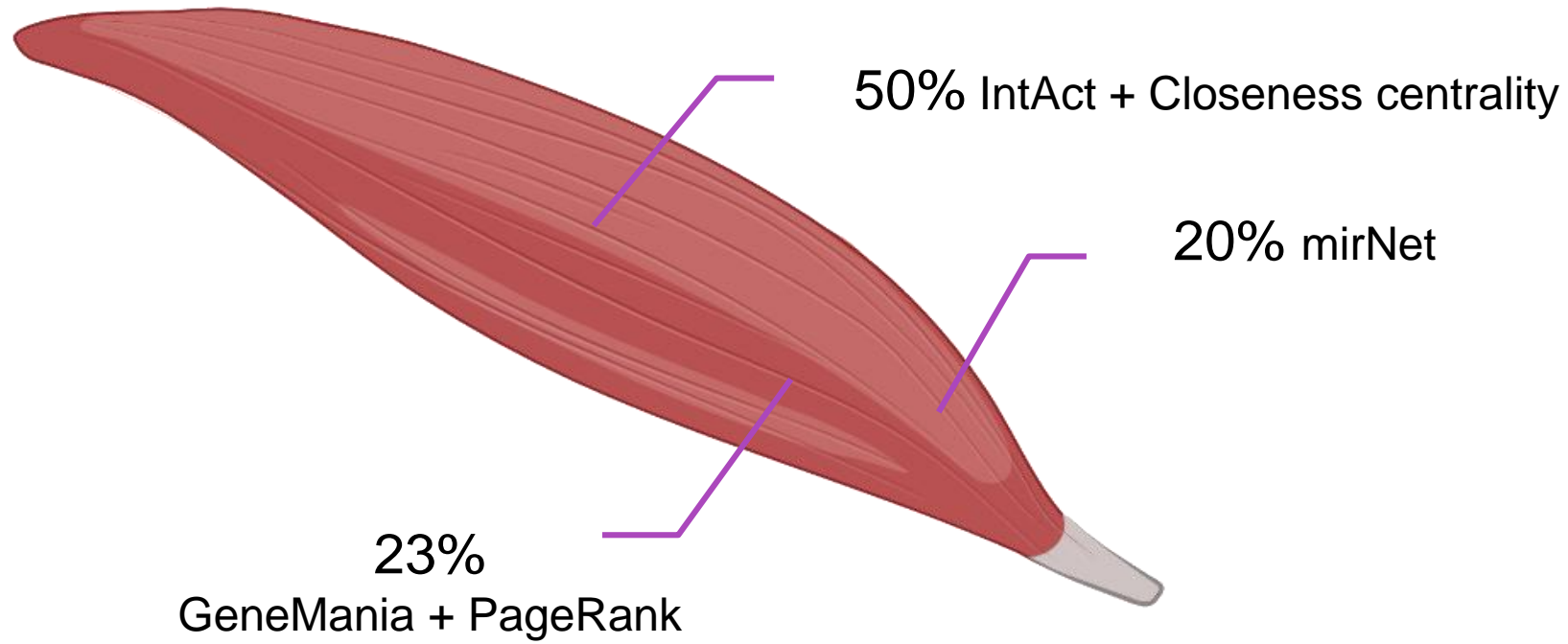
5 miRNAs
146 genes
163 edges



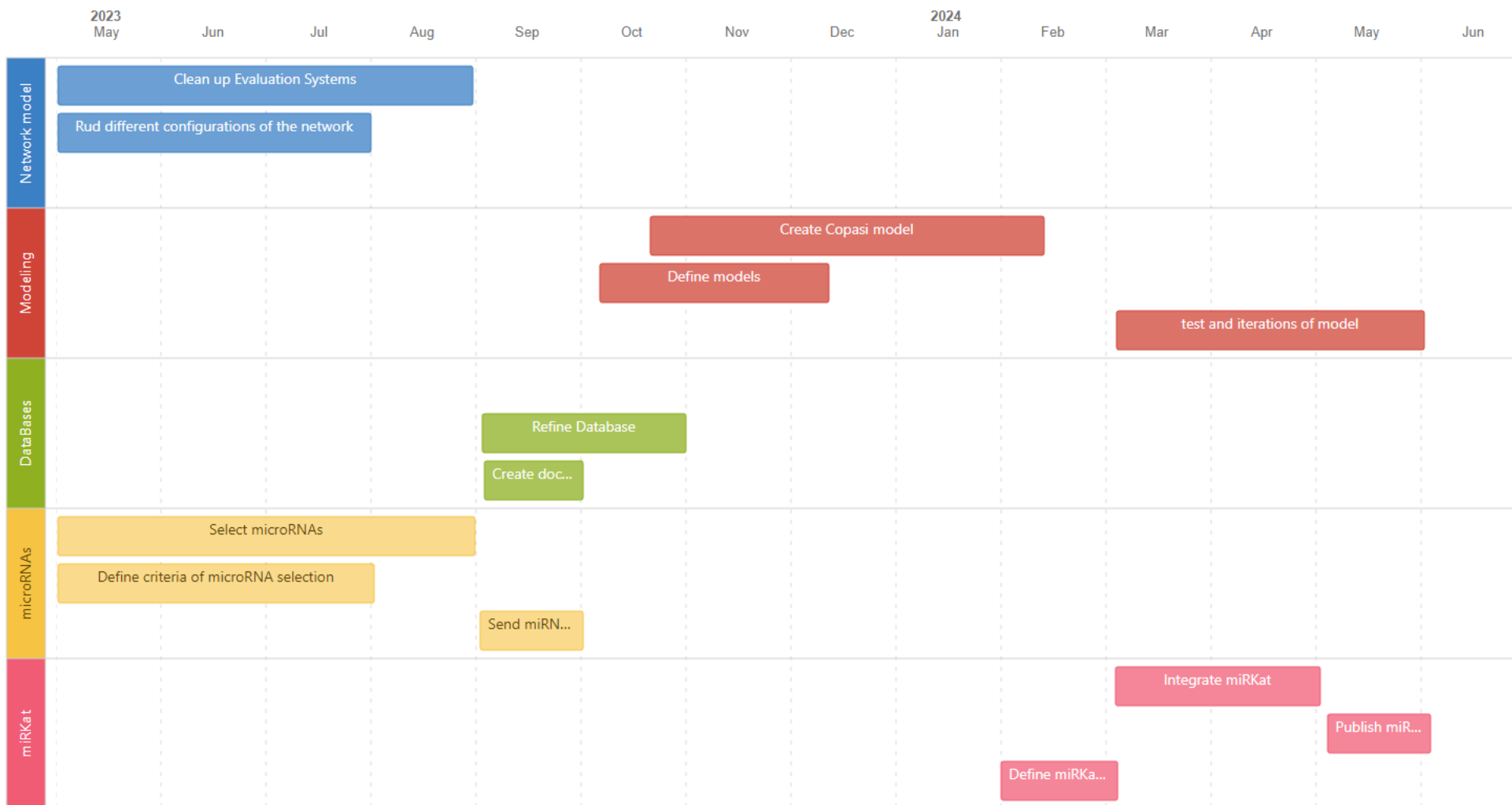








Differentially expressed?



Questions?

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Thank You



Acknowledgements

This presentation has emanated from research conducted with the financial support of Science Foundation Ireland under Grant number [18/CRT/6214]

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