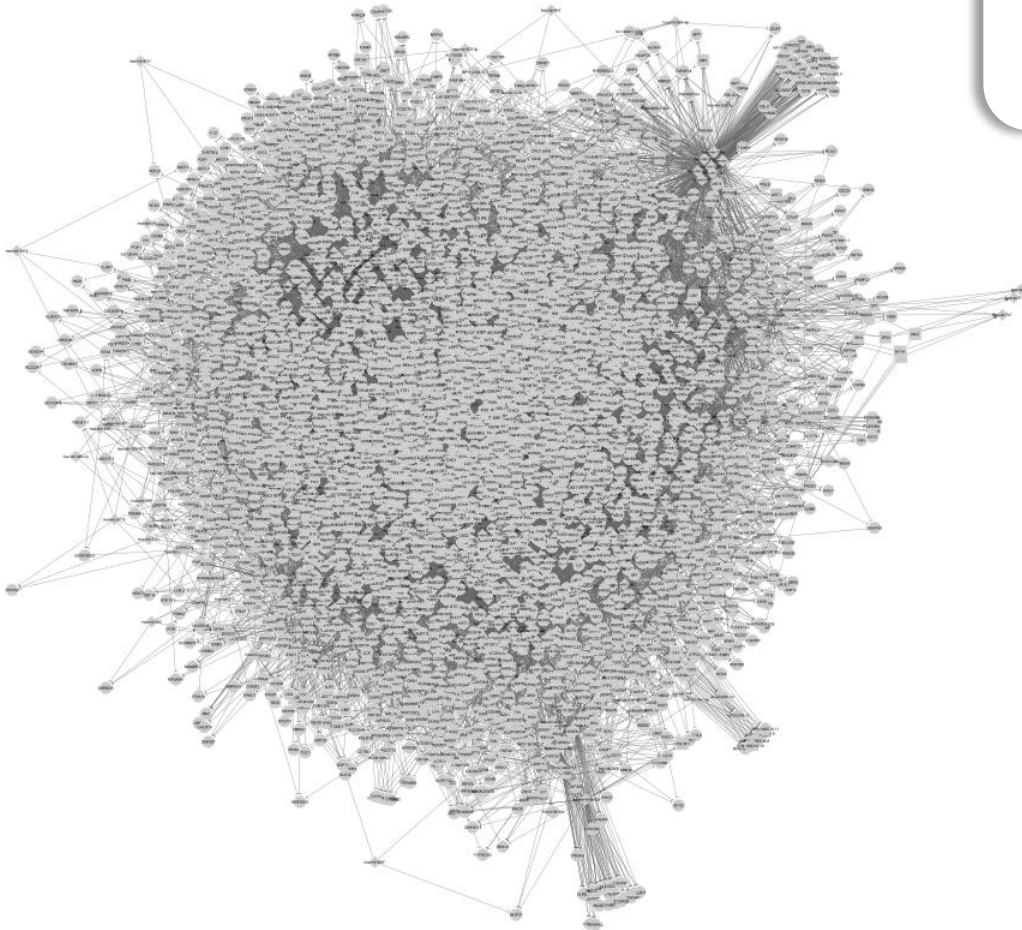


MIR@NT@N

meta-regulation network models

a framework integrating
transcription factors,
microRNAs and their
targets to identify sub-
network motifs in meta-
regulation network models



Antony Le Béhec
Life Sciences Research Unit
Pr. Evelyne Friederich Team



lucilinx

the Luxembourg Bioinformatics Network

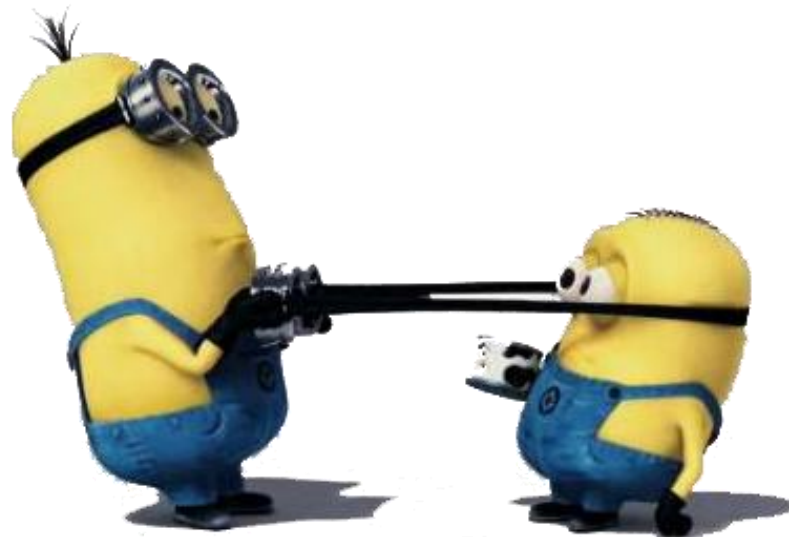
A single element does not support the function



A single element does not support the function
At least, 2 elements are needed...



A single element does not support the function
At least, 2 elements are needed...
... to create a function



The function is supported by the interaction between elements

Interactions between elements define the biological process
and some regulations control the stability of this process



KEGG
Reactome

JASPAR
PAZAR
Transfac

miRBase
microRNA.org
Argonaute

IntAct
BIND
VisAnt

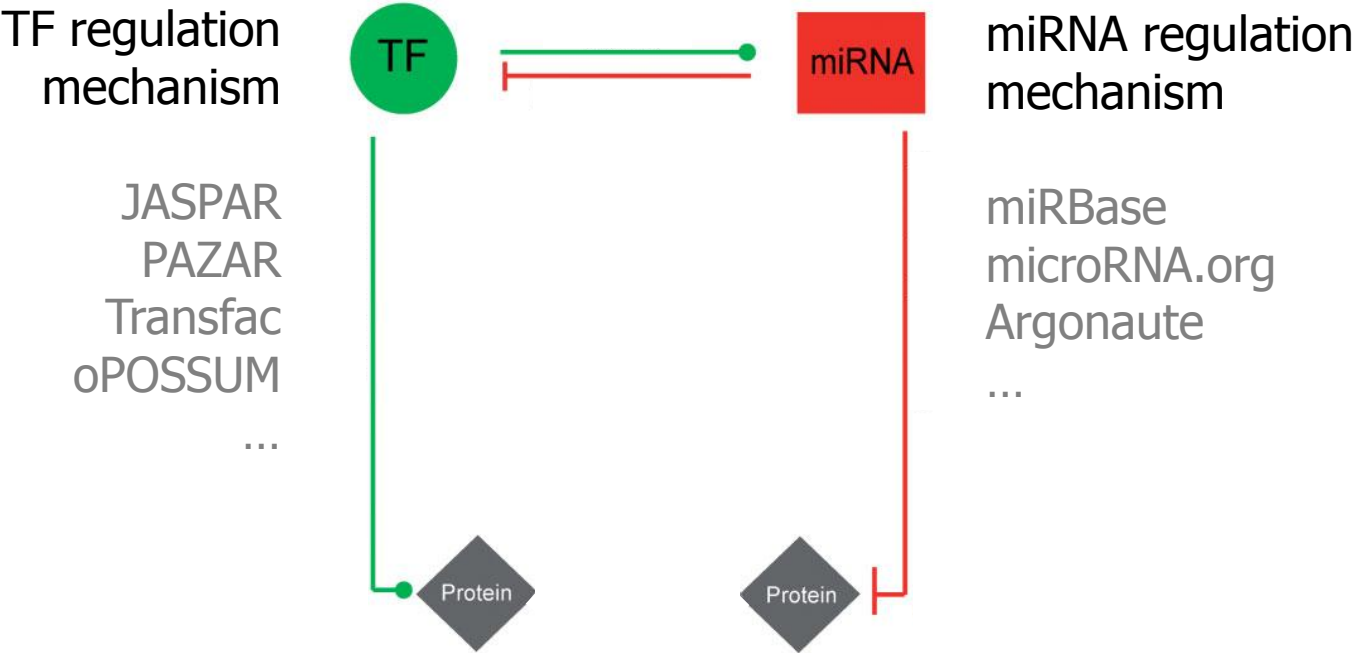
Meta-Regulation Network – microRNAs & TFs

Meta-regulation network model



Martinez and Walhout (2009)

at a **transcriptional** & **post-transcriptional** level



Enright et al. (2003)
Jones et al. (2004)

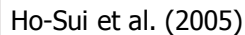
1: 1094248-1094330 [+]

8

TF→Gene



A PUBLIC DATABASE OF **TRANSCRIPTION FACTOR AND REGULATORY SEQUENCE ANNOTATION**

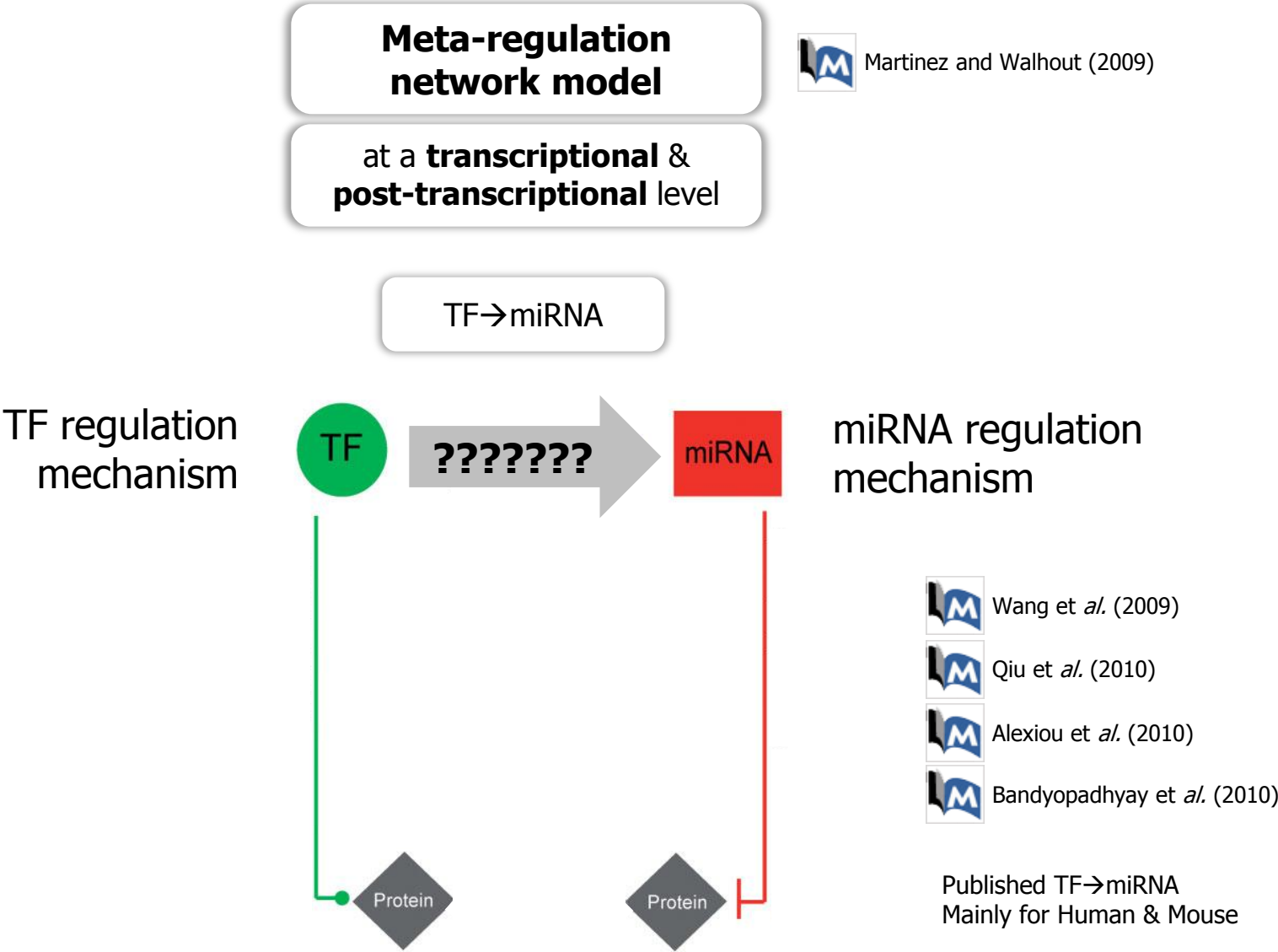


ID	name	species	class	Sequence logo
MA0001	AGL3	Arabidopsis thaliana	MADS	Click to view details
MA0002	RUNX1	Arabidopsis thaliana	RUNT	Click to view details
MA0003	TFAP2A	Homo sapiens	AP2	Click to view details
MA0004	Arnt	Mus musculus	bHLH	Click to view details
MA0005	Agamous	Arabidopsis thaliana	MADS	Click to view details
MA0006	Arnt-Ahr	Mus musculus	bHLH	Click to view details
MA0007	Ar	Rattus rattus	NUCLEAR RECEPTOR	Click to view details
MA0008	Athb-1	Arabidopsis thaliana	HOMEO-ZIP	Click to view details

at a **transcriptional & post-transcriptional** level



Meta-Regulation Network – microRNAs & TFs



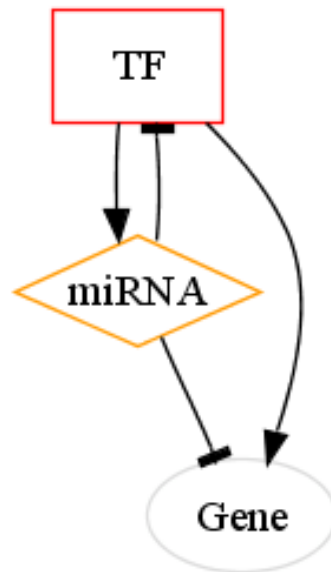
at a **transcriptional & post-transcriptional** level

TF→miRNA



TFBS Quality Score

miRBase



JASPAR
PAZAR
oPOSSUM

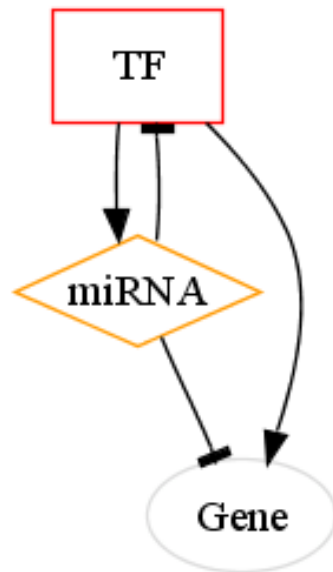
miRBase
MicroCosm
microRNA.org

Ensembl
UniProt

Full model available for **7 species**

Caenorhabditis elegans
Danio rerio
Drosophila melanogaster
Gallus gallus
Homo sapiens
Mus musculus
Rattus norvegicus

..

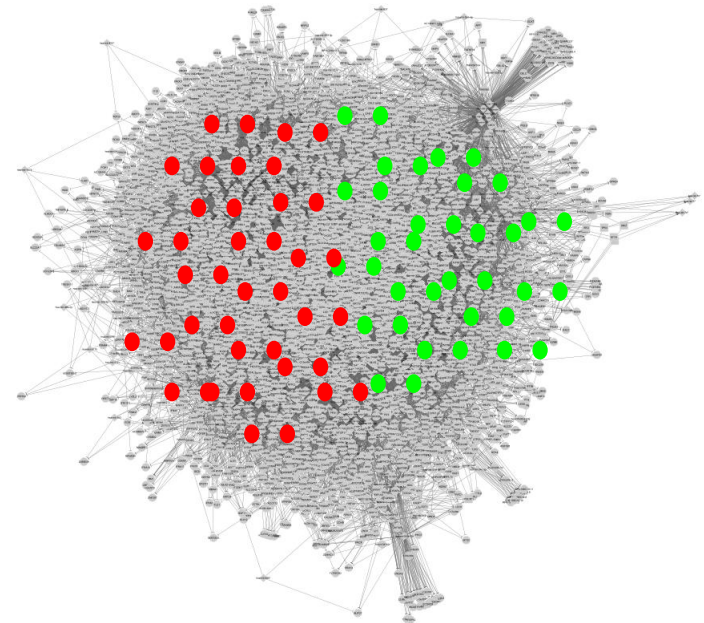


JASPAR
PAZAR
oPOSSUM

miRBase
MicroCosm
microRNA.org

Ensembl
UniProt

Meta-regulation network database



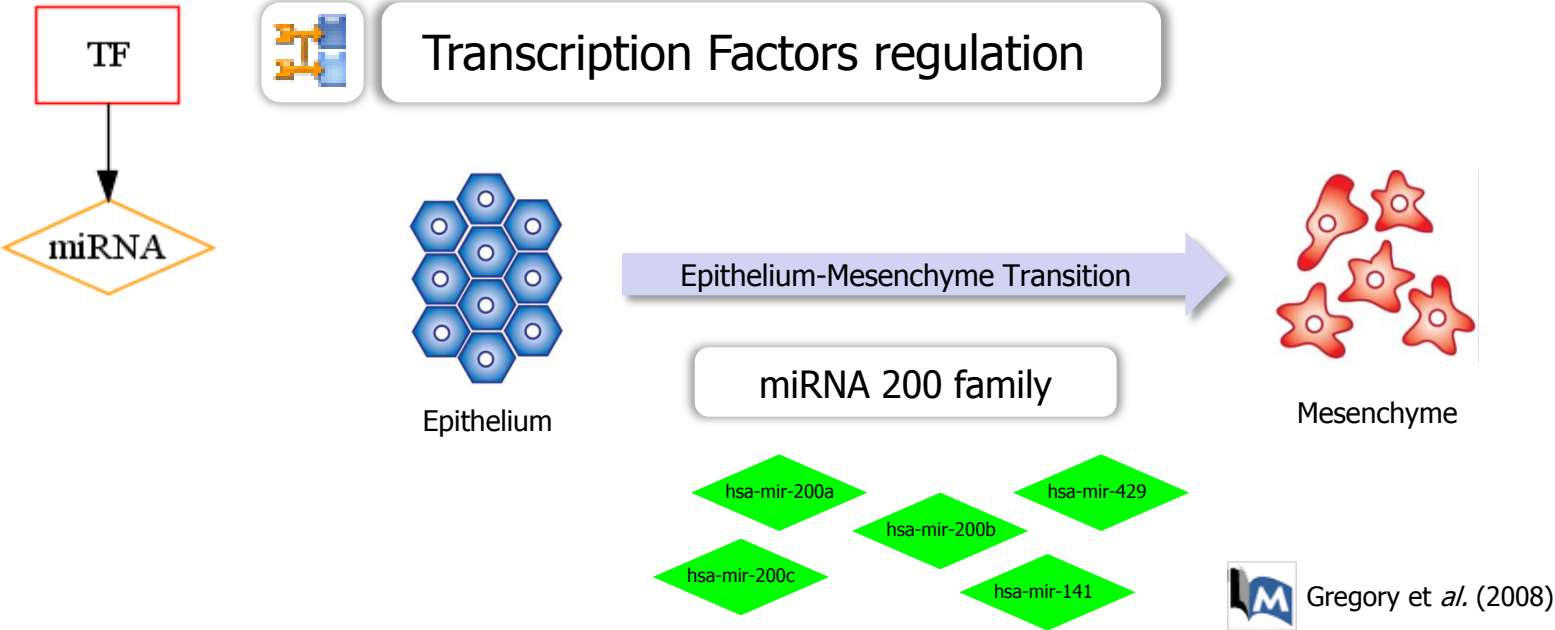
Contextualization
with TFs/miRNAs/Genes
up-regulated
down-regulated

focus on **major regulators** and **targets**
and detect **sub-networks motifs**



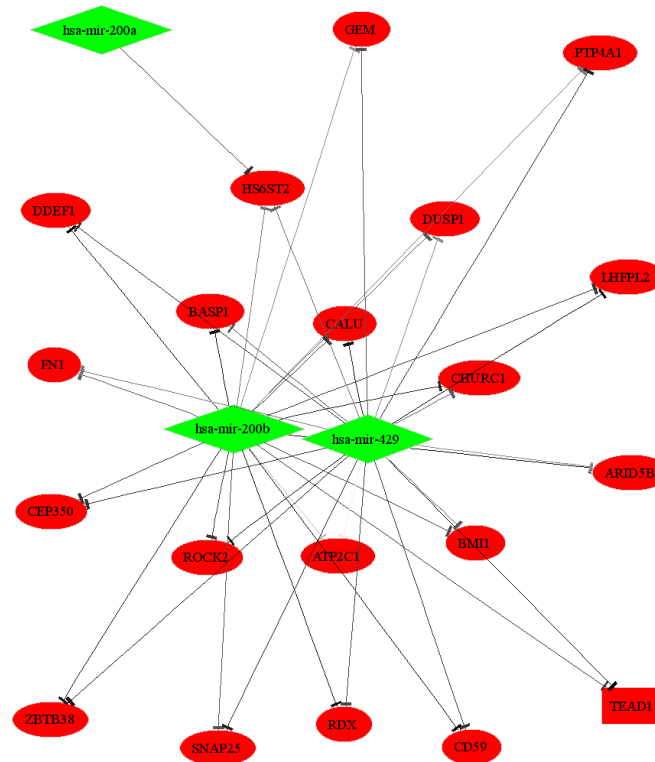
15

MIR@NT@N – major TF regulators on targeted miRNA









Cochrane et al. (2009)

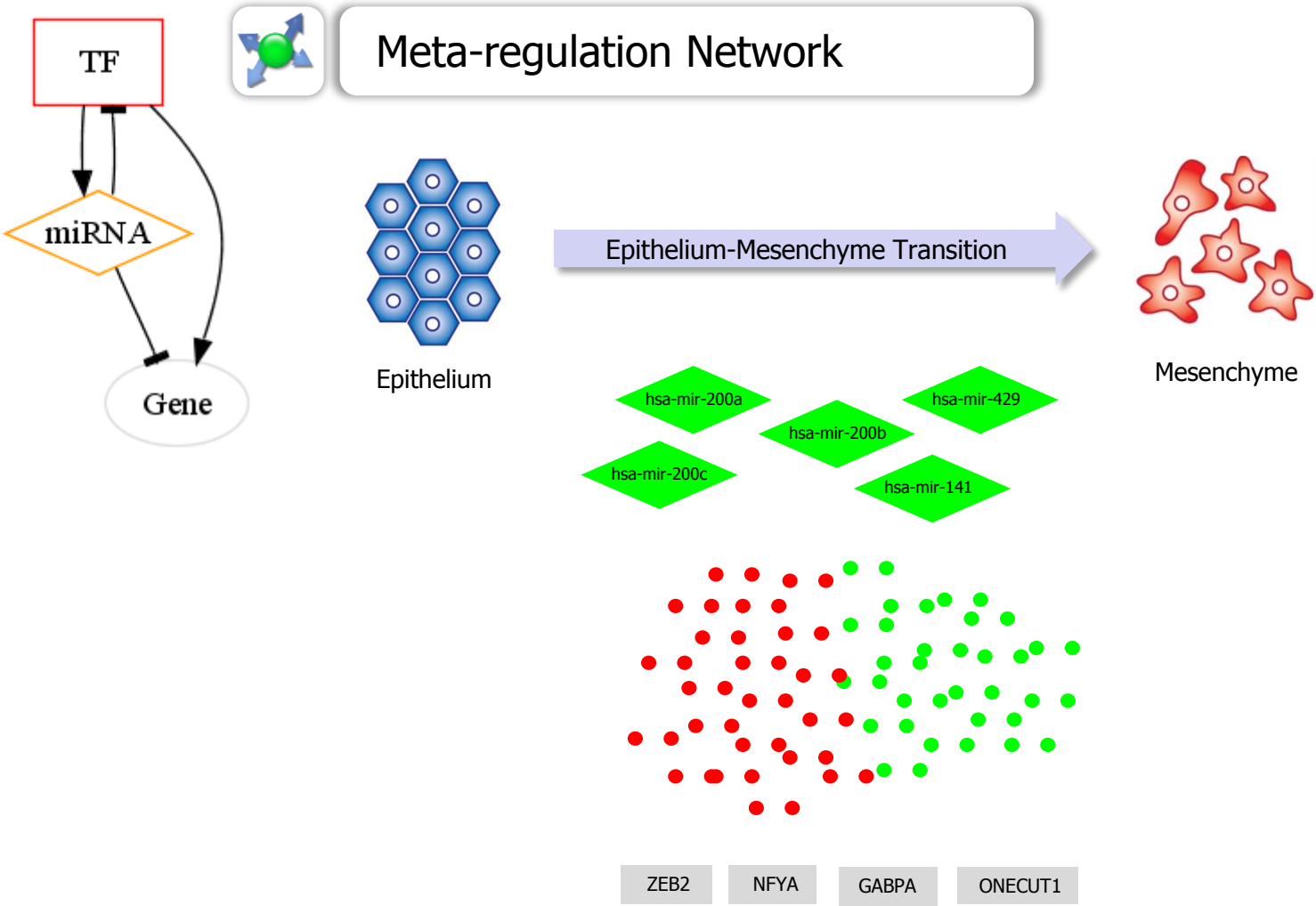


Wellner et al. (2009)



Zhao and Rivkees (2004)

MIR@NT@N – networks generation







(direct or indirect)



22



(direct or indirect)



23



Wang et al. (2009)
Qiu et al. (2010)

Published TF→miRNA regulations

43% TF→miRNA found by **MIR@NT@N**



Emmrich and Putzer (2010)
Sylvestre et al. (2007)



Bendoraitė et al. (2010)
Bracken et al. (2008)



Wang et al. (2008)



Chang et al. (2008)
Wang et al. (2008)



Mott et al. (2010)

MIR@NT@N – Future plans

Integrate **expression data** to improve regulation predictions
and increase the **quality** of generated networks

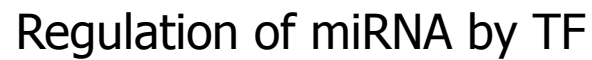
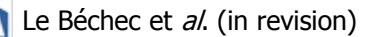
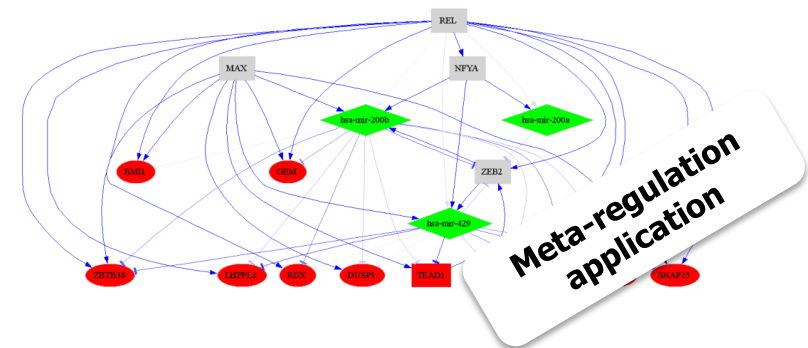


Take into account **Context/Time dimension**
to develop a **dynamic network approach**





miRNA and Transcription Factor Analysis Network



Thanks



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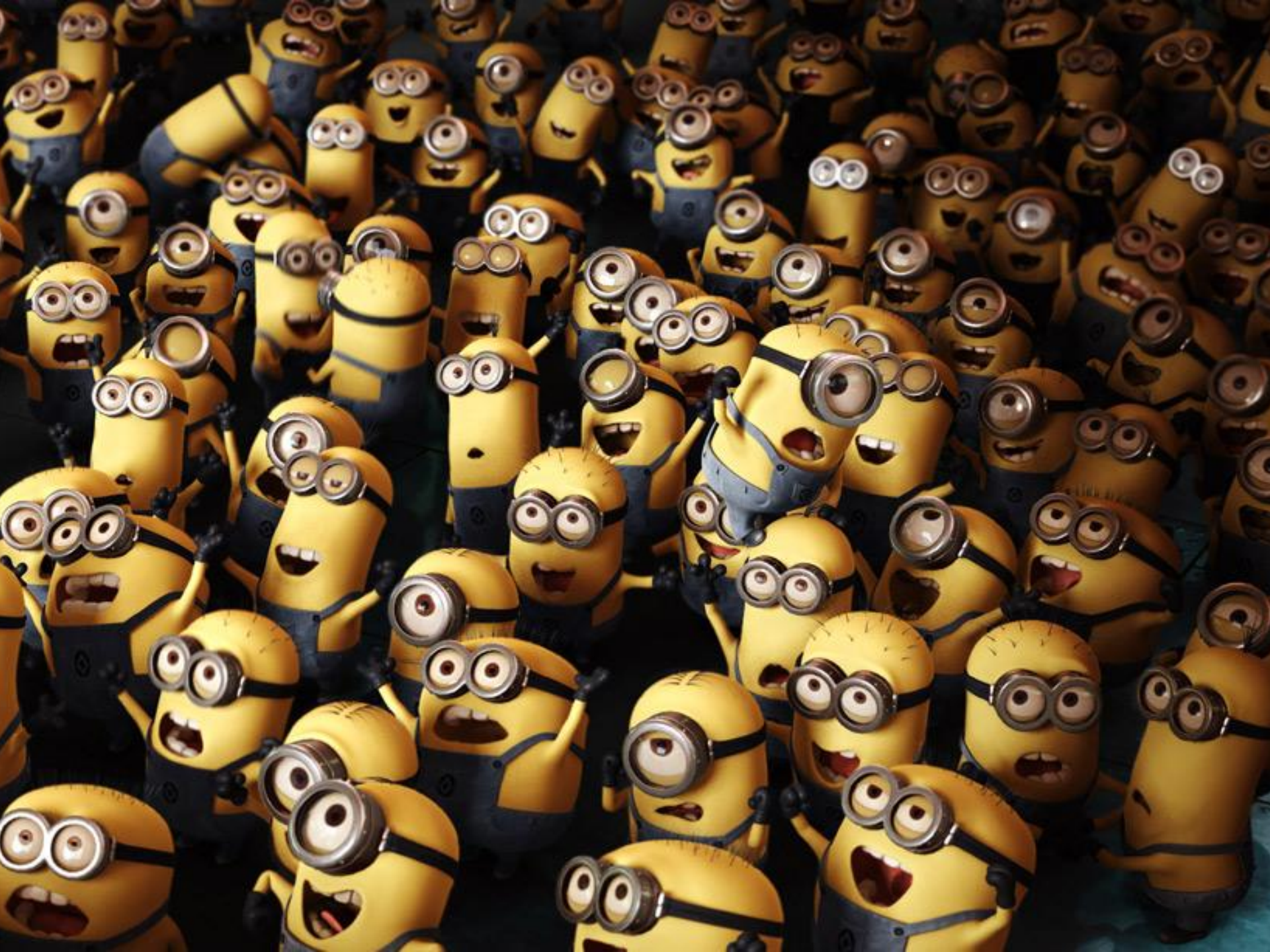
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IRCM
Dr. Anne Saumet



Fonds National de la
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CONTRE LE CANCER



Questions ?

