

Deus ex machina :
Intel·ligència Artificial
i BIOLOGIA COMPUTACIONAL

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Laboratori de Genòmica Computacional

Dept. de Genètica, Microbiologia i Estadística

Institut de Biomedicina de la Universitat de Barcelona



UNIVERSITAT DE
BARCELONA



Metrópolis, Fritz Lang (1927)



III JORNADA DELS INSTITUTS DE RECERCA PROPIS DE LA UB
INTEL·LIGÈNCIA ARTIFICIAL (IA): RECERCA I SOCIETAT

L'Era del «Big Data»



DADES



L'Era del «Big Data»

DADES



INFORMACIÓ

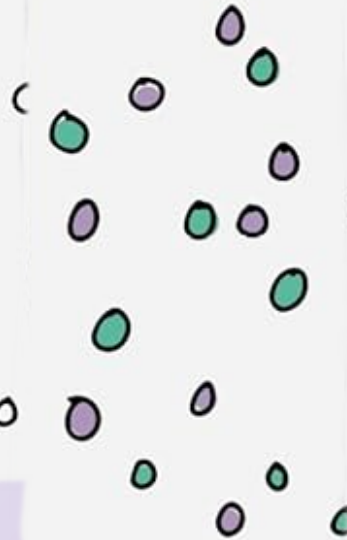


L'Era del «Big Data»

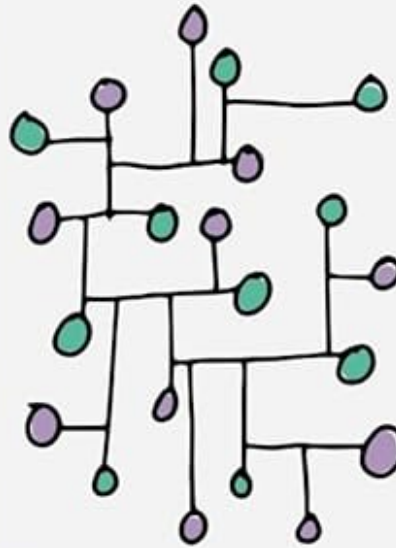
DADES



INFORMACIÓ



CONeixEMENT



L'Era del «Big Data»

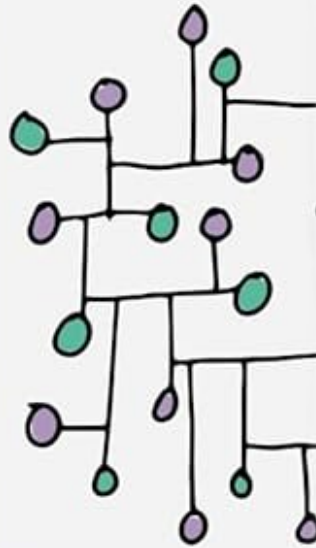
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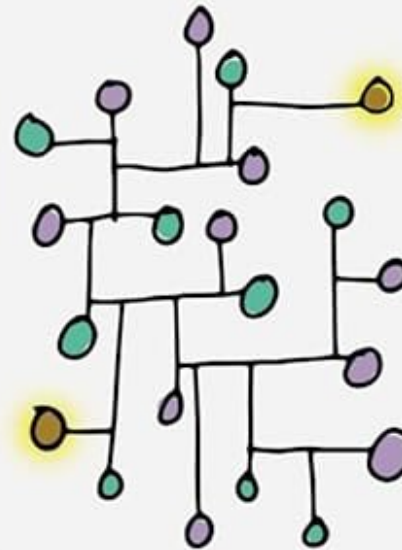
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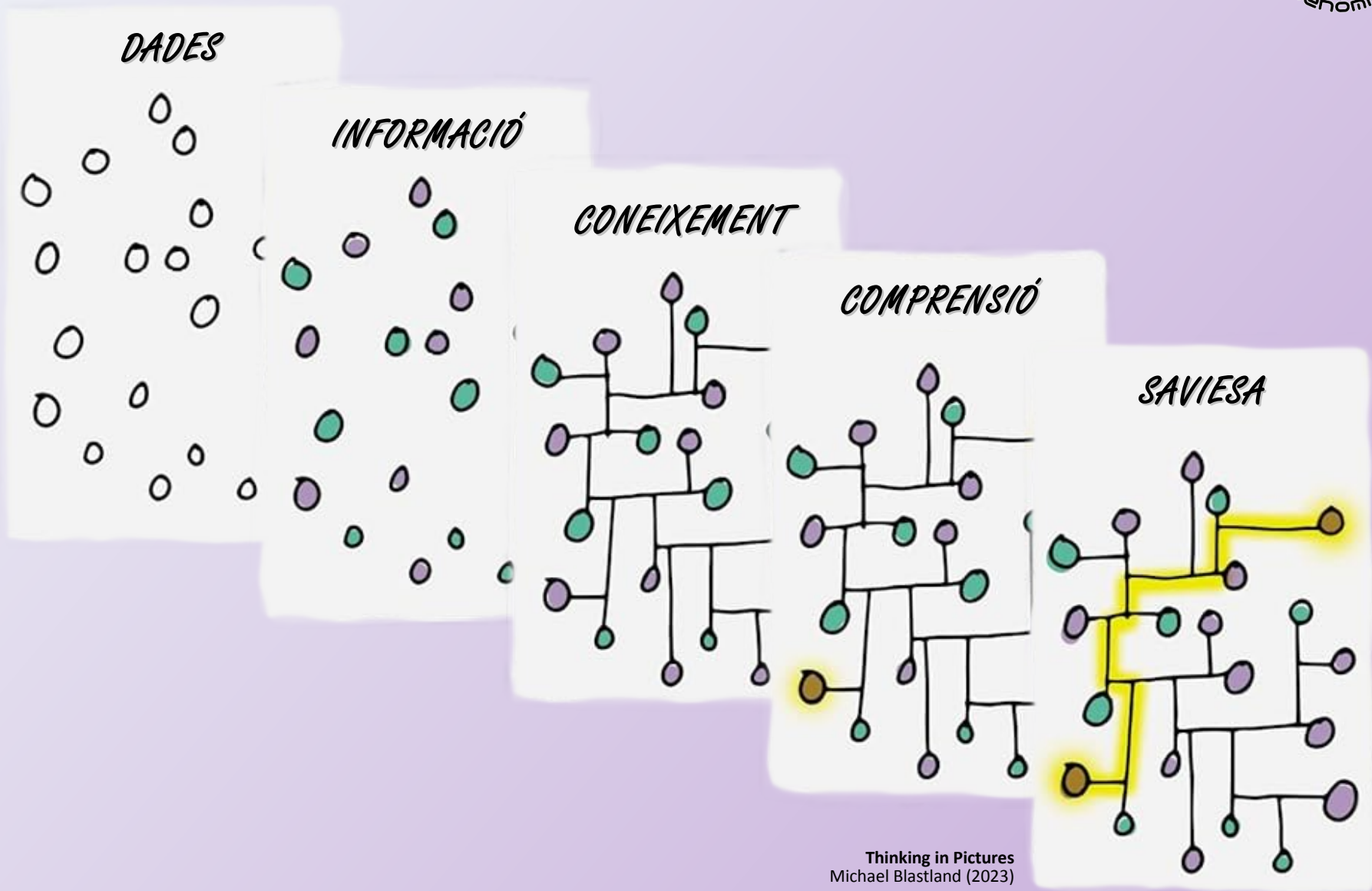
CONeixEMENT



COMPRESIÓ

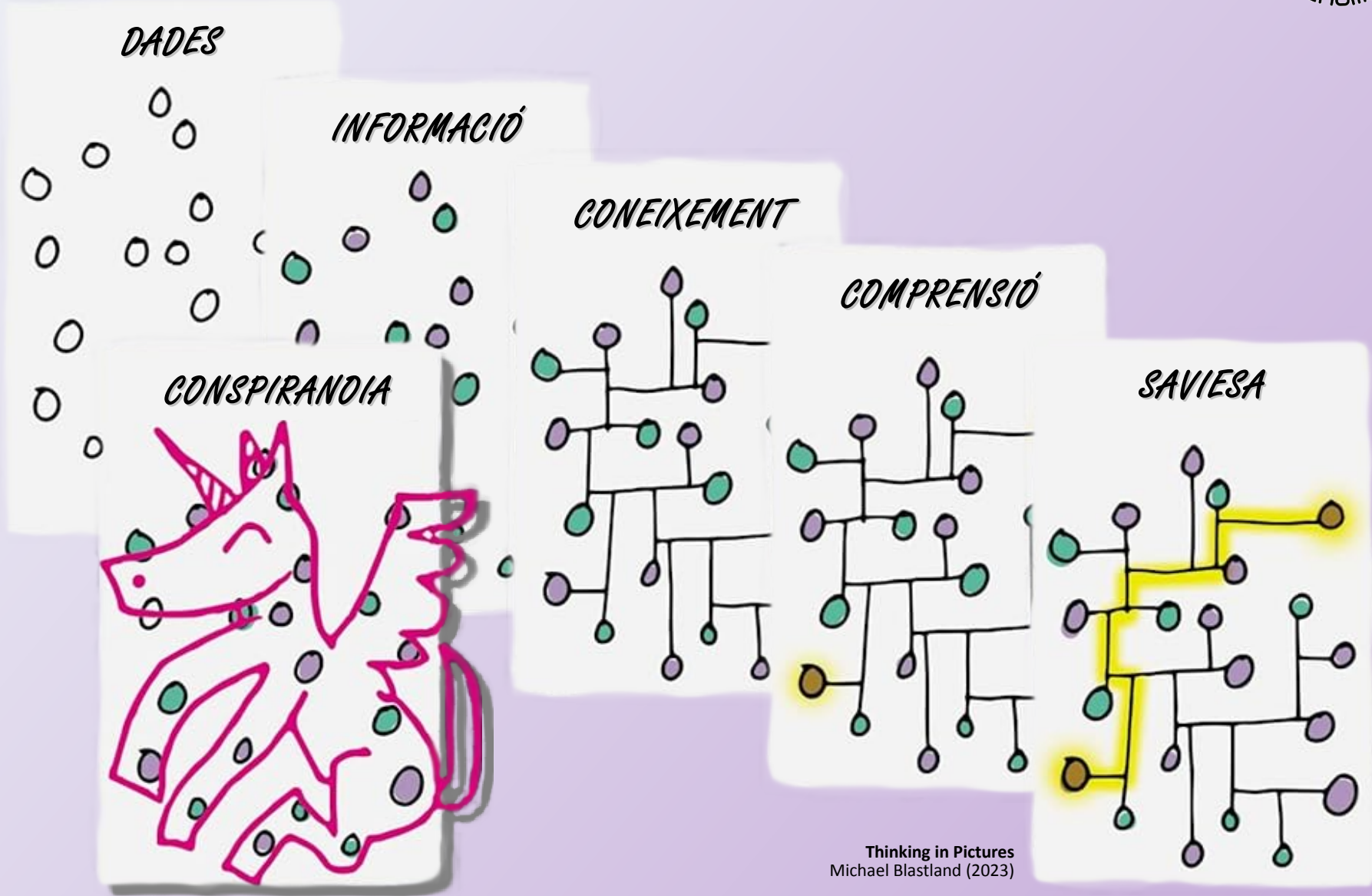


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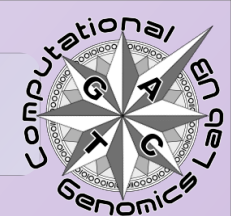
Thinking in Pictures
Michael Blastland (2023)

L'Era del «Big Data»



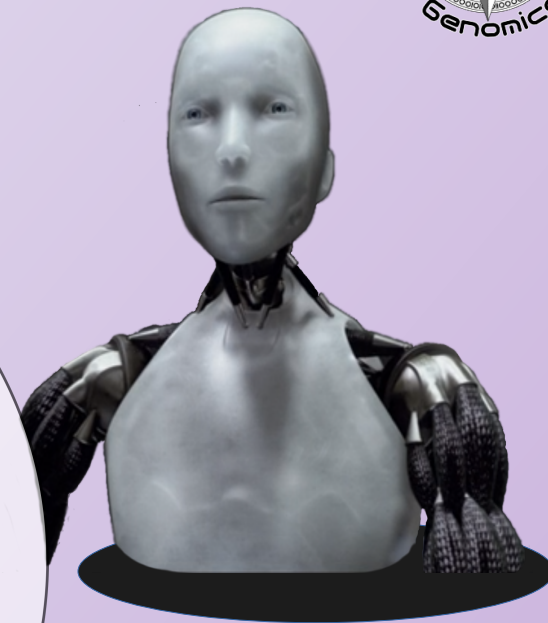
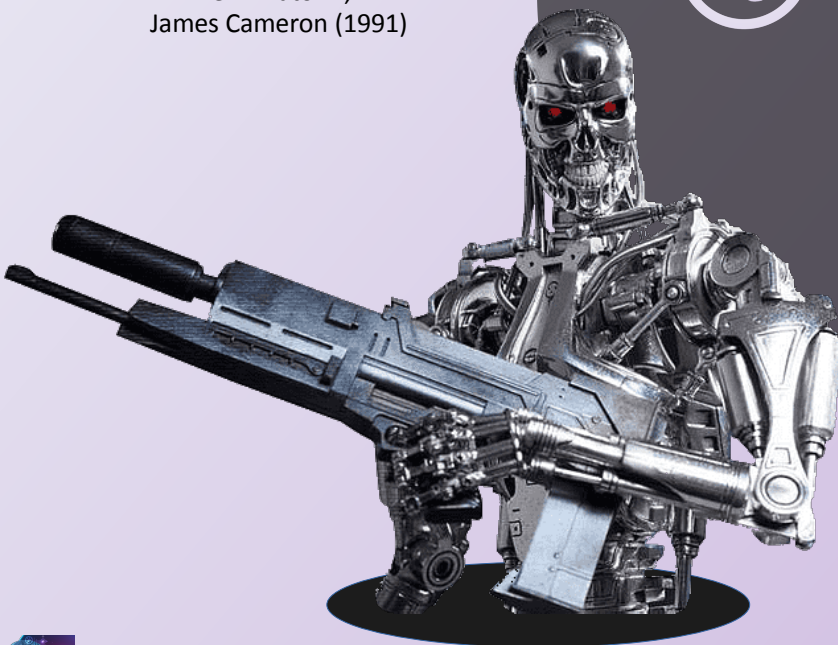
Thinking in Pictures
Michael Blastland (2023)

Els Perills de la Tecnologia



SkyNet

Terminator 2,
James Cameron (1991)



Sonny

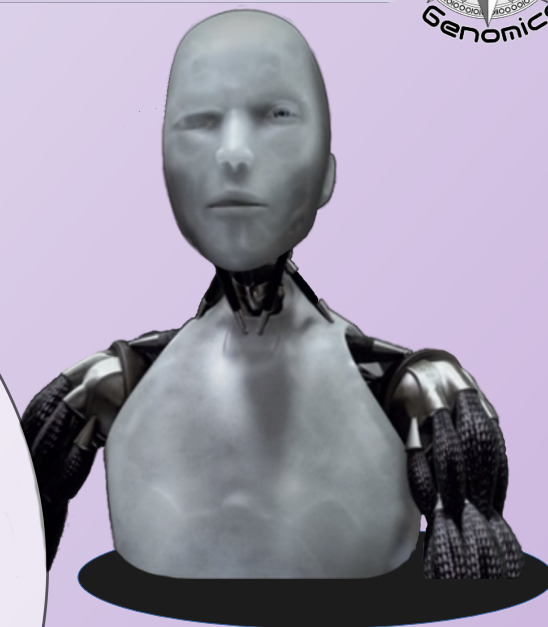
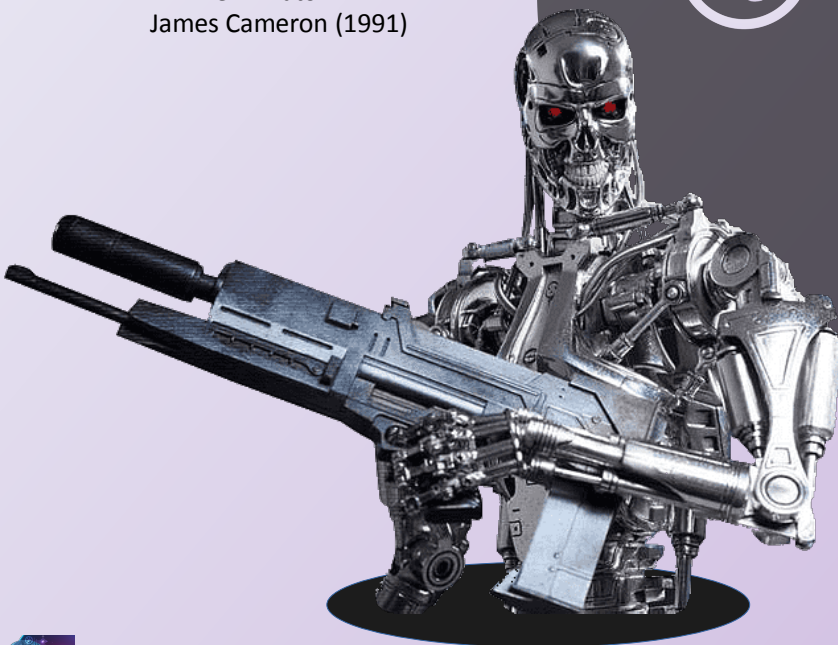
Jo Robot,
Alex Proyas (2004)

Els Perills de la Tecnologia



SkyNet

Terminator 2
James Cameron (1991)

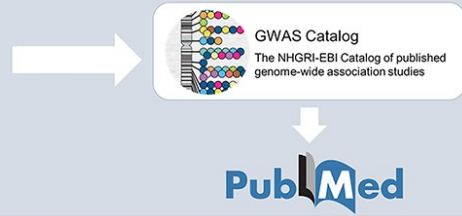


Sonny

Jo Robot
Alex Proyas (2004)

Biaixos en les Dades...

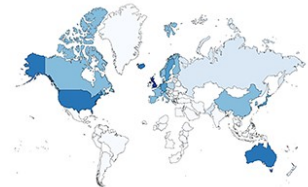
Ethnic, gender and other sociodemographic biases in genome-wide association studies for the most burdensome non-communicable diseases: 2005-2022



We mined the NHGRI-EBI GWAS Catalog (2005-2022) for the most burdensome non-communicable causes of death worldwide. We then compared: i) the geographic, ethnic, and socioeconomic characteristics of study populations, ii) the geographic and socioeconomic characteristics of the regions within which researchers were located, and iii) the extent to which male and female investigators undertook and led the research.



37.6%
of all authors had affiliations to US institutions.



The origin of samples was diverse:

34.5%
of data emanated from **UK** cohorts; the **US** and **Iceland** followed, contributing 16.3% and 9.6%.



91.2%
of complex trait GWAS has been performed in people of European ancestry.

> 95%
of samples were originated from high-income countries.

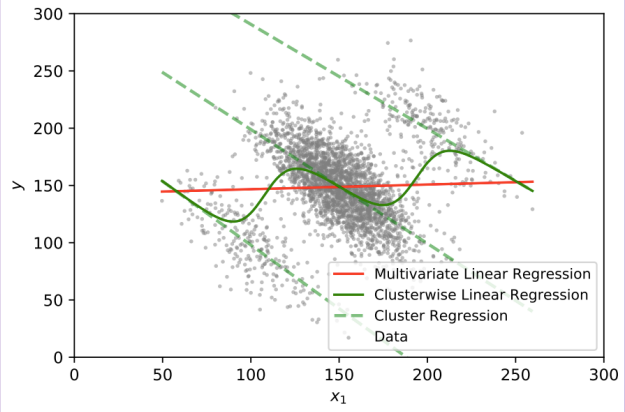
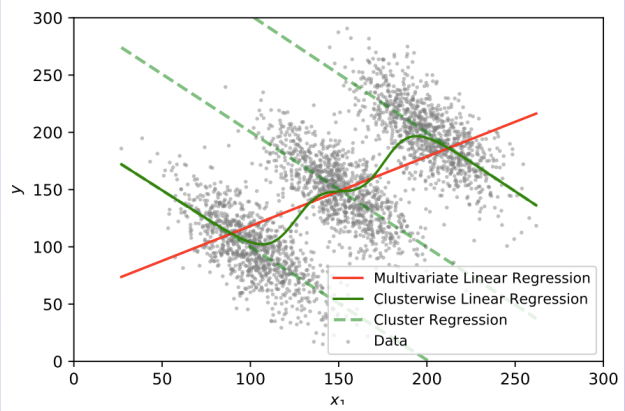


> 85%
of authors were affiliated to high-income countries.



Hugo Fitipaldi & Paul W Franks, *Human Molecular Genetics* (2023)

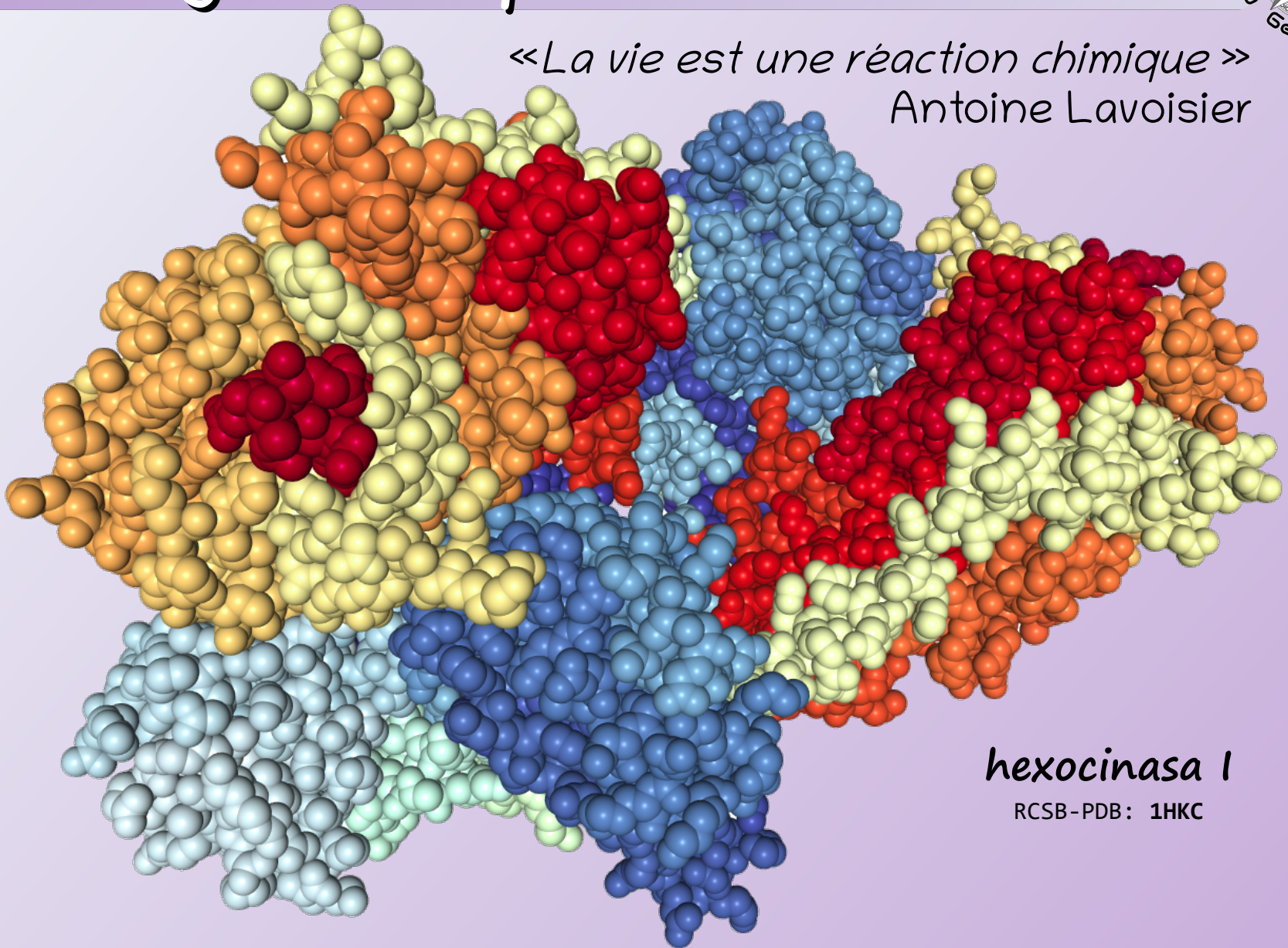
Ninareh Mehrabi et al, *ACM Computing Surveys* (2021)



Biologia i Complexitat



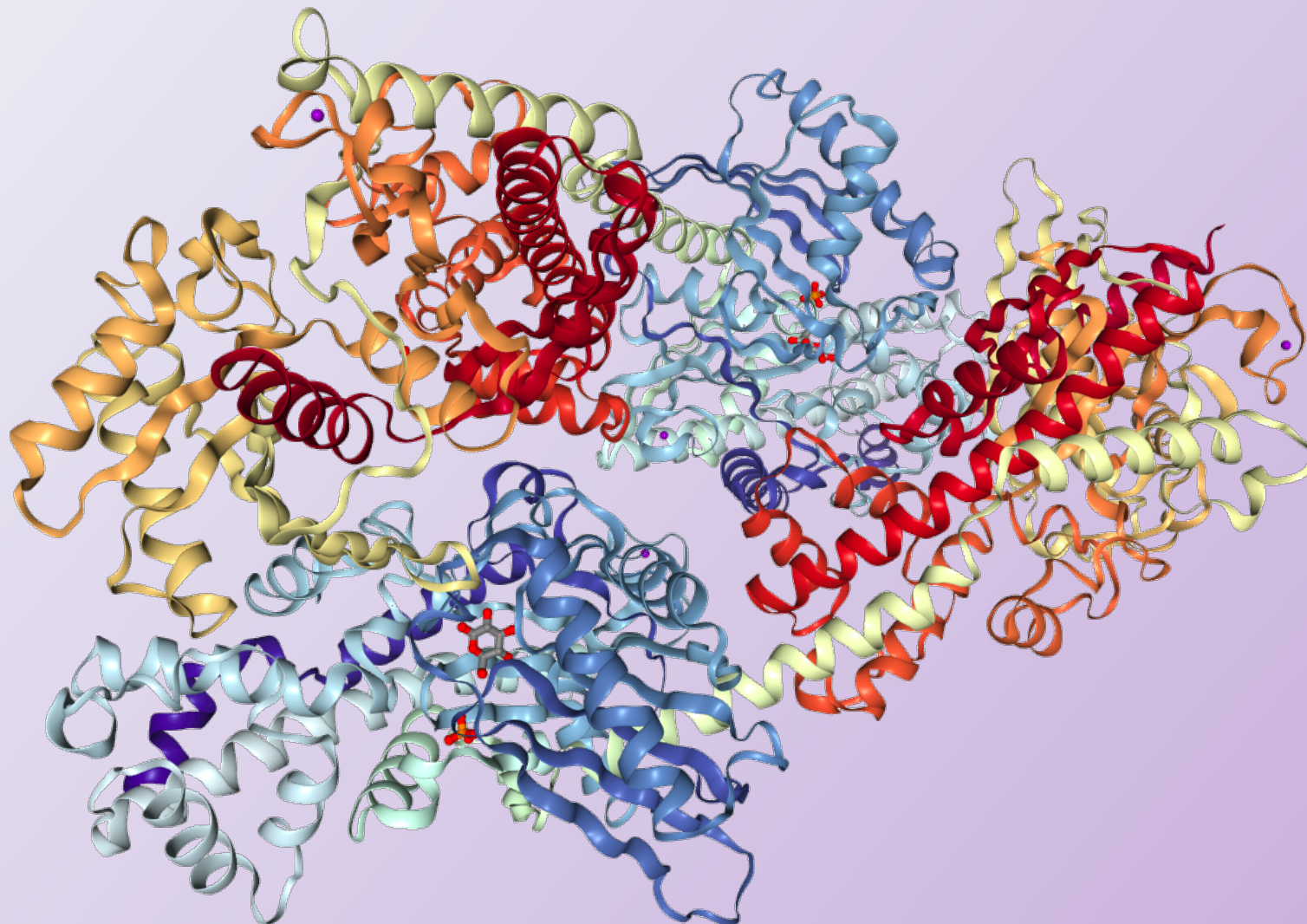
<<La vie est une réaction chimique >>
Antoine Lavoisier



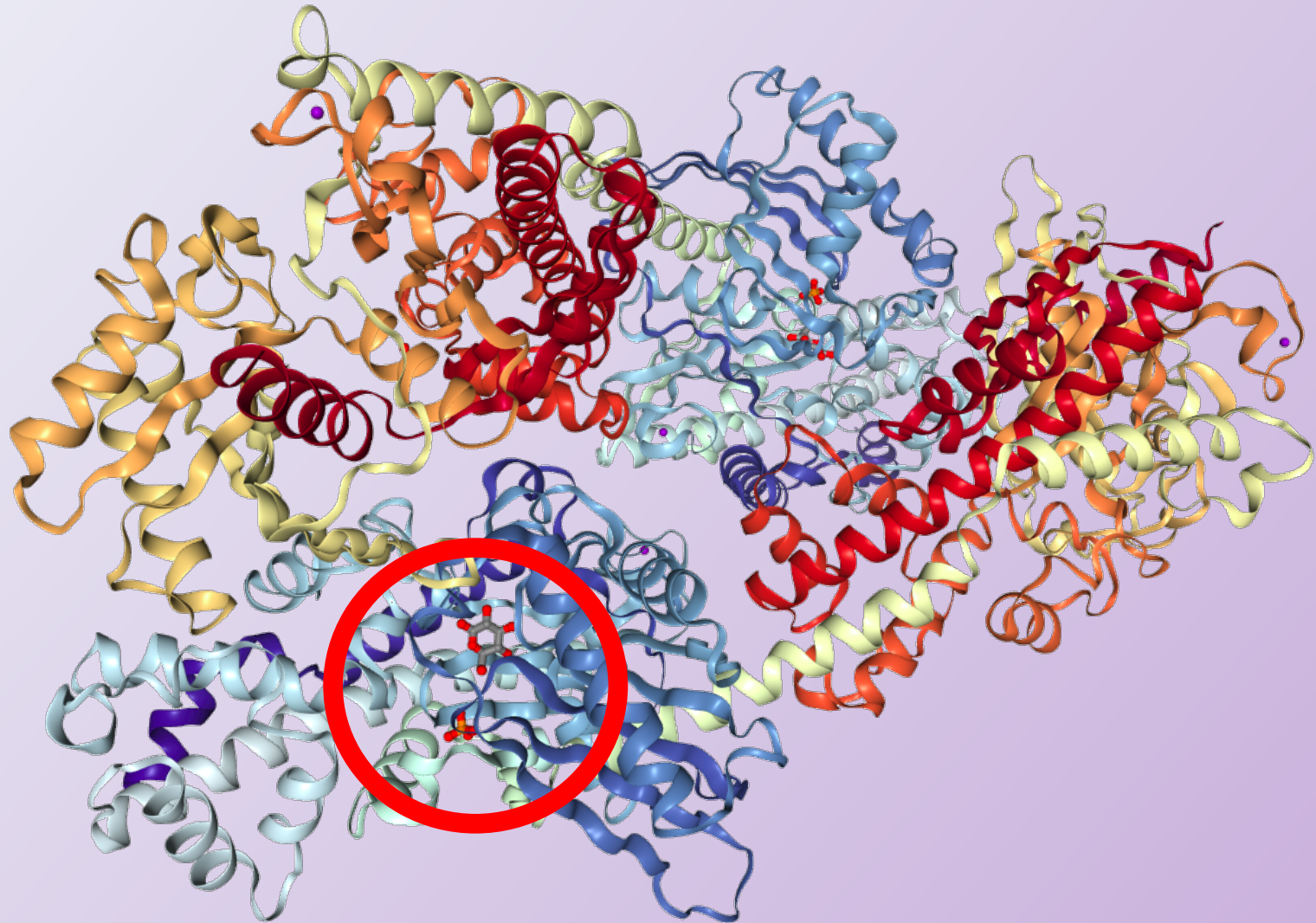
hexocinasa I

RCSB-PDB: 1HKC

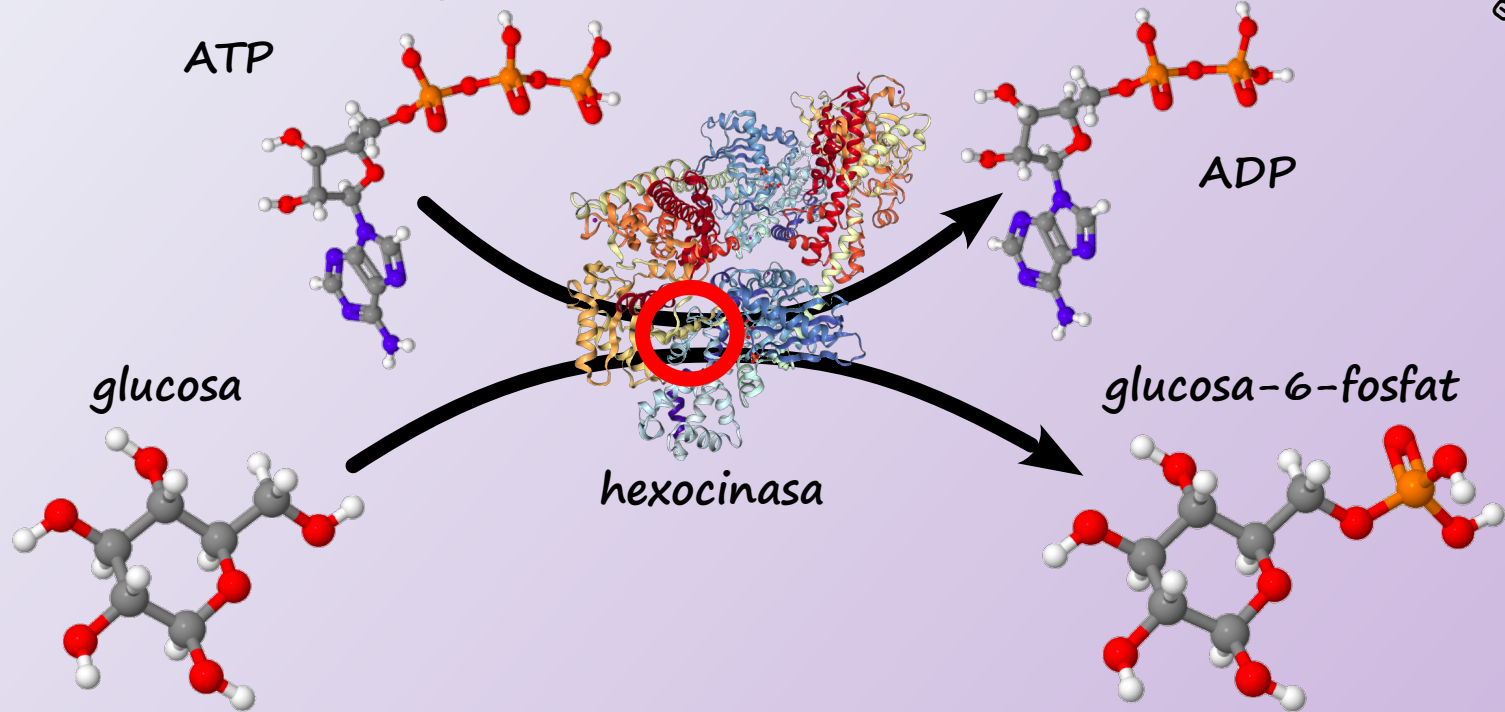
Models Biològics



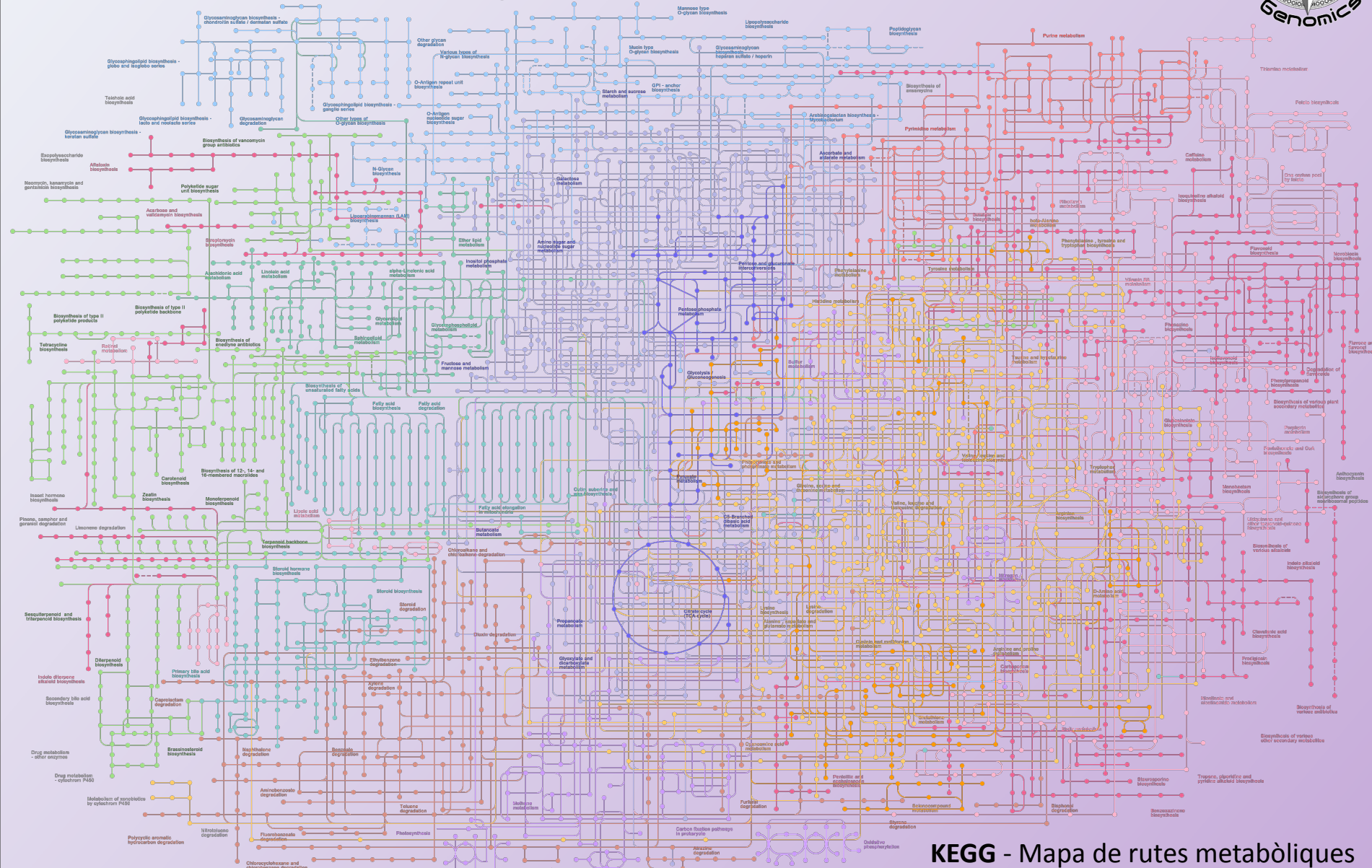
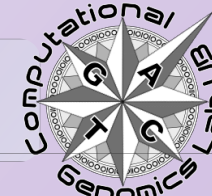
Models Biològics



Models Biològics: el Metaboloma



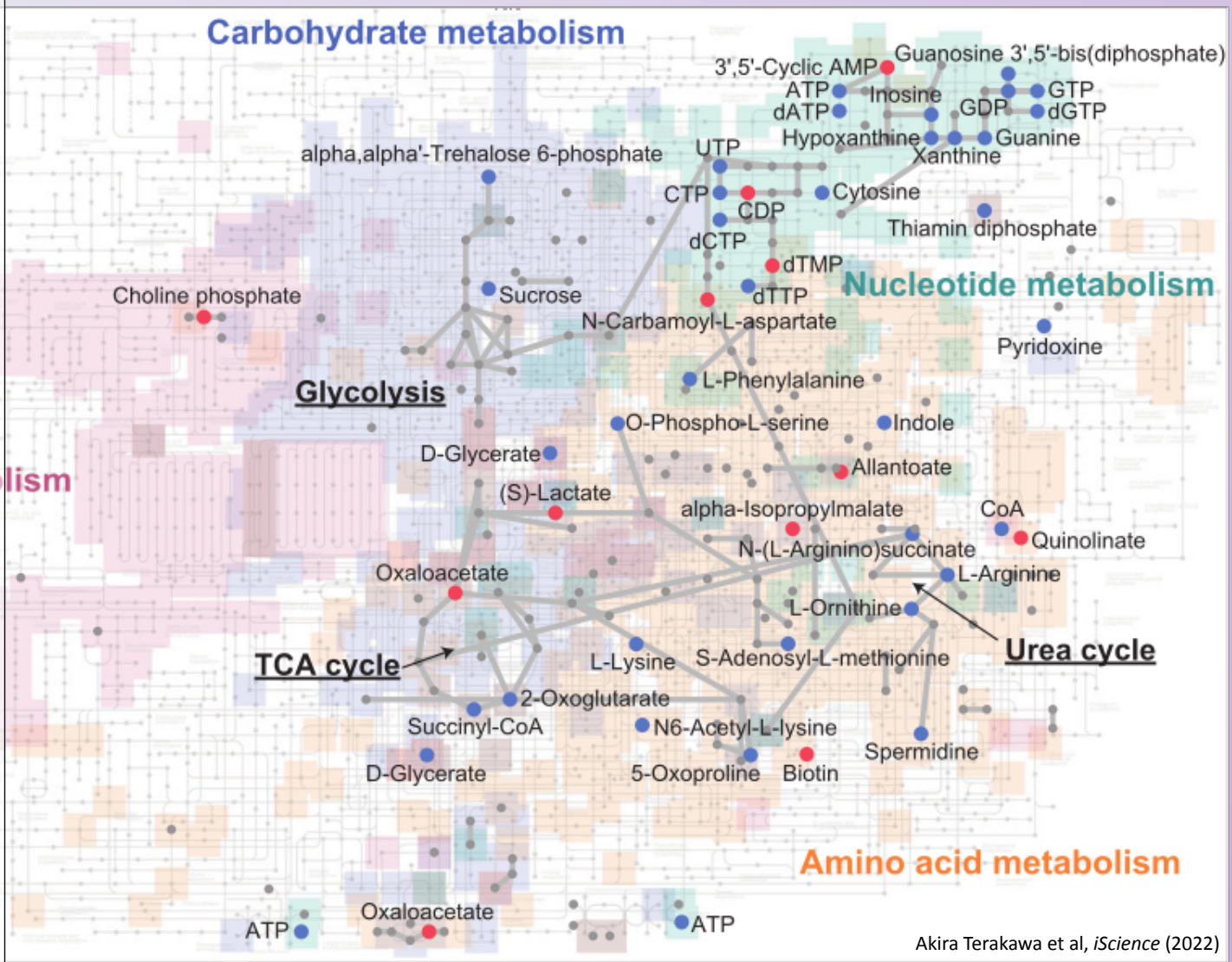
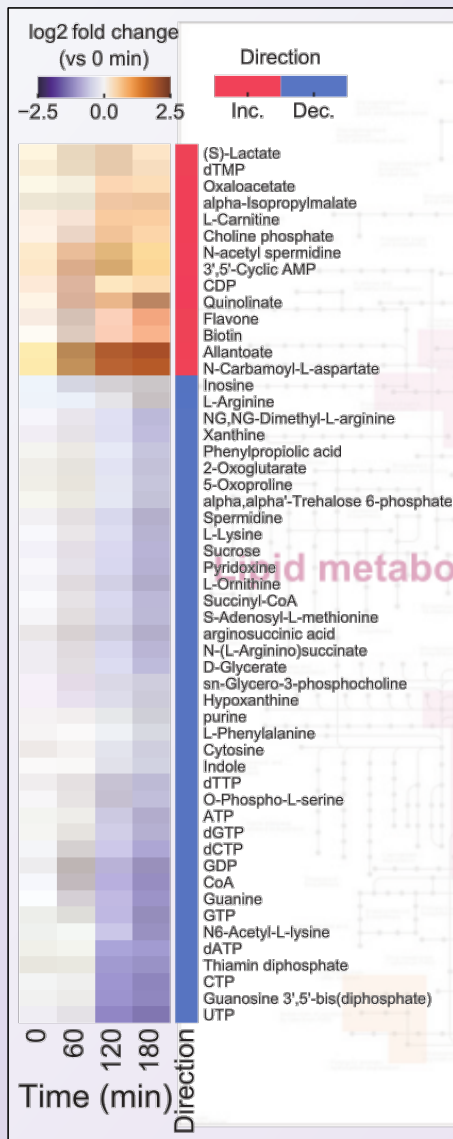
Models Biològics: el Metaboloma



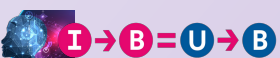
KEGG - Mapa de rutes metabòliques



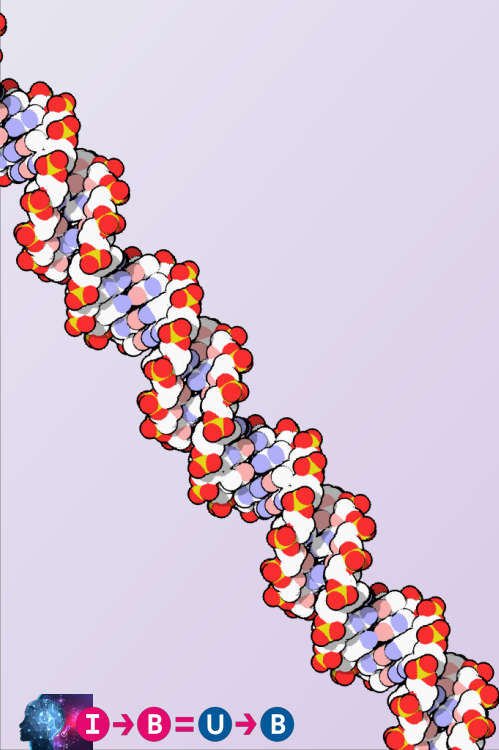
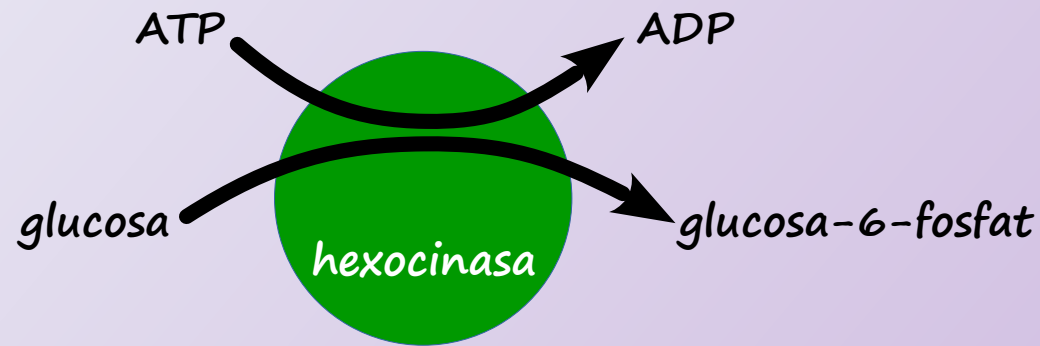
Models Biològics: el Metaboloma



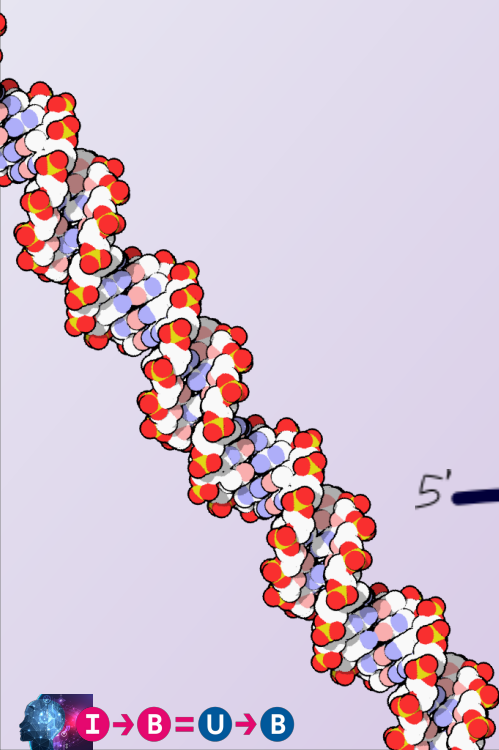
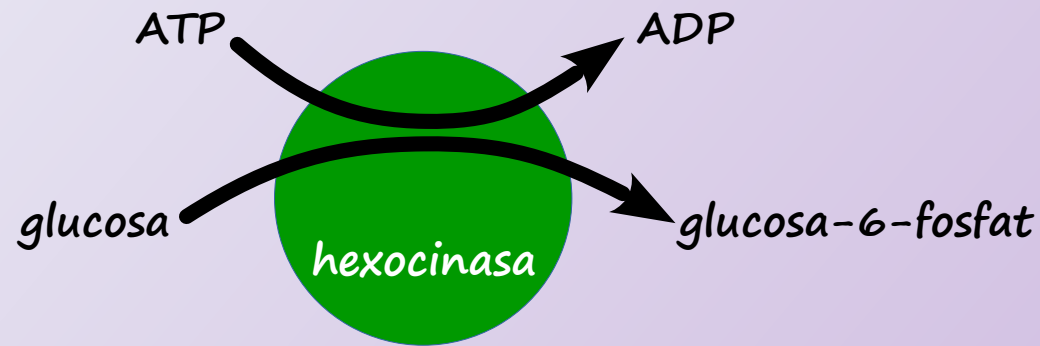
Akira Terakawa et al, *iScience* (2022)



Activant el Codi del Programa

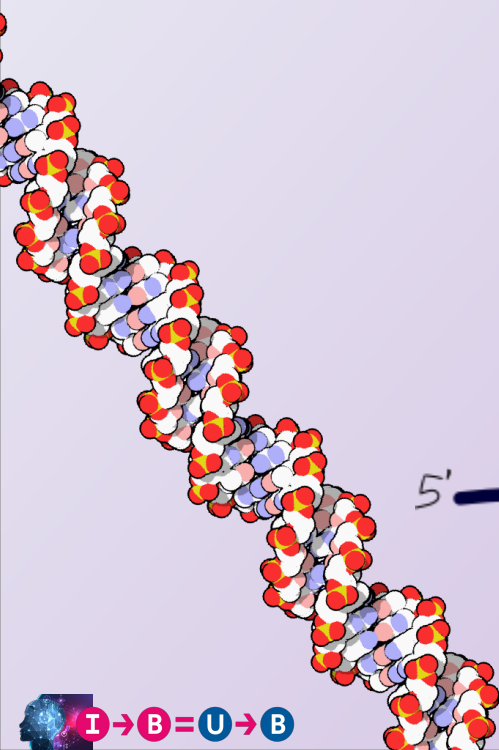
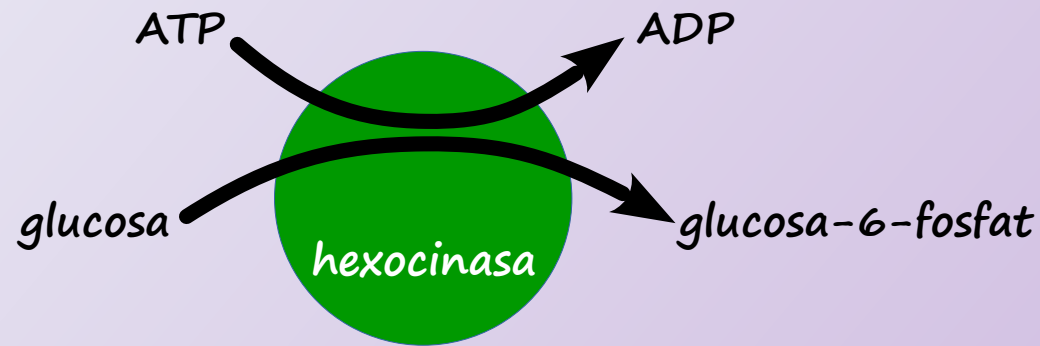


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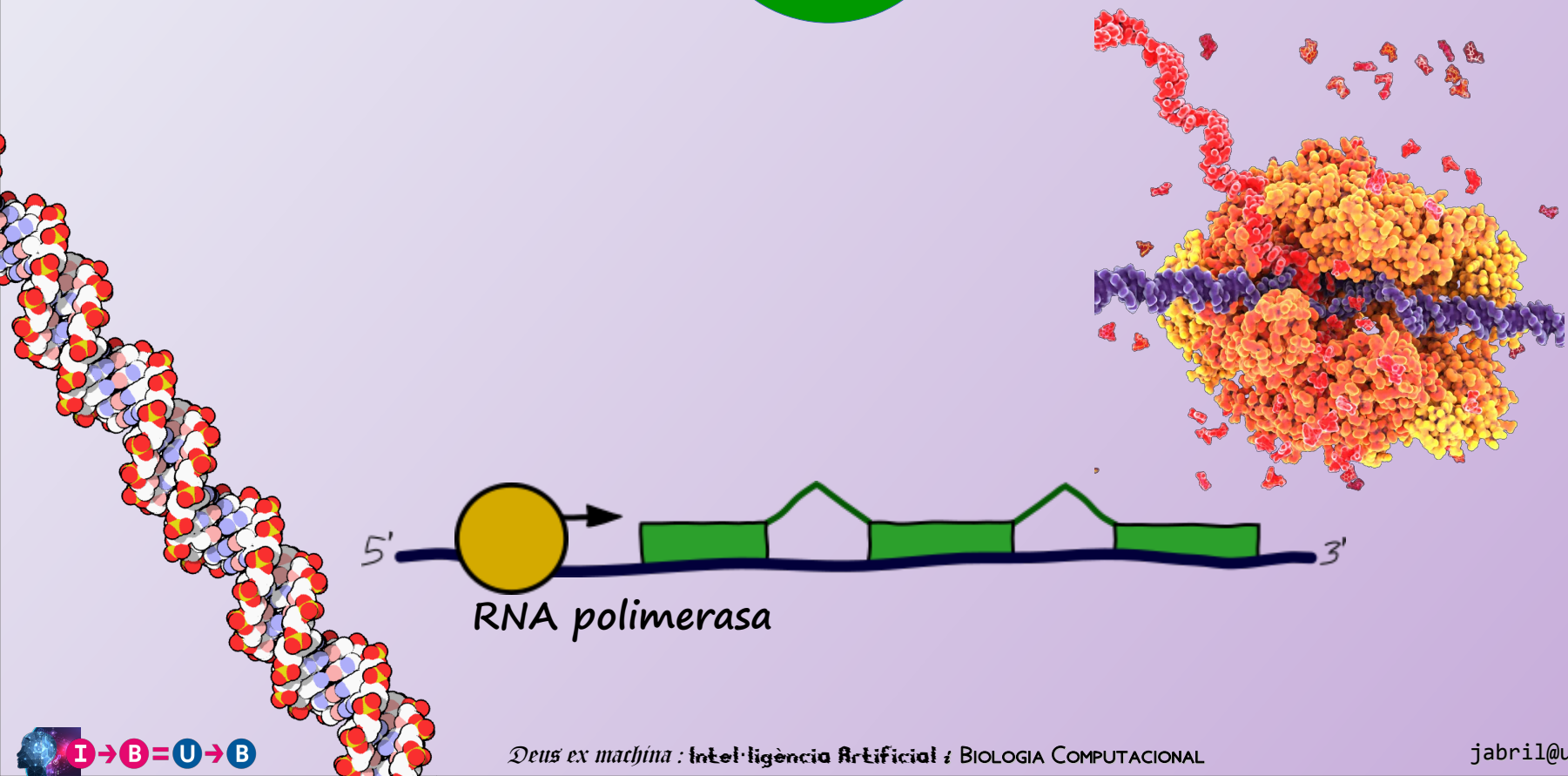
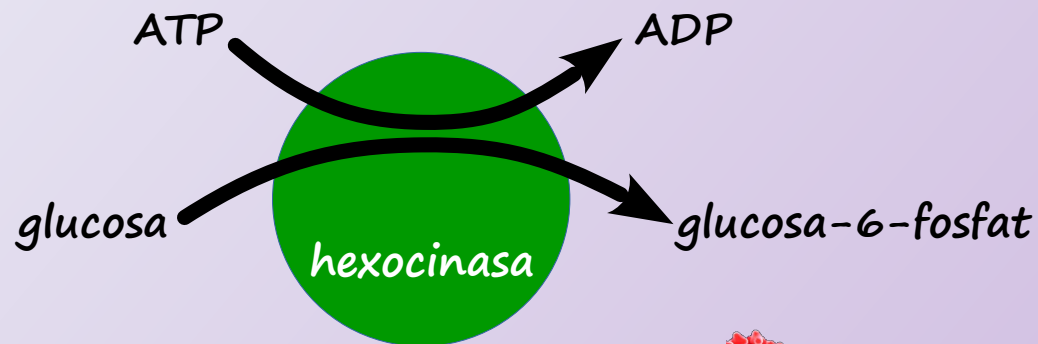


5' ————— 3'

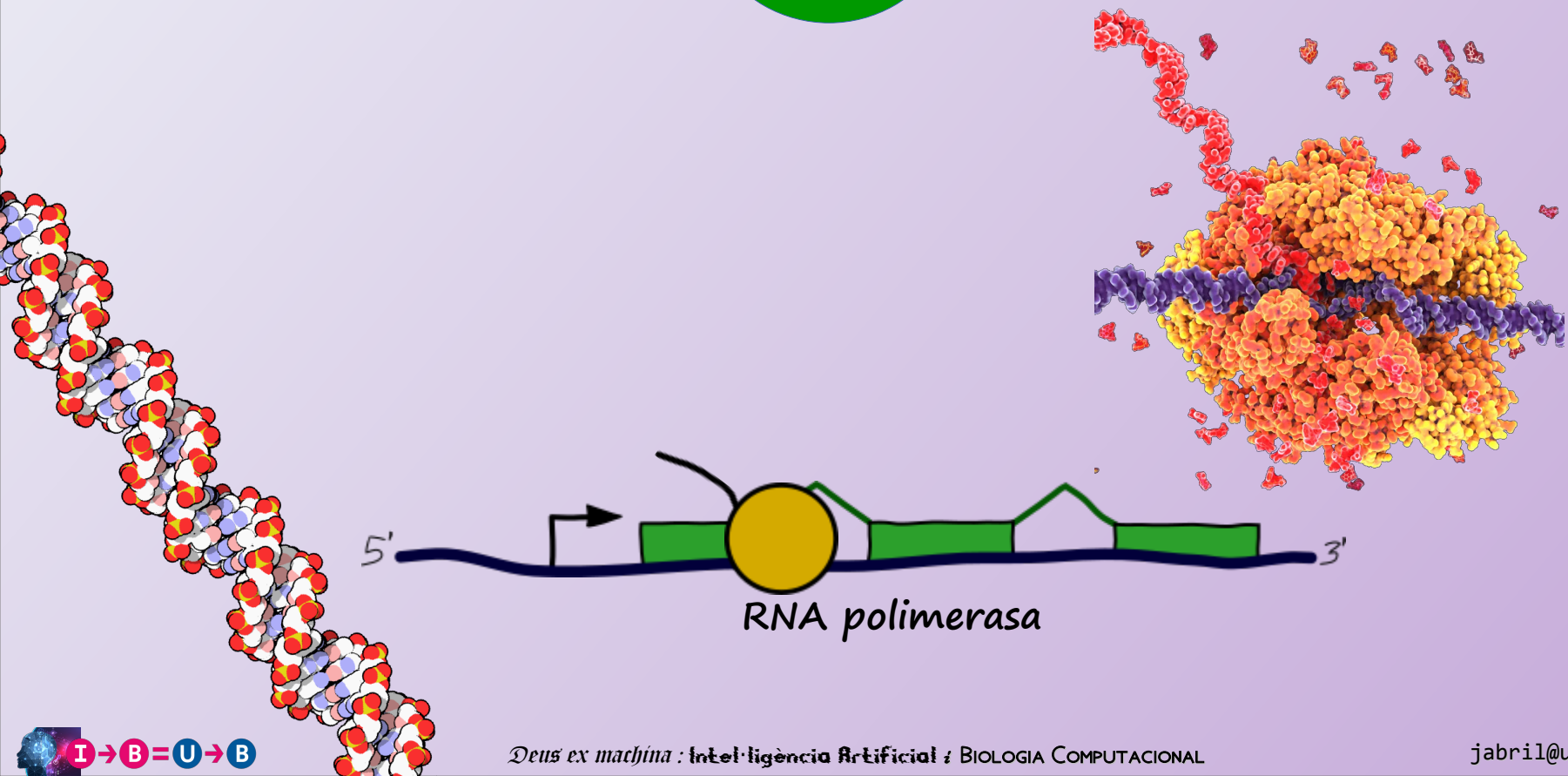
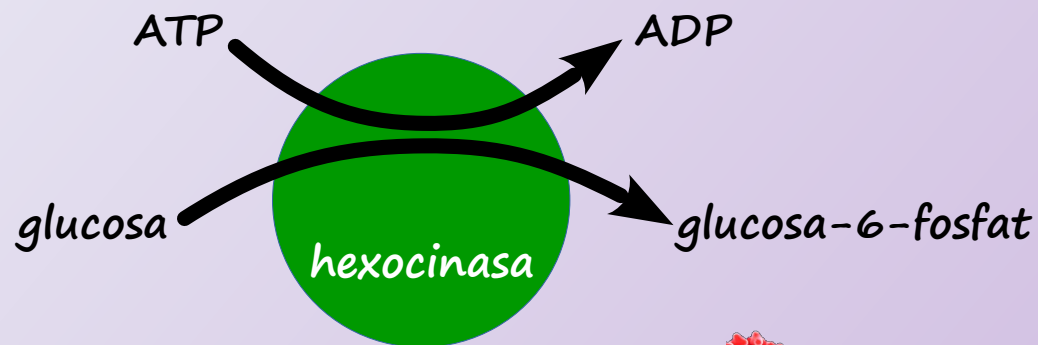
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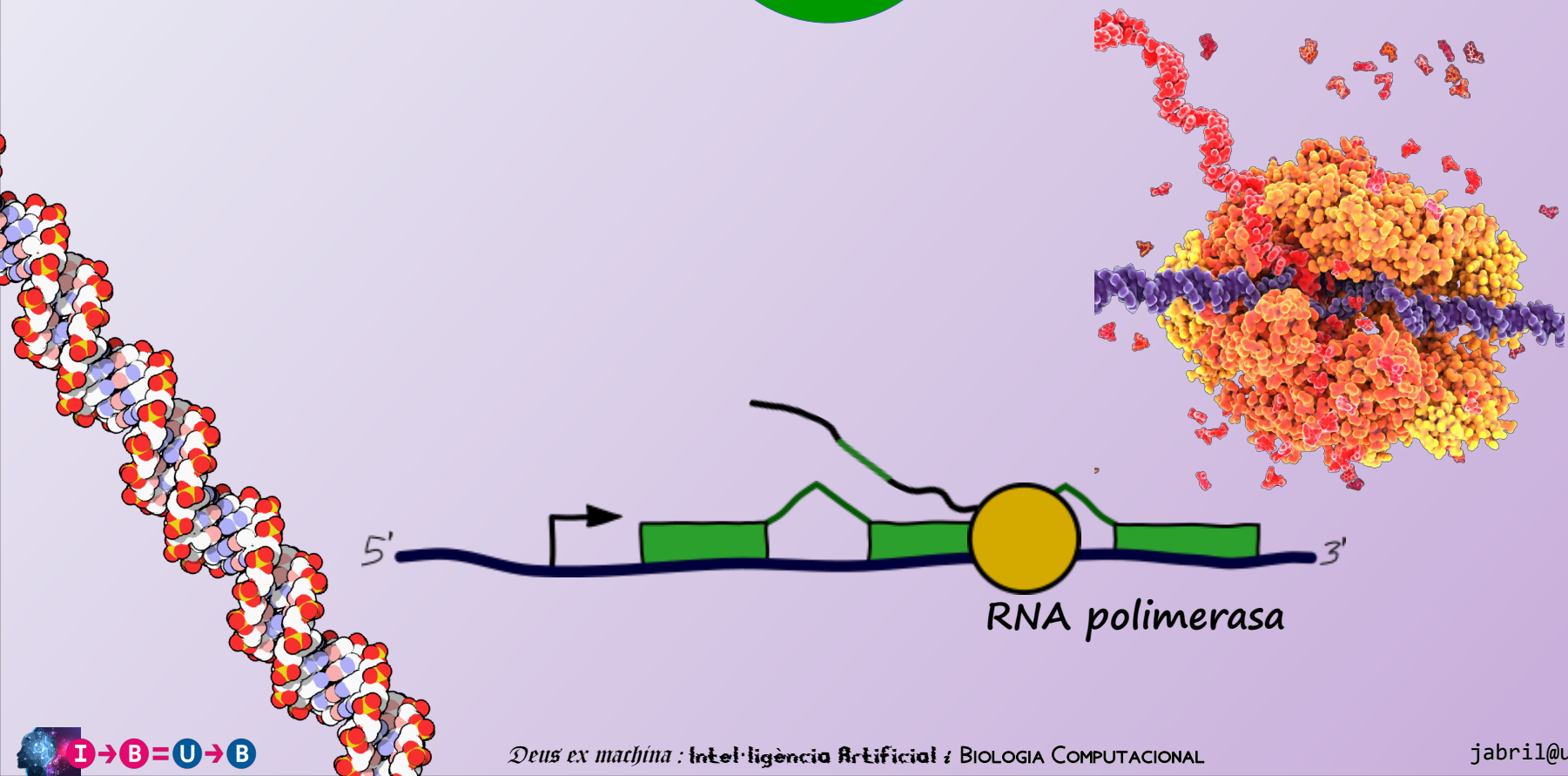
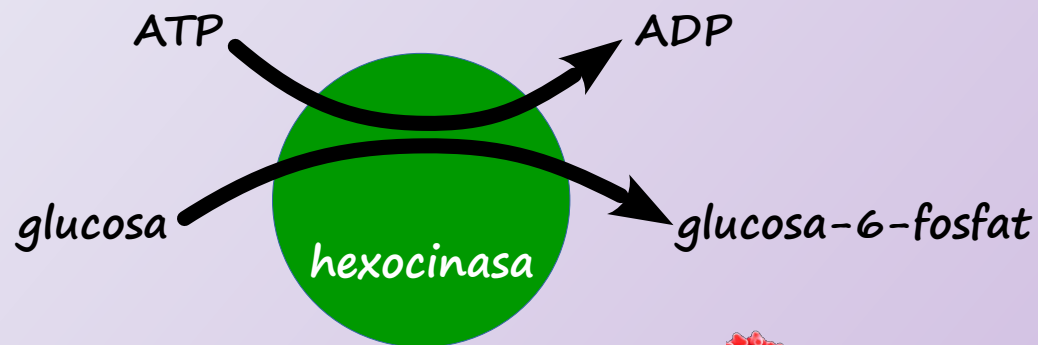
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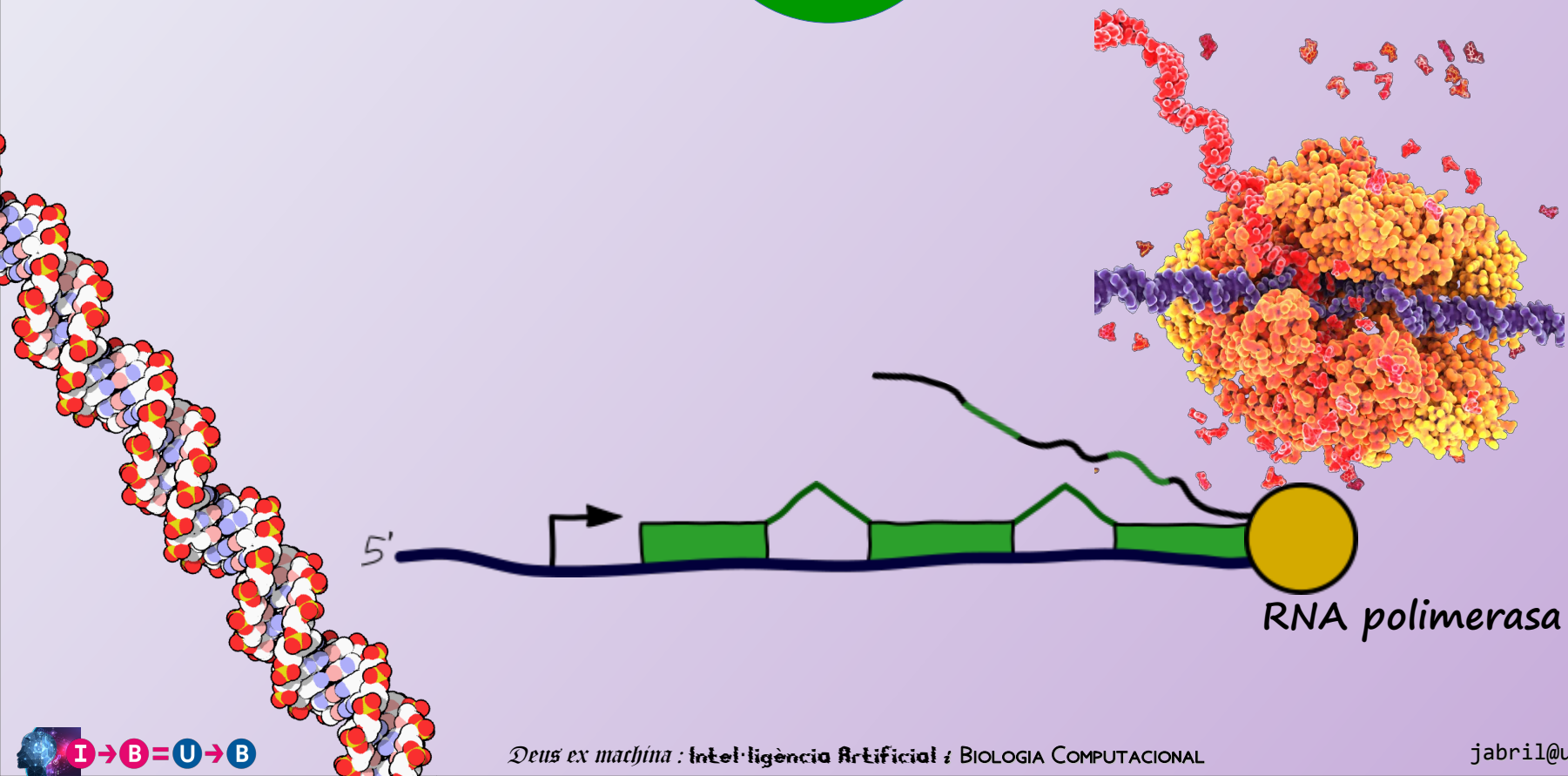
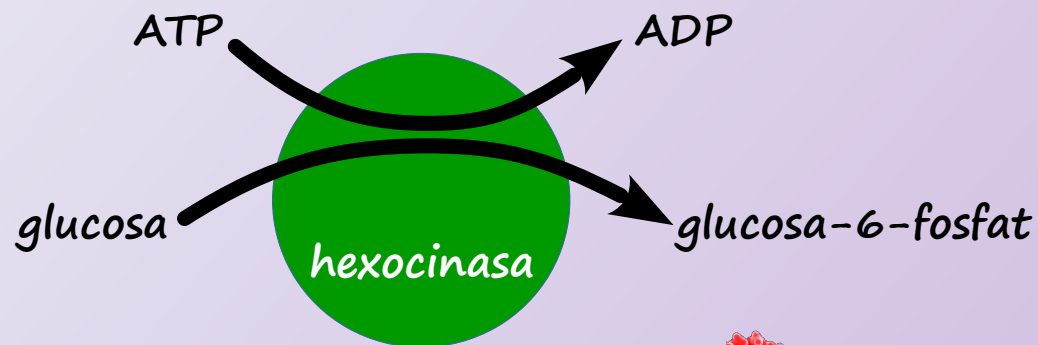
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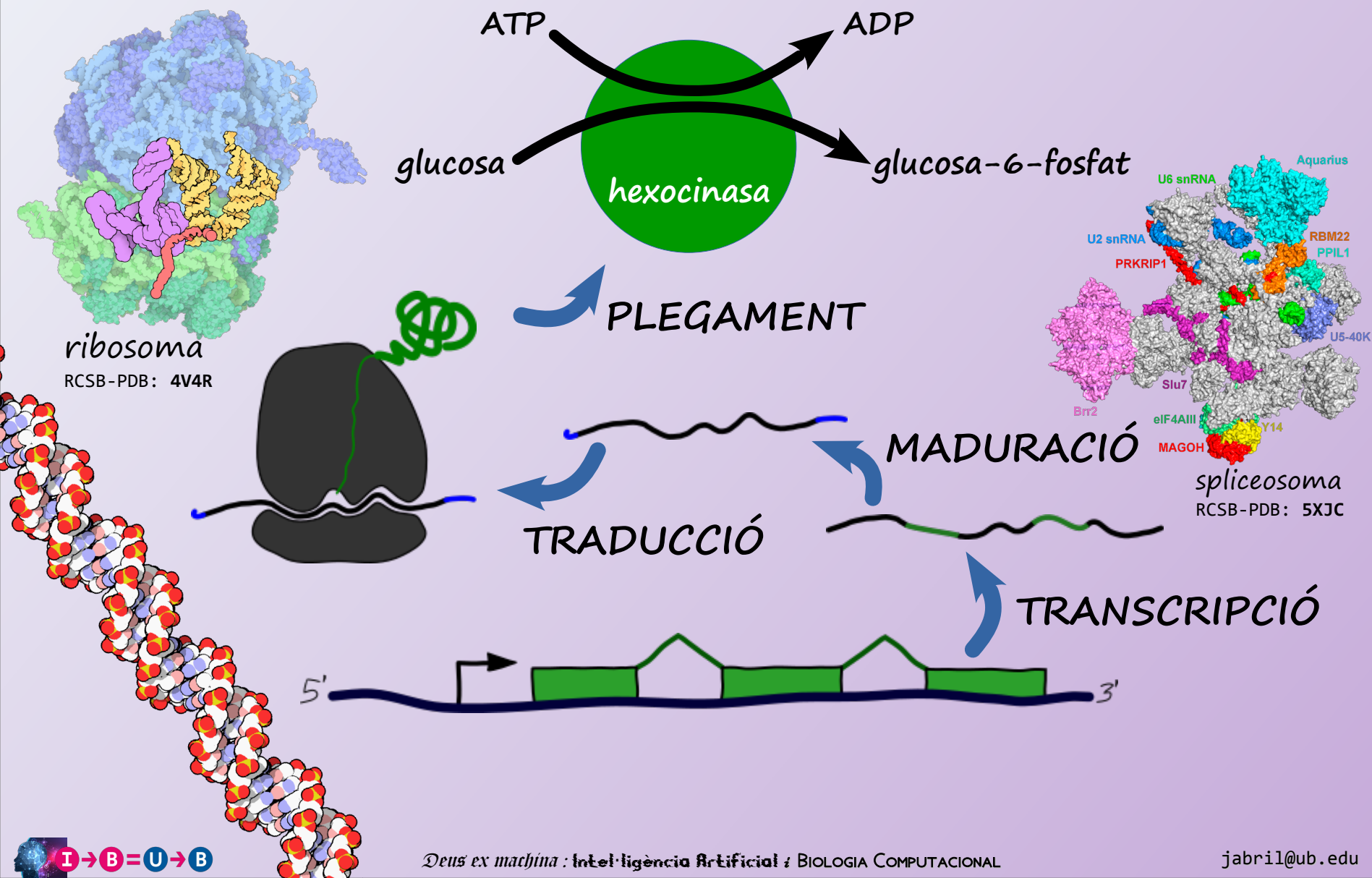
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Activant el Codi del Programa

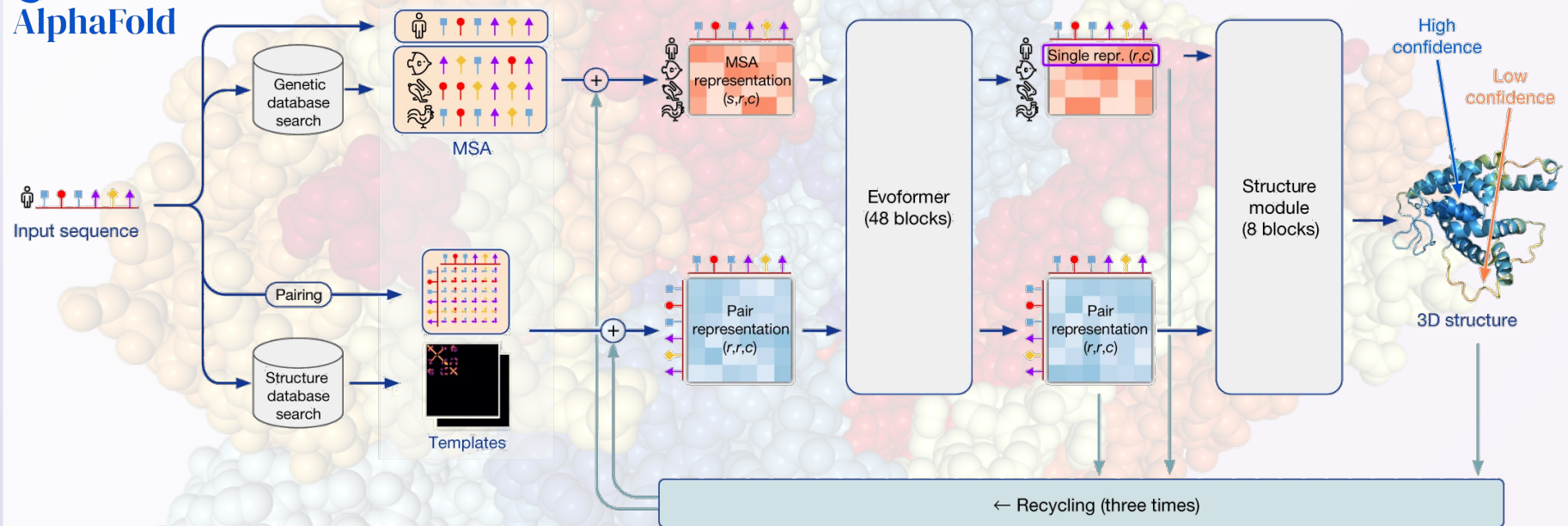


Activant el Codi del Programa



I.A. i el Problema del Plegament

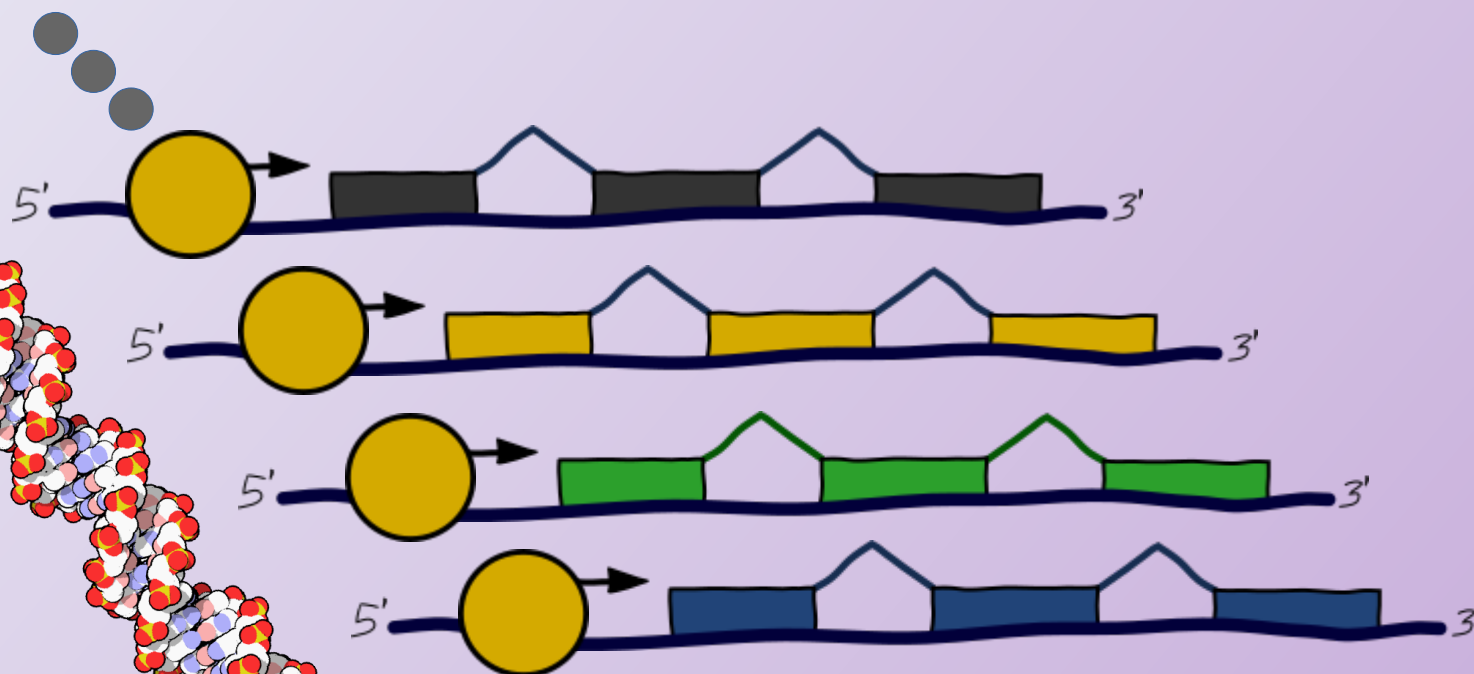
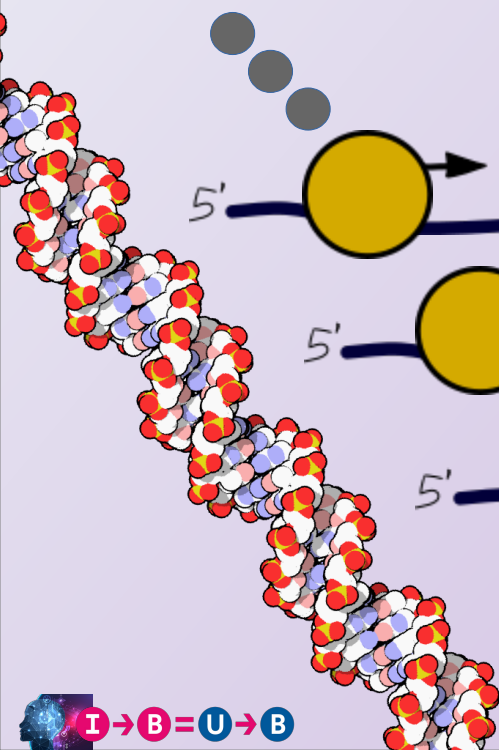
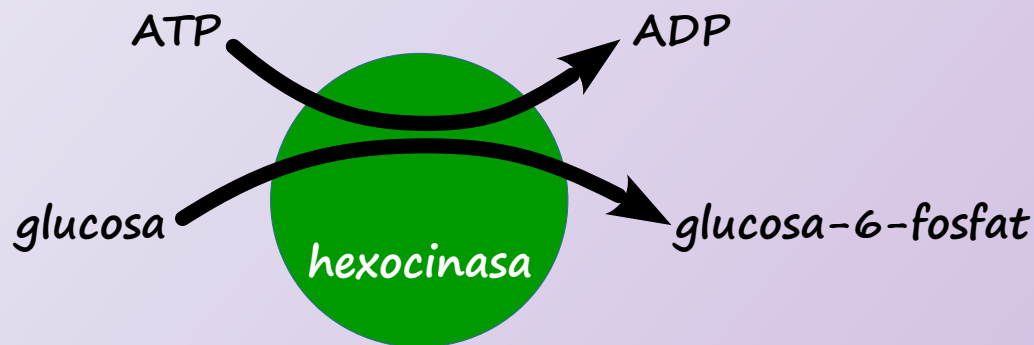
DeepMind
AlphaFold



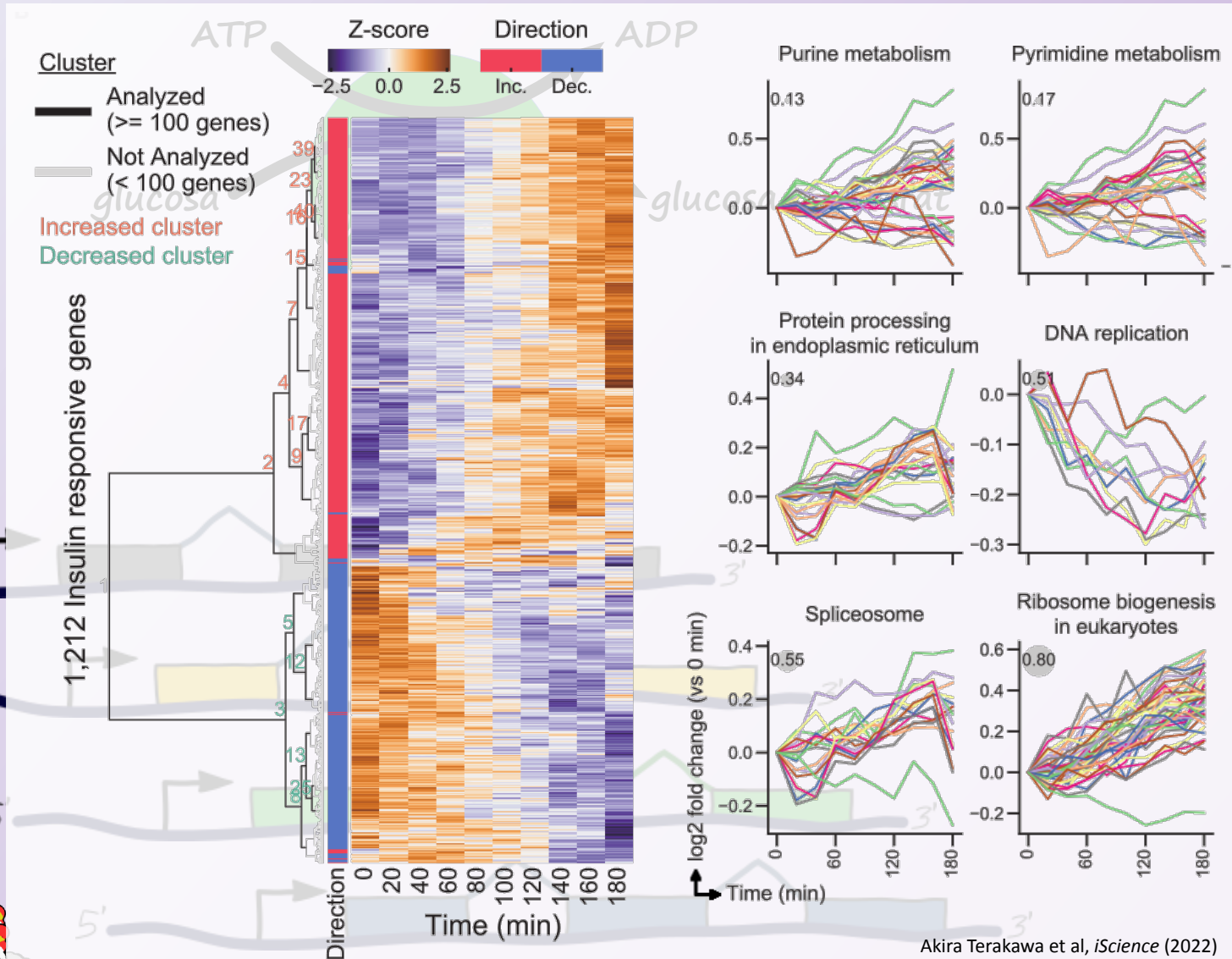
hexocinasa I

RCSB-PDB: 1HKC

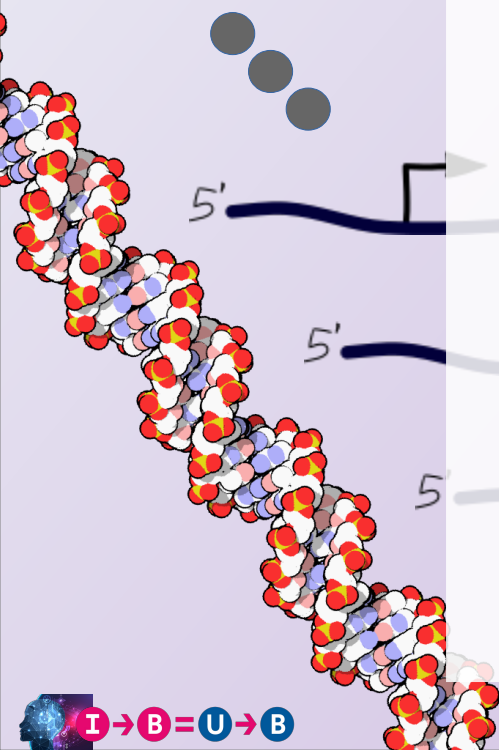
Modelant l'Expressió Gènica



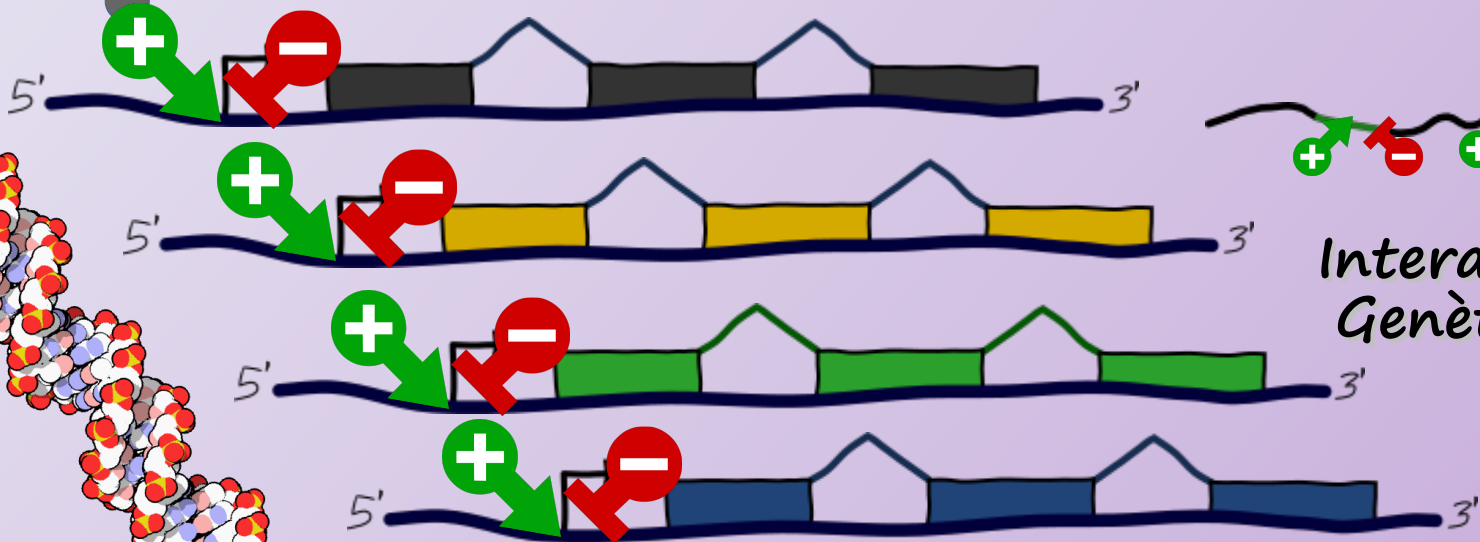
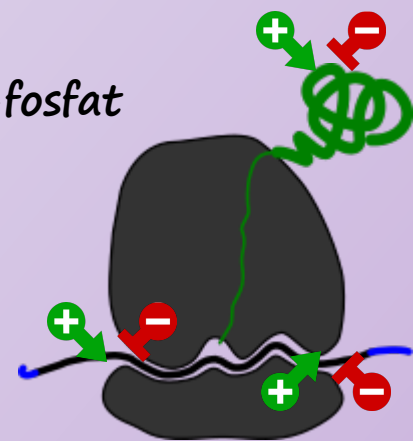
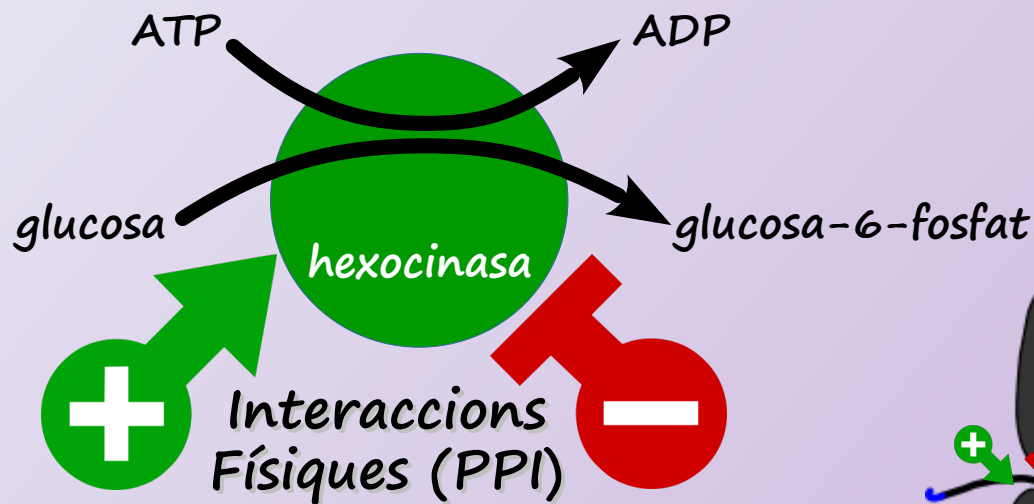
Modelant l'Expressió Gènica



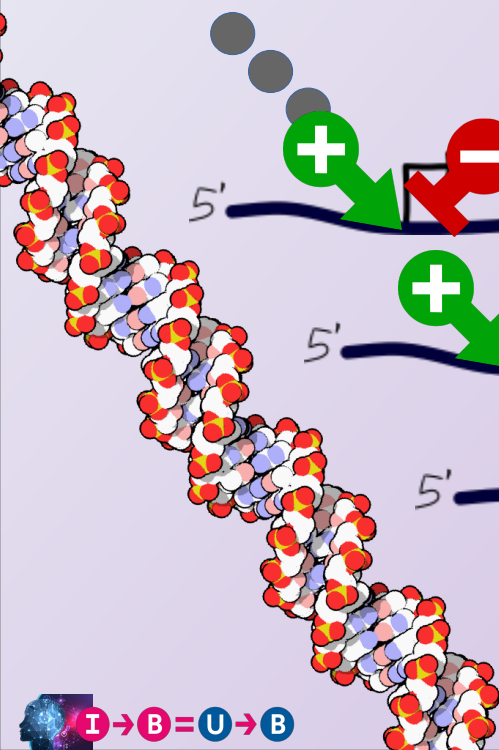
Akira Terakawa et al, *iScience* (2022)



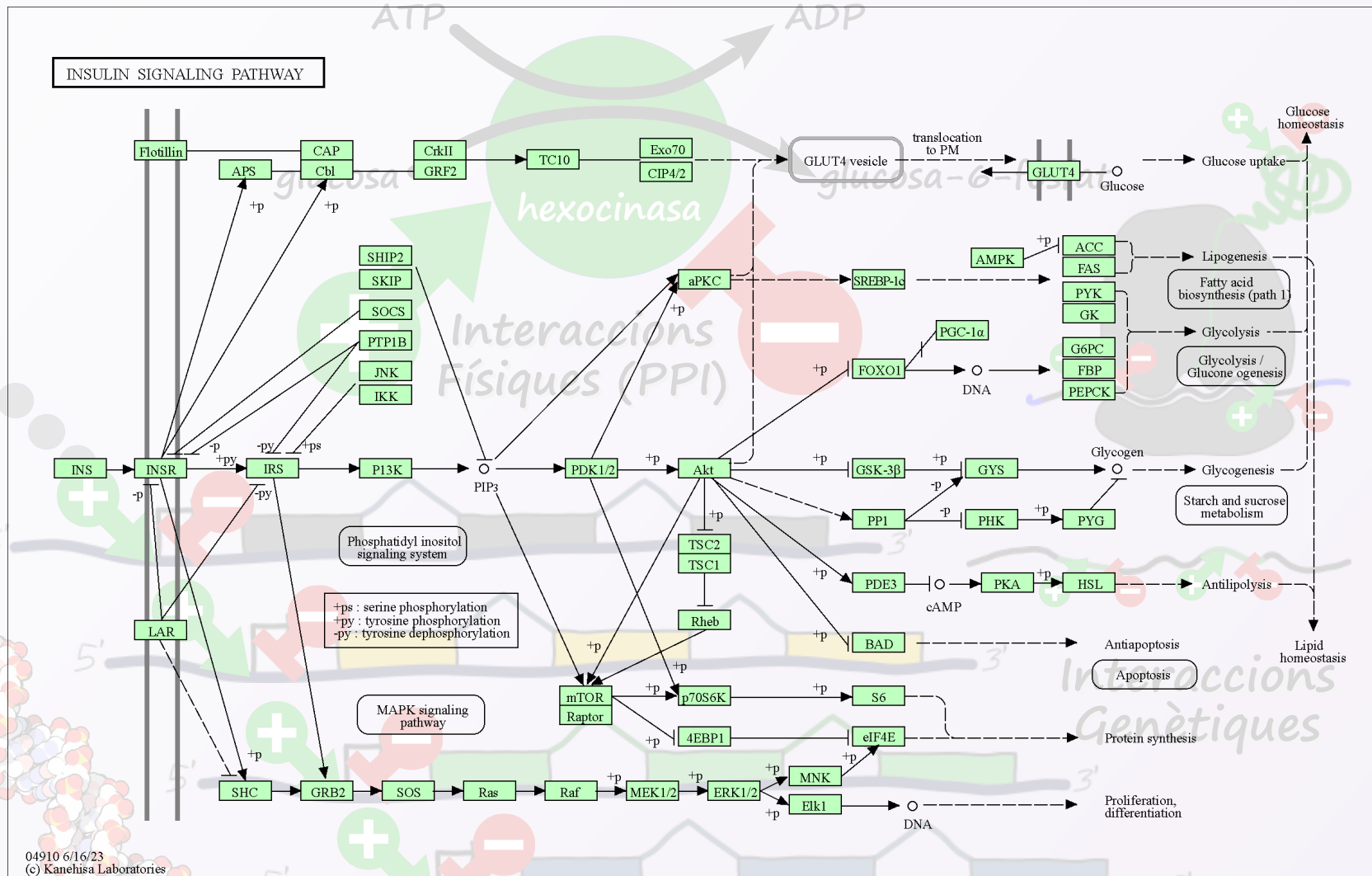
Modelant l'Interactoma



Interaccions Genètiques

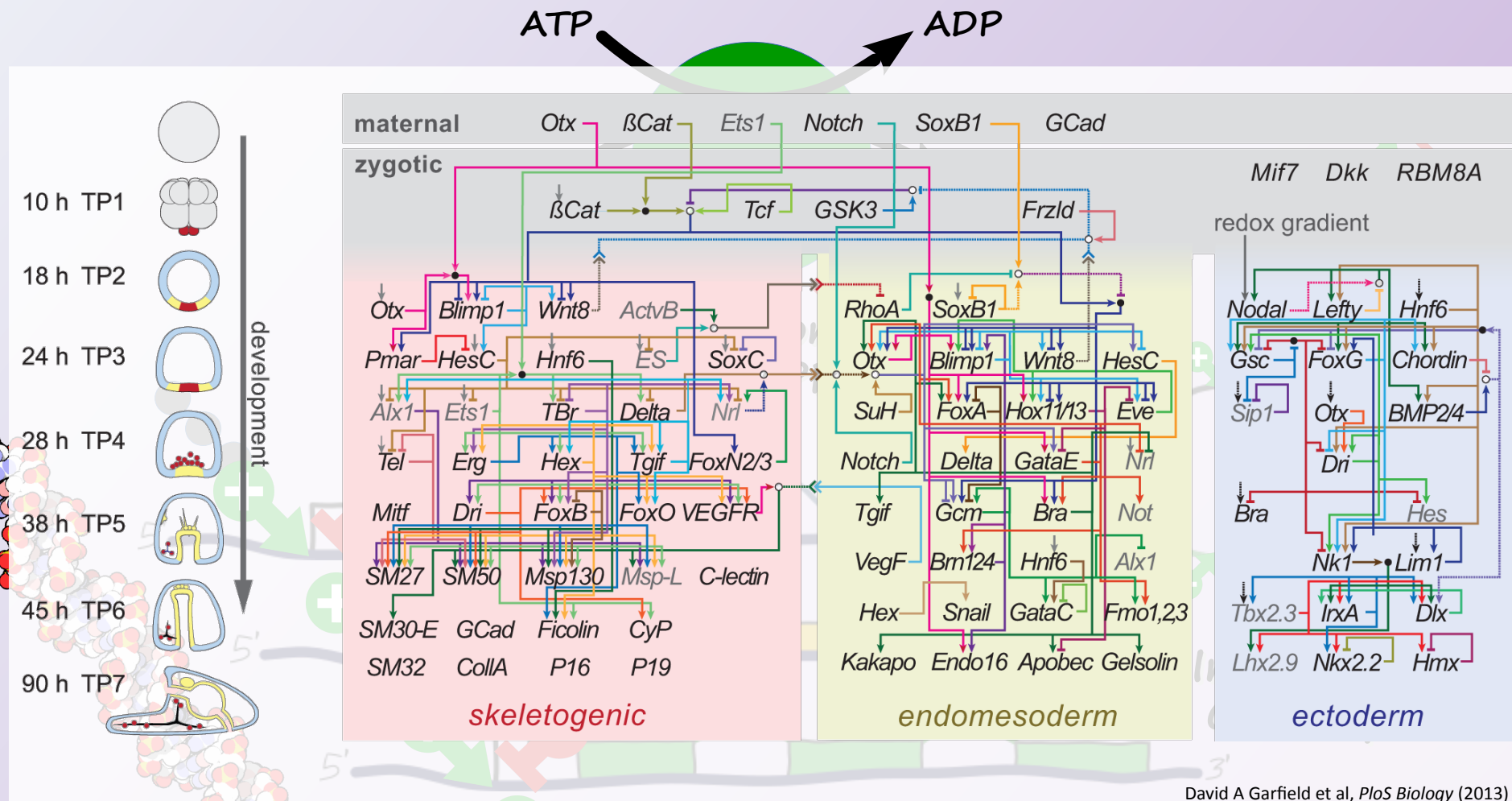


Modelant l'Interactoma



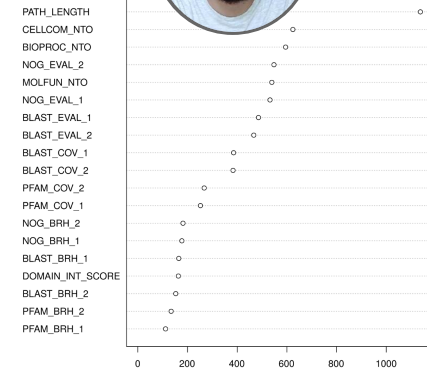
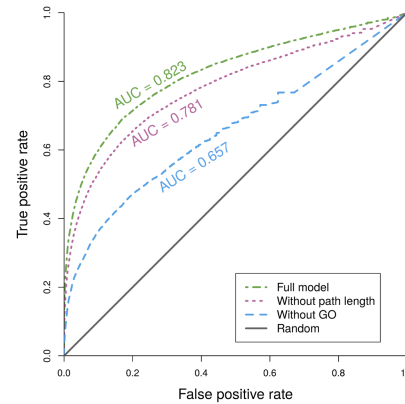
KEGG – Ruta de Senyalització de la Insulina (hsa04910)

Modelant l'Interactoma

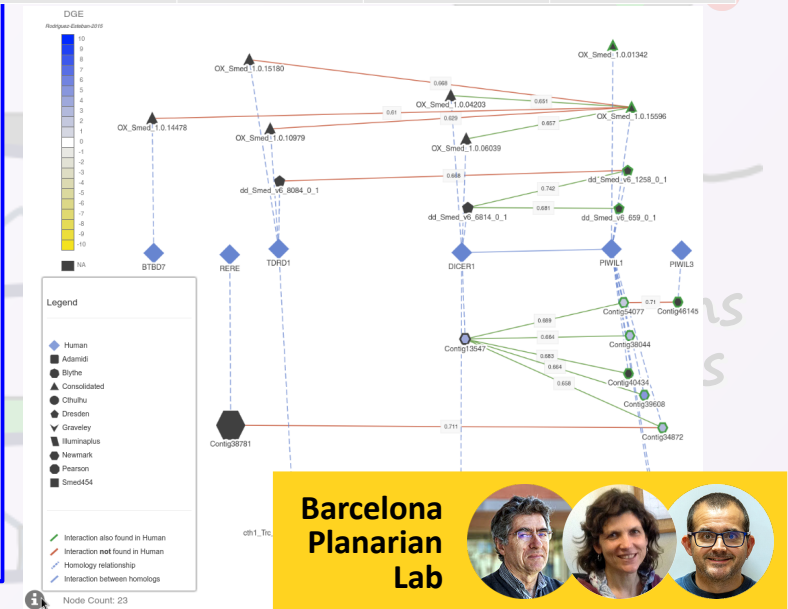
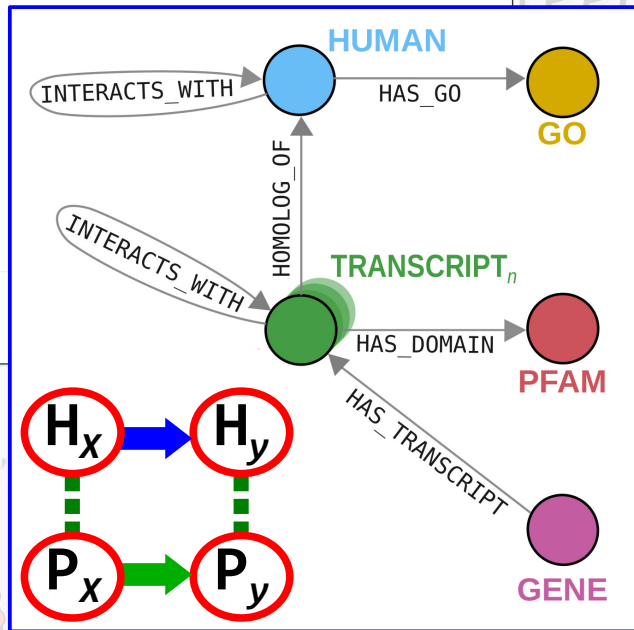


David A Garfield et al, *PLoS Biology* (2013)

Modelant l'Interactoma

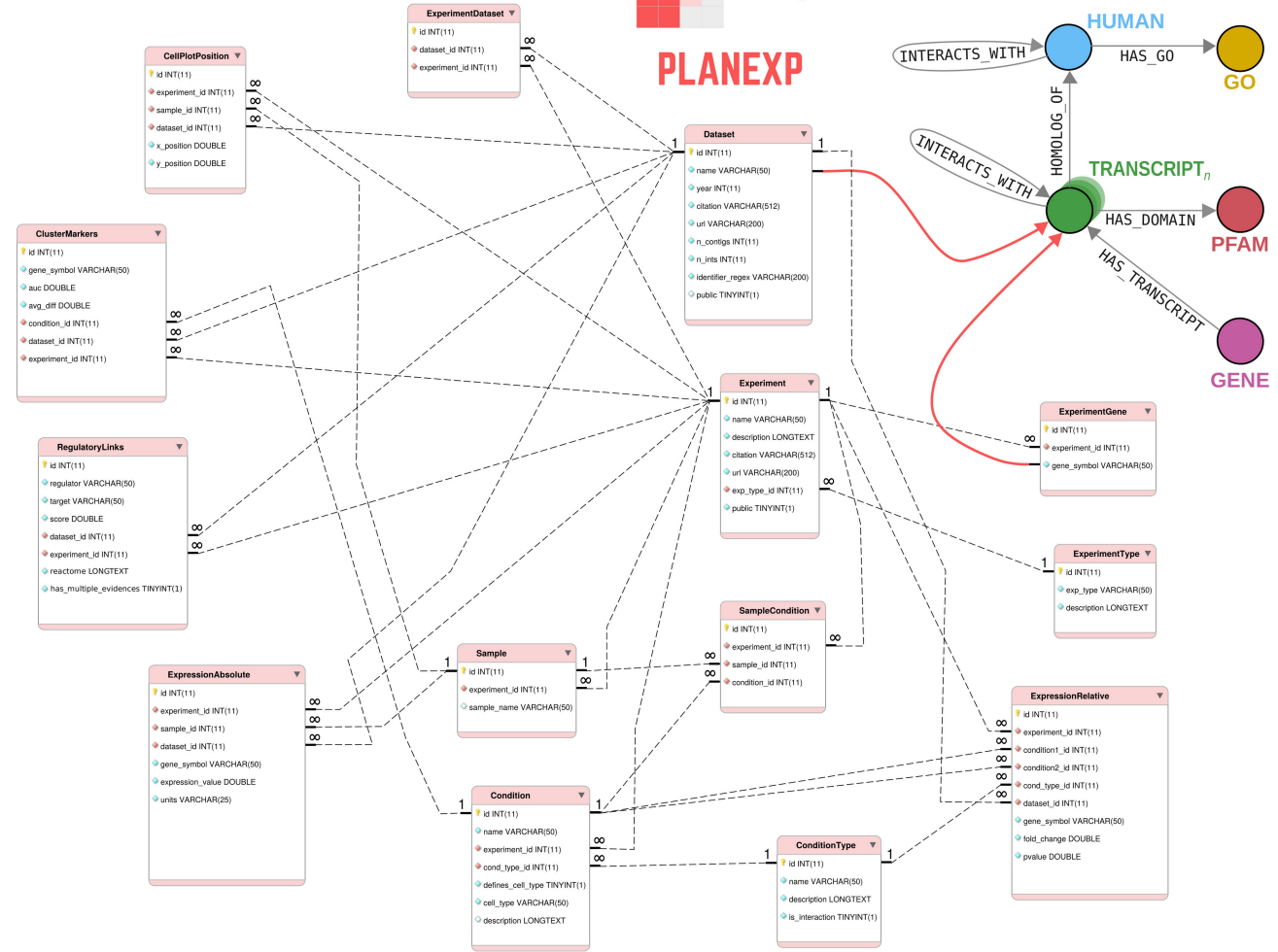
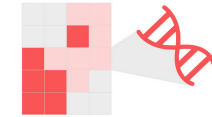
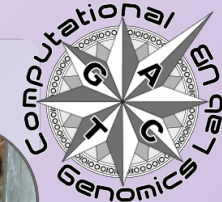
PRECISION	RECALL	SPECIFICITY	OOB error
0.35	0.34	0.99	2.67%



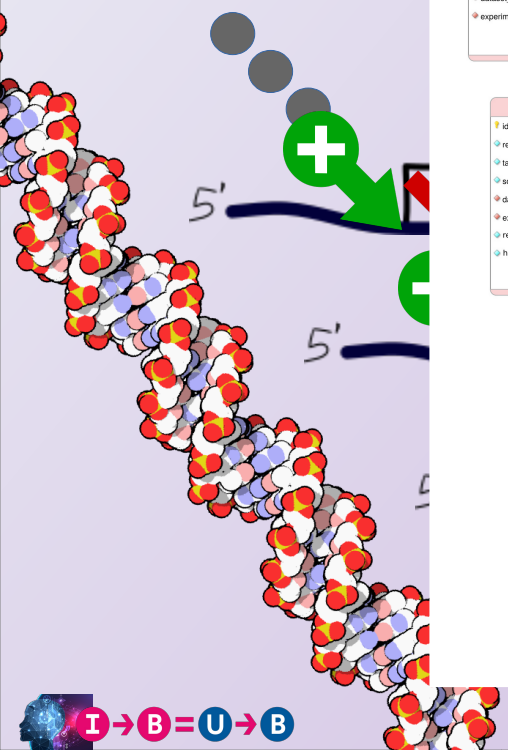
Barcelona Planarian Lab

Sergio Castillo-Lara & Josep F Abril, *Bioinformatics* (2017)

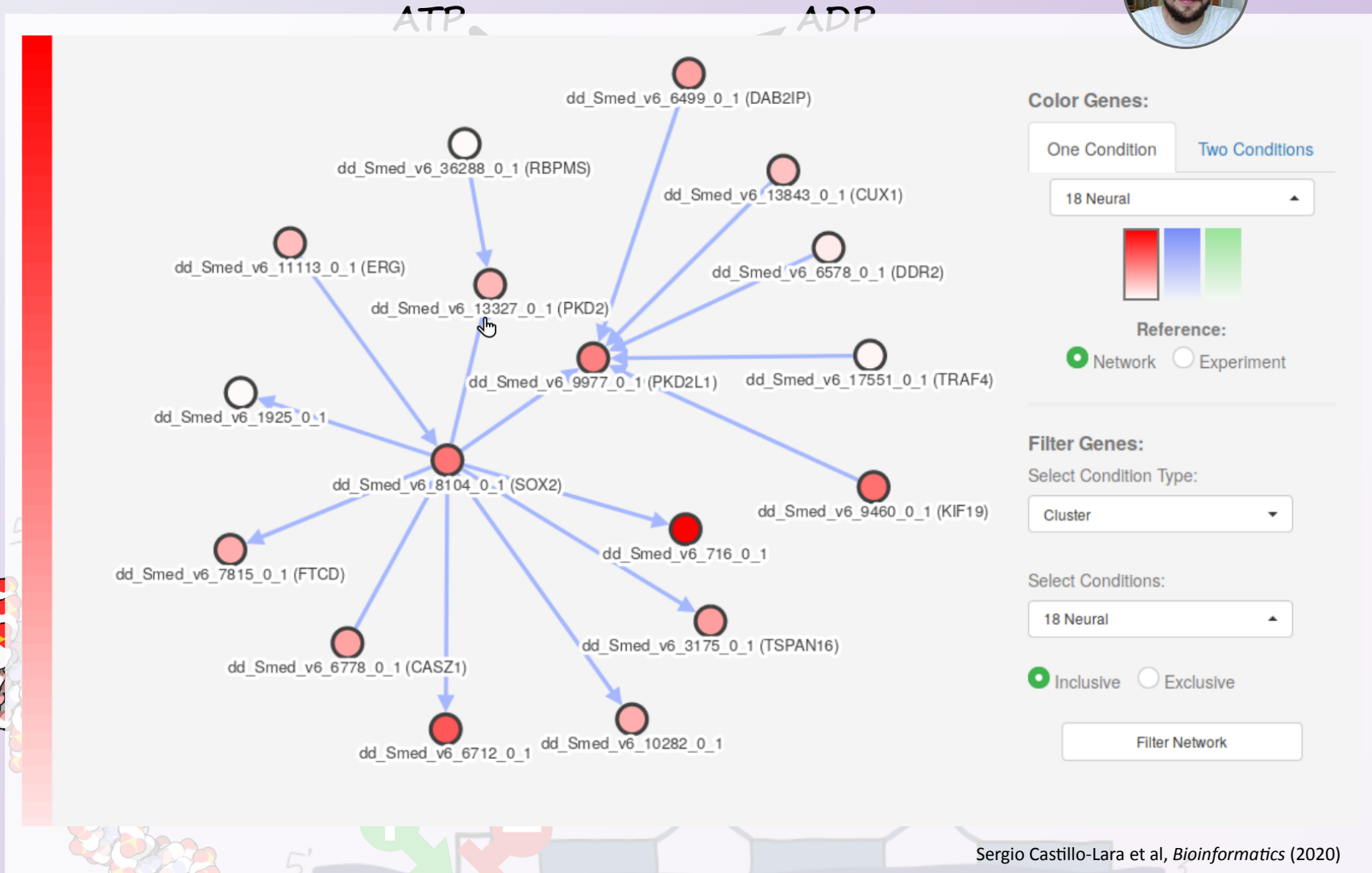
Modelant l'Interactoma



Sergio Castillo-Lara et al, *Bioinformatics* (2020)

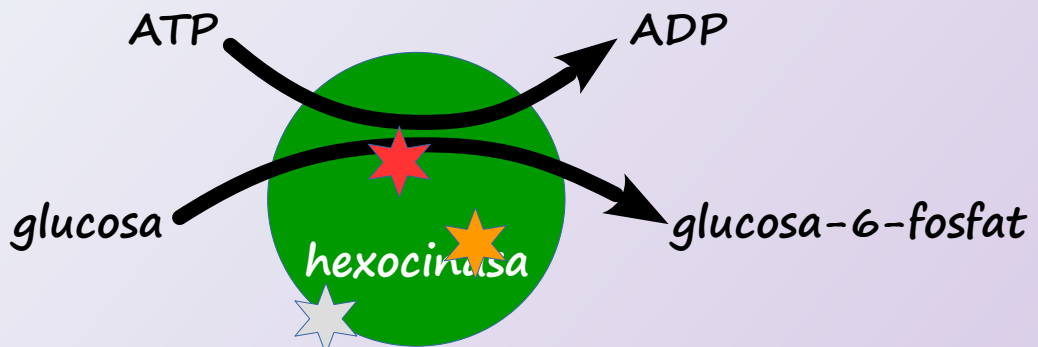


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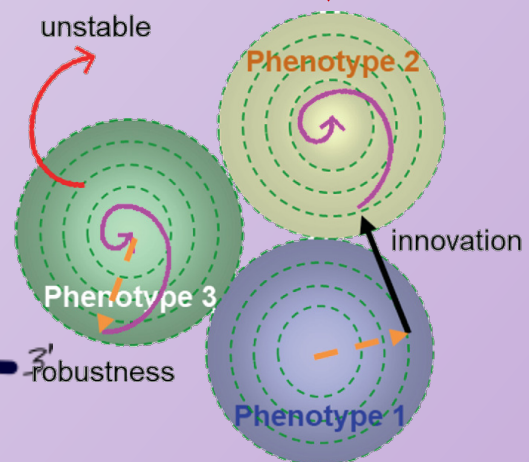
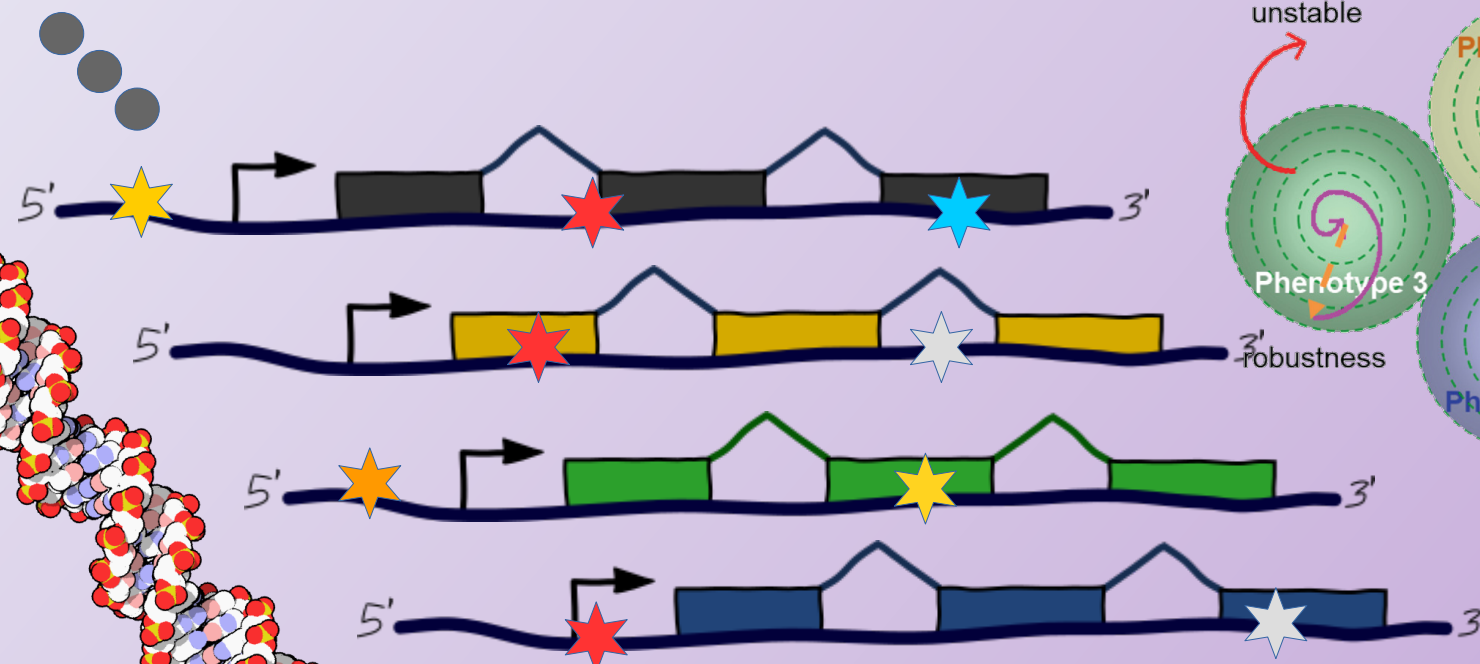
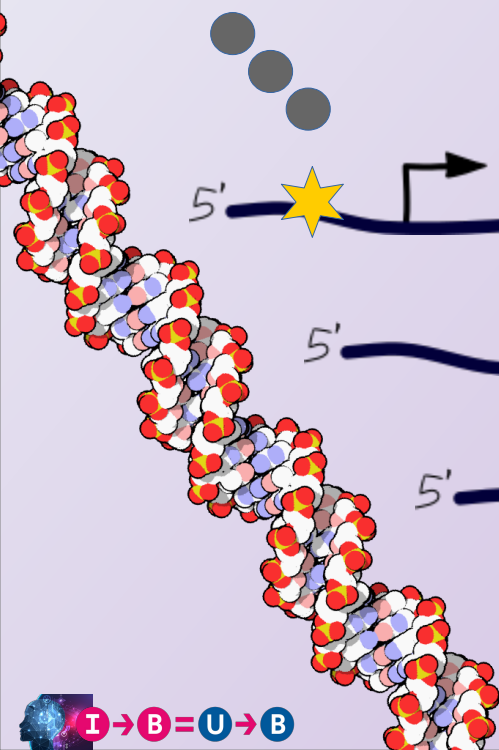


Sergio Castillo-Lara et al, *Bioinformatics* (2020)

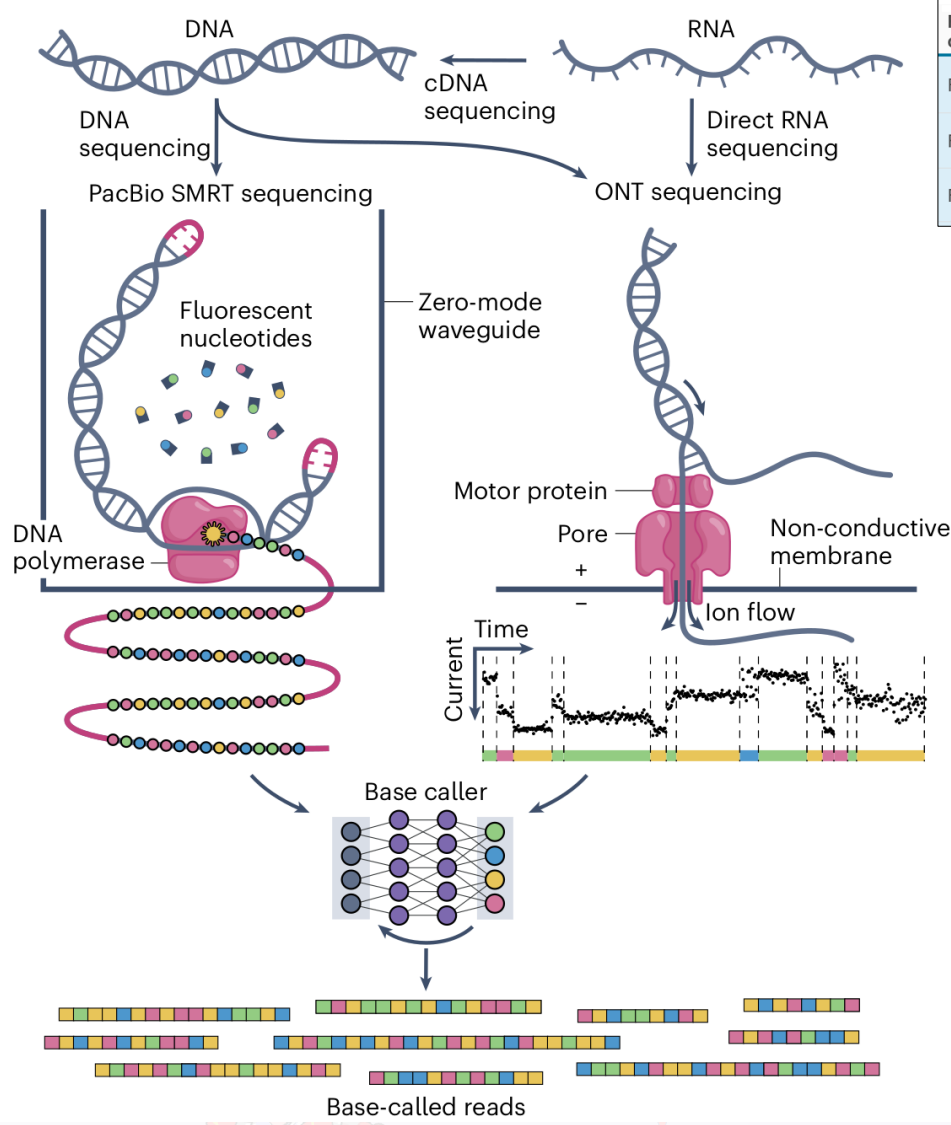
Capturant la Variabilitat de Seqüència



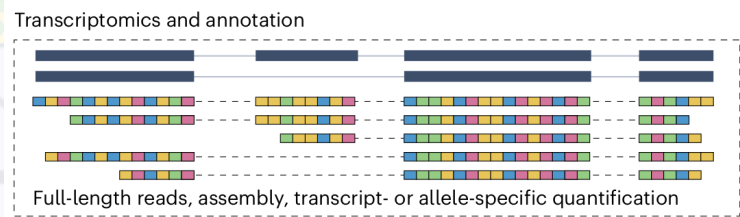
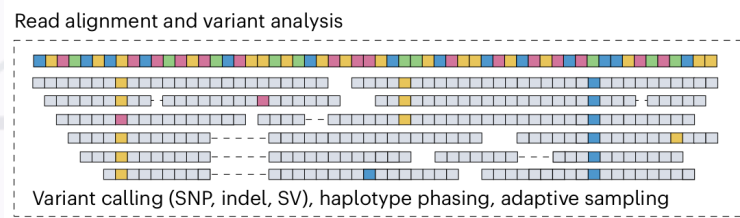
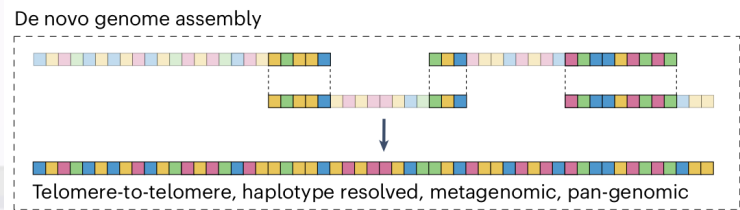
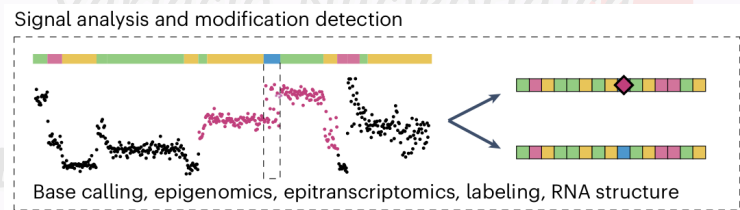
Mutacions
 Variació Nucleotídica
 Variació Aminoacídica
 Variació Estructural i Funcional



Capturant la Variabilitat de Seqüència



Flow cell	Kit	Sequencing & basecalling parameters	Sample	Raw read accuracy
R10.4.1	Ligation Sequencing Kit V14	400 bps, 5 kHz, HAC basecalling	Human HG002	99.0% (Q20)
R10.4.1	Ligation Sequencing Kit V14	400 bps, 5 kHz, SUP basecalling	Human HG002	99.5% (Q23)
R10.4.1	Ligation Sequencing Kit V14	400 bps, 5 kHz, Duplex basecalling	Human HG002	>99.9% (Q30)

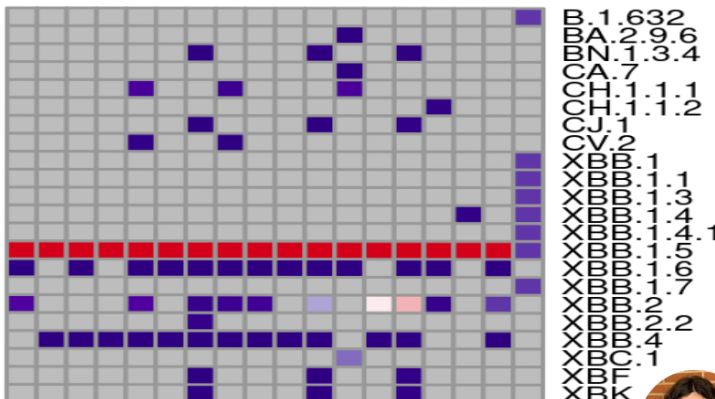
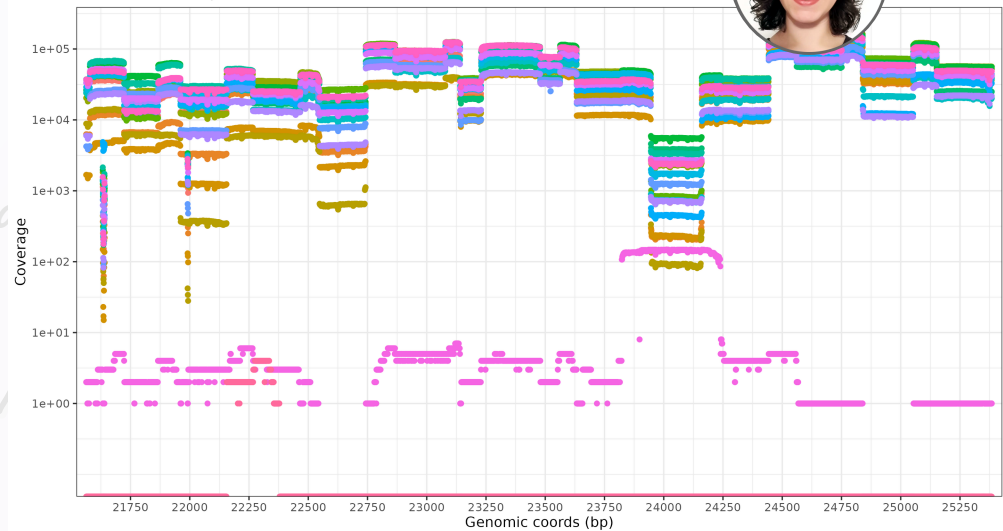
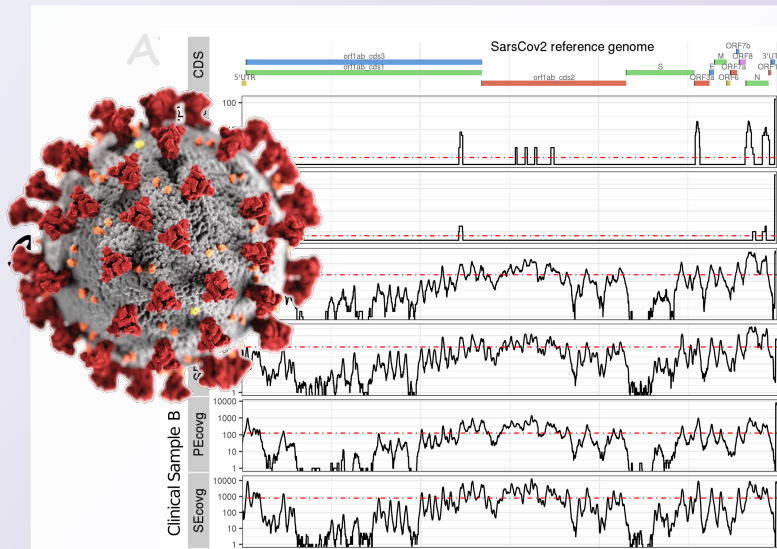
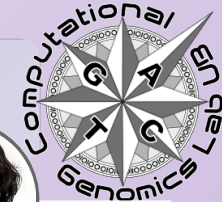


Sam Kovaka et al, Nature Methods (2023)



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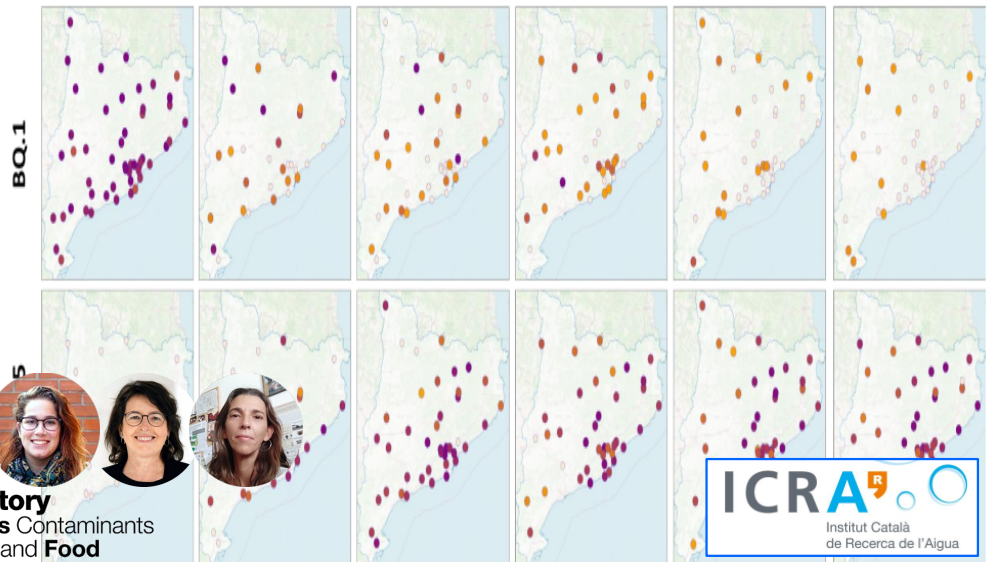
Capturant la Variabilitat de Seqüència



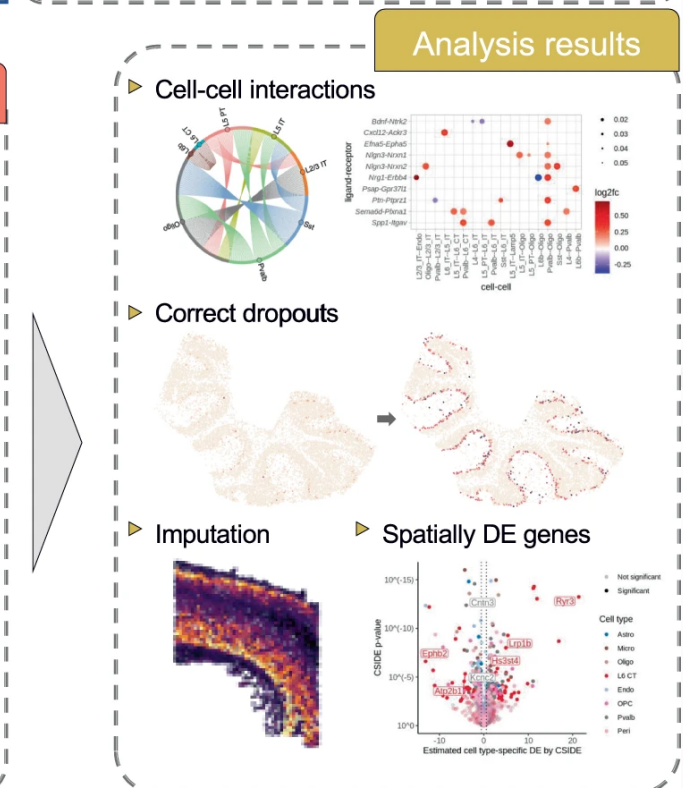
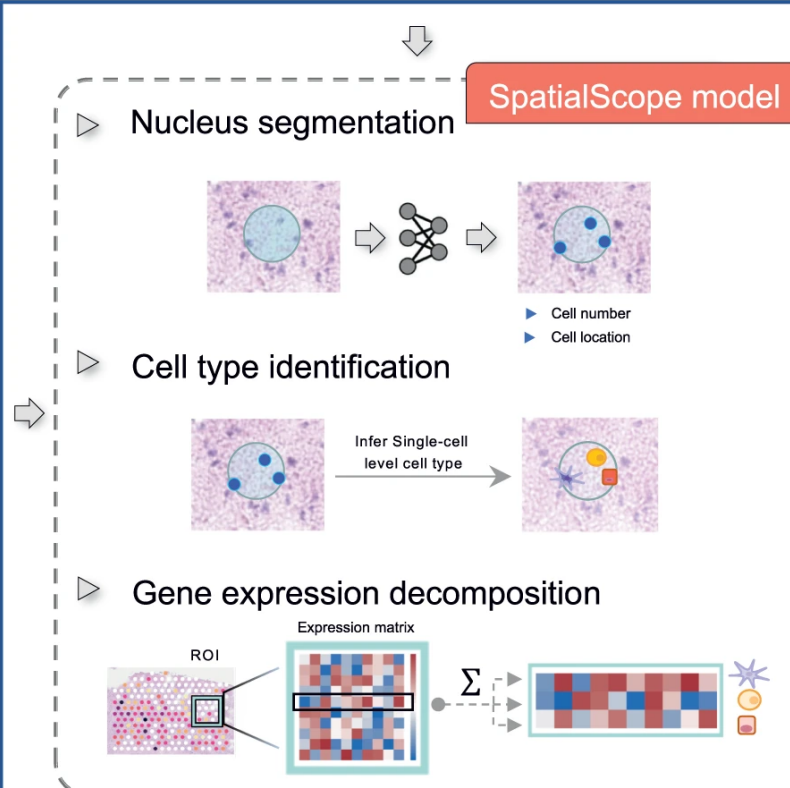
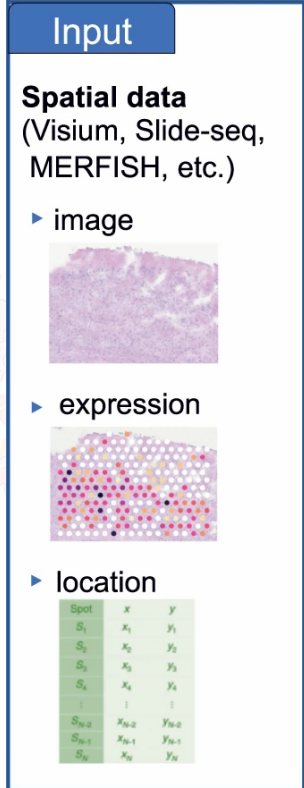
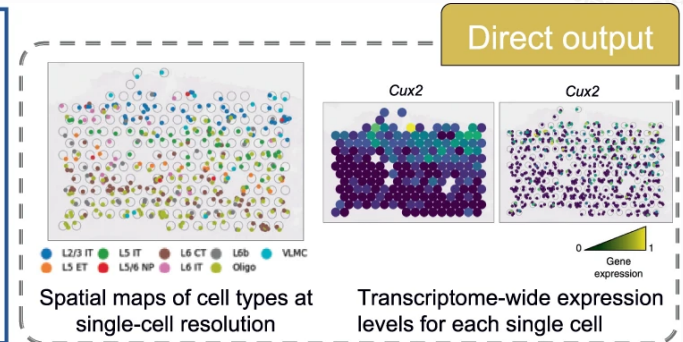
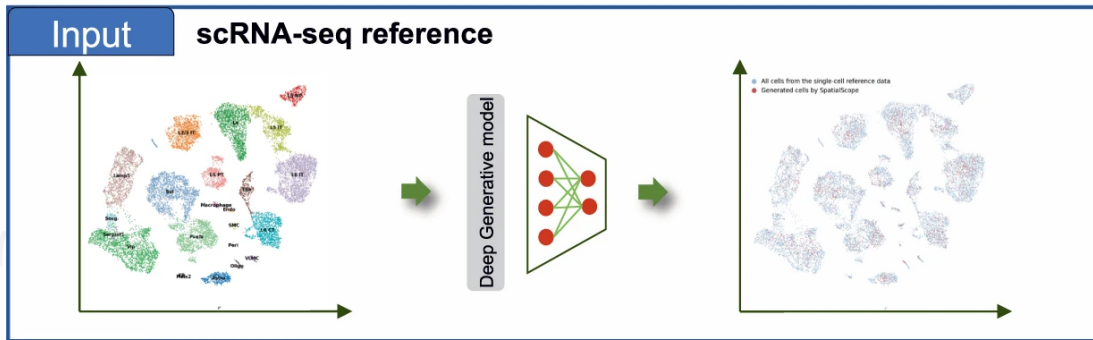
- DCNE-2023-08-
- DLDM-2023-08-
- DRP-2023-08-
- DBLN-2023-08-
- DDLO-2023-08-
- DDPA-2023-08-
- DDAM-2023-08-
- DDTR-2023-08-
- DDCP-2023-08-
- DDPA-2023-08-
- DDPA-2023-08-
- DDTR-2023-08-
- DDVC-2023-08-
- DDMA-2023-08-
- DDVG-2023-08-
- DDBS-2023-08-
- DDSF-2023-08-
- DDVC-2023-08-
- DDSL-2023-08-
- DDMAS-2023-08-
- DDGU-2023-08-
- DDMAN-2023-08-



Laboratory
of Viruses Contaminants
of Water and Food



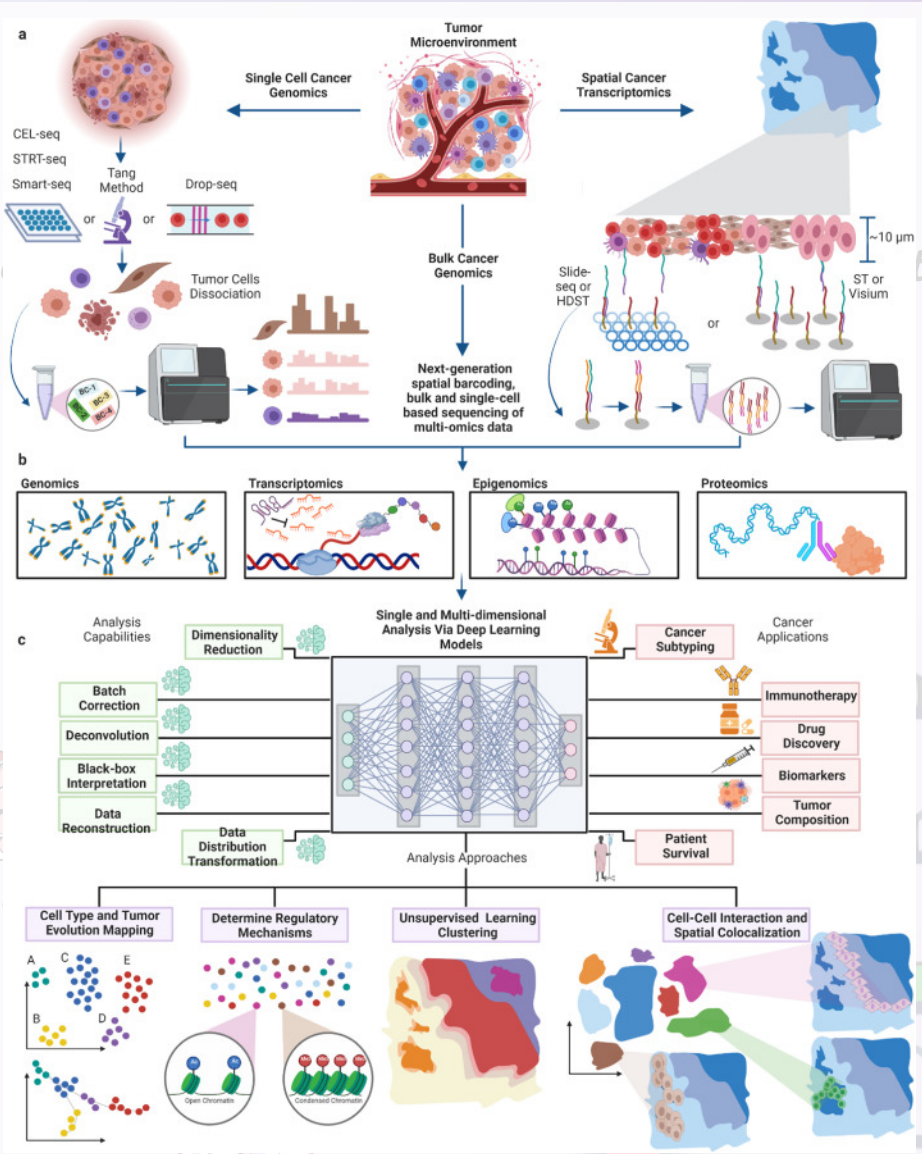
«Single Cell» i «Spatial-Transcriptomics»



Xiameng Wan et al, Nature Communications (2023)

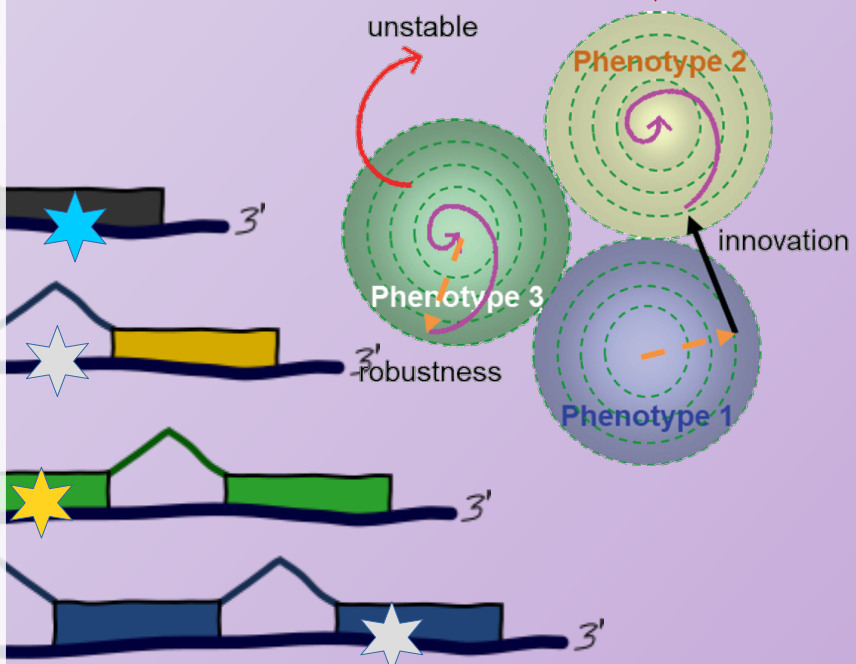
Desxifrant Malalties Complexes

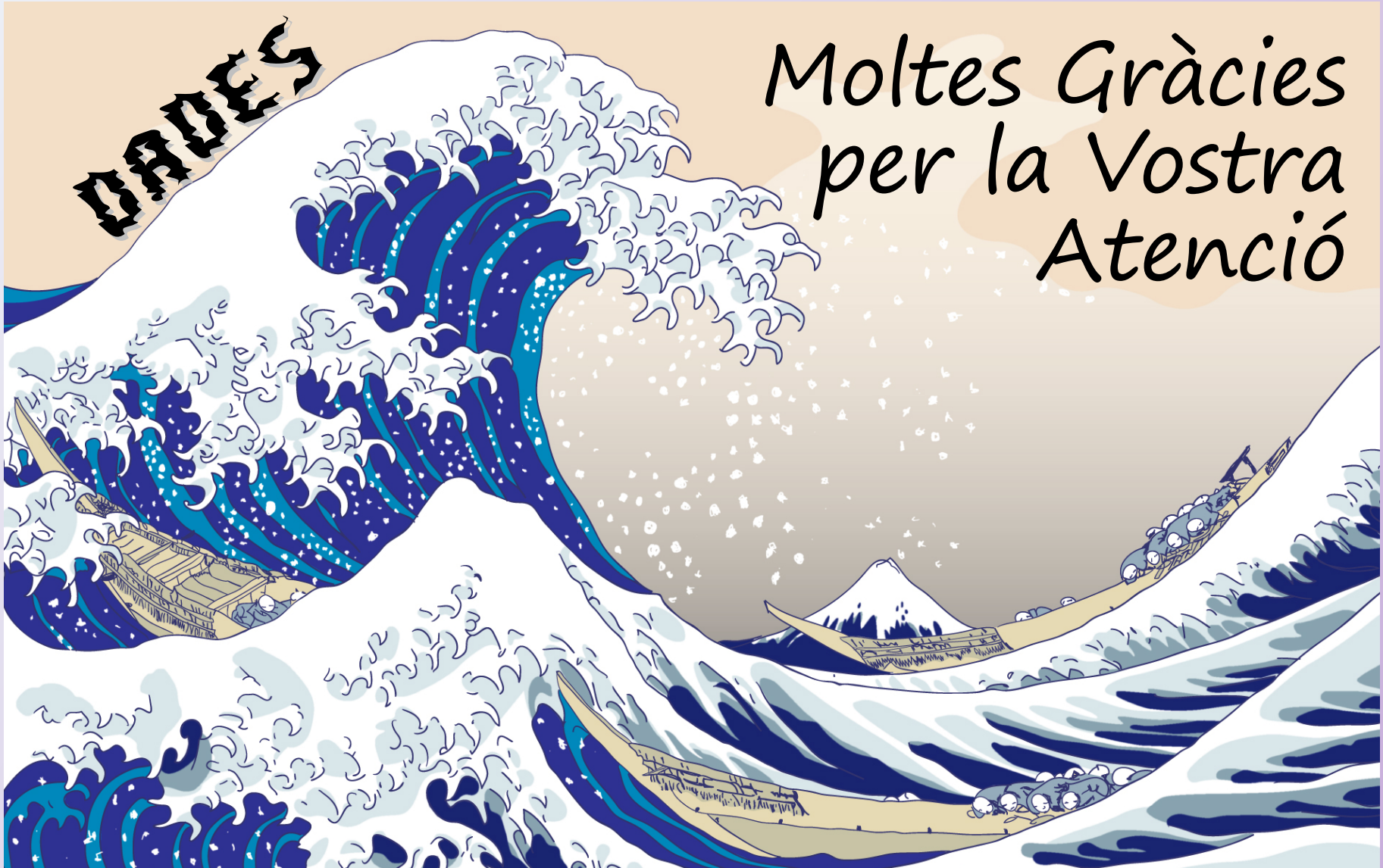
gluc



Raid Halawani et al, *Computers in Biology and Medicine* (2023)

Mutacions
Variació Nucleotídica
Variació Aminoacídica
Estructural i Funcional





Moltes Gràcies
per la Vostra
Atenció

La gran onada de Kanagawa, Katsushika Hokusai (1830)

