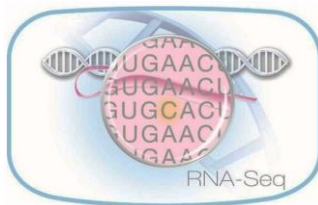




# Innovative tool to model the dynamic of genetic systems

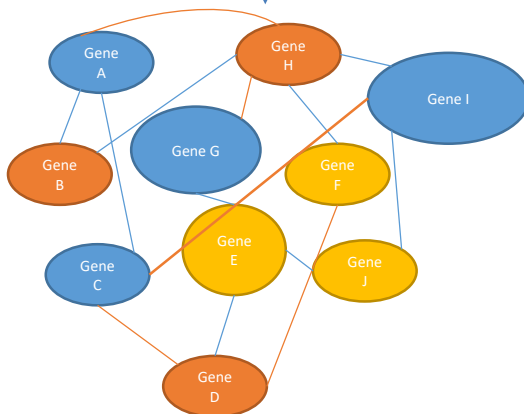
Source data, and corresponding source networks



WENA

Innovative software

Most dynamic gene-networks overtime



## MARKET CHALLENGES

Computational biology refers to the development of techniques for the collection, manipulation, and use of biological data to make discoveries and predictions.

Combining biology and computers, it aids in drug breakthroughs and consequent development during the various stages of clinical trials.

However, factors such as absence of standardization, limitations of individual methods, lack of skilled resources and personnel, shortage of data, and non-verified predictive models are expected to challenge market penetration.

## SUGGESTED APPLICATIONS

- Network-based integration of network layers and poly-omic data
- Disease target prioritization
- Data-driven dissection of molecular pathogenesis (rule & pattern discovery)

## DEVELOPMENT STATUS

Accurate model of the molecular and temporal dynamics of the Huntington's disease (HD) process in the mouse striatum and cortex.

Top predictions about genetic interactions validated in *C. elegans* models of neuronal dysfunction in HD.

Top predictions about genes centrally involved in the HD process validated in cellular models of the disease.

## INNOVATIVE SOLUTION

A team from Sorbonne Université has developed a modeling software and multilayer network approach that can handle complete molecular profile datasets (e.g. RNA-seq, proteomics, RNAi screens) to bring out what are the essential responses of biological systems to disease.

This software is based on a data-driven approach in which the dynamics of signaling systems is weighted across conditions (e.g. across layers of molecular regulation, across time-points). The software enables to visualize the temporal dynamics of genetic interactions and select top targets to optimize the development of new treatments.

## COMPETITIVE ADVANTAGES

- Comprehensive and quantitative analysis
- Ease of use & ease of data interpretation
- WENA enables to integrate up to 3 layers of molecular networks across up to 3 time-points
- Thresholding can be fine-tuned
- WENA enables to retain only 4-5 top genes for each phase of disease
- Cross-integration of molecular networks enable to maximize biological accuracy

## IP RIGHTS

Software registered in 2018