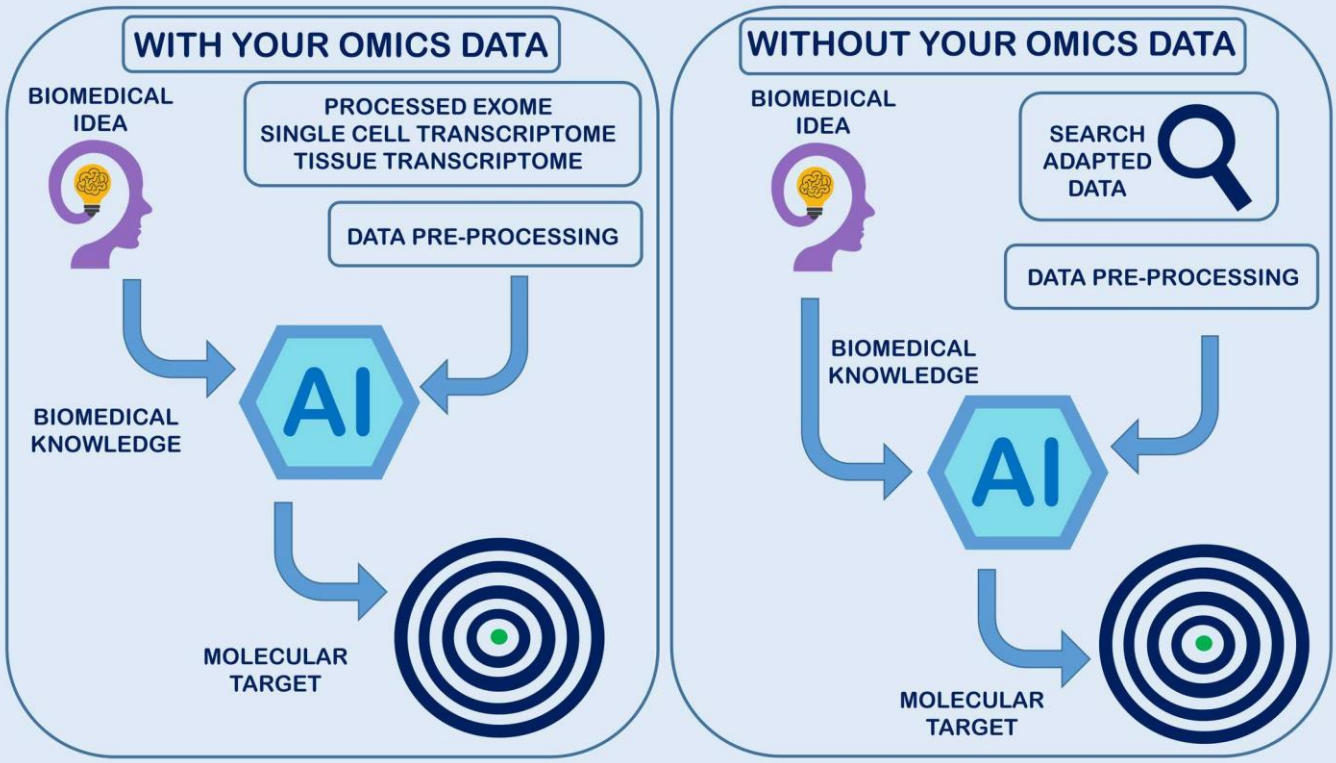
ciblomix
Biomedical AI

"Make sense of your omics data with biomedical knowledge"

SYNOPSIS:

Science and medicine generated omics experiments leading to the production of massive and heterogeneous data. The first difficulty is to solve the high dimensionality of the data, for which conventional statistical methods are not efficient because they lead to a large number of errors in this context. New high throughput sequencing technologies (NGS) generate heterogeneous complex data depending on whether they are studying the epigenome (genomic intervals), genome (variations), or transcriptome (quantification). Artificial intelligence (AI) which collecting biomedical knowledge assemble experimental data and solve their complexity.



DISCOVERIES

- Implication of the bone marrow microenvironment in Primary myelofibrosis (1)
- Implication of REL & inflammation in phase progression disease of chronic myelogenous leukemia (2)
- Prediction of parental imprinting genomic regions affected during hydatidiform moles (3)
- Prediction of liver cancer starting from lipid metabolism connected to inflammation in steatosis and NASH progression (4)

REFERENCES

(1) Inflammation as a Keystone of Bone Marrow Stroma Alterations in Primary Myelofibrosis. Mediators Inflamm. 2015;Epub 2015 Nov 12. **(2)** ASH2015: A Bio-Integrative Approach Identifies an Inflammatory Signature in Chronic Myeloid Leukemia (CML) Stem Cells That Is Highly Perturbed in CML Blast Crisis and Involves REL transcription Factor. **(3)** A bioinformatics transcriptome meta-analysis highlights the importance of trophoblast differentiation in the pathology of hydatidiform moles. Placenta. 2018 May;65:29-36. **(4)** Lipid Related Genes Altered in NASH Connect Inflammation in Liver Pathogenesis Progression to HCC: A Canonical Pathway. Int J Mol Sci. 2019 Nov 8;20(22).

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