

LUCID ANALYTICS - OUR MISSION



To empower Datalization through scientific and human intelligence.

Datalization (n,f) is the use of Data & Algorithms to expand the business and optimize or provide new revenue streams; it is the process of moving to a data driven organisation.











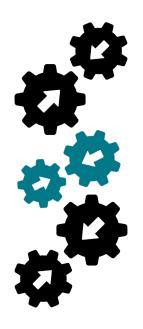


OPTIMAL SYNERGY OF TWO FIELDS



Scientific input into R&D projects in order to ensure and validate the quality of developed and deployed data model

Ensuring this thanks to our internal core expert team and our expert Lucid network





Development and implementation of data solutions with an expert software development team born in a scientific environment

Developing a solution is a point. Understanding the scientific need is another, this is why our Software development team is Science-born!







Open Source Empowering Science

- Avogadro: Open-source molecular editor for chemistry and drug discovery.
- TensorFlow and PyTorch: Machine learning libraries for scientific research.
- Astropy: Python library for astronomy research and data analysis.
- Open Science Grid: Open-source platform providing distributed computing resources for data-intensive research.
- GNU Octave: Open-source alternative to MATLAB, used for numerical simulations in science and engineering.
- OpenMM: Open-source toolkit for molecular simulations, especially in computational biology.
- GeoNode: Open-source platform for sharing geospatial data and maps, widely used in environmental and climate sciences.



STANDARDIZE study metadata across multiple laboratories

REQUIREMENT

Build a platform to support prospective study metadata acquisition, assisting different Omics laboratories to register studies / dataset in a central place via flexible data models facilitating analysis and following FAIR principles.

SERVICES PROVIDED

- Help Omics labs to register study metadata.
- FAIR-ification of studies and datasets (historical and prospective).
- Automation of analysis pipelines.
- Empower data analysists with programmatic access to data.
- Enable data reuse.

DELIVERABLES & BENEFITS

Web platform enabling study registration, searching and analysis. FAIR-ification of historical studies as well as prospective registration. Samples registration system.

Integration with existing services.





















MASTER results interpretation via NLP and LLM methods

REQUIREMENT

Generate a digital solution to level up the interpretation of gene expression signature analysis.

Create a gene expression signature annotation pipeline to simplify and aggregate multiple genesets together using NLP and LLM algorithms in order to create a new set of biological themes helping researchers to get a clear and efficient results interpretation.

SERVICES PROVIDED

- Easy-to-use Rshiny interface.
- Connexion to database of master expression programs via internal API.
- Calculation of a score for master expression programs.
- · Comprehensive visualization of differential expression analysis results.

DELIVERABLES & BENEFITS

NLP and LLM algorithms.

Developer documentation.

User documentation.

Rshiny web interface.

Interactive graphical visualizations.





