Single cell analytics

Commonly used acronym: *SCS*

Created on: 26-02-2024 - Last modified on: 11-03-2024

Organisation

Name of the organisation BioLizard

Department Single cell analytics

Country Belgium

Geographical Area Flemish Region

SCOPE OF THE METHOD

The Method relates to	Animal health, Environment, Human health: Food & agriculture
The Method is situated in	Basic Research, Regulatory use - Routine production, Translational - Applied Research
Type of method	Other: Data analytics

DESCRIPTION

Method keywords

Single cell analysis
single-cell
Data analysis
data exploration
transcriptomics
omics

Scientific area keywords

Single cell studies
Single cells

Data Science
data integration
machine learning
bioinformatics
multi-omics

Method description

Through leveraging our combined computational and biological knowledge, we have proven expertise supporting clients in:
(1) Tailored analysis of single-cell data that incorporates relevant biological information, including application of AI and machine learning,
(2) Studying the stochastic nature of gene expression and the organization of cell types in space and time,
(3) Providing strategic and analytical support for experimental design, processing and bioinformatic analysis of single cell sequencing data, including enabling different analysis packages, reviewing analysis results from different projects, and consulting on data analysis strategies for new single cell technologies,
(4) Augmenting in-house data by mining public databases for relevant information,
(5) Combining multi-omics approaches to improve your understanding of complex biological processes and regulatory elements ... And more!

Method status

History of use
Internally validated
Validated by an external party (e.g. OECD, EURL ECVAM,...)

PROS, CONS & FUTURE POTENTIAL

Advantages

- Single-cell sequencing data is extremely rich in information, and this complexity comes with computational and analytical challenges.
- BioLizard has developed customizable in-house pipelines that support the analysis of multi(modal)-omics single-cell data from a variety of different library preparation platforms. The modular nature of our platform allows for easy customization of the analysis workflow to suit your unique research setting.

- Moreover, our data exploration platform allows you to interactively visualize and investigate your results through an intuitive interface. We always ensure to align regularly with our clients to ensure that it’s clear how your data has been handled, and we maintain the highest standards for data security and privacy.

Challenges

Single-cell sequencing allows you to dive deeper into the biology of cells and research them on an individual level. This generates more data to process. To put things in perspective: bulk sequencing technology captures the average of a mixture of cells. Single-cell sequencing, on the other hand, can capture the transcriptome of up to 20 000 single cells. This implies a 20 000 fold increase in information to process, and this only considering transcriptomic data! This increase in data creates some challenges, like:

(1) Computational challenges: Do you have the processing power? Or the storage? Depending on the size of the dataset, you'll need 32 or up to 64 GB RAM and enough storage (sometimes up to 1TB). On top of that, it could be smart to have multiple CPUs to speed things up. We doubt the average office laptop could handle these requirements.

(2) Challenges with analytics: One thing is that it gets harder to pinpoint what's important and what's not when you have more information. Another thing is the risk of using the wrong statistical assumptions, which form false conclusions. As opposed to bulk sequencing methods, workflows for single-cell analysis are complex. It requires a certain set of statistical skills to identify the right approach.

(3) Challenges with experimental design: The experimental and computational departments often function as two separate entities within an organization. Both parties should interact and collaborate to obtain most of your single-cell sequencing data: starting from the experimental design! Regardless of the biological question that you might want to ask, computational and wet-lab professionals are there to help you build an approach to avoid lacking statistical power in the analysis.

(4) Challenges with interpretation: A large amount of data also makes interpretation difficult. Once data is processed, cleaned, filtered, and suitable analytical algorithms have been applied, how can someone correctly interpret this information? The (bio)-informatician – while capable in coding and analytics – often lacks the deep knowledge into the biological matters provided by researchers.

REFERENCES, ASSOCIATED DOCUMENTS AND OTHER INFORMATION

Links

- BioLizard Services - Single cell sequencing
- BioLizard - Bio|Verse Platform
- Statistical challenges faced when analysing single cell sequencing data
- Single-cell vs. bulk sequencing: which one to use when?
- Trends in single cell sequencing: High-throughput technologies
- Spatial transcriptomics and its added value
- Strategic AI for single cell sequencing & omics advances
- Trends in single cell sequencing: Atlases & public data
- Trends in single cell sequencing: Spatial transcriptomics

Other remarks

Single-cell sequencing data is extremely rich in information, and this complexity comes with computational and analytical challenges. Effective analysis of single cell data requires adequate computational resources, a strong biological background and a solid understanding of the appropriate biostatistical techniques - all of which BioLizard is ready to support you with. Whether you're looking for an end-to-end service, or an experienced partner to assist with single cell experimental design or apply top-tier data analytics to your existing data, we're ready to assist you.