

Who are Multicore Dynamics ?

Core expertise in the field of bioinformatics and the development of high performance computing solutions for medical science.

Multicore Dynamics have designed an integrated system incorporating highly parallel architecture together with advanced database technologies to support the ultra-rapid processing and in-depth analysis of biomolecular data originating from clinical studies. Our goal is to provide a flexible platform that extends existing boundaries and accelerates the path leading to new discoveries in health care.

Who can we help ?

Any one working in medical science with a requirement to analyse data. Whether you are a researcher, clinician or analyst, we have the expertise to understand your requirements and deliver solutions.

If you require -

- ◆ Fast, data-driven answers, we can help
- ◆ In-depth comparison of hundreds or thousands of molecular profiles, we can help
- ◆ A pipelined approach to the many processing steps, we can help
- ◆ Reliable quality checks and Access Control, we can help
- ◆ Predictive analytics for your data, we can help

How can we help ?

In medical research, there is a continual requirement to better understand the mechanisms of disease and translate the results from research into clinical practice. However, with the research path encumbered with limitations and bottlenecks, progress has often been constrained. The constraints lie in part, with the process and analysis technologies which until now, have been out of sync with the demands of the data or the goals of the Researcher.

System Summary

- ◆ Flexible choice of pre-defined processing steps
- ◆ Predictive modelling tools to profile diseased vs healthy subjects
- ◆ Simple and intuitive interface to update and re-process existing sample sets with further samples
- ◆ Database driven integration of clinical and omics data
- ◆ Reliance and performance driven, rapid processing of high dimensional datasets
- ◆ Auditing—full traceability of processes and actions performed
- ◆ Automated data checks prior to transformation
- ◆ Reproducibility of results
- ◆ Tools to visualize results
- ◆ Transformation pipeline focused on fast and error-free data manipulations
- ◆ Compatible with multiple machine instrument manufacturers
- ◆ Future development to include Persistent Homology providing another avenue for greater insight and clinical answers

A R i O N⁴
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Arion 4 Omics, Data Driven Intelligence for Clinical Studies

Scalable

Using synthetic data of varying size, we are able to simulate hardware load times. According to the size of a clinical study and depending on the desired performance goals, the hardware can be tailored accordingly. Should a future clinical trial dramatically increase in size, the hardware can be upgraded such that reliability and performance are not compromised.

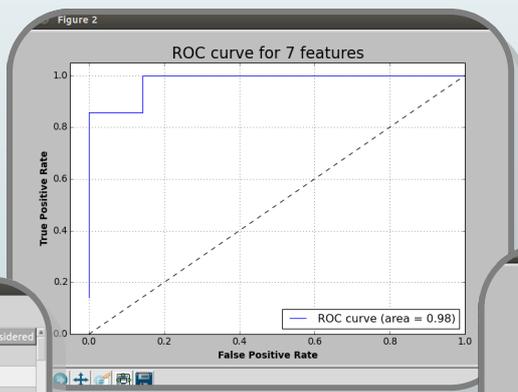
From thousands of mass spectrometry profiles to biomarkers within a day ?

In-order to accelerate the clinical discovery process and obtain answers from the underlying data, novel technologies that reduce the overall time from data acquisition, to the availability of processed results are sought. Using 50,000 samples, our benchmarked results show that initial biomarker discovery can be achieved in less than a day.

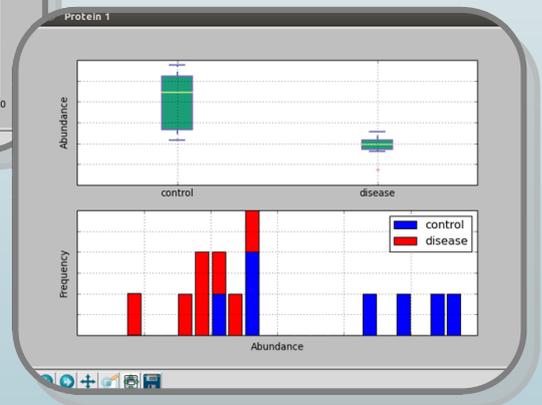
Additional methods of analysis such as our machine learning module, provide an alternative and fresh approach to the analysis process. Machine learning is quickly positioning itself as a primary diagnostic tool in modern healthcare as it promises to not only deliver biomarkers but provide data-driven, clinical decision making. Besides offering cost-effective techniques for the utilisation of bio-molecular data, it can assist physicians in their diagnosis and propose a suitable course of medication. As a predictive tool, it can quickly identify high risk patient groups and those most likely to be re-admitted.

Below : following data import and quality checks, the user may select which samples should be processed.

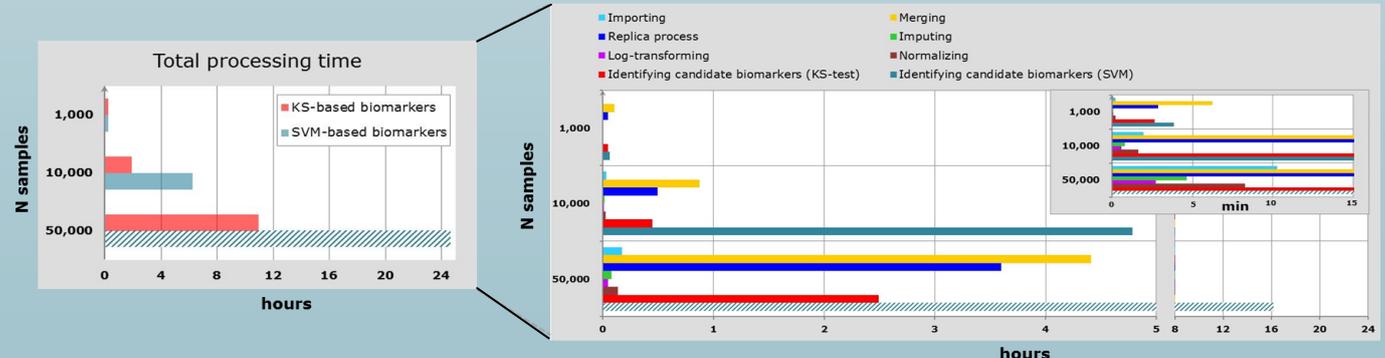
me tag	previous record	Batch number	er of proteins	er of peptides	ToBeConsidered
2016...	0:00:00	1	493	0	<input checked="" type="checkbox"/> true
2016...	0:00:30	1	481	0	<input checked="" type="checkbox"/> true
2016...	0:00:33	1	1562	0	<input checked="" type="checkbox"/> true
2016...	0:00:02	1	1559	0	<input checked="" type="checkbox"/> true
2016...	0:00:11	1	159	0	<input checked="" type="checkbox"/> true
2016...	0:00:13	1	436	0	<input checked="" type="checkbox"/> true
2016...	0:00:01	1	1975	0	<input checked="" type="checkbox"/> true
2016...	0:00:11	1	178	0	<input checked="" type="checkbox"/> true
2016...	0:00:15	1	1415	0	<input checked="" type="checkbox"/> true
2016...	0:00:13	1	191	0	<input checked="" type="checkbox"/> true
2016...	0:00:16	1	1146	0	<input checked="" type="checkbox"/> true
2016...	0:00:56	1	1154	0	<input checked="" type="checkbox"/> true
16...	0:00:05	1	1945	0	<input checked="" type="checkbox"/> true



Below : Box plots and histograms offer visual exploration of biomarkers.



Above : Receiver operating characteristics (ROC) curves associated with machine learning models, provide excellent diagnostic tools for medical research.



The view on the left shows the total processing time for 1,000 to 50,000 samples of synthetic protein data generated from an entire set of 152,493 human proteins from the UniProt database. The view on the right, shows benchmarked times for the individual steps.