Top-down systems biology approaches for "omics"-based tissue and biofluid analytics

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Top-down systems biology identifies molecular interaction networks in health and disease using system-wide data generated by high-throughput -omics technologies. The rapid advances in the post-genomic analytical technologies, most notably Mass Spectrometry (MS), has made possible to simultaneously analyze hundreds to thousands of metabolites in biological fluids and intact tissues at a relatively low cost. The ability to generate, model, and interpret such metabolic data in relation to benchmark patient clinical information, enabled by powerful bioinformatics platforms, makes personalized medicine a tangible proposition. The advancements in the field of metabolic phenotyping have focused primarily on instrument development and validation of the MS technologies.

However, despite the significant advances in these areas, the major barrier to its wider adoption and transition into main stream medicine and industry has been the challenge of interpreting and managing the huge data sets MS generates. The interpretation of metabolic data is dependent on the advances made by reconstruction of molecular networks via cellular bottom-up systems biology models.

This presentation outlines innovative bioinformatics solutions for emerging technologies of mass spectrometry imaging (MSI) and rapid evaporative ionization mass spectrometry (REIMS), targeting unmet medical needs of cancer network-driven diagnosis and rapid pathogen identification in sepsis. The translational bioinformatics platforms are presented that allow intuitive clinically-oriented interrogation of MS datasets in an integrated and streamlined fashion. These developments aim to overcome current methodological roadblocks for effective clinical translation of MS technologies since the existing workflows for data processing rely on a heterogeneous array of bioinformatic packages which are poorly optimized and only suitable for specialists in the field [1], [2].

References

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