

Integrative Analytics and Artificial Intelligence

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Background

The ability to saliently warehouse information and extract key features remains a pressing concern in health data research today. Such proficiencies should have functionality for allowing researchers the freedom to operate within a safe environment and yet discover new insights or confirm hypotheses. As data collections grow within the cancer research landscape they offer disparate datatypes all the way from single biomarker testing to whole genome sequencing. The cost of such high-throughput platforms has fallen dramatically allowing researchers the ability to acquire more information at the patient level; following tumour evolution over time or spatial heterogeneity. The tools required to warehouse and analyse this information must evolve also and employ techniques that place the heavy lift away from the individual.

Methods

The Cancer Integromics Research Application Framework (CIRAFm) is a robust architecture that fuses several cross-platform coding technologies that emulates a user-friendly interface as a front-end. The platform was created to offer the freedom for software and algorithm development making it very personable to individual requirements. This flexibility of creating differing applications allows the development of a framework for the modern 'big data' era, which is fast evolving. Ingesting information into this framework has allowed us to sculpt many analytical tools embracing artificial intelligence (AI) to explore spatial and temporal heterogeneity across several data types. These methods have explored natural language processing and evolutionary algorithms to highlight key markers and signatures of tumour pervasiveness.

Results

The framework embraces a 'plug and play' architecture where we have key applications to explore data mining and dynamic interaction. We have employed several programming architectures and key mathematical approaches to extend our understanding when applied to tumour biology. Such algorithms exploring alignment-free technology have allowed us to model the evolutionary trajectory of patient samples and use AI to highlight the biology within. We can then use genetic algorithms to mine these markers for their connectivity to other known biology and ascertain a better understanding of potential targets.

Conclusions

Integrative analytical methods tied to smart AI techniques are undoubtedly the future of health care data leading to novel insights and targeted discovery within the precision medicine age. We have seen a quick adoption of our platform as it harnesses the computer's ability to 'learn' to discover new insights and will offer better strategies to decipher key mechanisms in tumour biology in acceptable turnaround times.

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