Moving from NIPT to cancer screening - universality of low pass whole genome analysis

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Background:

In recent years, prenatal testing has been moving toward non-invasive methods to determine the fetal risk for genetic disorders, eliminating the risk of miscarriage associated with traditional invasive testing. Emerging high-throughput molecular techniques and the discovery of cell-free fetal DNA in maternal plasma initiated the implementation of innovative screening methods known as non-invasive prenatal tests (NIPT). Due to many advantages, adopting NIPT in routine clinical practice was rapid and global, and nowadays, numerous countries are integrating NIPT into publicly funded national health care systems. Since the non-invasive detection of fetal chromosomal aneuploidies employs cell-free DNA (cfDNA) biomarkers, we would expect the development to go hand in hand with other clinical applications, such as liquid biopsy-based cancer screening. However, unlike pregnancy, tumors are not temporally or spatially limited considering the human body, thus the development of cancer screening approaches presents a far greater challenge. A myriad of physiological, methodological, and analytical aspects should be considered, and it seems not to be humanly possible to evaluate and combine all these variables. Thus opening a new frontier for artificial intelligence that, we hope, will be the game changer in early multi-cancer detection.

Conclusion:

Here, we discuss the first-hand experience of our transition from prenatal testing to screening for malignancies in liquid biopsy samples, where our practical knowledge of cfDNA fragments from NIPT analysis was utilized to build a novel approach integrating a machine learning model for cancer prediction.

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