

Precision medicine for breast cancer: multi-omics towards predicting complete remission and avoiding surgery

Abstract

Breast cancer (BC) is the most common cancer and the second leading cause of cancer death in women. Many patients with BC can be cured with existing therapies, but side effects cause substantial physiological and psychological burden. Early prediction of individual risk and therapy response is essential for advancing personalized BC therapy. Toward the goal of avoiding over-treatment in low-risk patients, gene expression signatures can already identify patients who may safely avoid chemotherapy. Pushing personalization further, it seems realistic that integrating functional imaging in combination with multi-omics profiling will accurately identify a subset of BC patients who can safely forgo curative surgery. Here we pursue the hypothesis that integrative ML analysis of functional imaging (PET/MRI) and multi-omics profiling of tumor biopsies and liquid biopsy at early response can predictively identify patients that will achieve pathological complete response (pCR) following neoadjuvant chemotherapy (NACT), with the future perspective of avoiding resective surgery in these patients. PREDICTOME will develop a validated ML model for predicting pCR in BC towards safely omitting surgery in low-risk patients based on multi-omics dynamics during early NACT response. To this end, it will combine a large, well-characterized retrospective cohort with long-term follow-up data with the power of a prospective cohort, including multi-omics analysis of early molecular responses to.

Scientific disciplines:

106014 - Genomics (35%) | 102001 - Artificial intelligence (35%) | 302043 - Magnetic resonance imaging (MRI)

Keywords:

response prediction

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Further links about the involved persons and regarding the project you can find at

https://archiv.wwtf.at/programmes/life_sciences/LS20-065