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Non-invasive Prediction of BRCA Mutation Status in Ovarian Cancer Using Whole-body Tumor Burden Deep Learning

This multi-modal AI framework predict BRCA status preoperatively with high accuracy (AUC 0.916), to enable genetically-guided surgical triage and bridge the global gap in accessible precision oncology for underserved patient populations.

I. Technological Innovation

A dedicated ovarian cancer AI prediction framework has been constructed, adopting a multi-modal architecture that integrates whole-body CT tumor burden with comprehensive clinical phenotypic data. Based on the largest retrospective cohort to date combining preoperative imaging and clinical information, the model extracts 2.5D deep learning features across eight high-risk abdominal anatomical sites according to Suidan criteria, simultaneously capturing both inter-tumor and intra-tumor heterogeneity. This whole-body tumor burden analysis paradigm breaks through the limitations of traditional single-lesion delineation, establishing a robust non-invasive prediction engine for BRCA mutations.

II. Workflow Optimization

Embedded at the preoperative decision node, the system enables real-time, non-invasive BRCA risk stratification using routine CT imaging, directly addressing the global challenge where only 35% of patients undergo genetic testing due to cost and accessibility barriers. By providing individualized surgical triage guidance for cytoreductive surgery prior to formal gene sequencing, it ensures equitable access to precision oncology across diverse healthcare environments.

III. Model Innovation

We have shifted from single-lesion, experience-driven radiomics to a "whole-body tumor burden +clinical data" dual-driven paradigm, establishing a specialized AI development framework for ovarian cancer. This model supports tiered surgical and therapeutic decision-making—directing BRCA-mutant patients toward complete cytoreduction and targeted maintenance therapy while optimizing genetic testing resource allocation. By leveraging multi-site metastatic patterns (omental involvement, supradiaphragmatic lymphadenopathy, peritoneal dissemination, etc.), the model overcomes the heterogeneity bottleneck that caused prior deep learning attempts to fail (AUC of only approximately 0.48).

IV. Demonstrated Benefits

The system demonstrates robust diagnostic performance (AUC 0.916, sensitivity 86.9%, specificity 93.3%), offering a low-cost, easily accessible alternative to bridge the global BRCA testing gap. This tool enables genetically-informed individualized surgical triage, improves preoperative treatment planning, and reduces the economic burden of universal genetic screening. Moving forward, we will seek global multi-center collaboration to validate this AI tool across diverse populations.

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