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Patent Search

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Abstract:

The intra-tumor heterogeneity in the tumor sites comprises different genetic or molecular characterizations within the tumor sites, including one or more molecules, expressions, or mutations. The method predicts the survival of the subject based on the severity of the tumor. Detection of relatively low heterogeneity in regional ha indication of the low severity of the tumor. The test data and each training data vector further comprise at least one additional characteristic selected from the group the sex, age, genetic information, biomarker data, smoking status, medical history, or a combination thereof of the individual human. the biopsy sample is a fine nee endoscopic biopsy, or core needle biopsy. The annotated image comprises smaller patches, a subtype of the tumor, and the mgmt promotor methylation status as rr mgmt.

Complete Specification

Description: A METHOD AND A SYSTEM FOR MEASURING INTRA-SITE HETEROGENEITY IN A TUMOR USING ARTIFICIAL INTELLIGENCE

BACKGROUND

Technical Field

[0001] The embodiments herein generally relate to a method and a system for measuring intra-site heterogeneity in a tumor using artificial intelligence.

Description of the Related Art

[0002] Despite tremendous efforts in cancer therapy over the past decades, overall cancer mortality remains high and has not changed substantially. Cancer ther mainly challenged by heterogeneity is a hallmark of tumors and has a crucial role in the outcome of the malignancy, because it strongly impacts diagnosis at the gei and molecular level and challenges the design of effective therapies. There are two types of heterogeneity: inter-tumor and intra-tumor heterogeneity. Especially, in tumor heterogeneity closely associates with cancer progression and contributes to cancer drug resistance, leading to the failure of many new therapies to deliver meaningful survival benefits and the increase in the health economic cost of therapeutic development. Therefore, the understanding of intra-tumor heterogeneity i important for both researches on fundamental mechanisms of tumor evolution and clinical practices of cancer treatment.

[0003] The direct analysis of specific mutations can typically detect only a subset of the cases within a particular cancer type known to be associated with those sp mutations. Additionally, tumor-derived DNA is usually the minor species of DNA in human plasma; the absolute concentration of DNA in plasma is low. Therefore, tl detection of one or a small group of cancer-associated mutations in plasma or serum may achieve low analytical sensitivity even among patients with cancers know harboring the targeted mutations. Furthermore, it has been shown that there is significant intratumoral heterogeneity in terms of mutations even within a single tu

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