Integrated CAncer GEnome Score (iCAGES) for personalized cancer therapy

Technology #cu17137

This technology is an algorithm that leverages patient cancer genomic data to provide a personalized chemotherapy regimen.

Unmet Need: Personalized chemotherapy guided by unique cancer genome signatures

While it is well understood that cancer results from the acquisition of somatic mutations in the genome, only a small proportion of mutations, known as “drivers”, are responsible for oncogenesis. Identification and classification of these mutations are essential to delivering personalized therapy, as different mutations in the same gene may cause diverse clinical outcomes. However, existing computational tools are often ill-suited to analyze personal cancer genomes. As such, there is a need for improved methods of processing individual cancer genomes to enable personalized cancer treatment.

The Technology: Algorithm identifies cancer driver genes to provide prioritized drug treatment

This technology identifies cancer driver mutations in patient-specific cancer genomes and then leverages these mutations to provide a personalized treatment plan. To accomplish this, iCAGES first prioritizes personalized cancer driver mutations, which are then linked to mutation features of genes using a trained statistical model. Based on this information, iCAGES then generates a prioritized list of drugs targeting the potential driver genes for a personalized chemotherapy regimen. By optimizing treatment plans, this technology may help reduce side effects and improve treatment outcomes.

This technology successfully predicted patient response to drug treatment and long-term survival in analysis of a dataset from The Cancer Genome Atlas (TCGA).

Applications:

- Personalized cancer treatment
- Predicting side effects of cancer treatments based on patient’s genome
- Analysis of existing cancer genomic data sets for determining treatment efficacy
- Data collection for potential combination therapies
Advantages:

- Allows for personalized treatment plans specific to each patient
- Rapidly analyzes patient-specific cancer genomic data
- Identifies cancer mutations to predict the best precision therapies
- Incorporates treatments under clinical trials as options for therapy

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Related Publications:


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