Roy Chartier
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Computing for the Cure!

Dear Roy:

Thank you for a continued and significant support to our World Community Grid project – Mapping Cancer Markers. Most cancers (and other complex diseases) lack effective biomarkers to detect disease early, to identify high risk patients, and to predict optimal treatment strategy. The main challenge is learning from and using the enormous amounts of complex, multi-dimensional molecular data from tumor samples. Many methods have been introduced to generate biomarkers from these data, but only a few make it to clinical use. We lack systematic methods to find all useful signatures and to select the best one.

The Mapping Cancer Markers project aims to comprehensively and systematically discover clinically useful markers to aid early cancer detection, identification of high-risk patients, and prediction of treatment response. Finding all clinically useful markers would require processing thousands of patient samples and testing an astronomical number of marker combinations, which is not feasible even on the World Community Grid.

We use heuristics to reduce the search space, enabling us to tackle this challenge. However, the success of this research is only enabled by the World Community Grid participants like Cancer Computer, since validating the heuristics requires knowing the ground truth, which we would not be able to compute without this unique computational infrastructure.

Every year, numerous groups from around the world develop and publish gene signatures for various cancers. One of the challenges of interpreting these different findings is that most of these reports are not directly comparable to each other. The first phase of the Mapping Cancer Markers project has been designed to create a standard benchmark that we and other groups can use to estimate how useful the biomarkers are. By establishing a standard test and scoring system, we can evaluate any group of biomarkers. The results from the first phase of Mapping Cancer Markers will allow us to create such a test for existing and future gene signatures. The second phase will be geared towards finding clinically useful molecular signatures, initially focusing on gene signatures that can predict the occurrence of lung cancer. While we started MCM with lung cancer, as its survival rate improved only slightly over the past decades, we will tackle other cancers including ovarian, sarcoma, pancreas and breast.

Our goal is not only to find better signatures for these cancers – but to understand the characteristics of the search space across these signatures, so we can validate heuristic approaches to find clinically useful signatures with much less computing power. Then, we would be able to apply the approach to all cancers, and other complex diseases, and hopefully to significantly impact on patient survival.

The Mapping Cancer Markers project has explored over 7.5 trillion potential lung-cancer signatures, and to-date has explored 90 billion ovarian-cancer signatures. To do the same with our own computational resources, we would require 56 years for lung and 73 years for ovarian (75,000 CPU-years and 100,000 CPU-years, respectively).

The World Community Grid did not make our research faster or cheaper – rather, it enabled us to ask and start answering questions that would otherwise be impossible. So, thank you again for your support.

Sincerely,

Igor Jurisica, PhD, DrSc

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