

Judging the Archon Genomics X PRIZE for whole human genome sequencing

To the Editor:

The \$10 million Archon Genomics X PRIZE (AGXP) will be awarded to organizations that can swiftly and inexpensively sequence 100 human genomes at high degrees of accuracy and completeness. The Prize was conceived as an incentive to speed the development of technologies that will make possible personalized genomic medicine. Although the daunting task of making sense out of the myriad differences among human genomes remains, and the unraveling of features linked to or causal for medical and behavioral differences among our species is just beginning, the ability to obtain an accurate and full whole human genome sequence easily, quickly and cheaply must remain a near-term goal to enable such decipherment.

Since the AGXP was launched in 2006, there have been important advances in DNA sequencing technologies both in terms of speed and reduction in costs. However, no current human genome sequence is fully complete, fully accurate or certain to contain all rearrangements or information of chromosome phasing (haplotype). Highly repetitive and other regions remain difficult to sequence but are likely critical in defining heritable features. Hence the ideals of the Prize remain as critical for the future of human genetics and genetic medicine as ever.

The AGXP and *Nature Genetics* take this opportunity to announce the creation of a forum open to the worldwide genetics community to help further define appropriate standards for measuring the quality of whole human genome sequencing. The AGXP and its advisors have conceived of a set of tests and standards (known

collectively as the AGXP Validation Protocol (VP)) that will be used to evaluate the whole genome sequencing capability of any group wishing to be so tested.

The current AGXP VP will be posted online in the citable preprint archive *Nature Precedings* on 24 February 2011 for comment together with an invitation to send comments to the corresponding author. The archive displays comments on the draft, and more substantial related articles can be independently uploaded within the archive's Human Genome Standards topic collection. Updated draft versions of the AGXP VP will be posted periodically to reflect substantial community input. The community consensus AGXP VP achieved by the refereeing deadline of May 1st will be published in *Nature Genetics*.

The current AGXP VP proposes a sampling method that selects data from a small subset of the 100 human test genomes and uses that data as a measure of the accuracy, completeness and phasing capability of contestants. Sampling remains the method of choice, as the cost of sequencing the sample set itself remains a serious consideration and financial resources are limited. To ensure that the contest is fairly judged, the identity of the sample sets (that is, which of the test genomes are sampled and which segments) must remain a closed secret. Advice will be sought through the posting in *Nature Precedings* on ways to reduce costs. The Archon X PRIZE Foundation also seeks *pro bono* assistance from qualified interested parties for both physical characterization of the DNA sample sets and development of the required bioinformatic methodology.

Comments, criticisms and novel suggestions on the VP will be sought through the mechanism of *Nature Precedings*. The primary role of the VP is to enable the X PRIZE Foundation to declare a winner of the prize purse without controversy. The authors of this Archon Genomics X Prize VP recognize that there are weaknesses in the proposed approach owing to constraints imposed by the parameters of the competition. We are also limited from accepting suggestions that would add cost or make the judging procedure more complicated. Indeed, the best outcome of this consultation effort would be to receive suggestions that simplify the validation approach and reduce total cost. In addition, in order to characterize the test samples, advice and help is sought from the genetics community to participate in their preparation and physical characterization.

COMPETING FINANCIAL INTERESTS

The authors declare competing financial interests: details accompany the full-text HTML version of the paper at <http://www.nature.com/naturegenetics/>.

Larry Kedes^{1,5,6}, Edison Liu^{2,5},
C Victor Jongeneel³ & Granger Sutton^{4,5}

¹X PRIZE Foundation, Playa Vista, California, USA. ²Genome Institute of Singapore, Agency for Science, Technology and Research, Singapore. ³National Center for Supercomputing Applications and Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Champaign, Illinois, USA. ⁴J. Craig Venter Institute, Rockville, Maryland, USA. ⁵Members of the Archon Genomics X PRIZE Scientific Advisory Board. ⁶Senior Advisor to the X PRIZE Foundation. Correspondence should be addressed to L.K. (kedes@usc.edu).