Overtaken by events

Despite the small number of entries, the genomics X prize is to be commended for attempting to push the boundaries of DNA sequencing technology.

The sparse list of contenders for the Archon Genomics X Prize shows how far sequencing technology has come — and how far it still has to go. Barring any late surprises, only two teams will have signed up by the registration deadline of 31 May to compete for the US$10-million prize for the first to sequence 100 centenarians’ genomes in 30 days or less at a cost of $1,000 per genome (see page 546). The sequences must have no more than one in a million errors, be 98% complete and have correct haplotype phasing — a determination of which parent contributed each portion of a chromosome. It is not possible at present to meet this combination of goals with any single technology, but that does not explain why so few are reaching for it.

One reason why more teams are not lining up for the prize is that the promise of a genomic medical revolution is not being stalled by any lack of data. At genetic-medicine conferences, such as the University of California’s OME 2013 precision-medicine conference, held on 2 and 3 May in San Francisco, or the Big Data in BioMedicine conference held from 22 to 24 May at Stanford University in California, you will hear the same refrain: “We have more data right now than we know what to do with.” Figuring out how to interpret genetic data — and, more crucially, how to prove their value to patients and health-care systems — is the most pressing challenge in genomics today. Researchers can already sequence the protein-coding regions of a genome for less than $1,000. Getting more data on regions of the genome that they do not yet know how to interpret will not help to advance the goal of proving the medical worth of big data.

Interpretation and analysis — making sense of the data — is now the real prize. Hence the launch of a spate of bioinformatics challenges (see page 547) as researchers compete to surmount that hurdle. They include Sequence Squeeze, a contest to develop the best sequence-data-compression algorithm; the Assemblathon, for the best program to assemble a genome sequence from scratch; the DREAM Challenges to analyse and predict biological interactions among gene products; the CLARITY genome-interpretation challenge; and contests at the annual Beyond the Genome meeting. Michael Schatz at the Cold Spring Harbor Laboratory in New York, who has curated many of these contests, is planning more challenges this year, including one at Cold Spring Harbor later this autumn. Bioinformatics contests have the advantage that they do not require physical manufacturing infrastructure, so they are more accessible to more would-be solvers around the world.

There are other reasons why the genome X prize is a harder sell than other X prizes. The sequencing field is much more mature than were other industries that have been the focus of successful X prizes. Whereas there was no space-tourism industry before dozens of teams competed for the Ansari X Prize in 2004, for instance, there is already a thriving commercial market for sequencing. So any company that could meet the goals laid out in the prize already has its incentive — and it would be worth a lot more than $10 million. The value of the market leader in sequencing, Illumina of San Diego, California, is currently $8.8 billion.

And it is very unlikely that anyone other than a well-financed lab or large company could attempt the current challenge. That also sets it apart from other competitions — the Google Lunar X Prize, for example — in which teams of professionals or even hobbyists can make a respectable showing. The thriving do-it-yourself biology movement, by contrast, cannot mount a credible challenge to the large life-sciences companies. The attempt is even beyond most biotech start-ups. The UK-based biotechnology company Oxford Nanopore, for example, which is trying to commercialize a promising technology pioneered by highly respected researchers, has raised at least $150 million in grants and investment since 2008 — but has yet to show that its technology can be used to sequence a complete human genome.

That is not to say that the genomics X prize does not matter. The X Prize Foundation should be commended for revising the challenge, initially laid out in 2006, as the field evolved. It has also done a valuable service by working for two years with many partners, including Nature Genetcs, to outline a judging scheme that can independently assess the quality and accuracy of a genome sequence and that is agnostic about the sequencing technology used. The foundation deserves kudos for prompting the field to reach farther; if past history is any guide, genomics will reach that goal sooner than now seems possible.

Still less equal

Japan’s government must stick by its promise to help women’s careers to prosper.

In 2010, there were 1,552 children waiting to get places in childcare centres in Yokohama, by far the highest number of any city in Japan. Over the next three years, the city’s (female) mayor, Fumiko Hayashi, spent 37 billion yen (US$362 million) on building new infrastructure, including 144 childcare centres. Now the waiting list is zero.

Many female scientists, as well as women working in other sectors, celebrated the news. They know that help with child-rearing responsibilities is essential for a mother to have a successful career. But even better were the reverberations, which reached all the way up to the prime minister, with an indication that change might become more widespread.

On 20 May, after touring one of the childcare centres with Hayashi, Prime Minister Shinzo Abe said that the “Yokohama model” should