Well, I have been digging around a lot into Nanopore sequencing recently.

This started as preparation for a lecture I gave at the Bodega Applied Phylogenetics course a few weeks ago on “The Evolution of DNA sequencing.”

In preparation for my talk I posted my slides from last years talk and asked people on Twitter whether they had any suggestions. I got back some really useful comments and incorporated them into the talk and did my best to give credit on the slides themselves. I note – I was particularly intrigued by the comments about Oxford Nanopore sequencing:

Giving my annual “Evolution of DNA sequencing” talk tonight for #Bodega15 (2014 here http://t.co/9ekWcyTUl7) highlights of last year anyone?

— Jonathan Eisen (@phylogenomics) March 8, 2015

@phylogenomics great! Encyclopedic. To round out Moleculo “bleeding edge”, could add 10X. Didn’t see Hi-C seq and extensions (Dovetail). — Carlos Bustamante (@cdbustamante) March 8, 2015

@cdbustamante @phylogenomics http://t.co/0Z8DiT5l1c http://t.co/dlGWpiV0WY

— Nick Loman (@pathogenomenick) March 8, 2015

@pathogenomenick @cdbustamante thanks – was going to ask you directly for good@nanopore refs — Jonathan Eisen (@phylogenomics) March 8, 2015

@phylogenomics @cdbustamante @nanopore let me know if you want more!

— Nick Loman (@pathogenomenick) March 8, 2015

@pathogenomenick @cdbustamante @nanopore well, if you have slides from a talk you want to point me to … — Jonathan Eisen (@phylogenomics) March 8, 2015

@phylogenomics Actual data from Nanopore? — Keith Bradnam (@kbradnam) March 8, 2015

And in looking at the links people sent I became more intrigued. There were actual papers using the Nanopore thumb drive miniION sequencer. I really thought the system was not ready for primer time. But clearly I was wrong. So I incorporated some of this information into my talk (and added the caveat
that I was impressed with the minION papers even though I was biased a bit against the Oxford Nanopore company \textit{due to their really lame ratio of M:F speakers at their recent meetings}. Even with my bias, the technology still looked OK. For the final talk see \textit{Evolution of DNA Sequencing 2015 Version}.

Anyway – this talk has made me now much more intrigued about Oxford Nanopores. And here is another thing to look at: \textit{A firsthand perspective of trialling mobile DNA sequencing – GigaBlog}. A nice blog post by Sam Minot from Signature Science, LLC and Andy Kilianski from the Edgewood Chemical Biological Center. The post is about a new paper of theirs in \textit{Gigascience}: Bacterial and viral identification and differentiation by amplicon sequencing on the MinION nanopore sequencer.

While clearly the MinION has a way to go in terms of quality and development, I can now state that I want one. Or many. Or like lots of many of them.

\textbf{UPDATE 4/27}

A new minION paper is out:


\textbf{Abstract}

Background Long-read sequencing technologies were launched a few years ago, and in contrast with short-read sequencing technologies, they offered a promise of solving assembly problems for large and complex genomes. Moreover by providing long-range information, it could also solve haplotype phasing. However, existing long-read technologies still have several limitations that complicate their use for most research laboratories, as well as in large and/or complex genome projects. In 2014, Oxford Nanopore released the MinION® device, a small and low-cost single-molecule nanopore sequencer, which offers the possibility of sequencing long DNA fragments. Results The assembly of long reads generated using the Oxford Nanopore MinION® instrument is challenging as existing assemblers were not implemented to deal with long reads exhibiting close to 30% of errors. Here, we presented a hybrid approach developed to take advantage of data generated using MinION® device. We sequenced a well-known bacterium, Acinetobacter baylyi ADP1 and applied our method to obtain a highly contiguous (one single contig) and accurate genome assembly even in repetitive regions, in contrast to an Illumina-only assembly. Our hybrid strategy was able to generate NaS (Nanopore Synthetic-long) reads up to 60 kb that aligned entirely and with no error to the reference genome and that spanned highly conserved repetitive regions. The average accuracy of NaS reads reached 99.99% without losing the initial size of the input MinION® reads. Conclusions We described NaS tool, a hybrid approach allowing the sequencing of microbial genomes using the MinION® device. Our method, based ideally on 20x and 50x of NaS and Illumina reads respectively, provides an efficient and cost-effective way of sequencing microbial or small eukaryotic genomes in a very short time even in small facilities. Moreover, we demonstrated that although the Oxford Nanopore technology is a relatively new sequencing technology, currently with a high error rate, it is already useful in the generation of high-quality genome assemblies.

\textbf{Update 5/5}

Erika Check Hayden has an an article about the minION in \textit{Nature News}.