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Paper review 1 Intro to Bionformatics 1

Giordano, F. et al. De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. Sci. Rep. 7, 3935 (2017).

I thought this paper did a good job of providing a very succinct description of how both of the sequencing technologies (PacBio and ONP) operate, generate base calls, and attempt to correct errors. It was nice that they used and described both hybrid and non-hybrid assembly pipelines, this is something I had not picked up on in previous literature. I was impressed to see how well the ONP did in comparison to the PacBio system considering the drastic difference in costs between the two platforms. It was interesting to see how poor the performance of the ONP was when attempting to sequence homomers, thankful there were bioinformatic methods to overcome this problem but at the cost of speed. This seems to be a area where ONP can make major improvements on either the technical or bioinformatic side. I wonder how well both of these platforms would preform in a much larger genome with a higher % of repetitiveness, such as in plants where genome size and ploidy level can vary greatly. Still I think that after reading this paper that even with its problems with homomers, ONP minion seems like a sequencing system that just about any molecular laboratory could/should add to its inventory.