Improved Read Lengths and Quality with PeakTrace Basecalling Software

The DNACF is eager to announce the incorporation of PeakTrace software in our Sanger sequencing pipeline. PeakTrace is a sequencing basecaller with improvements beyond the previous ABI KB basecaller. The pairing of PeakTrace software with the recent sequencing fee reduction ($4.75/reaction) allows the DNACF to continue provide sequencing services that are an exceptional value for MU researchers.

Improvements in trace resolution and better basecalling algorithms provide several advantages:

- Read lengths improved by up to 50%
- Lower error rates with improved read lengths of 20% in alignable Q20+ bases
- Better baseline normalization enhances peak profiles
- Sharper peak resolution at the end of traces

PeakTrace has been validated using established metrics outlined in Ewing et al. (1). Algorithms used by PeakTrace don’t simply make adjustments to the KB basecaller data but begin with the raw signal intensity of the .ab1 file to generate an improved trace profile using proprietary methods. Contact the DNACF (dna-core@missouri.edu) with any questions.

References