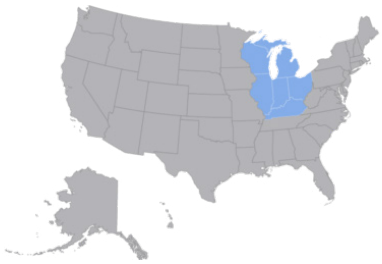
amd MIDWEST



October 2019

Inbox clutter?

Welcome to the first issue of our Monthly newsletter!! The last thing we want is to create another monthly opportunity to trash an email. So you can rest assured we will be posting helpful resources and upcoming events, well worth the electrons that were inconveniently moved about to send you this.

Upcoming Events

- **AMD Academy application** - https://www.surveymonkey.com/r/AMDAcademy2020 - November
- **CLIAC Meeting** - November 6-7
- **APHL Annual Conference**
  session proposals - Due November 1

Resources

- **The AMD-Midwest Regional Website:** https://staph-b.github.io/midwest-region/
- **The StaPH-B Website:** https://staph-b.github.io/

Bioinformatics Demystified

As your personal bioinformaticians, we will discuss a topic applicable to sequencing and bioinformatics in each newsletter so you can better relate to these modern technologies.

Next-Generation Sequencing (NGS) explained

NGS is an umbrella term for modern DNA sequencing technologies. NGS sequencing technologies can rapidly sequence DNA in parallel, and they are faster and more cost effective than the first generation of sequencing technologies that preceded them.

So what's the difference between NGS and whole genome sequencing (WGS)?

WGS is the process of sequencing all of an organism's genetic material i.e. its chromosome and plasmids. Not all sequencing is WGS. For example, using a method commonly referred to as targeted amplicon sequencing, we can use NGS to sequence only specific parts of the genome we're interested in, such as virulence or antibiotic resistance genes.

In summary: NGS is a technology, WGS is a technique, and we can use NGS to perform WGS.

2019 AMD 2-Day Meeting Recap

AMD 2 Day was the next iteration of AMD Day, a small conference hosted by CDC's Office of Advanced Molecular Detection on September 23 and 24. The meeting was focused on the future use of sequencing technologies in public health. Many talks and posters were focused on metagenomics and the use of long-read sequencing.

Meta-what?

Metagenomics is the sequencing of a bacterial community, which is a (often complex) mixture of different bacterial species. Rather than sequencing a single isolate, metagenomics allows us to learn more about the different species living in the community we're interested in. As we obtain more primary specimens, metagenomics will be useful because it provides us with a snapshot of everything in our specimen. However, using metagenomics is still a ways in the future, as it is expensive and requires significant skill to analyze metagenomic data. We would expect to see metagenomics become more widely used in public health as sequencing becomes cheaper and techniques for analyzing metagenomic data become more accessible.

How long is a long read?

The Illumina platform has been a workhorse in public health and it's hard to beat 99.9999% accuracy. However, shorter reads (150 - 300 base pairs) make reconstruction of genome difficult and inaccurate. Longer reads (1,000 - 2 million base pairs or longer) help resolve genome structure, which allows us to identify plasmids and gene orientation. This technology is still expensive and less accurate (95% - 98% accuracy), but it has been useful in various applications, including mobile laboratories where sequencing can be done in the field.