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Indiana CTSI Access Technology Program presents:

"WideSeq as a Next Gen Sequencing Replacement for Sanger Sequencing"

Speaker: Philip SanMiguel, Ph.D., Director
Purdue Genomics Core
Purdue University

Friday, September 9
12:00 pm – 1:00 pm

Please register to receive the ZOOM meeting link:
https://iu.zoom.us/meeting/register/tZcqcO-srT8tH9eC8o60qXAZouWmXnvRXGY0

Description: WideSeq, a service offered by the Purdue Genomics Core, spans the gap between small Sanger and large Illumina sequencing tasks. This allows, for example, sequencing of an entire plasmid construct at an affordable cost. Any double-stranded DNA template up to around 100 kb can generate useful results. Various use cases will be discussed. Sanger sequencing costs orders of magnitude more per base of sequence generated than Illumina Next Generation sequencing. But the costs of Illumina sequencing are in units of "runs", rather than individual reads or bases. Even the smallest Illumina run generates vastly more sequence than is useful or cost-effective to deploy against a Sanger-level task. The Purdue Genomics Core gathers samples submitted to it, constructs Illumina libraries from them to be run on a MiSeq once per two weeks. Some informatics, like de novo assembly, are performed and the results returned as a web page.

Disclosure Summary

The Access Technology Program provides investigators access and guidance in using novel technologies and Core Services. Services and views presented belong solely to the vendor; they do not necessarily reflect the views of the Indiana CTSI, Indiana University, Purdue University or University of Notre Dame.

Access Technology Program
Indiana Clinical and Translational Sciences Institute