

*Computational Pan-Genomics:
Algorithms and Applications*
MSU Presentation

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Abstract:

As the cost of sequencing DNA continues to drop the number of sequenced genomes rapidly grows. In the recent past, the cost dropped so low that it is no longer prohibitively expensive to sequence multiple genomes for the same species. This has led to a shift from the single reference genome per species paradigm to the more comprehensive pan-genomics approach, where populations of genomes from one or more species are analysed together.

The total genetic/genomic content of a population is vast, requiring algorithms for analysis that are more sophisticated and scalable than existing methods. Furthermore, existing algorithms are generally not intended for analysing populations, let alone without a reference, and so they are inappropriate for pan-genome analysis.

The focus of this work is the exploration of new algorithms and their applications to pan-genome analysis, both at the nucleotide and genic resolutions.