

Genome Sciences Seminar

Thursday, 6.23.22 | 3:30 | Foege Auditorium

remote viewing option: https://depts.washington.edu/gsrestrc/remote.htm



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"Long-read sequencing methods for studying centromere organization, evolution, and function"

Reference genome assemblies have historically excluded repetitive satellite DNA sequences found within and near centromeres, limiting the ability to study these regions using modern genomic and epigenomic tools. Recently, long-read sequencing and assembly methods have enabled reconstruction of complete centromeric and pericentromeric sequences, providing an unprecedented opportunity to study their organization, evolution, and function. In order to fully leverage these complete assemblies, we have created and applied new sequence analysis tools to reveal the organization and evolutionary relationships of human satellite DNA sequences. We also developed DiMeLo-seq, a long-read, single-molecule method for mapping protein-DNA interactions, and we applied it to measure the density of CENP-A containing nucleosomes across human centromeres. These efforts revealed strong associations between low CpG methylation, high CENP-A density, and the very recent expansion of underlying satellite repeats, raising important questions about the molecular and evolutionary mechanisms responsible for these associations.

https://www.altemoselab.org/home

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Seminar website at http://www.gs.washington.edu/news/seminars.htm

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