

GENETICS, BIOINFORMATICS, AND SYSTEMS BIOLOGY COLLOQUIUM

THURSDAY MARCH 17
12:00PM PST

ON ZOOM!

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PASSWORD: **GENOME**

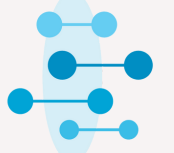
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”””FINALLY FINISHING THE HUMAN GENOME”””

Since its initial release in 2000, the human reference genome has covered only the euchromatic fraction of the genome, leaving important heterochromatic regions unfinished. Addressing the remaining 8% of the genome, the Telomere-to-Telomere (T2T) Consortium has finished the complete sequence of a human genome, T2T-CHM13, that includes gapless assemblies for all chromosomes, corrects errors in the prior references, and introduces over 200 million bp of novel sequence. The completed regions include all centromeric satellite arrays, recent gene-rich segmental duplications, and the short arms of all five acrocentric chromosomes, unlocking these complex regions of the genome to variational and functional studies for the first time.

Organization Committee: J. Gleeson, J. Sebat
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