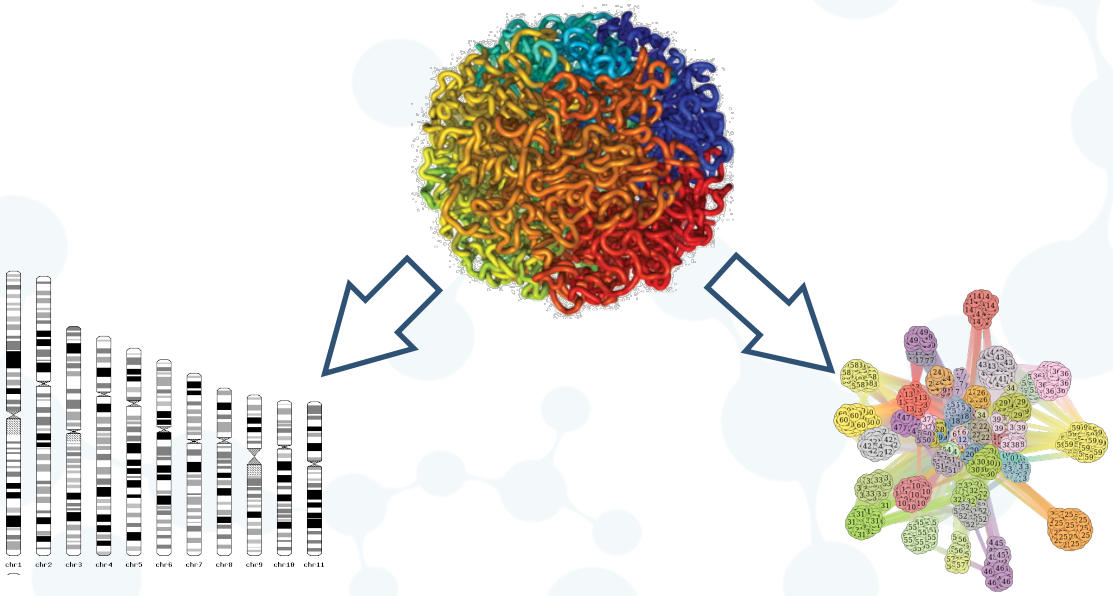
From Contigs to Chromosomes:

How Hi-C is transforming genome and metagenome assembly

Chromosome conformation capture methods like Hi-C measure the 3D organization of DNA *in vivo* using a combination of crosslinking, proximity-ligation, and paired-end sequencing.

Because this method captures genomic contiguity on intact chromosomes, the resultant information can be used to generate end-to-end chromosome-scale scaffolds for large genomes. Since Hi-C junctions form within intact cells, any sequences interacting by Hi-C must have originated from the same species/ strain in a mixed population, enabling metagenomic deconvolution.



Capturing genomic proximity information *in vivo* removes several major obstacles in genome and metagenome assembly, improving the quality and efficiency of genomic discovery efforts.

Friday, March 2nd, 2018
2:30-3:30 pm
3503 Thomas Hall (Stephens Room)

Ivan Liachko, Ph.D.
Founder, Phase Genomics, Inc.