PHASE GENOMICS

4000 Mason Rd
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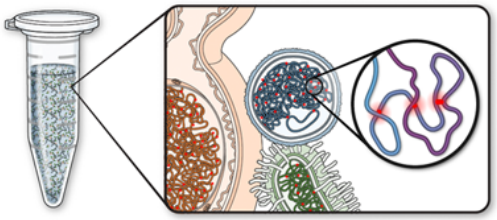
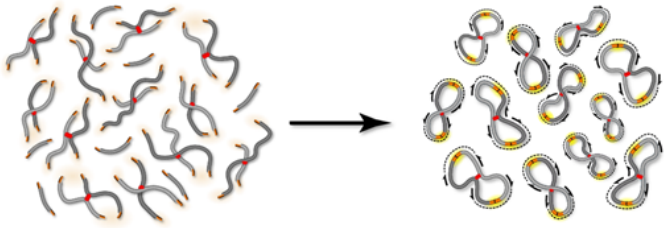
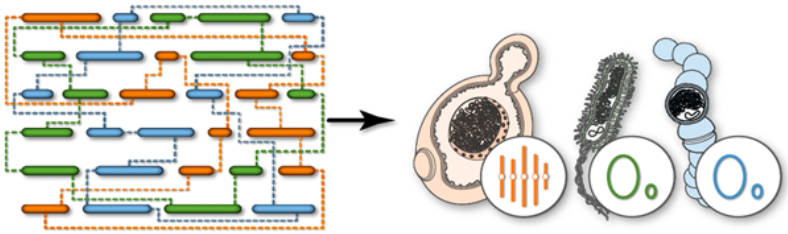
ProxiMeta™ Hi-C Metagenome Deconvolution



In vivo crosslinking traps intra-cellular DNA contacts, including inter-chromosomal and plasmid-genome interactions. Because crosslinking is performed *in vivo*, inter-cellular interactions are negligible.



Crosslinked loci are fragmented and proximity ligated, creating chimeric junctions between sequences originating from the same cell. Paired-end sequencing of these junctions yields proximity signal that is used to group sequences by cellular origin.



Intracellular proximity signal is used to deconvolute metagenomes by grouping sequences into species- and strain-specific clusters. Multi-chromosome genomes can also be assembled, and plasmids can be assigned to host organisms.

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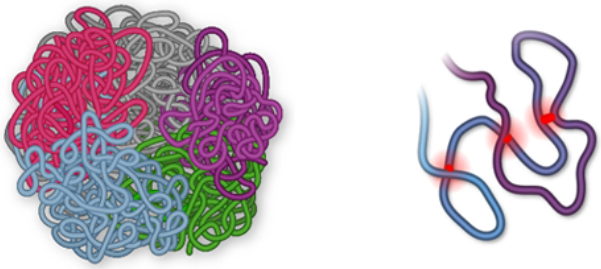
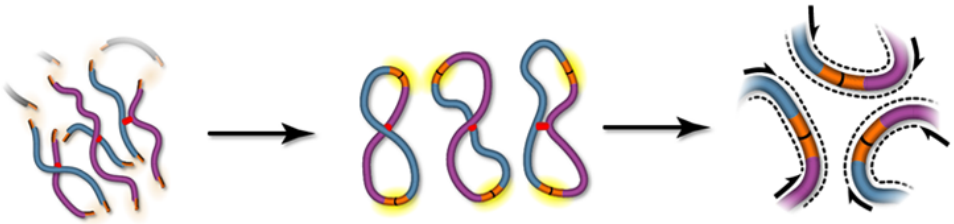
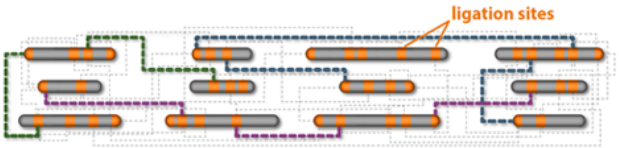
Proximo™ Hi-C Chromosome-Scale Scaffolding



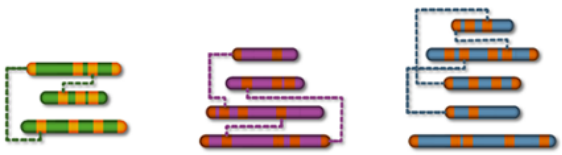
Physical proximity of nuclear DNA is inversely correlated with genomic distance. Chromatin proximity is captured through *in vivo* crosslinking, preserving contiguity information across entire chromosomes.



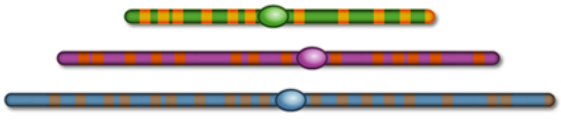
Crosslinked chromatin is fragmented and junctions are extracted. Fragmented junctions are proximity ligated and paired-end sequenced. Sequencing data encapsulates the chromatin proximity signal.



Proximity data establishes relationships among contigs at ligation sites.



Contigs are placed into chromosome groups based on proximity signal...



...then ordered and oriented by proximity signal onto chromosome-scale scaffolds.