What Hi-C can and cannot tell us about functional genomic architecture.

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Abstract

Nuclear architecture and underlying genomic functions, such as transcription, have been correlated for decades, but whether one is the cause or consequence of the other remains an open question. Since 2002, the use of molecular biology approaches (namely 3C) have complemented microscopy approaches to give an unprecedented view of how the genome tends to fold, particularly when coupled with high-throughput sequencing (Hi-C). I will give a historical overview of the evolution of the technology, and what biological insight we have gained from **correlations** of C-based data with functional studies. I will then more critically discuss what sort of information cannot currently be gleaned from these experiments, and the recent approaches that we and others have launched to fill these gaps.

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