

The dark side of the genome: revealing the native transposable element/repeat content of eukaryotic genomes

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The majority of genome assemblies to date fail to represent the true structure of native genomes. This lack of completeness is largely due to the inability to assemble the variable (often significant) fraction of nuclear genomes that is composed primarily of repeated sequences (with either a structural function such as satellite DNA and simple sequence repeats or “selfish DNA” such as high-copy transposable elements – TEs) – herein defined as the “dark side of the genome”. To address this problem, we developed a method to detect and quantify the dark side of the genome and used it to infer the genomic composition and dynamic evolution of the majority of native repeats and TEs present within several test eukaryotic genomes.

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