The genomes of many animals, plants and fungi are tagged by DNA methylation of cytosine. To understand the biological significance of this epigenetic mark it is essential to know where in the genome it is located. New techniques are making it easier to map DNA methylation patterns on a large scale and the results have already provided surprises. In particular, the conventional view that DNA methylation functions predominantly to irreversibly silence transcription is being challenged. Not only is promoter methylation often highly dynamic during development, but many organisms also seem to target DNA methylation specifically to the bodies of active genes [1].

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[1] Suzuki MM, Bird A. DNA methylation landscapes: provocative insights from epigenomics. Nat Rev Genet. 2008 Jun;9(6):465-76. doi: 10.1038/nrg2341. Review. PubMed PMID: 18463664.