



## CpG% and the epigenetic programming

**CpG%** and the epigenetic programming. The top of the figure shows a hypothetical distribution of (C+G)% and CpG% above a gene. It further indicates that intergenic CpGs are methylated and CpGs in the regulatory regions are generally unmethylated. For an intuitive overview, the methylation pattern is represented on the two strands above the chart. The lower part of the figure shows the importance of epigenetic reprogramming that leads, among other mechanisms, to cell types in some eukaryotic organisms. The patterned lines depict an interpretation of DNA methylation across cell generations. The significance of the geometric shapes used for illustration is shown in the lower left corner.

