GENETICS, SOFTWARE

READING BEHIND THE LINES

23.08.2006

-moblog– Eran Segal et al. describe in Nature a genomic code for correct nucleosome attachment of genomic DNA. DNA must be positioned for access to functional sites of gene activity where 147 bases are wrapped around each nucleosome core. AT is favored where phosphodiesterase backbones face inward and GC where it faces outward. Distance between nucleosomes may be variable – as the accompanying editoral by Timothy Richmond explains (the enigmatic histone H1 question). Do genomes use nucleosome DNA preference to target transcription factor towards appropriate sites? This might expain why current transcription factor models are rather poor as they are using only sequence binding matrices. It reminds me to steganograpy, algorithmic procedures that can be used to hide secret messages in in pictures without affecting the visual impression. Yea, yea.