Genome-wide DNA Conformational Flexibility in Yeast

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Motivation
The conformation of DNA and its sequence dependence are mainly determined by the chemical structures of the base pairs and their interactions. The torsional flexibility of DNA helix has been proved to be a sequence-dependent property expressed as fluctuations of the twist angle, which measures the rotation of a base pair about the axis perpendicular to the base plane. In 1989 Sarai and co-workers proposed a computational model of DNA flexibility on the basis of base pairs interactions and the results agree with available experimental observations. Flexible regions are known to mediate DNA-protein binding processes and are suggested to play a role in specific interactions of DNA metabolism; recently, evidence has been reported on a relationship with DNA replication origin, DNA repair, DnaseI cleavage and regulatory elements’ binding. DNA flexibility is also involved in chromosome instability.

Methods
The potential local variations in the DNA structure may be estimated by analysing the dinucleotide degree values calculated by an algorithm working on overlapping windows, summed and averaged. The resulting genome-wide continuous signal is processed in order to extract peaks, which are then studied by means of motif discovery and enrichment analysis.

Results
The first complete yeast flexibility map shall be introduced. The flexibility signal shall be described, then the analysis on peaks shall be reported. The complete yeast genome have been scanned to identify functional elements associated to peak loci, focusing on linguistic structures (repeats, motifs) and proximal genes, for which their evolvability as well as orthology to human genes shall be discussed. Finally, enriched loci have been compared to the most recent data on nucleosomes, yeast fragility markers, replication termination regions, evolutive and experimental breakpoints. Browsable data shall be soon available.

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