

Variation of different local and global parameters  
for the four datasets

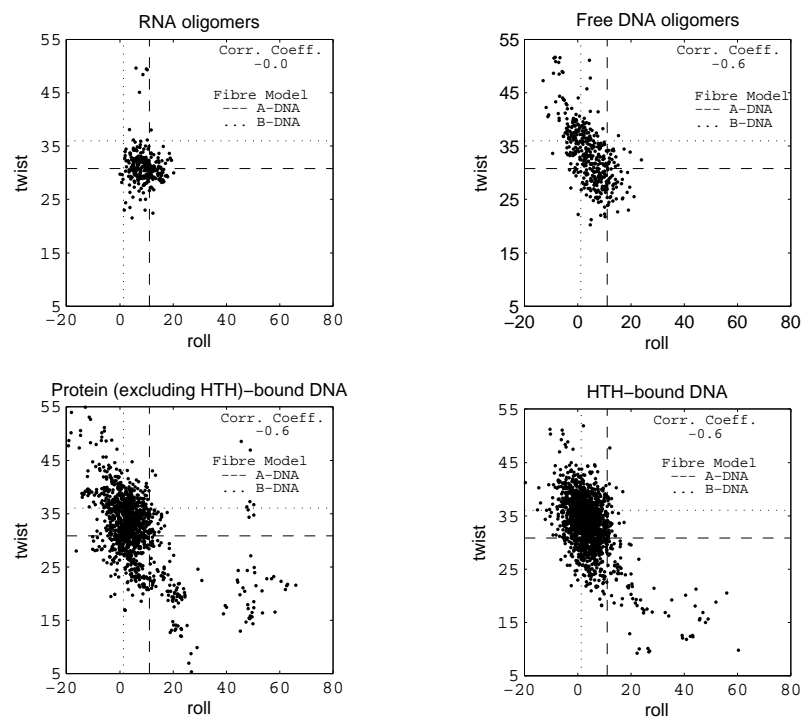


Figure 1: Twist versus Roll for the RNA, free DNA oligomers, protein (excluding HTH)-bound DNA and HTH-bound DNA datasets. Dashed and dotted lines have been drawn to highlight the values for the A and B-DNA fibre models.

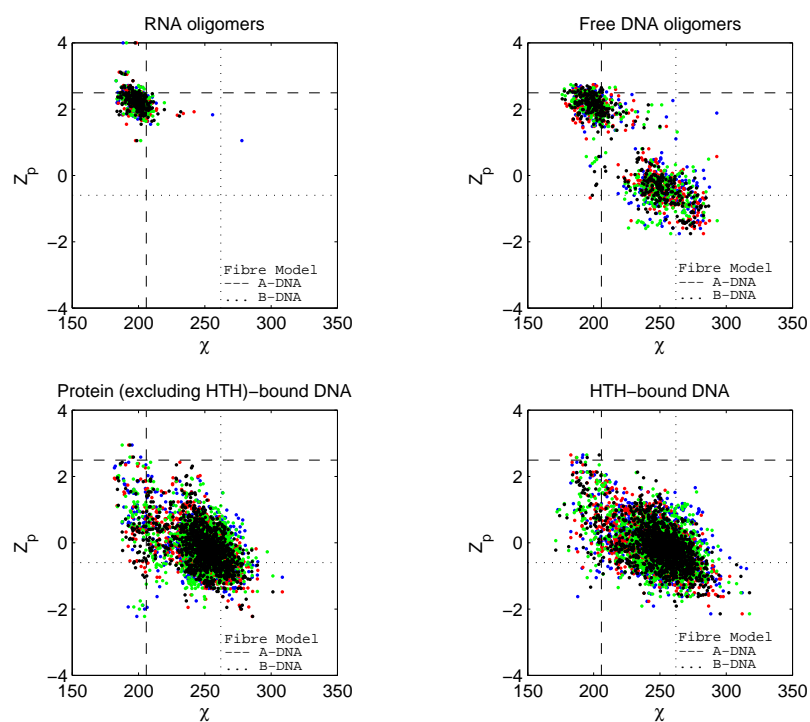


Figure 2:  $Z_p$  versus backbone torsion angle  $\chi$  for the four datasets. The four nucleotides constituting a basepaired dinucleotide step corresponding to a particular  $Z_p$  value have been colour coded as follows: 5'-end Strand 1 - blue; 3'-end Strand 1 - Red; 5'-end Strand 2 - Green; 3'-end Strand 2 - Black.

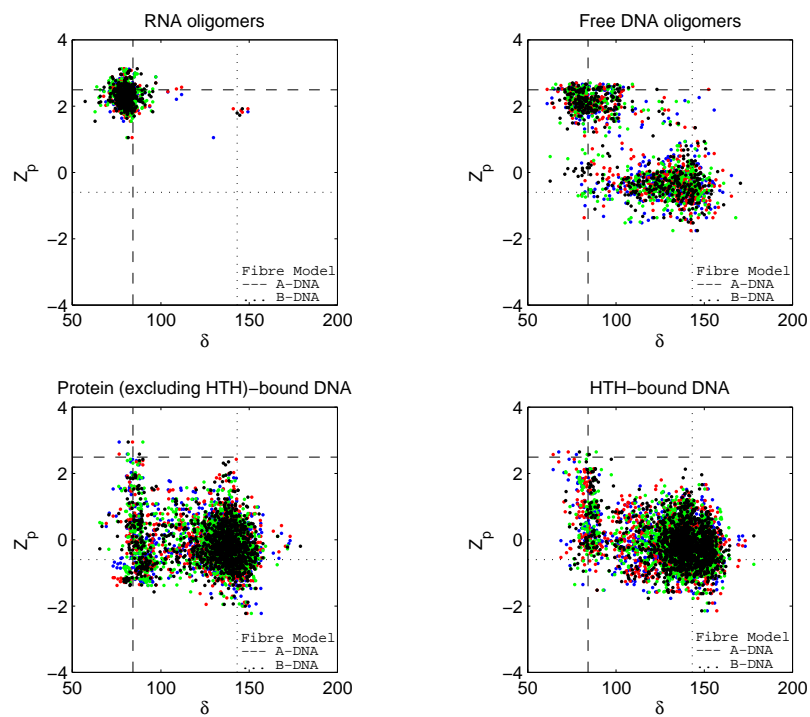


Figure 3:  $Z_p$  versus backbone torsion angle  $\delta$  for the four datasets. The four nucleotides constituting a basepaired dinucleotide step corresponding to a particular  $Z_p$  value have been colour coded as follows: 5'-end Strand 1 - blue; 3'-end Strand 1 - Red; 5'-end Strand 2 - Green; 3'-end Strand 2 - Black.

Table 1: Mean and standard deviation values (in parentheses) for global helical basepair orientation parameters and groove widths. The linear global helical axis has been fitted to the backbone  $C_1'$  atoms. For the complex and HTH datasets, structures which are curved or whose geometry of curvature could not be assigned are excluded, since a linear global helical axis cannot be fitted to such structures.

	Fibre-model		RNA	Free		Complex Excl. TEH <sup>†</sup>	HTH Excl. TC <sup>‡</sup>
	A-DNA	B-DNA		A-like ( $Z_p > 1.3 \text{ \AA}$ )	B-like ( $Z_p \leq 0.8 \text{ \AA}$ )		
Inclination ( $^\circ$ )	19.3	2.0	15.4 (4.8)	16.5 (5.1)	2.0 (3.5)	6.4 (6.2)	5.9 (6.5)
Helical twist ( $^\circ$ )	32.7	36.0	32.7 (6.1)	32.1 (3.7)	35.9 (6.0)	34.1 (4.6)	34.0 (4.8)
X-displacement ( $\text{\AA}$ )	-4.5	0.6	-4.3 (1.2)	-4.3 (0.9)	0.1 (0.8)	-1.1 (1.1)	-0.9 (1.3)
Helical rise ( $\text{\AA}$ )	2.6	3.4	2.7 (0.3)	2.7 (0.3)	3.3 (0.1)	3.2 (0.1)	3.2 (0.2)
Smallest P-P distance ( $\text{\AA}$ ) (across minor groove)	17.0	11.7	15.7 (0.6)	15.8 (0.6)	11.1 (1.5)	12.4 (1.7)	12.5 (1.8)
Smallest P-P distance ( $\text{\AA}$ ) (across major groove)	8.2	17.2	11.1 (2.0)	11.6 (2.7)	17.1 (0.9)	17.3 (1.7)	17.1 (1.3)

<sup>†</sup>TEH - TBP, Endonuclease and Hyperthermophile chromosomal protein SAC7D containing structures (excluded)

<sup>‡</sup>TC - TBP and CAP containing structures (excluded)