

# Supplementary IIIId: Context dependent prediction in DNA sequence using neural networks. Fourier, mouse genome, GC/AT content, high frequencies.

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This file contains the second of two sets of plots based on the Fourier analysis showing the L2-norm of the Fourier coefficients in a running window. This first set covers the frequency range from 200 to 45000 using a window length of 1000 (and a step size of 100); this second file/set covers the frequencies from 40000 to 140000 and used a window length of 5000 (and step size of 100). Note that, since the window length is here five times larger than for the lower frequency range (first set), the scale of the amplitudes (y-axis) is five times higher than there.

## Fourier plots, GC/AT content, frequency range 40000 to 140000

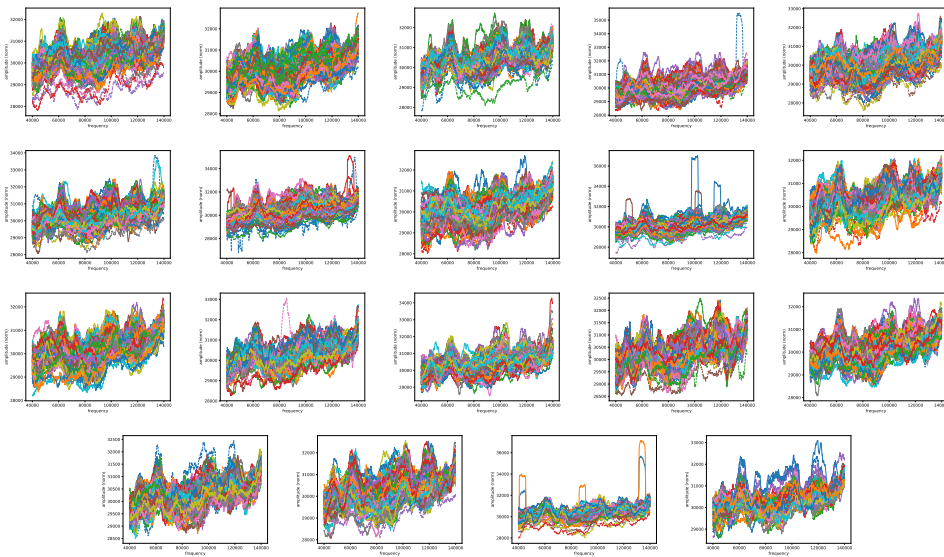


Figure 1: Mouse GC/AT content. Fouriers on GC/AT content arrays, higher frequency range. Each plot covers one chromosome, listed in increasing order (chr1 to chr19). The genome string is divided in adjacent segments of 1Mb (per chromosome); each plot shows the results for all segments in the chromosome (with ratio of qualified positions  $> 0.9$ ).