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

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This file contains the first 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); the second set covers the frequencies from 40000 to 140000 and used a window length of 5000 (and step size of 100) and is placed in a separate file.

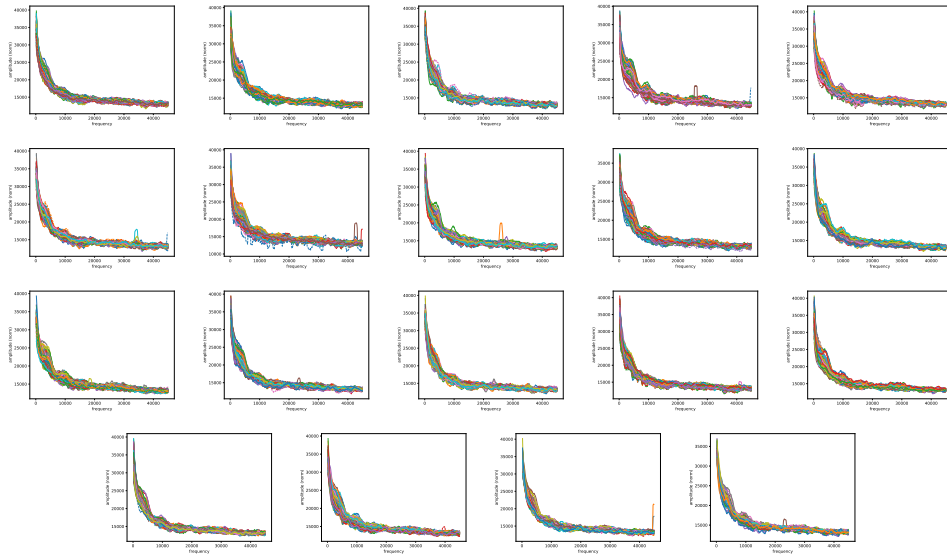# Fourier plots, GC/AT content, frequency range 200 to 45000

Figure 1: Mouse GC/AT content. Fouriers on GC/AT content arrays, low 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).