Supplementary IIIa: Context dependent prediction in DNA sequence using neural networks. Fourier, mouse genome, LSTM50, low frequencies.

Christian Grønbæk, Yuhu Liang, Desmond Elliott, and Anders Krogh

April 16, 2022

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.

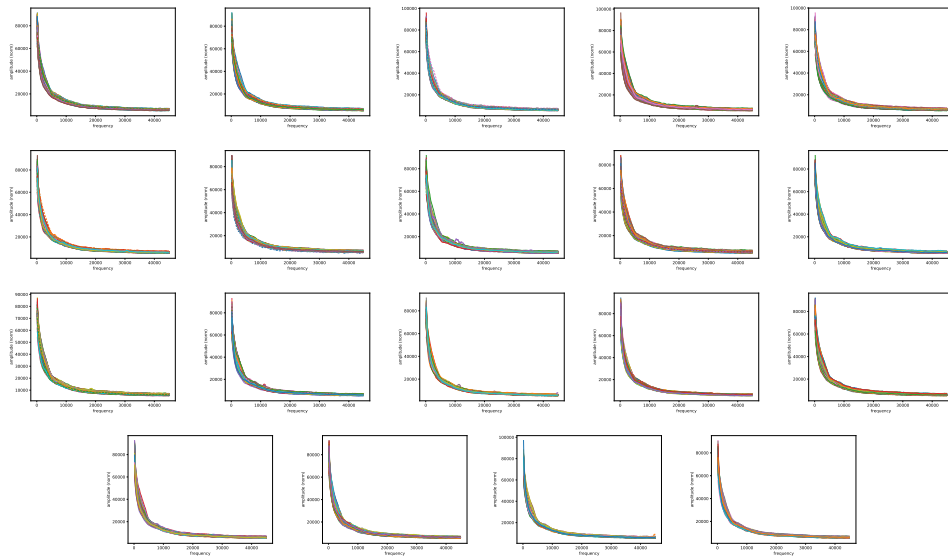# Fourier plots, LSTM50 predictions, frequency range 200 to 45000

Figure 1: Mouse LSTM50. Fouriers on reference-base probability, 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).