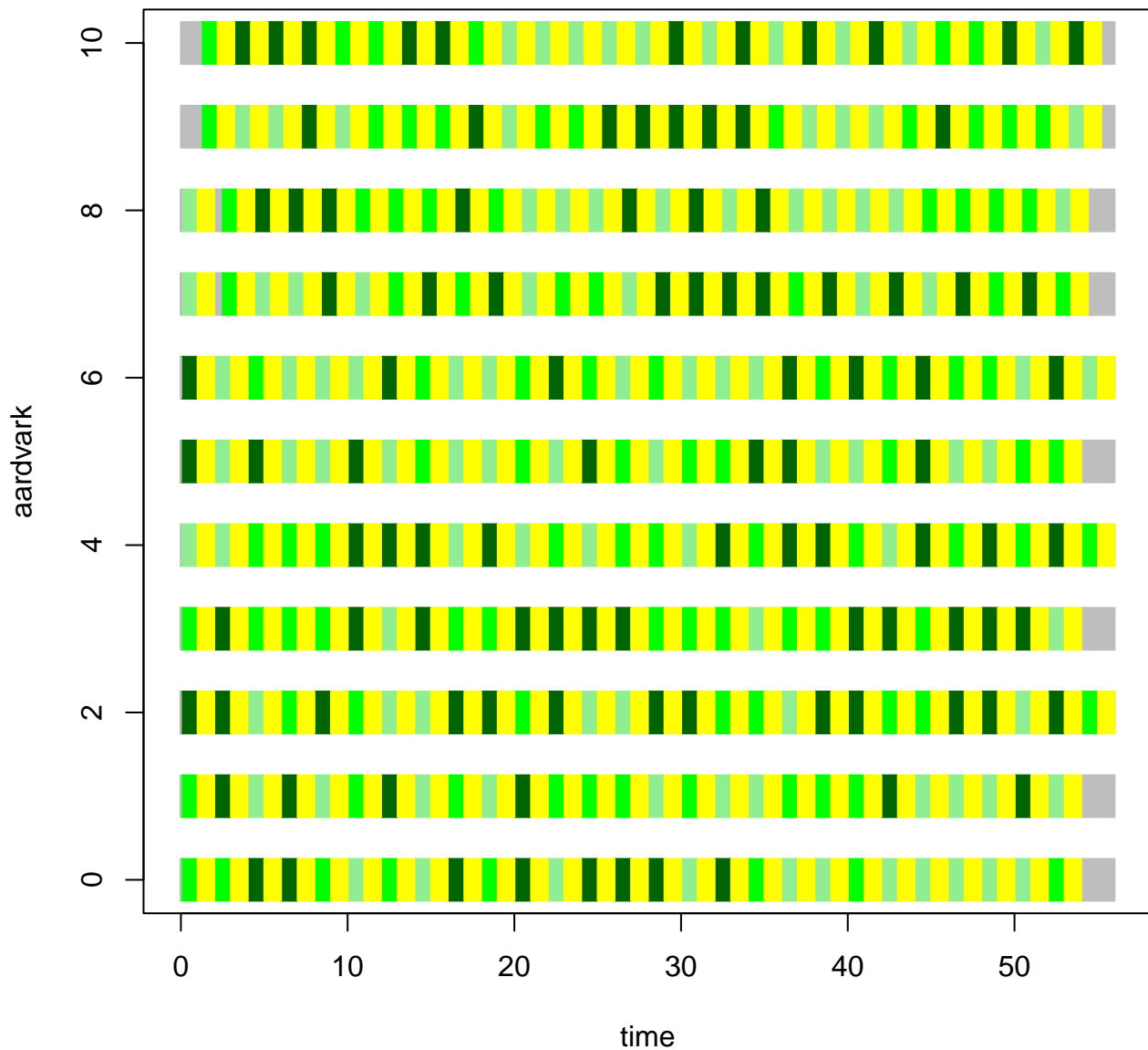


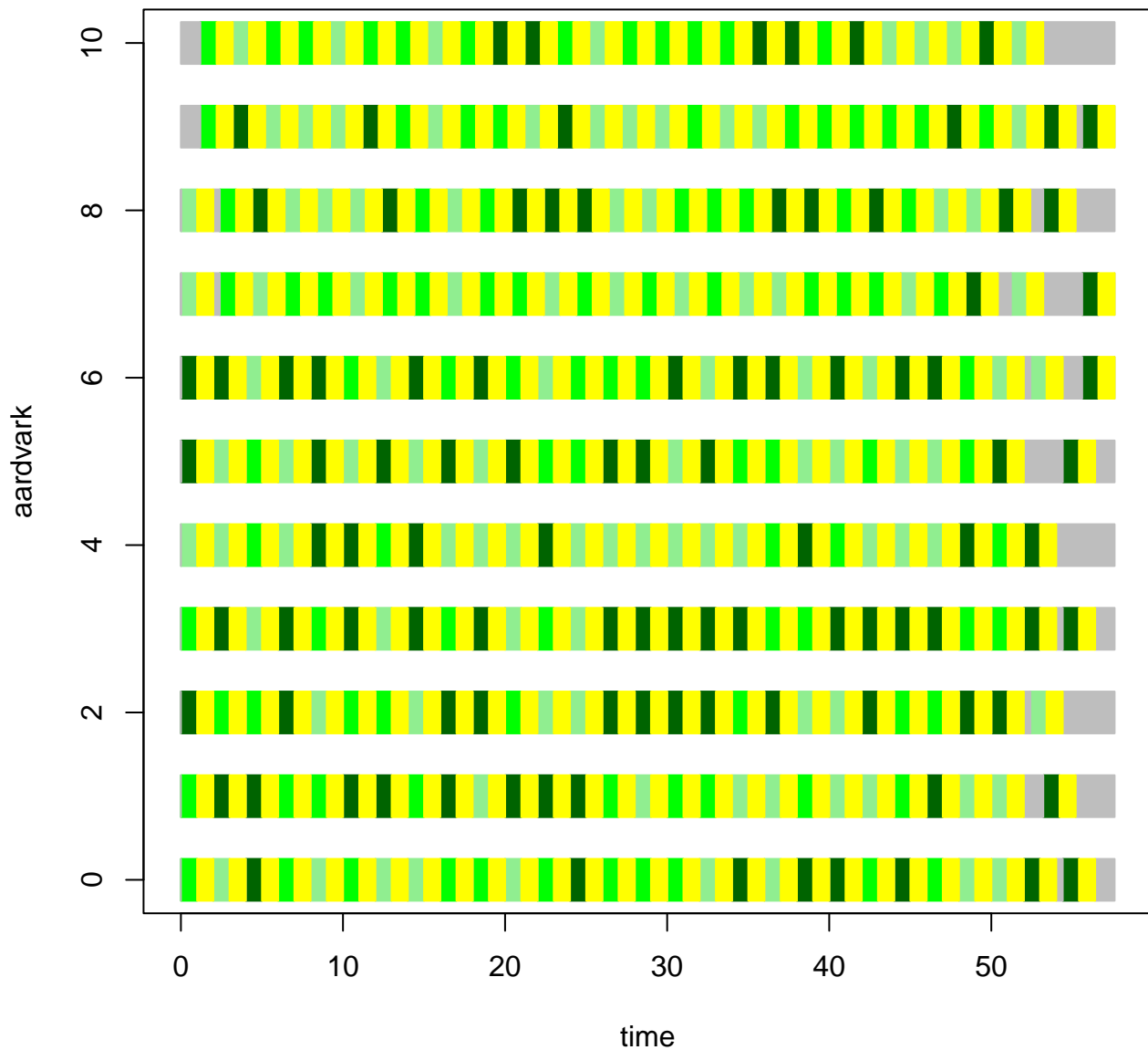
Figure 1 displays a heatmap visualization of gene expression data across 51 samples (columns) and 12 genes (rows). The columns are labeled 0 to 50 at the bottom. The rows show varying patterns of color (yellow, green, dark green, light green, and grey) across the 56 columns, indicating different expression levels or states for each gene across the 51 samples.

aardvark

Plot for output_1.csv



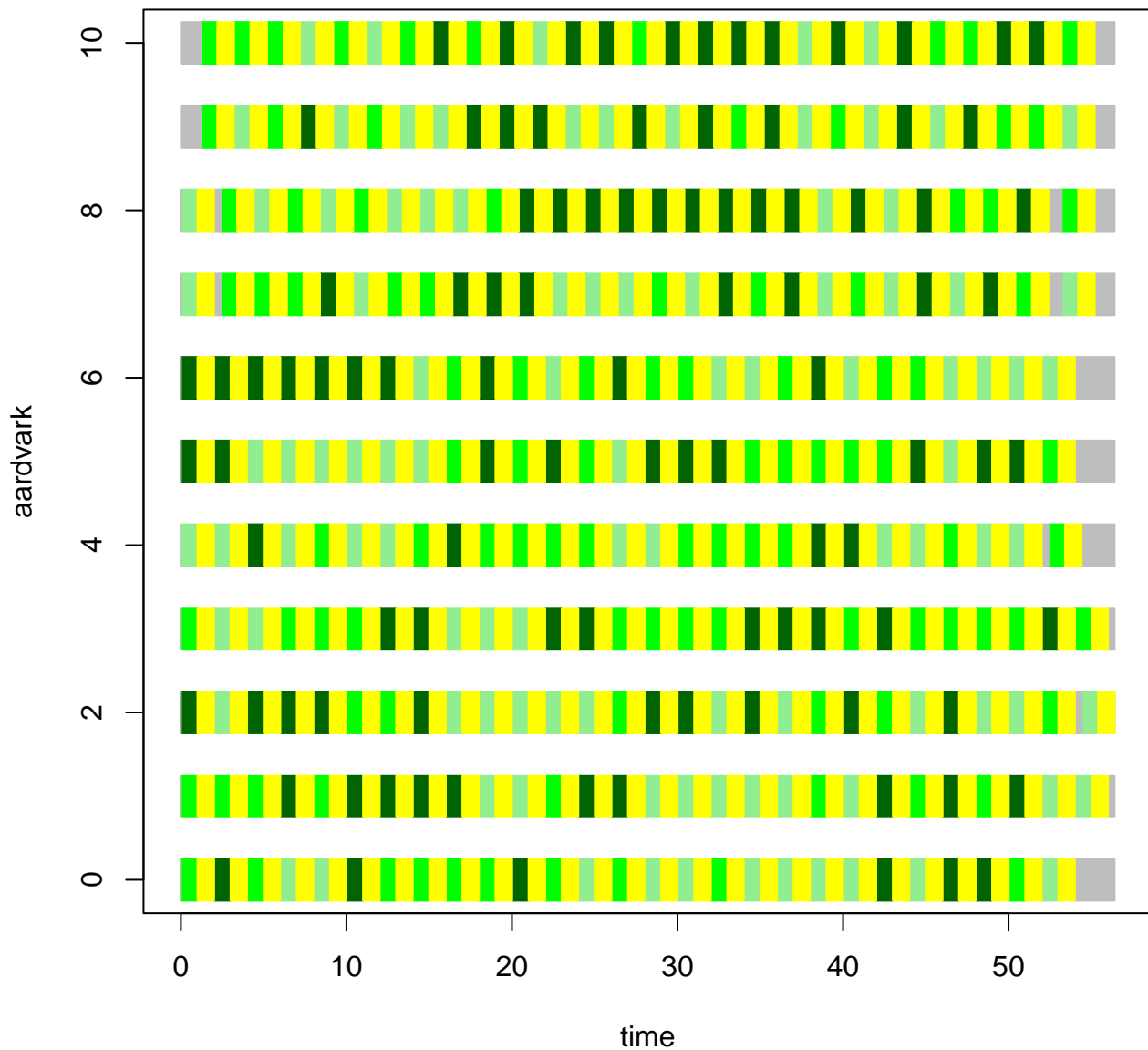
Plot for output_2.csv



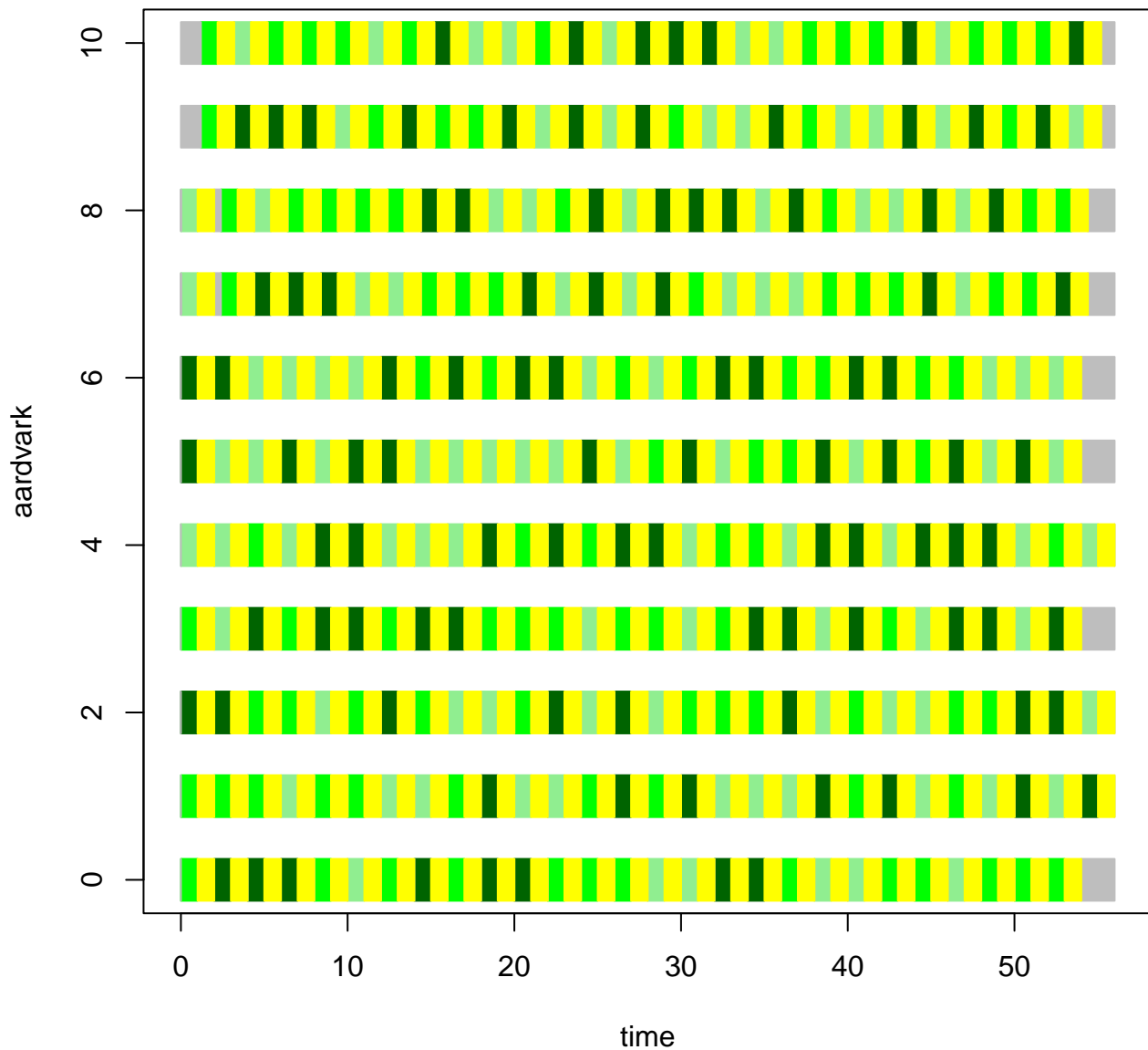
0 10 20 30 40 50

time

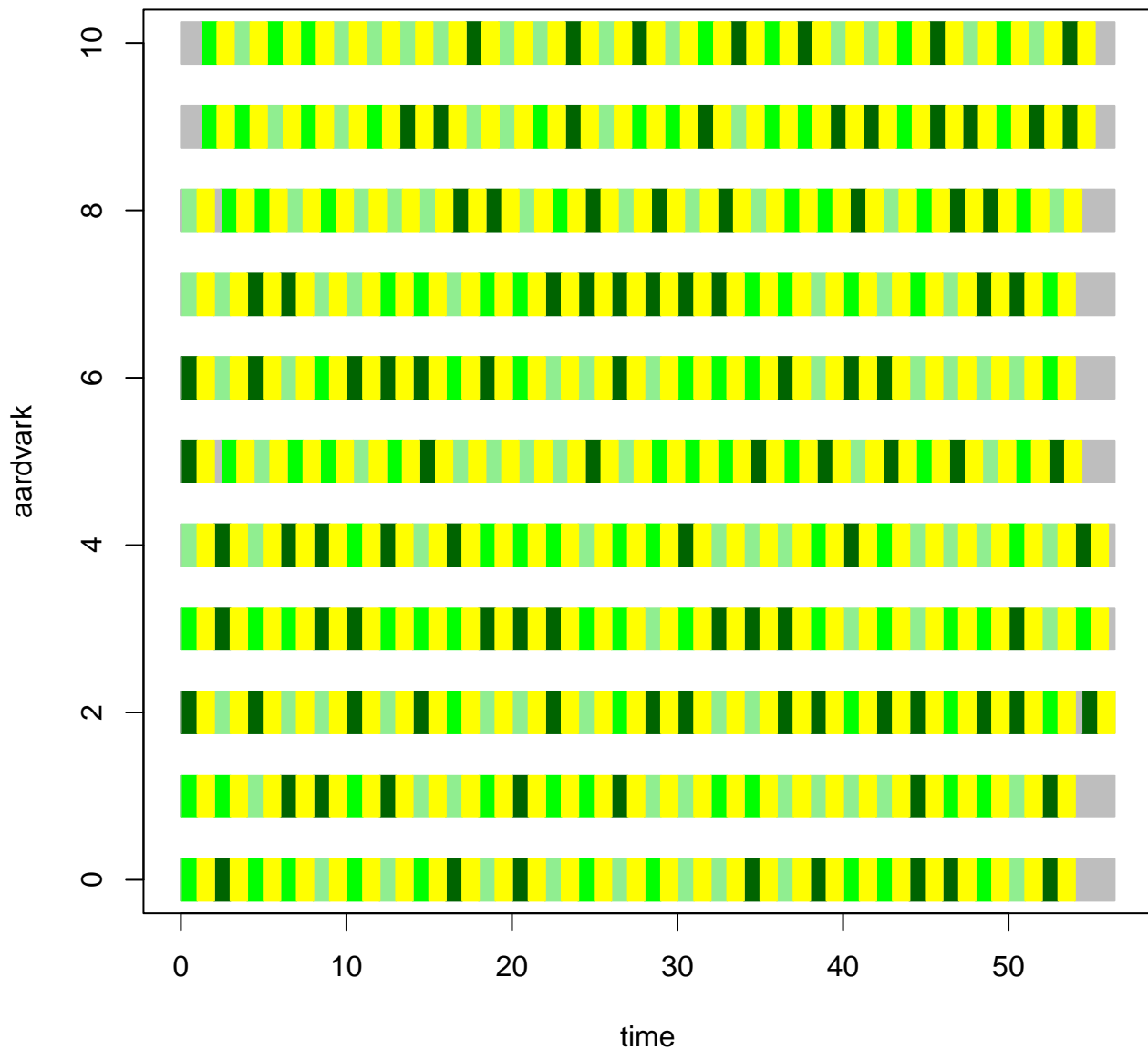
Plot for output_4.csv



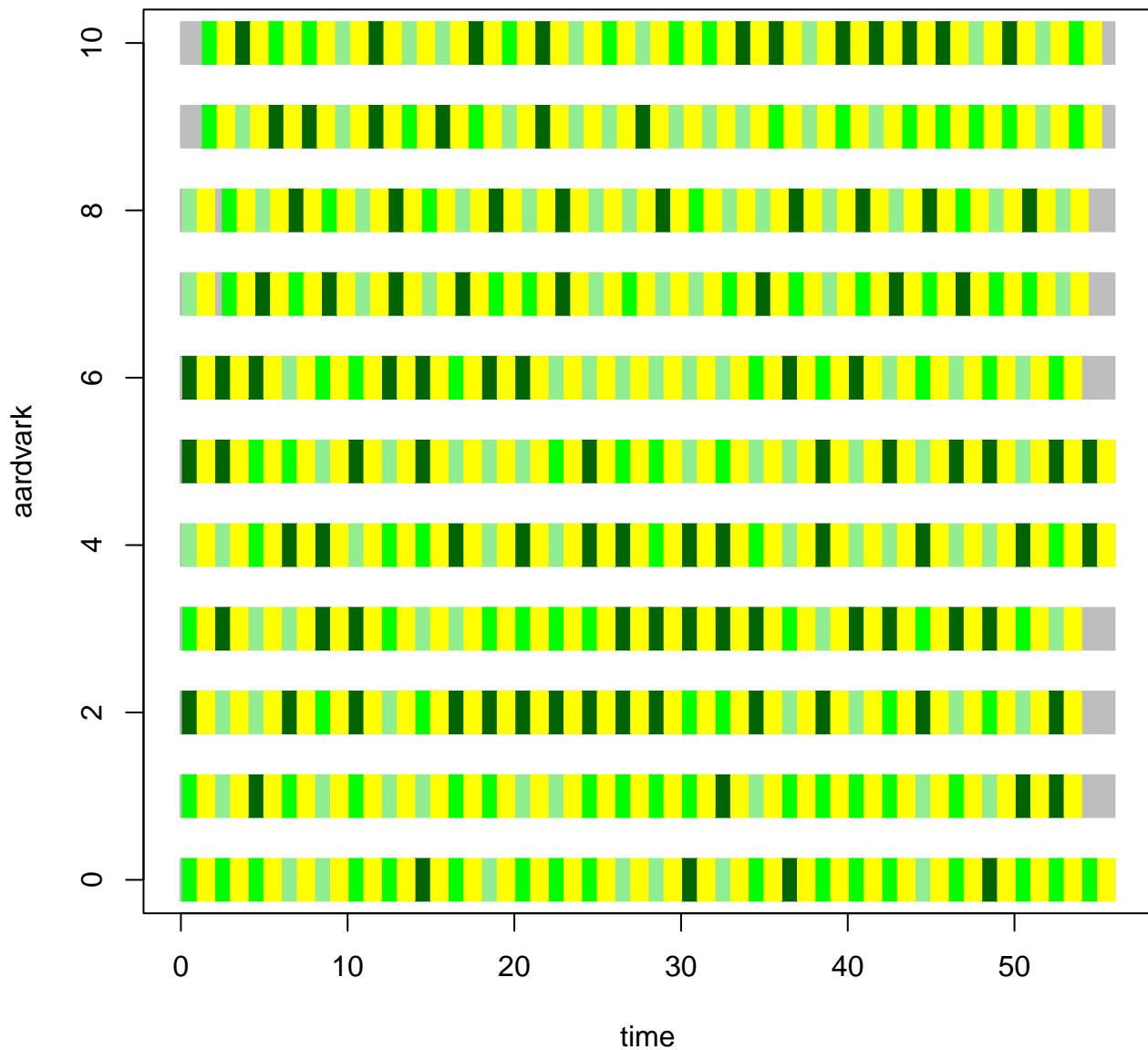
Plot for output_5.csv



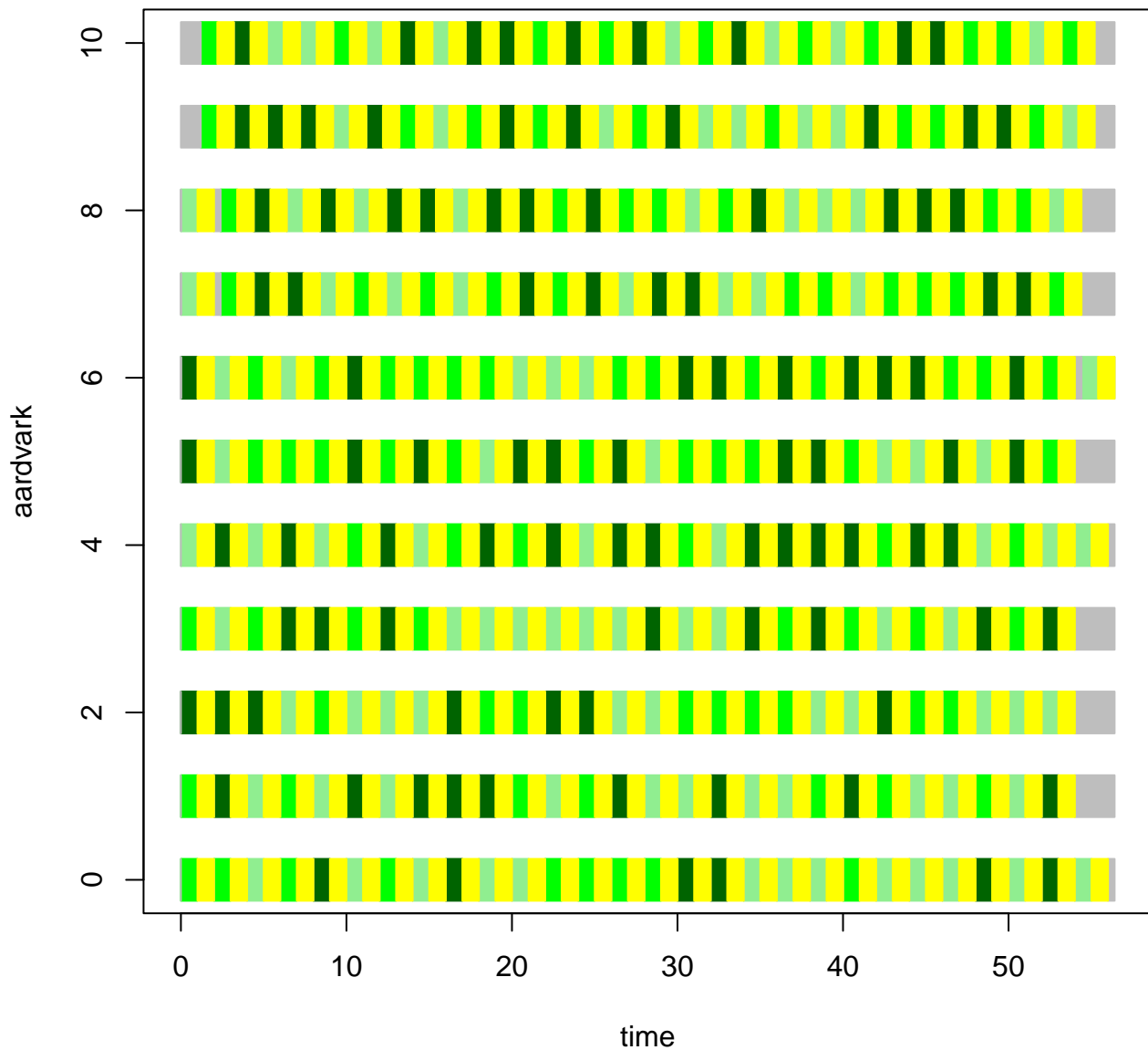
Plot for output_6.csv



Plot for output_7.csv



Plot for output_8.csv



The figure displays a 12x100 grid of colored squares. The colors are black, white, and gray. The sequence is generated by a cellular automaton rule. The first row is all black. The second row is all white. The third row is all gray. The remaining rows show a complex pattern of black and white squares, with gray squares appearing at the ends of some rows.

0 10 20 30 40 50