



Figure 1 is a line graph showing the percentage of individuals in each life history strategy (LHS) across seven life stages (1 to 7). The y-axis is labeled 'Individuals (%)' and ranges from 0 to 100. The x-axis is labeled 'Life stage' and ranges from 1 to 7. The legend includes: Fast (red dashed), Slow (blue solid), High (green dotted), Low (purple dash-dot), D (yellow solid), SF (cyan solid), CC (pink solid), CC_High (green dotted), High_Ten_High (red dashed), and High_Ten_Low (blue solid). The graph shows that the 'Fast' strategy starts at approximately 40% at life stage 1 and increases to 100% by life stage 7. The 'Slow' strategy starts at approximately 60% at life stage 1 and decreases to 0% by life stage 7. The 'High' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7. The 'Low' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7. The 'D' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7. The 'SF' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7. The 'CC' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7. The 'CC_High' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7. The 'High_Ten_High' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7. The 'High_Ten_Low' strategy starts at approximately 20% at life stage 1 and increases to 100% by life stage 7.

[illegible]

The graph plots 'Normalized CPU time (%)' on the y-axis (0 to 100) against 'Problem size, n' on the x-axis (10, 20, 30, 40, 50, 60, 70, 80, 90, 100). The legend identifies the following algorithms: Dijkstra (blue line with circles), Bellman-Ford (green line with squares), Floyd-Warshall (red line with triangles), and others (various colored lines). The graph shows that as the problem size increases, the CPU time for most algorithms increases, with some algorithms showing a sharp increase at n=100.

Figure 1 is a line graph showing the normalized weight of various features for different models. The y-axis is labeled 'Normalized weight, 0% to 100%' and the x-axis is labeled 'Model' with values 1 through 8. The legend includes: Blue (P), Red (T), Green (D), Yellow (C), Cyan (G), Magenta (P), Dark Green (P), Red (P), and Red (P). The graph shows that the weight of features varies significantly across models, with some features being dominant in certain models and others being less so.

[illegible][illegible]

Figure 1 is a line graph showing the normalized relative content (%) of various amino acids in the plasma of rainbow trout over an 8-day period. The y-axis represents the normalized relative content (%) from 0 to 100. The x-axis represents time in days from 1 to 8. The legend identifies the following series: Phe (blue solid line), Arg (red solid line), His (green solid line), D (black solid line), Glu (blue dashed line), Gln (red dashed line), Asp (green dashed line), Phe_Tiss_0.1 (black dotted line), Phe_Tiss_0.2 (blue dotted line), and Phe_Tiss_0.3 (red dotted line). The graph shows that several amino acids, particularly Glu, Gln, and Asp, show a significant increase in relative content over time, while others like Phe and Arg remain relatively stable or show a slight decrease.

