Color Plate 1

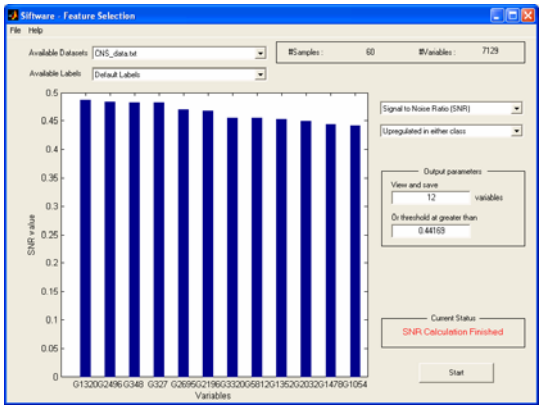

Fig. 1.6. 12 genes selected as top discriminating genes from the Central Nervous System (CNS) cancer data that discriminates two classes – survivals and not responding to treatment (Pomeroy et al. 2002). The NeuCom software system is used for the analysis (www.theneucom.com) and the method is called "Signal-to-Noise ratio"

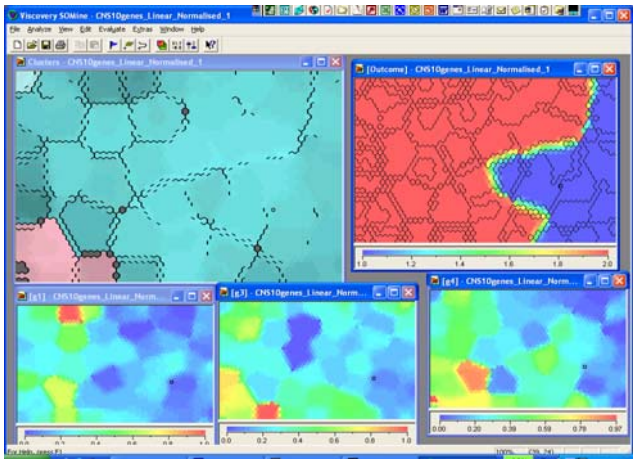

Fig. 4.5. SOM output derived from 60 samples and 12 input gene expression variables from the CNS data (Pomeroy et al. 2002) (See Fig. 1.6) - the top left map; in the top right map the class labels are mapped (class survival in the left blob, and class fatal – on right side); the bottom three maps show the contribution of gene G1, G3 and G4 respectively – none of them on its own can discriminate correctly the samples and a good discrimination is achieved through their interaction and pattern formation. The software system ViscoverySOMine was used for this experiment (http://www.somine.info/)