

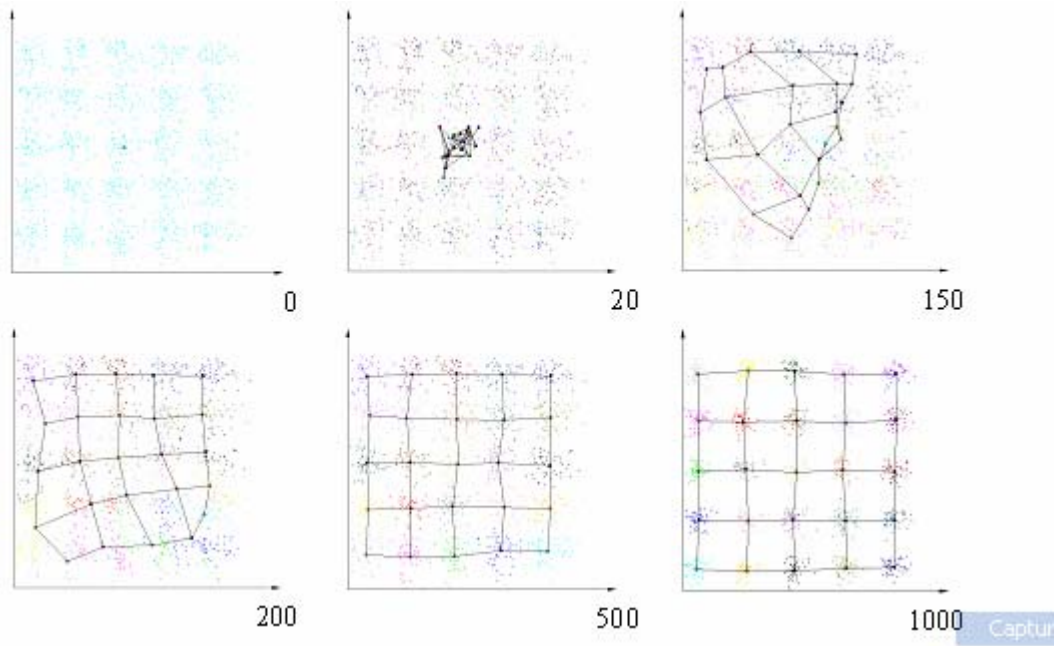


Figure 3: The positions of the cluster centers (or prototypes) during the execution of the ASOM algorithm for a specific architecture (5×5 grid architecture). The numbers at lower right-hand corner indicate the number of iterations.

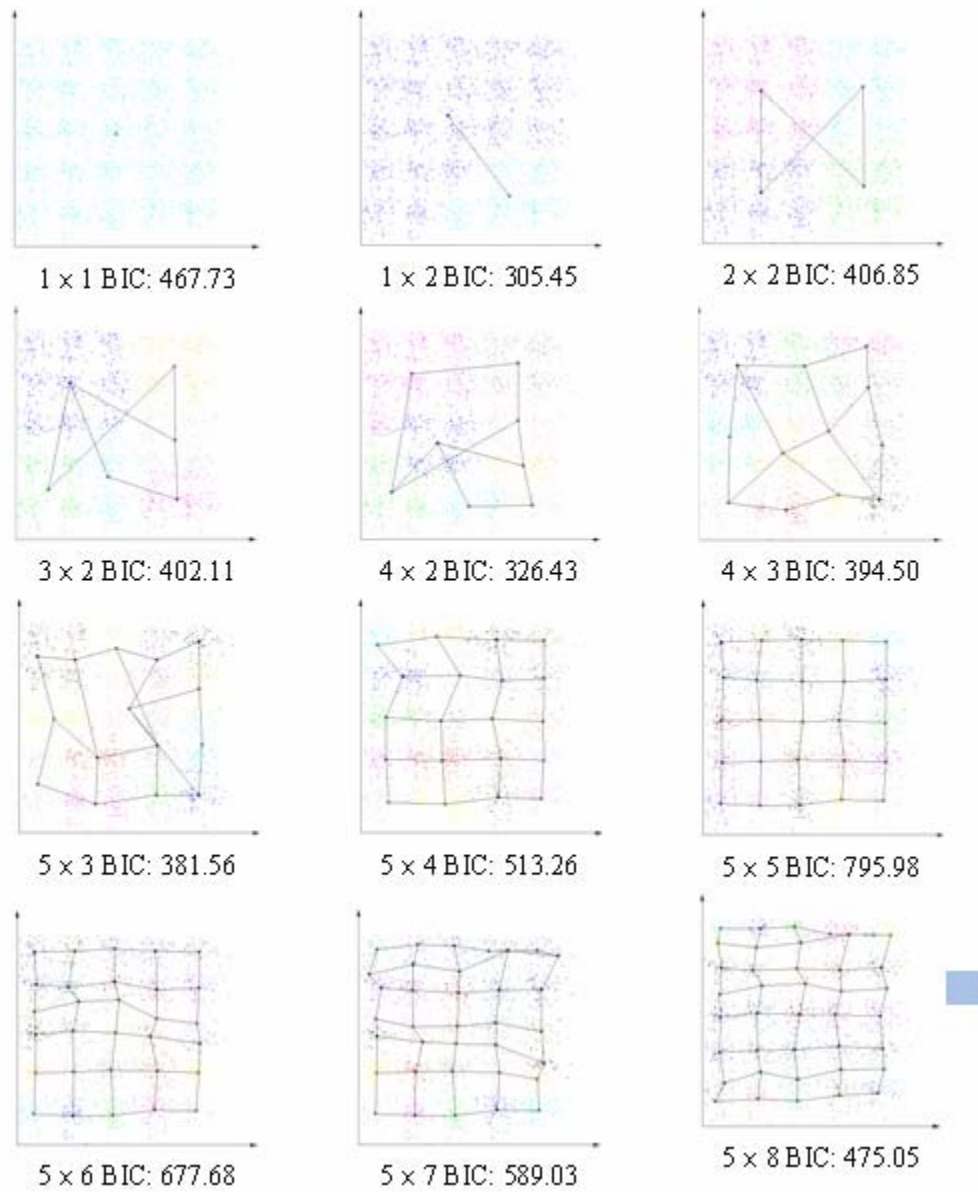


Figure 4: Experiments with data consisting of points in two-dimensional space are shown above. The maximum number of rows and columns were set to 8. The reference vectors are shown as large black dots, and the neighboring cluster centers are connected by an edge. 5×5 squared array. The numbers at lower right-hand corner indicate the architecture and corresponding BIC score.

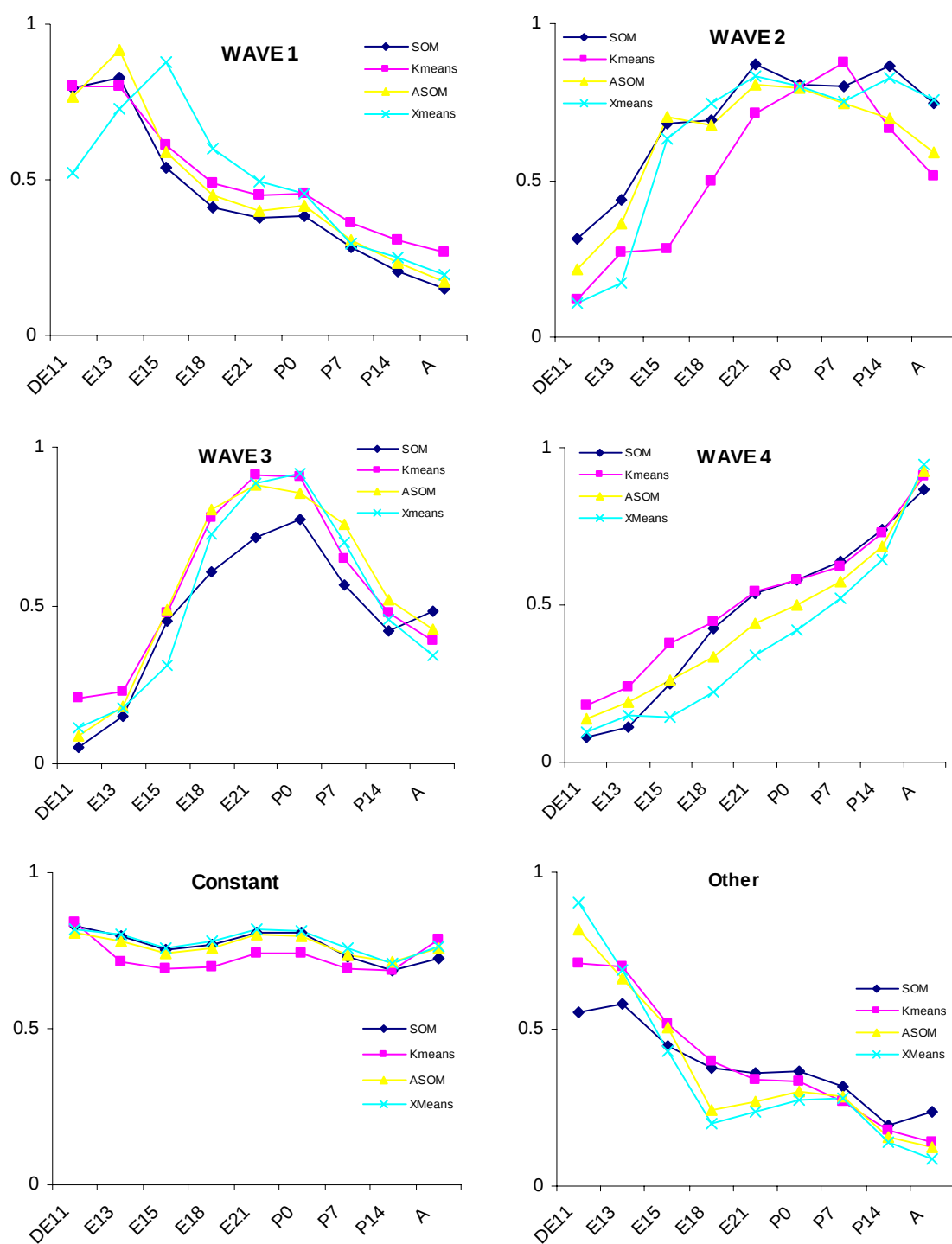


Figure 5: Mean normalized gene expression levels of gene clusters generated by ASOM, SOM, Kmeans, XMeans.

Table 1: Enrichment of ASOM clusters by function category from the gene ontology (GO) database.

Cluster	# of Genes	Enriched functional category(total genes)	Clustered genes	-log10 (p-value)
1	42	nucleic acid binding (37)	16	12
		DNA binding (27)	15	15
2	130	cell proliferation (77)	34	9
		cell cycle (66)	33	10
3	20	cell proliferation (77)	10	5
		cytokinesis (14)	6	6
4	53	helicase activity (17)	11	9
		DNA helicase activity (16)	8	5
5	26	amino acid metabolism (26)	10	9
		transferase activity (67)	7	3
6	86	nucleic acid binding (37)	10	3
		DNA binding (27)	8	3
		transcription regulator activity (37)	8	3
		transcription factor activity (10)	5	3
7	88	cytoplasm organization and biogenesis (79)	15	3
		organelle organization and biogenesis (76)	15	3
8	78	transferase activity(TA) (67)	15	4
		TA, transferring glycosyl groups (15)	5	3