In this paper, FOM was repeatedly applied to 100 sub-samples, where each run considers 95% of the patterns of the original dataset. The 100 runs were combined to obtain the figures shown below. Similar to the automatic methods, the sub-sample scheme allows to analyse the invariance to perturbations of the input. The variability of the adjusted FOM introduces more information about the quality of the clustering solution. The black lines in all plots, panels (a) to (f), connect the median values of the distribution.

Panel (a) of Figure 9 and panels (a) to (f) of Figures 10 and 11 show the results of applying FOM to gene expression datasets from Table II. The (x) axis shows number of cluster and the (y) axis shows the adjusted FOM index (adj. FOM) that informs the adjusted FOM points to the presence of structure when the root mean square deviation in the left-out condition averaged over all left out conditions has a plateau of similar minimum values. The number of clusters is detected when the adjusted FOM has an elbow point.

Fig. 9. FOM output. In these cases FOM was performed using EAC-av as clustering algorithm. Results could only be calculated for (Y), which has 79 condition. The rest of the dataset have 1000 and 2000 conditions/genes and the processing time exceeded 8 hours per iteration, thus it was not possible to finish the analysis.
Fig. 10. FOM output. In these cases FOM was performed using PKNNG-av as clustering algorithm.
Fig. 11. FOM output. In these cases FOM was performed using Spectral Clustering combined with Gaussian kernel as clustering algorithm.