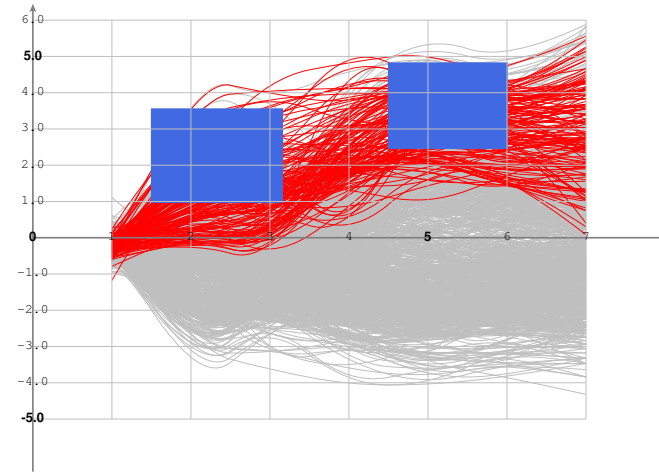
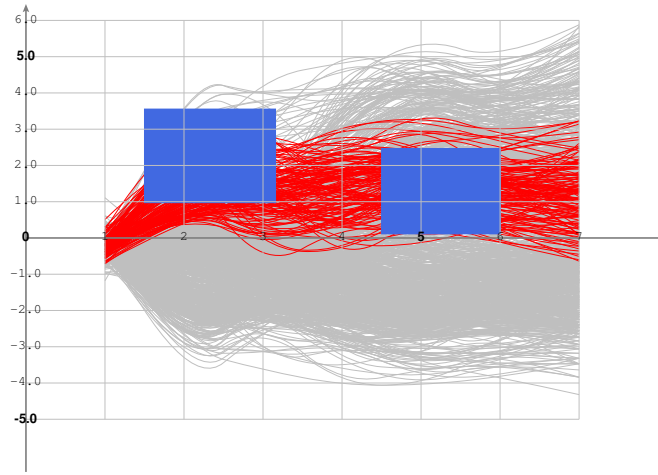


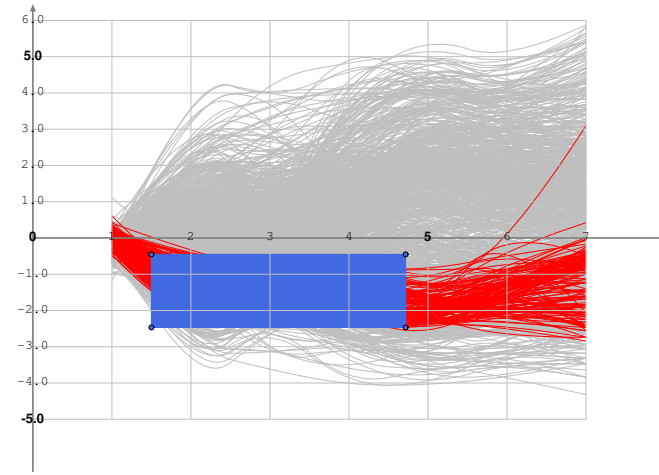
(a) Early up-regulation



(b) Sustained up-regulation



(c) Up- and down-regulation



(d) Down-regulation

Figure 1: We depict query results from a Yeast Sporulation data set. In the first query ((a)), we have 150 genes with early up regulation expression. Functional analysis reveal that these genes are mostly related to meiosis, mitotic cell cycle and metabolism. We make this query more specific by creating a new time box ((b)). Now, our query returns genes that have a sustained up-regulation expression. These are mostly related to meiosis and mitotic cell cycle. By applying a move operation on the second time box, we query for genes with up regulation followed by down-regulation ((c)). These genes have functional relation to metabolism. Lastly, we delete the second time box and move the first time box down to obtain genes with down regulation expression. These genes are mostly related to mitochondrial genes. These functional analysis are in accordance to the analysis performed in the original study [?].