hsa-mir-148a modulated patient survival negatively, and it also indicates that the genes that are not regulated by hsa-mir-148a are not related to survival.

We can use this Bayesian GGM approach as an alternative method to identify target genes for microRNAs. For the group of triplets with Bayes factors supporting the three-way model, casual model, and zero effect model, we can set the gene as one of the target genes of the microRNA in the triplet. We compare the targets of the 437 microRNAs determined by this approach with the targets of microRNAs in the microRNA.org database released in August 2010 (`www.microrna.org/microrna/getDownloads.do`). Target predictions on the website are based on mirSVR (Betel et al., 2010), which is a development of the miRanda algorithm. Of the 437 microRNAs, 222 have target predictions in the database. We calculate the percentage of our target prediction within the target prediction by mirSVR method and find a mean of 56%. This means that the predicted targets by our method are similar to the targets predicted on the basis of the structure of microRNAs.

14.5 Discussion

In this chapter, we have determined the associations among microRNA, gene expression, and patient survival time in TCGA GBM data. We took one feature from a platform to compose a triplet and applied an objective Bayesian model selection approach for GGM to determine significant interactions. In the objective Bayesian model, we used the HIW g-prior, which corresponds to the implied fractional prior in fractional Bayes factors. We calculated the Bayes factors for the data from each triplet given the eight models. Triplets were grouped according to which of the eight graphical models were supported by their Bayes factors. Among the models involving microRNA, the number of triplets in the group supporting the causal model was the highest (Figure 14.3). This result is consistent with the fundamental biological relationship that microRNA modulates gene expression, which then affects patient survival.

Table 14.2 shows that the number is small (14) for the microRNAs involved in the group of triplets with Bayes factor supporting the independent model and the microRNA model. This indicates that although microRNA can directly affect patient survival without modulating gene expression, this is a rare situation.

The GGM estimates for the triplets with the highest Bayes factors compared with the null model are calculated and plotted. For the microRNAs shown in the figures, the estimation results are similar to the results obtained by Srinivasan et al. (2011). By integrating microRNA and gene expression information, we have a better understanding of the relationship among microRNA expression, mRNA expression, and patient survival. We identified some microRNAs that