

CHAPTER 5 CONCLUSIONS AND SUGGESTIONS

5.1 Conclusions

The presence of HERVs, whether in inter- or intragenic regions, is extremely significant to the expression of nearby genes, because of their potential regulatory sequences maintained. However, there is no tool facilitating who are interested in the mentioned issue. HERV Profiler has thus been developed in this work to be responsible for the point. HERV Profiler can facilitate investigations of neighboring HERVs of interested genes by two main features. Visualizing neighboring HERVs of the genes is the first feature provided by HERV Profiler. There are several beneficial characteristics of the neighboring HERVs collected and shown in the visualizing tables. Furthermore, graphical displays are also provided when users get stuff with many characters shown. Another advantageous feature is HERV profiling. The objectives of this feature are to find over-represented HERV types among a gene list and rank genes in a gene list based on their possessing HERVs. Users can retrieve the profiles to analyze outside the tool as well.

In conclusion, HERV Profiler is a powerful tool which can be used in the investigations on the neighboring HERVs of the interested genes. It can be used to observe whether HERVs are likely related to the differentially expressed genes under a study condition. Moreover, HERV Profiler can purpose interesting HERV types and genes based on the hypothesis of being over-represented of the neighboring HERVs.

5.2 Suggestions

(1) The HERV locations relative to genes collected in the HERV Profiler database were limited to only the regions of exons and introns. It could be more beneficial to users in the studies on protein-coding genes if the regions of coding sequences (CDS) and untranslated sequences (UTRs) would be additionally specified and collected in the database.

(2) In the case studies related to SLE, HERV Profiler can be used to purpose candidate HERV types and genes that may be affected by those HERVs under the SLE condition. Therefore, there should be the wet experiments specially designed and performed to prove the candidate HERVs and genes to make the conclusion stronger.