In the publication, iMir utilizes the first version of Cutadapt [step 1], which removes adapter sequences from RNA reads; the standalone miRanalyzer (prerequisite: Bowtie 0.12.8, The ViennaRNA package 1.8.5 and Weka 3.5.3) [steps 2 and 3], which aligns reads to a reference genome; DESeq 1.9 [step 5], which calculates differential expression in its pipeline; gplot(no version given, but 3.0.1.1 is the latest) [step 5], which is used to create diagrams for differential analysis; limma (no version given, but 2.1.1 is the latest) [step5], which is used for performing quantile normalization for differential analysis. Newer versions of these software are available on CGC (Cutadapt 1.1.5, Bowtie2 2.2.6, and DESeq2 1.18.1). Cutadapt and Bowtie are the only two tools that are available in HIVE. ViennaRNA package, gplot, limma and miRanalyzer are not available in CGC. To solve this issue, CGC has tools such as MicroRazerS and RazerS 3 (version 2.3.2) for analyzing miRNA, which replicates steps 2, detection of known miRNAs. All tools are readily available online, and separate emails have been sent to both CGC and HIVE to inform the absence of the tools listed above.