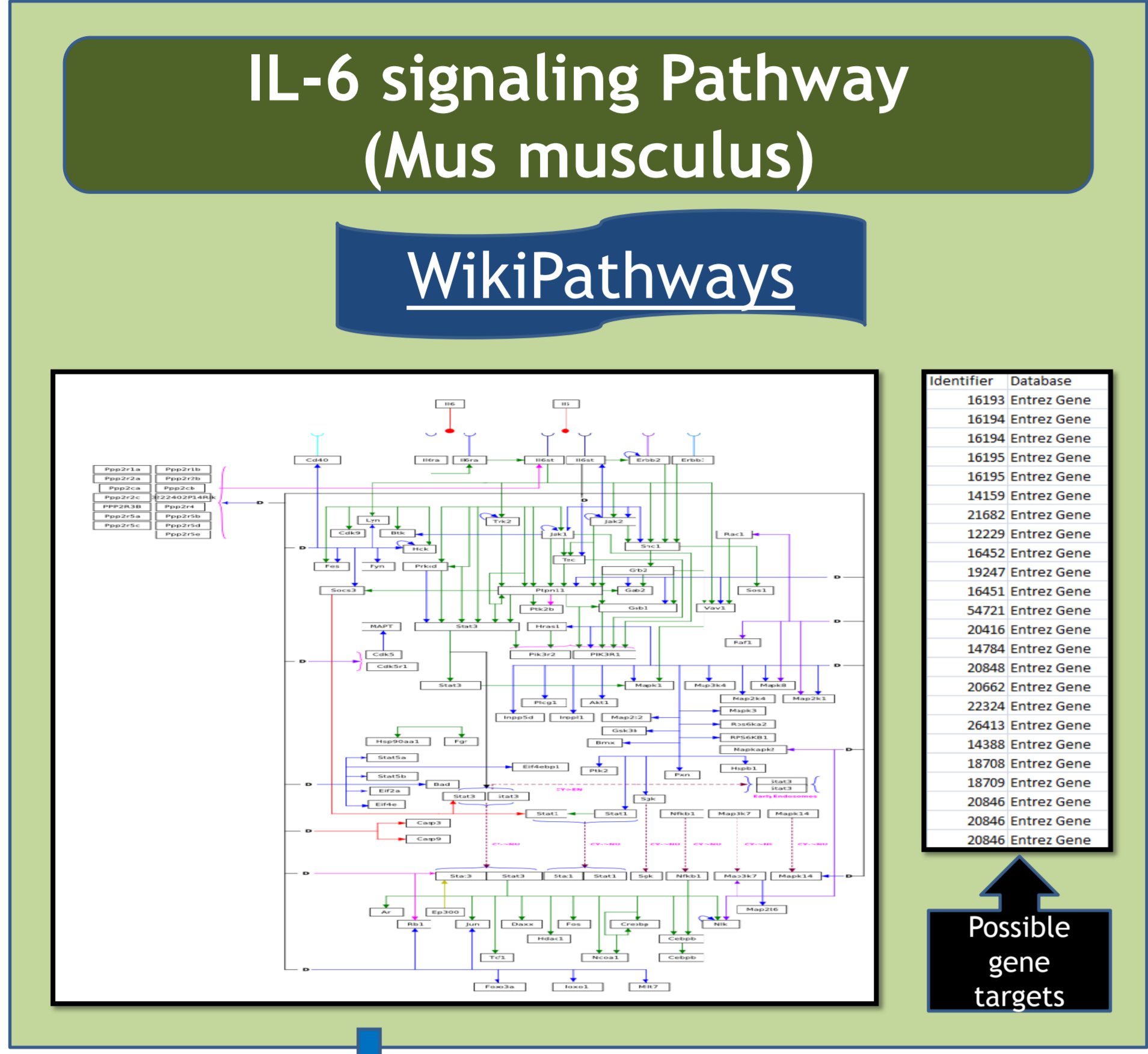


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MicroRNAs are highly conserved and small non-coding RNA molecules. They inhibit protein expression through translational repression or complete degradation and gene silencing. We integrated validated and predicted miRNAs in biological pathways available on [WikiPathways](http://www.wikipathways.org), using miRNA databases. We linked the validated miRNA targets to the genes in the pathways, using [BridgeDb](http://www.bridgedb.org) for identifier mapping. BridgeDb is a software framework that serves as middleware between relational databases, files and mapping services. The resulting pathways can be used to investigate miRNAs expression results from microarray and sequencing technologies. We developed a Bioconductor package (to be submitted) that uses the existing BridgeDb REST web services from R.

We verify the miRNA targets in the pathways by co-evaluating miRNA and mRNA microarray expression data from a mouse heart failure model. We did this using [arrayanalysis.org](http://www.arrayanalysis.org), which currently has quality control and normalization modules. We added modules for statistical and pathway analysis. Pathway visualization was done using [PathVisio](http://www.pathvisio.org) which required connecting R to Java, for which a new XMLRPC interface was developed.

**Conclusion:** we have developed a reusable approach to integrate information about miRNA in pathways and use these for analyses.



This work is a combined effort by the exchange students of Manipal University, India in collaboration with Dept of Bioinformatics-BiGCaT, Maastricht University, Netherlands.

