**Questions to the database:**

* Which miRNA is in which interaction? (values + cut off)
* Which miRNAs are on the edges between the nodes (not only the counts) (value cut off)
* Which genes interact with each other? (+values: with min/max this value /min.correlation filter, p-value, multiple sensitivity corr. MRCorr )
* Which gene interacts with which miRNA? (+values: with min/max this value)
* Which subgraph is possible with selected genes/miRNAs + value cut offs
* Which gene-gene, gene-miRNA interaction is in which cluster?
* Which of these interactions could be important to cancer (survival analysis, clinical data)?
* Which of the genes are hubs? *Definition of hub*! (Eigenvektor centrality, Betweenness centrality, Node degree)
* Biomart (Gene infos / type, lcRNAs, XChromosome inactivation, Paraspeckels)
* Expression data in samples (Heat Map, Environment plot)
* Survival plots (Kaplan Mayer) von genes
* *Sponge gene in other cancer types? in which other cancer types is it*
* Sponge run between cancer type and interactions\_genegene !!!Parameter!!!
* *Future to do:(Gene ontology)*