**Databases and non coding RNAs**

***In silico* prediction of miRNA:gene interactions** (<http://www.microrna.gr/microT-CDS/>)

1. Pick 2 of your favorite Homo sapiens genes and one of the following: CLOCK, MTOR, SIRT1, AKT1, BRCA1, ADIPOQ, PALB2, TNF, TP53, IGF1
   1. Use microT-CDS to predict interactions with your genes and microRNAs
   2. How many interactions are predicted with score >0.8 for your genes?
   3. Can you find interactions with a 9mer seed binding site for each of your genes? With an 8mer?
   4. Can you find binding sites that are conserved in >8 species? In which species are they conserved?
   5. Pick 1 interaction that you find interesting for each gene. Can you describe it? (miRNA involved, number of binding sites, prediction score, conservation for binding sites, regions, etc).
   6. Can you find pathologies that are associated with your selected miRNAs (1 for each gene)? Which are the 2-3 most common?

**Finding experimentally identified miRNA:gene interactions from online databases (**[**http://www.microrna.gr/tarbase/**](http://www.microrna.gr/tarbase/)**)**

1. Search TarBase v8 for experimentally identified interactions of your previously selected genes. Are there such interactions for all your genes?
   1. Are there interactions that are experimentally identified and also predicted?
   2. Find an interaction validated with >3 techniques. Can you find in which tissues/cell lines were these experiments performed?
   3. Are there any negative interactions?
   4. Can you filter them and keep only High Throughput interactions?
   5. Can you keep only interactions supported by PAR-CLIP or Luciferase Reporter assays? Are interactions validated with these two methodologies available for all your genes?

**Identifying miRNA – regulated pathways** [**http://www.microrna.gr/miRPathv3/**](http://www.microrna.gr/miRPathv3/)

1. Use miRPath v3 to analyze the effect of a miRNA of your choice on molecular pathways. Repeat the analysis with interactions derived from DIANA-microT-CDS and DIANA-TarBase. When using interactions from microT-CDS can you also change the score threshold (e.g. 0.75 or 0.6)? Do your results change?
   1. Use again miRPath v3 to analyze the combined effect of hsa-miR-107, hsa-miR-103, hsa-miR-15a, on molecular pathways. Try the different types of miRNA combination: genes union and pathways union.
   2. Click on a pathway and see the targeted genes. How many genes are contained in more than one lists?
   3. Go to KEGG Pathways: <http://www.kegg.jp/kegg/pathway.html> Select 3 of your favorite pathways. Use DIANA-miRPath reverse search module to find the miRNAs having most interactions in these pathways. Use predicted as well as experimental interactions (microT-CDS and miRPath). Are there common miRNAs in these analyses?