

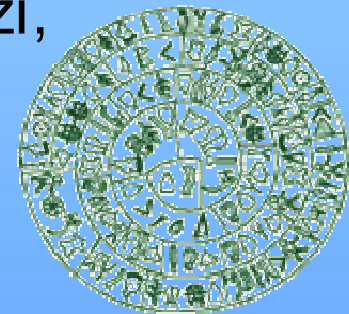


# Development of a miRNA target prediction tool using profile hidden Markov models

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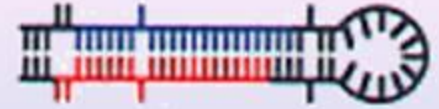


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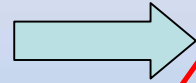


**IMBB**  
**FORTH**

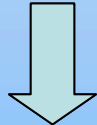
# Targetprofiler prediction flowchart



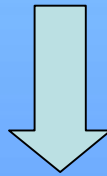
Scanning 3'UTRs  
using sliding  
window



- **Filtering:**
  - conserved in seed region
  - total un-conserved count
  - max conservation stretch
  - 7mer-m8 match
  - long loop stretches



1. Trained HMM  
model  
score >5.9



1. Candidate  
miRNA target  
(Experimental Verification)



PC cluster

# Where are we in comparison to other target prediction tools



Correlation of target predictions with changes in protein production for five miRNAs (*miR-1*, *miR-16*, *miR-30a*, *miR-155*, *let7b*)

prediction algorithm	number of predicted targets mapped to Refseq	number of targets measured by pSILAC	number of down-regulated targets ( $\log_2FC < -0.1$ )	fraction of down-regulated targets ( $\log_2FC < -0.1$ )
TargetScanS	2842	622	381	61%
PicTar	3289	629	386	61%
rna22 on 3'UTRS	4112	723	255	35%
rna22 on 5'UTRS	607	79	20	25%
PITA top 600	3000	325	139	43%
PITA top 1000	5000	572	226	40%
miRbase	3347	658	288	44%
miRanda	8605	1533	715	47%
Diana-MicroT3.0	1678	294	194	66%
Targetprofiler filt. hig	1879	284	190	67%
Targetprofiler filt. low	2398	477	288	61%



# Conclusions



- Computational target prediction – need for improvement
- pSILAC ~5000 proteins, 5 miRNAs
- Targetprofiler on the web
- Experimental verification



**THANK YOU!**

**FOR YOUR ATTENTION!**