



## Integrative Bioinformatics and Systems Biology



Dr. Mohamed Hamed

## LECTURE PLANNING

Lecture: 12 lectures, 3 hrs each.

Total workload: 42 hrs : 36 hrs of lectures and tutorials and 6 hrs of self studies.

Entrance requirements: basic knowledge of biology and computer science.

Literature: Lecture slides, tutorial handouts and problem sets will be provided.

## INTEGRATIVE BIOINFORMATICS AND SYSTEMS BIOLOGY

COURSE ABBREVIATION: INT-BIO

LANGUAGE: ENGLISH

USED MEDIA: POWERPOINT PRESENTATION

Module: Lecture and tutorial.

By: Dr. Mohamed Hamed

Head of the Integrative OMICs Analysis Group in Rostock University medical center, Rostock University, Germany.

## MOTIVATION AND COURSE OBJECTIVES

The main challenge of modern systems biology is unraveling the holistic picture of the complex molecular interactions that occur on different molecular levels (genomic, transcriptomic, epigenomic, proteomic, etc). Therefore, the needs to integrate/jointly analyze biological data from different high-throughput technologies emerged in order to identify biomarkers for early diagnosis and prognosis of complex diseases and facilitating the development of novel treatment approaches.

This course aims at teaching students how to perform data-specific computational analyses as well as integrative analysis approaches, combining knowledge from different OMICs-based datasets. Both, theoretical and practical aspects will be covered. Students will have the opportunity to work both independently during tutorials and in teams during the research project.

## COMPETENCES TO BE DEVELOPED

Students will get practical and extensive hands-on experience on:

- R scripting language and bioconductor packages.
- Data-specific computational analysis and pipelines for the vast amounts of biological data produced using high-throughput technologies.
- Developing and applying integrative bioinformatics methods that could be utilized in all biology-related areas of interest.
- Basics of machine learning methods as tools for integrating biological features from heterogeneous Omics data.
- Students will be developing their own research projects, interpreting the obtained results, writing a manuscript, scientifically discussing the results.

## ASSESSMENT

- Students need to finalize a research project applying all/ most of the learned methods and skills during the course. Novelty and extending the learned methods is highly encouraged and will be well graded.
- The outcomes of each research project should be compiled in a high scientific quality research article that is ready for submission in a peer-review journal.
- All projects will be presented, discussed and scientifically reviewed in the last lecture.

### R language mini-course 1

-Introduction to the course

-Basics of R language and statistical methods.

-R studio IDE

### R language mini-course 2

-Advanced R statistics

-Bio-conductor packages

### R language mini-course 3

-Case study:

Microarray analysis using R

### Introduction to integrative bioinformatics

-Importance of data integration

-Different methods for biological data integration

-OMICs data types, and TCGA repository

-Databases of diseases-related genes and miRNAs

### Transcriptomic analysis

-From microarrays to RNA-seq

-RNA-seq analysis

-Linking to Ontologies and pathways

-Drug signature databases: CMAP and LINKS

### Non-coding RNAs

-Small and long non-coding RNAs

-miRNA sequencing analysis

-miRNA databases

-lncRNAs analysis

### Network- based integrative methods

-TFmiR analysis

-Network motif analysis

-Central hubs identifications

- Network visualization (Cytoscape )

### Epigenetics

-Introduction to the epigenetic landscapes of normal and tumor cells

-DNA methylation, Co-methylation analysis

-DMRs identifications

### Chip-seq experiments and/or GWAS

-Computational analysis of Chip-Seq data and/or

-Downstream analysis of genetic variants

### Integrative analysis based on machine learning.

-Introduction to machine learning in bioinformatics.

-Unsupervised methods: Clustering biological data  
-PCA analysis

### Supervised machine learning methods

-Classification and regression analysis

-Model selection and evaluation of learning methods

-Outlook at deep neural networks applications in bioinformatics

### PROJECTS DISCUSSION AND CLOSURE

-Projects presentation.

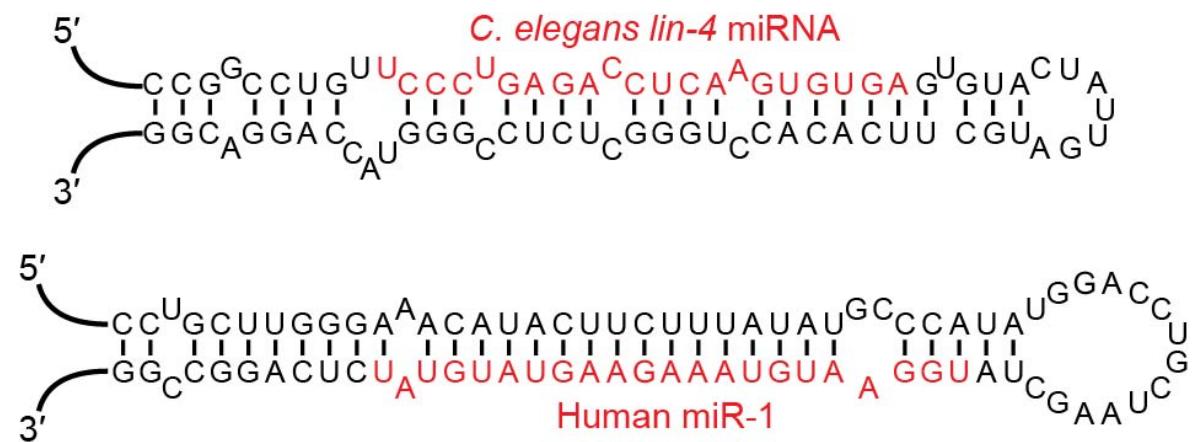
-Reviews of the potential manuscripts

# Lecture 7

## Practical miRNA-Seq using R

# Structure

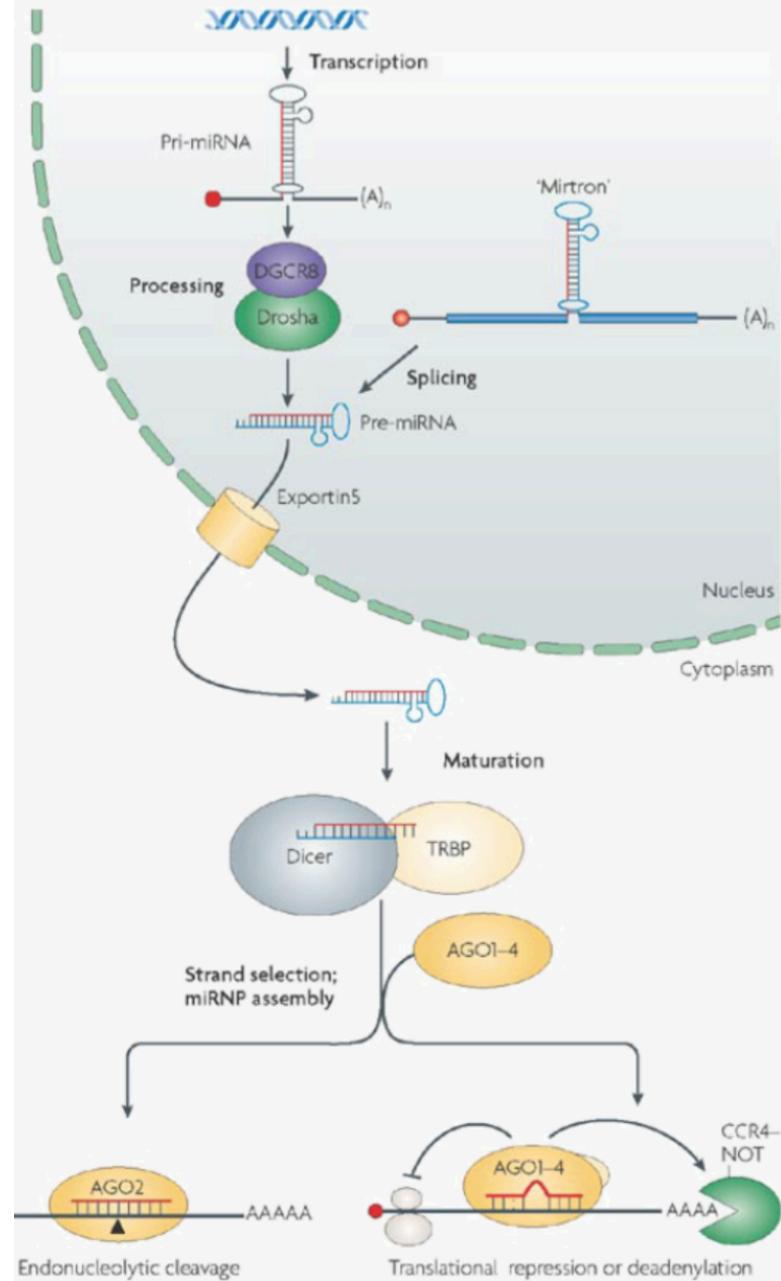
- Small non-coding RNAs (17-23 nucleotides length)
- Very stable and conserved across organisms
- Per ~120 base precursor molecule transcribed from the genome usually two mature forms are build and exported from nucleus, -3p and -5p



# From Precursor to mature miRNAs

- Transcription of the pre-miRNAs is done via the RNA-Polymerase II
- The pre-miRNAs can contain multiple miRNA sequences in their hairpin structure
- The typical hairpin-structure is due to two symmetrical strands.
- The pre-miRNAs are exported from the nucleus to the cytoplasm via Exportin5
- DICER splices out the loop-structures of the pre-miRNA.

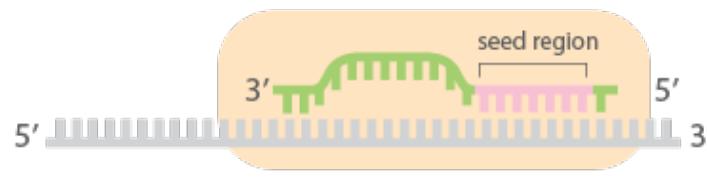
Result is the mature miRNA



# Gene repression by miRNAs

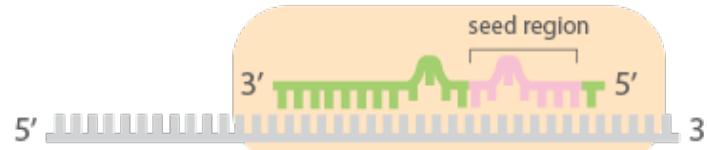
- miRNAs often repress target genes through translational silencing of the mRNA or through degradation of the mRNA, via complementary binding to specific sequences in the 3' UTR region of the target gene's transcript.

## miRNA Seed Region Binding



abm<sup>®</sup>

Perfect binding to mRNA

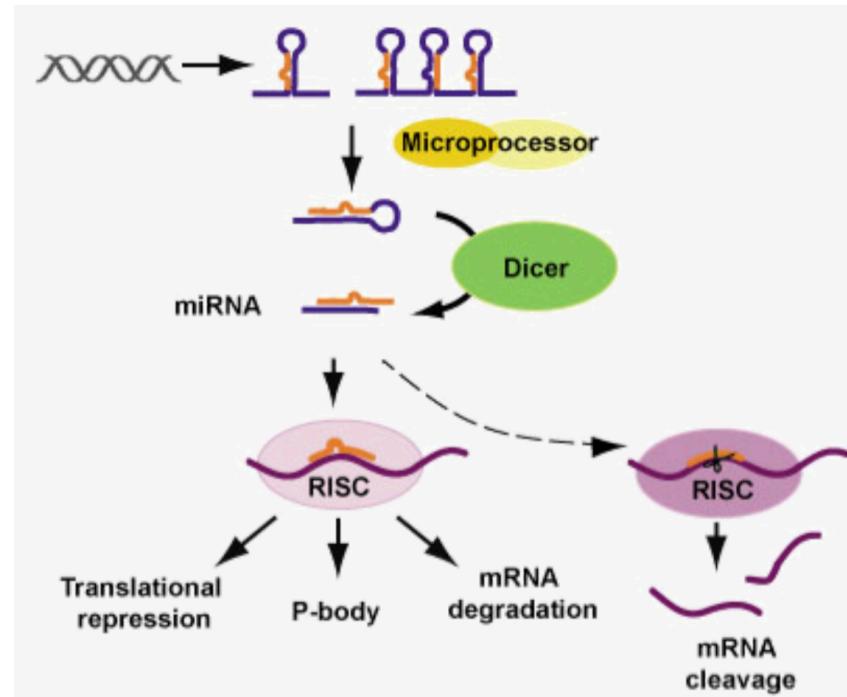


Translational  
Inhibition

Imperfect binding to mRNA

# Biology

- There are more than 20,000 miRNAs in >100 species are known
- In *homo sapiens*, there are more than 2000 annotated miRNAs
- These build 0.0002% of the human genome
- These miRNAs are regulating more than 70% of genes and majority of biochemical pathways



# Potential

- miRNAs are tissue specific molecules : expressed specifically in tissues and body fluids .
- Can explain the regulatory mechanisms of complex biological and cellular functions.
- Their biological functions still not completely revealed.
- Have high potential as diagnostic and prognosis biomarkers.

# Potential

- A miRNA can target a plethora of mRNAs, creating a post-transcriptional regulatory network that has a critical role not only in cellular functions but also in pathological processes especially in human cancerogenesis.
- A considerable amount of literature has been published on miRNA-related mutations and on the impact of somatic mutations on miRNA functions.
- These studies have reported that genetic variants within miRNAs or their target sites can alter miRNA function in cancers and have been associated with cancer risk, treatment efficacy and patient prognosis, as well as genomic phenotypes.

# miRNA Nomenclature

- precursor miRNAs
  - Organism identifier, 3 letters
  - miR (some older “let”)
  - miR identifier (may be specific for family)
  - Single character for similar sequences which usually denotes family members
- mature miRNAs
  - -5p
  - -3p
  - Former: \*

hsa-miR-181c-5p

# miRNA Nomenclature

miRNA Names	Notes on Nomenclature
hsa-miR-XX vs. mmu-miR-XX vs. rno-miR-XX	The first three letters indicate the organism the miRNA is found in. hsa = human, mmu = mouse, rno = rat.
hsa-mir-XX vs. hsa-miR-XX	Capitalization indicates whether it is the mature or precursor miRNA. mir = precursor sequence, miR = mature sequence.
hsa-miR-XX-5p vs. hsa-miR-XX-3p	The guide and passenger miRNAs processed from the pre-miRNA. The guide miRNA is found in higher abundance than the passenger miRNA. Older alternative to the -5p and -3p nomenclature.
hsa-miR-XX-1 vs. hsa-miR-XX-2 vs. hsa-miR-XX	Mature miRNA sequences that are identical, but are originally transcribed from different genes and have distinct precursor sequences. As the sequences are identical, they may be referred to without the numerical suffix.
hsa-mir-XX-1 vs. hsa-mir-XX-2	Precursor miRNAs that are different, but are processed into an identical miRNA.
hsa-miR-XXa vs. hsa-miR-XXb	Closely related mature miRNAs (differ by only one or two nucleotides).

# NGS applications

## DNA

Whole human genome sequencing  
Exome sequencing  
Gene panel sequencing  
Pathogene sequencing

SNP calling  
INDEL calling  
Copy Number Variations  
Genomic Rearrangements

## Others

interactions of proteins with DNA (ChIP seq)  
interactions of proteins with RNA (PAR-CLIP)  
Bisulfite sequencing (methylation)

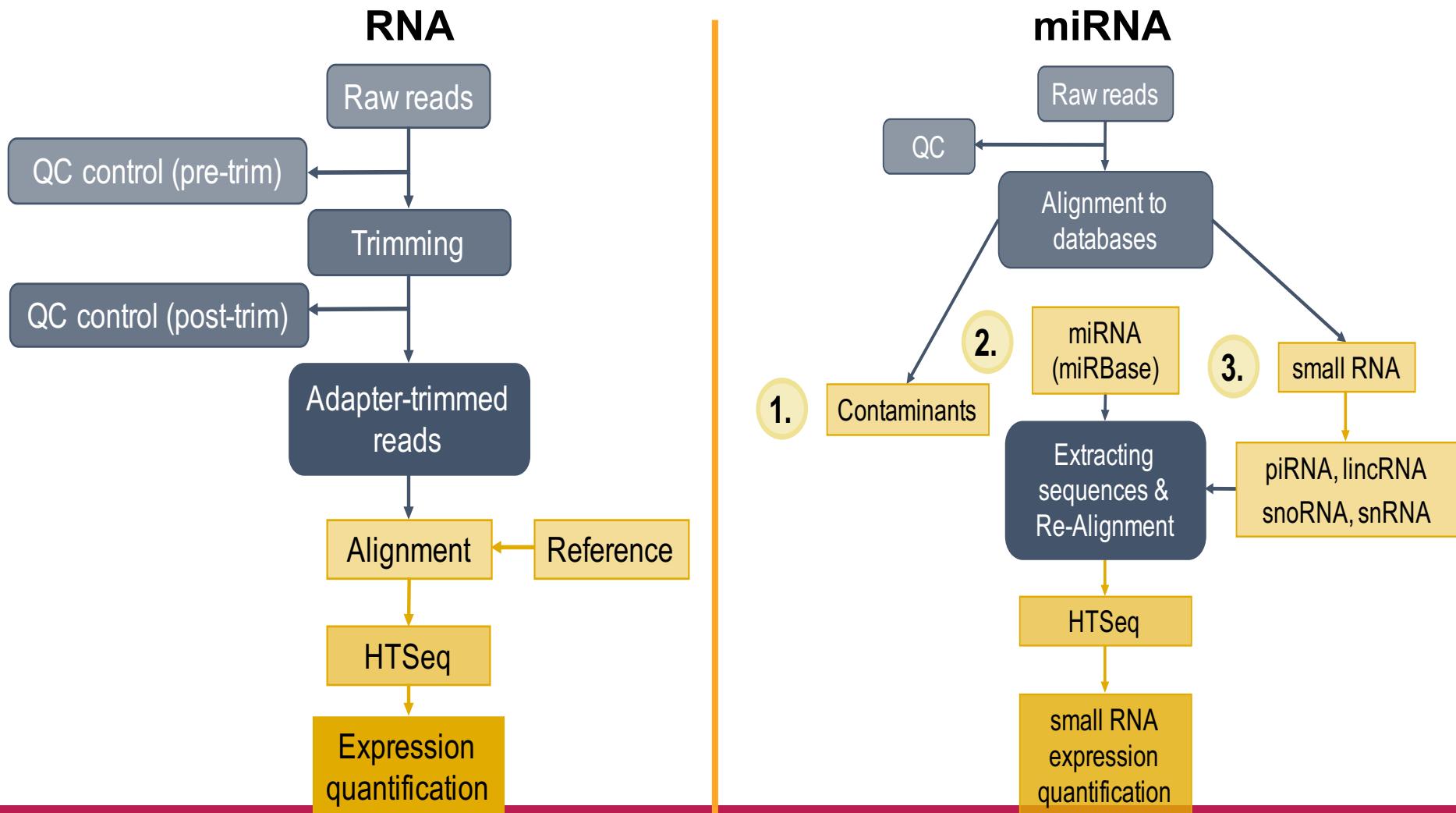
## RNA

Transcriptome sequencing  
miRNOMe sequencing

Expression level  
Alternative splicing events  
Fusion genes

# A pre-processing pipelines in practice

13



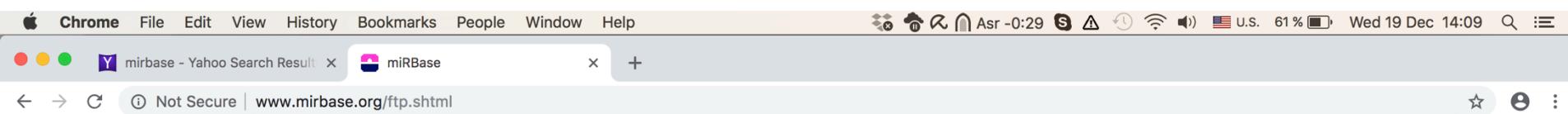
# Detecting novel miRNAs (miRDeep)

- Basic idea of miRDeep: miRDeep detects miRNAs by analyzing how sequenced RNAs are compatible with how miRNA precursors are processed in the cell

## Functionality:

- Run miRDeep on own data to detect known and novel miRNAs
- Quantification of miRNAs
- Estimation of false positive rate of novel miRNAs

# miRNA annotation



## miRBase

MANCHESTER 1824

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### miRBase Sequence Download

- ▶ [Go to the FTP site](#)
- ▶ [Previous releases](#)
  
- ▶ [README](#) Release notes - read these first!
- ▶ [miRNA.dat](#) all published miRNA data in EMBL format
- ▶ [hairpin.fa](#) Fasta format sequences of all miRNA hairpins
- ▶ [mature.fa](#) Fasta format sequences of all mature miRNA sequences
- ▶ [miRNA.diff](#) Changes between the last release and this
- ▶ [miRNA.dead](#) List of entries that have been removed from the database

### Genome coordinates

<a href="#">aae.gff3</a>	<a href="#">ame.gff3</a>	<a href="#">ath.gff3</a>	<a href="#">bmo.gff3</a>	<a href="#">bta.gff3</a>	<a href="#">cbr.gff3</a>	<a href="#">cel.gff3</a>	<a href="#">cfa.gff3</a>
<a href="#">cre.gff3</a>	<a href="#">dme.gff3</a>	<a href="#">dps.gff3</a>	<a href="#">dre.gff3</a>	<a href="#">ebv.gff3</a>	<a href="#">fru.gff3</a>	<a href="#">gga.gff3</a>	<a href="#">hcmv.gff3</a>
<a href="#">hsa.gff3</a>	<a href="#">kshv.gff3</a>	<a href="#">mdo.gff3</a>	<a href="#">mghv.gff3</a>	<a href="#">mml.gff3</a>	<a href="#">mmu.gff3</a>	<a href="#">osa.gff3</a>	<a href="#">ptc.gff3</a>
<a href="#">ptr.gff3</a>	<a href="#">rno.gff3</a>	<a href="#">sme.gff3</a>	<a href="#">tni.gff3</a>	<a href="#">vvi.gff3</a>	<a href="#">xtr.gff3</a>	<a href="#">zma.gff3</a>	

Comments, questions? Email [mirbase@manchester.ac.uk](mailto:mirbase@manchester.ac.uk)



# Predictions of miRNA Target interactions

Based mainly on two methods:

- inverse correlation between the expression profiles of the miRNA and the potential target genes
- Sequence similarity

# Predictions of miRNA Target interactions

- Main/ common algorithms for predicting miRNA targets

miRNA	Target Gene		Predictions										
			DIANA-microT	Micro Inspector	miRanda	Mir Target2	mi Target	NB miRTar	Pic Tar	PITA	RNA 22	RNA hybrid	TargetScan/ TargetScanS
Mature ID	Symbol	RefSeq	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hsa-let-7f	ADRB2	NM_000024	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	COL3A1	NM_000090	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	CYP19A1	NM_000103	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	GDF6	NM_001001557	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	LIN28B	NM_001004317	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	TGFBR1	NM_004612	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	COIL	NM_004645	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	SLC20A1	NM_005415	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	ABCC5	NM_005688	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	PBX3	NM_006195	●	●	●	●	●	●	●	●	●	●	●
hsa-let-7f	IGF2BP3	NM_006547	●	●	●	●	●	●	●	●	●	●	●

# Survey on miRNA useful tools/dbs

- <http://www.tamirna.com/resources/usefulmicrornatools.html>

# microRNA target prediction tools

## miRDB

miRDB is an online database for miRNA target prediction and functional annotations. All the targets in miRDB were predicted by a bioinformatics tool, MirTarget, which was developed by analyzing thousands of miRNA-target interactions from high-throughput sequencing experiments. Common features associated with miRNA target binding have been identified and used to predict miRNA targets with machine learning methods. miRDB hosts predicted miRNA targets in five species: human, mouse, rat, dog and chicken.

## TargetScan

TargetScan predict regulatory targets of vertebrate microRNAs (miRNAs) by identifying mRNAs with conserved complementarity to the seed (nucleotides 2-7) of the miRNA. An over-representation of conserved adenosines flanking the seed complementary sites in mRNAs indicates that primary sequence determinants can supplement base pairing to specify miRNA target recognition.

## PicTar

PicTar is a computational method for identifying common targets of microRNAs. Statistical tests using genome-wide alignments of eight vertebrate genomes, PicTar's ability to specifically recover published microRNA targets, and experimental validation of seven predicted targets suggest that PicTar has an excellent success rate in predicting targets for single microRNAs and for combinations of microRNAs.

## RNA-hybrid

RNA-hybrid predicts multiple potential binding sites of miRNAs in large target RNAs. In general, the program finds the energetically most favorable hybridization sites of a small RNA in a large RNA.

## miRIAD

miRIAD is a web search tool developed with the primary purpose of integrating relevant information concerning intragenic miRNAs and their host genes.

## DIANA-mirPath

DIANA-mirPath can utilize predicted miRNA targets (in CDS or 3'-UTR regions) provided by the DIANA-microT-CDS algorithm or even experimentally validated miRNA interactions derived from DIANA-TarBase. These interactions (predicted and/or validated) can be subsequently combined with sophisticated merging and meta-analysis algorithms.

## miRTar.human

miRTar is a tool that enables easily to identify the biological functions and regulatory relationships between a group of known/putative miRNAs and protein coding genes. It also provides perspective of information on the miRNA targets on alternatively spliced transcripts.

## miRmap

Includes experimentally verified miRNAs and their targets, also contains RNAhybrid and TargetScan target prediction module.

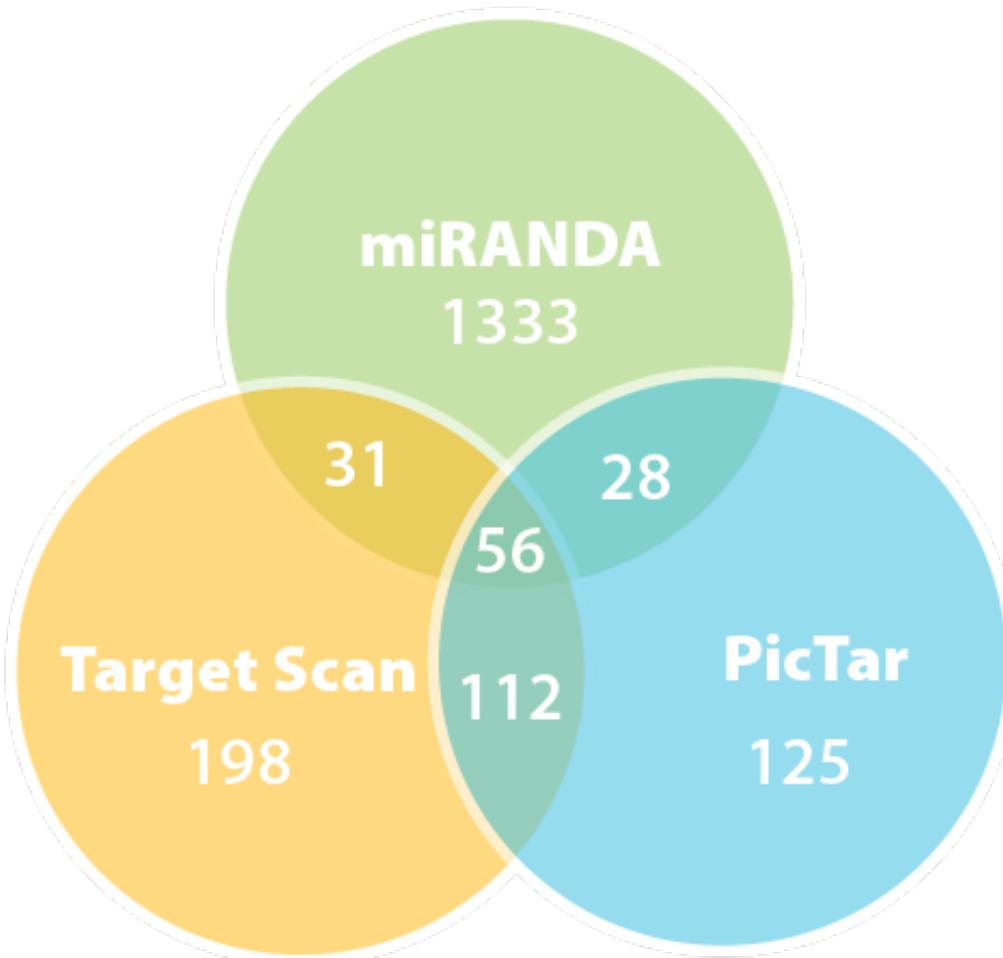
## StarMir

Software for statistical folding of nucleic acids and studies of regulatory RNAs based on CLIP data (sequence, thermodynamic and target structure features).

## ComiRNet

# Shortlisting the miRNA targets

To narrow down a list of potential miRNA targets, one can combine the results of multiple target prediction programs. The most likely targets are shared amongst all sets of results.



# miRNA Target databases I

Search

## miRTarBase



Home

Search

Browse

Statistics

### miRTarBase: the experimentally validated microRNA-target interactions database

As a database, miRTarBase has accumulated more than three hundred and sixty thousand miRNA-target interactions (MTIs), which are collected by manually surveying pertinent literature after NLP of the text systematically to filter research articles related to functional studies of miRNAs. Generally, the collected MTIs are validated experimentally by reporter assay, western blot, microarray and next-generation sequencing experiments. While containing the largest amount of validated MTIs, the miRTarBase provides the most updated collection by comparing with other similar, previously developed databases.

# miRNA Target databases I



Home Search Browse Statistics Help Download Contact Us

Release 7.0

## miRTarBase Download

[MTI.xlsx](#) All published miRNA target interaction data in EXCEL format

## MTI PubMed Abstract Manually Curation Corpus

[MTI-PubMed\\_corpus.txt](#) Manually curation of miRNA and target genes, and their relations in PubMed abstracts [README](#)

## MicroRNA Target Sites Provided by Original Literatures

[MicroRNA\\_Target\\_Sites.xlsx](#) Manually curation of miRNA and target sites, and the target sites were provided by original literatures

## Catalog by Species

<a href="#">ath_MTI.xls</a>	Arabidopsis thaliana
<a href="#">bmo_MTI.xls</a>	Bombyx mori
<a href="#">bta_MTI.xls</a>	Bos taurus
<a href="#">cel_MTI.xls</a>	Caenorhabditis elegans
<a href="#">cfa_MTI.xls</a>	Canis familiaris
<a href="#">cgr_MTI.xls</a>	Cricetulus griseus
<a href="#">dme_MTI.xls</a>	Drosophila melanogaster
<a href="#">dre_MTI.xls</a>	Danio rerio

# miRNA Target databases II

The screenshot shows the miRecords website. At the top, there's a green header bar with the "miRecords" logo. Below it is a grey navigation bar with links: "Validated Targets", "Predicted Targets", "Download Validated Targets", "Submit Data", "Documentation", "Disclaimer", "siRecords", and "Biolead.org". On the left side, there's a box titled "Updated!" containing the message: "miRecords was last updated on April 27, 2013." Below this is a larger box titled "About miRecords" which contains detailed text about the database's components and history. On the right side, there's a large green "Download" button with the text "Thanks for your interest in the miRecords data. The current release (April 27, 2013) of the Validated Target dataset can be downloaded [here](#)."

**Updated!**  
miRecords was last updated on April 27, 2013.

**About miRecords**

miRecords is a resource for animal miRNA-target interactions. miRecords consists of two components. The *Validated Targets* component is a large, high-quality database of experimentally validated miRNA targets resulting from meticulous literature curation. The *Predicted Targets* component of miRecords is an integration of predicted miRNA targets produced by 11 established miRNA target prediction programs.

As of April 27, 2013, the *Validated Targets* component of miRecords hosts 2705 records of interactions between 644 miRNAs and 1901 target genes in 9 animal species. Among these records, 2028 were curated from "low throughput" experiments.

The *Predicted Targets* component of miRecords integrates the predicted targets of the following miRNA target prediction tools: [DIANA-microT](#), [MicroInspector](#), [miRanda](#), [MirTarget2](#), [miTarget](#), [NBmiRTar](#), [PicTar](#), [PITA](#), [RNA22](#), [RNAhybrid](#), and [TargetScan/TargetScanS](#).

**Download**

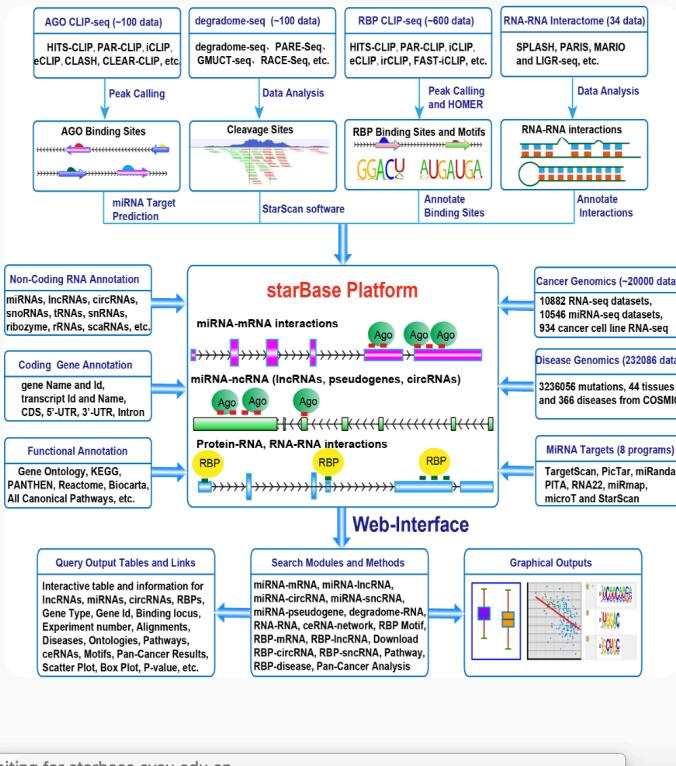
Thanks for your interest in the miRecords data. The current release (April 27, 2013) of the Validated Target dataset can be downloaded [here](#).

# miRNA Target databases III

Home miRNA-Target ▾ Degadome-RNA ▾ RNA-RNA ▾ ceRNA-Network ▾ RBP-Target ▾ RBP-Motif RBP-Disease Pathway ▾ Pan-Cancer

Web API Help ▾ starBase2

## Welcome to starBase!



**starBase v3.0 is an open-source platform for studying the miRNA-ncRNA, miRNA-mRNA, ncRNA-RNA, RNA-RNA, RBP-ncRNA and RBP-mRNA interactions from CLIP-seq, degradome-seq and RNA-RNA interactome data.**

In summary, starBase v3.0 identifies more than 1.1 million miRNA-ncRNA, 2.5 million miRNA-mRNA, 2.1 million RBP-RNA and 1.5 million RNA-RNA interactions from multi-dimensional sequencing data.

Accompany with gene expression data of 32 types of cancers which are derived from 10,882 RNA-seq and 10,546 miRNA-seq data, starBase v3.0 allows researchers performing Pan-Cancer analysis on RNA-RNA and RBP-RNA interactions. starBase v3.0 also provides platforms to perform the survival and differential expression

### starBase Citations

- >1800 Citations in Google Scholar
- Average Daily Usage: ~5000 visits from ~500 unique researchers
- Average Annual Usage: >1,000,000 visits from >100 countries

### Statistics of starBase v3.0 (2018 update)

- Species: 23 Species
- CLIP-seq data: >700 datasets
- Degadome-seq: 100 datasets
- RNA-RNA interactome: >30 datasets
- RNA-seq data: >10,800 samples from 32 cancer types
- miRNA-seq data: >10,500 samples from 32 cancer types
- Disease data: >3,236,000 mutations from 366 disease types
- miRNA-ncRNA(CLIP): >1,100,000 interactions
- miRNA-mRNA(CLIP): >2,500,000 interactions
- RBP-mRNA: >1,208,900 interactions
- RBP-ncRNA: >117,000 interactions
- RNA-RNA: >1,530,000 interactions
- miRNA-ncRNA(degradome): >32,000

# microRNA databases

## miRBase

The miRBase database is a searchable database of published miRNA sequences and annotation. Each entry in the miRBase Sequence database represents a predicted hairpin portion of a miRNA transcript (termed mir in the database), with information on the location and sequence of the mature miRNA sequence (termed miR). Both hairpin and mature sequences are available for searching and browsing, and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also available for download.

## miRBase Tracker

An easy-to-use online database that keeps track of all historical and current miRNA annotation present in the miRBase database.

## FirePlex Discovery Engine

The FirePlex Discovery Engine assembles a list of the most important microRNAs and associated genes from the scientific literature for any keyword or topic, putting years of research at your fingertips in seconds.

## miROrtho

miROrtho contains predictions of precursor miRNA genes covering several animal genomes combining orthology and a Support Vector Machine. It provides homology extended alignments of already known miRBase families and putative miRNA families.

## DIANA tools

DIANA-TarBase v8.0 is a reference database devoted to the indexing of experimentally supported microRNA (miRNA) targets. Its eighth version is the first database indexing >1 million entries, corresponding to ~670 000 unique miRNA-target pairs. The interactions are supported by >33 experimental methodologies, applied to ~600 cell types/tissues under ~451 experimental conditions. It integrates information on cell-type specific miRNA-gene regulation, while hundreds of thousands of miRNA-binding locations are reported.

## miRCancer : microRNA Cancer Association Database

miRCancer provides comprehensive collection of microRNA (miRNA) expression profiles in various human cancers which are automatically extracted from published literatures in PubMed. Search by cancer names or the on-site sequence analysis tools is possible.

## miRWalk

The new version of miRWalk stores predicted data obtained with a machine learning algorithm including experimentally verified miRNA-target interactions. The focus lies on accuracy, simplicity, user-friendly design and mostly up to date informations.

## omiRas

omiRas provides an interface to generate a miRNA-mRNA interaction network for user selected microRNAs. Interactions between genes and miRNAs are determined by the intersection of 7 databases (TargetScan, miRanda, PICTAR, PITA, miRDB, TarBase, miRConnect).

# Useful tools for miRNA research

**DIANA TOOLS**

HOME SOFTWARE PUBLICATIONS CONTACT

**WEB SERVICES**

**Web Services at DIANA-LAB**  
DIANA-LAB enables access to the tools and data resources via Web Service Technologies. REST services are now provided for [mirPath](#), [microT v4](#), [microT-CDS](#) and [Tarbase v6.0](#). All REST Services can be accessed directly from the website, programmatically, by downloading our [DIANA Taverna Plug-in](#). Our REST Services have also been deposited in the BioCatalogue repository, where detailed information for their usage is provided ([here](#)).

**SOFTWARE TO DOWNLOAD**

**DIANA Taverna Plug-in**

**WEB APPLICATIONS**

**microCLIP**  
An AGO-CLIP-guided algorithm for the identification of transcriptome-wide miRNA-target interactions.

**TarBase v.8 - NEW!**  
A database of experimentally supported miRNA:gene interactions.

**microT-CDS - UPDATED!**  
Search for targets of annotated miRNAs based on the popular microT-CDS algorithm.

**MirPath v.3**  
A miRNA pathway analysis Web server.

**LncBase v.2**  
Elaborated info for predicted & exp. verified miRNA-IncRNA interactions.

**Automated Pipelines**  
Pipelines to analyse user data from small scale & high-throughput experiments.

**MR-microT (beta) UPDATED!**  
Near-real time miRNA target prediction on the Cloud.

**mirPub**  
Search for miRNA-related publications.

**miRGen v.3**  
Accurate characterization of miRNA promoters & their regulators.

**MirExTra v.2.0**  
Uncovering microRNAs and transcription factors with crucial roles in NGS expression data.

**Older Versions**

# Enrichment analysis of miRNA



[BMC Bioinformatics](#). 2010; 11: 419.

Published online 2010 Aug 9. doi: [10.1186/1471-2105-11-419](https://doi.org/10.1186/1471-2105-11-419)

PMCID: PMC2924873

PMID: 20696049

## TAM: A method for enrichment and depletion analysis of a microRNA category in a list of microRNAs

Ming Lu,<sup>1</sup> Bing Shi,<sup>1,2</sup> Juan Wang,<sup>1</sup> Qun Cao,<sup>1</sup> and Qinghua Cui<sup>✉1</sup>

► Author information ► Article notes ► Copyright and License information [Disclaimer](#)

This article has been [cited by](#) other articles in PMC.

### Abstract

Go to:

### Background

MicroRNAs (miRNAs) are a class of important gene regulators. The number of identified miRNAs has been increasing dramatically in recent years. An emerging major challenge is the interpretation of the genome-scale miRNA datasets, including those derived from microarray and deep-sequencing. It is interesting and important to know the common rules or patterns behind a list of miRNAs, (i.e. the deregulated miRNAs resulted from an experiment of miRNA microarray or deep-sequencing).

# Enrichment analysis of miRNA



## Description

**miRTrail** allows you to easily analyse for potential relationships between a set of miRNAs and a set of mRNAs.

This enables you to assess possible important implications of the miRNAs on the given disease.

In its actual implementation, miRTrail supports human RNAs. Future versions may integrate RNAs of other species.

**UPDATE:** miRTrail now offers support for:

- mouse and zebrafish
- custom miRNA - target mRNA interactions

Uses **GeneSymbols** as identifiers for the mRNAs and **miRBase** for the microRNAs, respectively.



**YOUR TURN  
START WITH THE TUTORIALS**