## The case...

- Manos is a PhD student in BSRC A. Fleming, GR, starting his research on microRNAs.



## The case...

## The case...

MicroRNAs (miRNAs) are short ribonucleic acid (RNA) molecules, on average only 22 nucleotides.


## The case...

MicroRNAs (miRNAs) are short ribonucleic acid (RNA) molecules, on average only 22 nucleotides.


## Target prediction???

Need to f nd some papers!


Prof. says: "they bind to complementary sequences on
target messenger RNA transcripts (mRNAs), usually resulting in translational repression and gene silencing".

## The case...

MicroRNAs (miRNAs) are short ribonucleic acid (RNA) molecules, on average only 22 nucleotides.


## Target prediction???

Need to f nd some papers!


Prof. says: "they bind to complementary sequences on target messenger RNA transcripts (mRNAs), usually resulting in translational repression and gene silencing".


Found some papers in Google!

## The case...

MicroRNAs (miRNAs) are short ribonucleic acid (RNA) molecules, on average only 22 nucleotides.


## Target prediction???

Need to f nd some papers!


Prof. says: "they bind to complementary sequences on target messenger RNA transcripts (mRNAs), usually resulting in translational repression and gene silencing".


Found some papers in Google!


DIANA microT

TargetScan

## The case...

MicroRNAs (miRNAs) are short ribonucleic acid (RNA) molecules, on average only 22 nucleotides.


## Target prediction???

Need to f nd some papers!

|  | Prof. says: "they bind to |
| :--- | :--- |
| complementary sequences on |  |
| ens | target messenger RNA |
| transcripts (mRNAs), usually |  |
| resulting in translational |  |
| repression and gene silencing". |  |



Found some papers in Google!

Good Idea!!
DIANA microT
TargetScan

## The case...

MicroRNAs (miRNAs) are short ribonucleic acid (RNA) molecules, on average only 22 nucleotides.

Computational verified

## Target prediction???

Need to f nd some papers!

Prof. says: "they bind to complementary sequences on target messenger RNA transcripts (mRNAs), usually resulting in translational repression and gene silencing".


Found some papers in Google!


Good Idea!!
DIANA microT
TargetScan

Find more papers, write notes, generate ideas, re-structure the domain... locations, experimentally suggested microRNA transcripts, micl expression levels in several tissues, SNPs and TFBSs near micr version of miRGen is the first attempt to build a widely accessib user-friendly database that connects TFs and miRNAs through experimentally supported functional relationships.
miRNAs incorporate into the RNA-Induced Silencing Complex and guide it to specific miRNA Recognition Elements (MREs) on the mRNA molecules of target genes. Most MREs are known to be located in the 3'UTR of protein coding genes.
microRNAs
?!
$l_{\text {microRNA }}^{\text {targets }}$

microRNA target prediction

$$
\text { Grimson et al. - Molecular cell - } 2007
$$

! $\rightarrow$ MicroRNA targeting specificity in mammals determinants beyond seed pairing.pdf

Describes several important features that affect miRNA targeting such local AU content, proximity of binding sites to one another etc
The features are implemented in TargetScan 4.2

$$
\text { Friedman et al. - Genome Research - } 2009
$$

$Q \rightarrow$ Most mammalian mRNAs are conserved targets of microRNAs Most mammalian mRNAs are conserved targets of microRNAs.pdf

## Mindmaps

- Graphical representations of elements
- concepts, ideas, notes, tasks, or other items related to a topic of study.
- Mindmapping elements are organized in hierarchical branches.
- However, everything is built around a central topic.
- Elements are arranged in a non-linear fashion.
- This encourages a brainstorming approach to planning and organizational tasks, and idea generation.


## Mindmaps

- Mindmap usage
- project and task management
- links to files, executables, source of information,
- knowledge base
- organization (notes, refs), essay writing and brainstorming.
- Mindmaps vs Semantic Networks, TopicMaps
- No explicit structured elements to model relationships. Radial hierarchies.
- Visual mnemonics: colors, icons and informal visual representations.


## Mindmaps

- Visual methods like mindmaps have been used for centuries
- learning
- problem solving
- recording knowledge
- visual thinking


## Mindmap in paper!



## FreePub

- FreePub, a creativity support tool to collect and organize scientific material using mindmaps.
- Creativity cycles:
- set up domain of interest using mindmaps,
- browse mindmaps and launch search tasks to gather relevant documents from several data sources,
- identify supporting material for those documents (e.g., blog posts, presentations),
- import and organise all retrieved information in mindmaps.


## FreePub architecture



## Searching facilities

## - Vertical search

- Retrieve relevant documents from several data sources.
- Vertical = tailored to certain types of information resources (e.g., DBLP, CiteseerX, PubMed, ...).
- Horizontal search
- Retrieve supporting material to retrieved docs.
- Horizontal = generic search engines (e.g., Google).
- Examples: doc itself, abstract, slide presentation, blog entries.


## Vert. search facilities: problems

- Wrapping?
- Data sources should be easily integrated.
- Web scrappers
- Capture data source search capabilities.
- Simplify Web information extraction.
- WebHarvest (http://web-harvest.sourceforge.net/)
- Provides several types of processors (e.g.,html-toxml, xpath, etc).
- Users define a sequence of extraction operations on Web pages based on path expressions.


## Vert. search facilities: problems

## Cleaning?

- Ambiguities in conf/journal names.
- Maintain a list of (name, acronym) pairs.
- Use string edit distance to determine similarities.
- Min number of edit operations (INS, DEL, REPL) needed to transform one string into the other.
- L('VLDD', 'VLDB Conf')= 6: replace `D' with `B', and insert `',`C', `o', `n', ‘f'.
- 'Very Large Database Conf' and 'VLDB Conf, both are matched to ('Very Large Database Conference', 'VLDB) catalog entry.


## Vert. search facilities: problems

- Duplicate elimination?
- Follow an entity resolution blocking technique.
- Divide objects into groups and only compare objects within the same group, to avoid redundant comparisons.
- Records in different groups are unlikely to match.
- Partition the result list of each data source into groups (key = date for each group)
- Maintain a (key, \{list of docs\}) structure
- Check pairs (o1, o2) only for o's that share the same key (date).


## Hor. search facilities: problems

- Support material?
- Doc itself, e.g.:
- title AND filetype:pdf OR doc
- Parse the doc to identify title
- Abstract, e.g.:
- Parse doc for "Abstract" tag.
- Many data sources do provide abstract!
- Slide presentations, e.g.:
- Title AND filetype:ppt
- Parse doc for certain terms (e.g., outline) (under impl).


## Hor. search facilities: problems

- Support material?
- Title AND author names
- Google Blog Search
- Technorati (http://technorati.com/) (under impl.)


## Using FreePub

- User selects mindmap elements.
- Freepub extracts keywords from these elements.
- Metasearch orchestration.
- Vertical search: find relevant documents.
- Horizontal search: find supporting material.
- Two modes for keyword exrtaction
- Normal mode.
- Semantic query expansion mode.


## Semantic query expansion



## Semantic query expansion

- All elements in the neighbourhood of userselected elements are considered as documents.
- The level of neighbourhoud is user defined.
- E.g., level 1 means that the neighbourhood of a selected element includes only directly adjacent nodes.
- To each document d, we assign weights docWeight_d according to the type of corresponding elements.


## Semantic query expansion

## DocWeight=1

 (hot topic node)Continuous training and correctio clustering and the expansion pror When having performed one train testing phase, check if the cluste solution gave us good results anc correct the clustering.

DocWeight=0.8
(subtopic node)

## Semantic query expansion

- How to determine expansion terms?
- Doc terms are cleaned (i.e., punctuation and stopwords are removed).
- docSize(d) = number of terms for document d.
- Compute freq(t,d): occurences of $\mathbf{t}$ in each $\mathbf{d}$ (i.e., term frequency), and $\operatorname{docFrec}(\mathbf{t})$ : num of docs containing $\mathbf{t}$.
- Compute w(d,t) = freq(t,d)*docFreq(t)*docWeight(d) / docSize(d).
- Term weight $\mathbf{W}(\mathbf{t})$ : the average of $\mathbf{w ( d , t )} \mathbf{t}$.


## Semantic query expansion

Terms are sorted according to $\mathbf{W}(\mathbf{t})$.

- Use the TOP-K terms to expand the initial query.


## Some screenshots



## Some screenshots

Freepub vo. 1 beta

## otions

Support Material


Algorifuns for Molerulux Biology | Full text | Lexming from
in a recent pubjication we described a two-classmachine
learning approach for miRNApre diction using the naive Bayes classiffer [131. Four criteria were used to select a pool of negative examplesfrom candidate stem loops. stem length out of the ranqe http://wowv.almob.org/content/3/1/2

## Some screenshots

| Q TargetScan | Describes several important features that affect miRNA targeting such local AU content, proximity of binding sites to one another etc |
| :---: | :---: |
|  | The features are implemented in TargetScan 4.2 |
|  | $\begin{aligned} & \text { Friedman et al. - Genome Research - } 2009 \\ & \text { Q } \rightarrow \text { Most mammalian mRNAs are conseved targets } \\ & \text { of microRNAs Most mammalian mRNAs are } \\ & \text { conserved targets of microRNAs.pdf } \end{aligned}$ |

Learning from positive examples when
the negative class is undetermined
FreePub Publications microRNA gene identification (2008) JYousef Malik, Jung Segun, Showe Louise, Showe Michael

Presentations
[Pres.] Joseph_Wang_L $\rightarrow$ Malik Yousef, Hsiuan-Lin Wu, ar can identify patients with early

Nal" ive Bayes for microRNA target predictions - machine learning for
FreePub
Publications microRNA targets (2007)
JMalik Yousef, Segun Jung, Andrew V.
Kossenkov, Louise C. Showe, Michael
K. Showe Bioinformatics

## FreePubCollecting and Organizing Scientific Material Using Mindmaps

Theodore Dalamagas, IMIS Institute /'Athena' R.C., Athens, Greece
Tryfon Farmakakis, School of Informatics, University of Edinburgh, Scotland Manolis Maragkakis, BSRC 'A. Fleming', Greece

Artemis G. Hatzigeorgiou, BSRC 'A. Fleming', Greece
http://web.imis.athena-innovation.gr/projects/mm/



