

2012

RegulonIT - A web based tool for regulon, gene, and co-expression data

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RegulonIT - A web based tool for regulon, gene and co-expression data

by

Aravindh kumar Balakrishnan

A thesis submitted to the graduate faculty
in partial fulfillment of the requirements for the degree of
MASTER OF SCIENCE

Major: Computer Science

Program of Study Committee:

Leslie Miller, Co-major Professor

Eve Wurtele, Co-major Professor

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Iowa State University

Ames, Iowa

2012

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DEDICATION

I would like to dedicate this thesis to my sister, Anitha Balakrishnan and to my parents for their unconditional support and encouragement throughout my work.

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ACKNOWLEDGEMENTS

I would like to take this opportunity to express my gratitude to everyone who helped me throughout my Master's degree and during the course of my thesis. Firstly, I would like to thank my advisors, Dr. Leslie Miller and Dr. Eve Wurtele for their guidance, encouragement and support throughout the period of this research work. I would also like to thank my committee member, Dr. Simanta Mitra for taking the time to review my thesis and giving suggestions for improvement. Further, I would like to thank Dr. Yaping Feng, Jonathan Hurst and Dr. Ling Li for providing biological data for my research work and for testing the RegulonIT web application. I would also like to thank Nick Ransom, Dr. Yi Wang and Manhoi Hur for helping me integrate the RegulonIT tool with external web services. I would also like to warmly thank my sister, parents and my roommates for their continuous encouragement, advice, and support during my education. Finally, I would like to express my gratefulness to the Virtual Reality Application Center for the research assistantship that provided support for me during my graduate studies at Iowa State University.

ABSTRACT

One of the greatest challenges in the field of biology today is the determination of unknown gene function. A number of web applications are currently being developed which aim at providing gene related information, such as gene expression and co-expression data for individual genes. Integrating gene expression networks with external data sources may give researchers additional information about these genes.

A regulon is a collection of highly co-expressed genes which can be identified by clustering a network of genes obtained from transcriptomic analysis. Regulon analysis offers a potential way to evaluate functions of genes in a given gene family or for developing hypothesis about the function of unknown genes. Hence, it is important that information about regulons, genes, and co-expression data be available to all biologists in a user friendly manner. Currently, information about regulons and its associated genes are not easily accessible, and in order to view regulon information, manual look up into flat files such as text files is required. In order to avoid this, we come up with an application which aim at providing regulon, gene, and co-expression data for three important species in a user-friendly manner using a web interface.

RegulonIT is a web based tool that aims at providing information about regulons and other gene related information. Currently, the tool provides regulon, gene and co-expression information for three species (*Arabidopsis thaliana*, *Saccharomyces cerevisiae* and *Homo sapiens*) for very large transcriptomic datasets using a web interface. RegulonIT is a user friendly platform independent web tool and is available at <http://metnetdb.org:9090/regulonit>.

CHAPTER 1. GENERAL INTRODUCTION

1.1 Overview

RegulonIT is a software application which currently provides regulon, gene and co-expression information for three species (*Arabidopsis thaliana*, *Saccharomyces cerevisiae* and *Homo sapiens*) for very large transcriptomic datasets using a web interface. The tool includes features like search, sort, filter and viewing correlation matrix. It also provides integration with external websites and web services like TAIR (The Arabidopsis Information Resource), yeast genome, KEGG (Kyoto Encyclopedia of Genes and Genomes), MetNet and MetaOmGraph for enabling interactions with external data sources. The software has been designed for easy addition of new datasets in an user friendly manner. The web server is supported by a database containing experimental data, annotations and GO(Gene Ontology) terms for all three species for different datasets. The database has been designed to make it possible to store pre-calculated co-expression results for faster processing of user queries.

1.2 Features

This section gives a brief description about the different features that are available with the RegulonIT web tool. These features are available in a form like layout where the user is prompted to enter an input. The form takes input using text boxes, drop down list boxes, check boxes or radio buttons depending on the functionality of the page. When the input is entered and the submit button is clicked, the request is sent to the server and once the business logic is processed, a response is sent back to the user in the form of a table.

1.2.1 Search

This feature allows the user to enter a search criteria, select a dataset and view information about regulons or genes at a selected correlation co-efficient.

There are two main search features in this application

- Search by Regulon
- Search by Gene

1.2.2 Sort

The search feature returns information in the form of a table and the table usually contains a large number of rows. The Sort feature allows the user to sort these rows in the table by ascending or descending order.

1.2.3 View Correlation matrix

This feature allows the user to view correlation matrix for a set of genes. A correlation matrix provides information about the correlation co-efficient between all pair of genes in a given set. If there are 'n' genes under consideration, then the final output will be a 'n*n' matrix represented in the form of a table.

A correlation matrix can be viewed in our application by two ways:

- Using the Search feature for getting gene information in the form of a table, selecting the genes in this table, and then generating the matrix.
- Entering a set of genes manually in a text area and then generating the matrix.

1.2.4 Search by multiple genes

This feature allows the user to enter more than one gene and view information about these genes simultaneously.

1.2.5 Data management

It is also possible for a privileged user to add a new species or add a new dataset for an existing species. This can be done only by administrators of this application.

1.2.6 Integration with external websites

This feature enables the user to interact with external websites and web services. Currently, the tool has interactions with TAIR, yeast genome, gene cards, KEGG, MetNet and MetaOmGraph.

1.3 Implementation resources

The application has been implemented using open source technologies like Java EE, Struts 1.3, AJAX(Asynchronous JavaScript and XML, Javascript), JDBC(Java Database Connectivity) and Apache Axis. The database used is MySQL 5.0.77 which is available in the MetNet server and the web server used is Tomcat 5.5.

1.4 Thesis organization

The thesis is organized as follows:

Chapter 2 contains the manuscript for the journal paper. This chapter has been prepared according to the format specified by BMC Bioinformatics journal. Dr. Leslie Miller provided suggestions for choosing the resources to be used for developing the web based tool. Dr. Eve Wurtele helped with the manuscript by providing biological information. Dr. Yaping Feng provided regulon, gene and co-expression data for the species.

Chapter 3 discusses the project implementation in detail. It describes the components of the Struts framework and the different resources that have been used for developing the RegulonIT project.

Chapter 4 provides conclusive remarks for the thesis.

CHAPTER 2. REGULONIT - A WEB BASED TOOL FOR REGULON, GENE AND CO-EXPRESSION DATA

A paper to be submitted to the BMC Bioinformatics Journal.

Aravindh kumar Balakrishnan, Yaping Feng, Leslie Miller, Eve Syrkin Wurtele

Abstract

Background

One of the greatest challenges in the field of biology today is the determination of unknown gene function. A number of web applications are currently being developed which aim at providing gene related information, such as gene expression and co-expression data for individual genes. Integrating gene expression networks with external data sources may give researchers additional information about these genes.

A regulon is a collection of highly co-expressed genes which can be identified by clustering a network of genes obtained from transcriptomic analysis. Regulon analysis offers a potential way to evaluate functions of genes in a given gene family or for developing hypothesis about the function of unknown genes. Hence, it is important that information about regulons, genes, and co-expression data be available to all biologists in a user friendly manner. Currently, information about regulons and its associated genes are not easily accessible, and in order to view regulon information, manual look up into flat files such as text files is required. In order to avoid this, we come up with an application which aim at providing regulon, gene, and co-expression data for three important species in a user-friendly manner using a web interface.

Results

RegulonIT is a software application which provides regulon, gene, and co-expression information for very large transcriptomic datasets using a web interface. It is currently focussed on *Arabidopsis thaliana*, *Saccharomyces cerevisiae*, and *Homo sapiens*. The tool includes features like viewing Pearson correlation matrix for genes in a regulon, analysis of gene expression by exporting data from RegulonIT into MetaOmGraph (www.metnetdb.org/MetNet_MetaOmGraph.htm), as well as standard features like search, sort, filter, and download. For instance, the user could search by regulon to find the number of genes present in the regulon, and view information about each and every gene in the regulon. The user could also generate a Pearson correlation matrix for all genes present in the regulon. The tool also allows the user to integrate the results with external data websites and web services like TAIR (The Arabidopsis Information Resource, www.arabidopsis.org), yeast genome (www.yeastgenome.org), KEGG (Kyoto Encyclopedia of Genes and Genomes, www.genome.jp/kegg), MetNet (www.metnetonline.org) and MetaOmGraph (www.metnetdb.org/MetNet_MetaOmGraph.htm) for enabling interactions with external data sources. The RegulonIT software has been designed to enable extensibility, and new species and datasets can be added in an user friendly manner. The web server is supported by a database containing experimental data, annotations, and GO(Gene Ontology) terms for all three species for different datasets. The database has been designed to store pre-calculated co-expression results for rapid processing of user queries.

Conclusions

RegulonIT is a user-friendly platform independent web tool which provides biologists an easy way to access regulon, gene, and co-expression information for very large transcriptomic datasets. This tool may help biologists in developing hypothesis about gene functions or associating genes which participate in the same biological process. The RegulonIT software is available at <http://metnetdb.org:9090/regulonit>.

2.1 Background

2.1.1 Gene co-expression and the significance of clustering

Genes which are highly correlated are biologically significant, since they may participate in the same biological processes or share similar functionalities(1)(2)(3). Gene co-expression networks derived from gene expression level data are being widely used for analysing the system-level functionality of genes(3). Cluster of genes obtained by clustering a co-expression network, formed by using gene expression data from several experiments, are often functionally related(1)(2)(4).

The expression data obtained from transcriptomic analysis can be transformed into a co-expression network where genes are represented as nodes. For this, the Pearson correlation coefficient between all pair of genes is calculated using gene expression data, as the absolute value of Pearson correlation is often used in gene expression cluster analysis(1)(2)(3). Two nodes are connected by an edge if the correlation co-efficient between them is higher than a threshold correlation co-efficient. Bin Zhang et al.(3) used the idea of soft thresholding for converting gene expression data into a co-expression network. Using simulated data, they provide evidence that weighted networks can yield better results than unweighted networks. Unweighted networks use hard thresholding, where the threshold correlation co-efficient is determined by analysing the density of networks. With increasing Pearson cut-off correlation, the number of edges decreases, and consequently the number of nodes in the network decreases. The correlation at which the network density is minimum is considered to be the threshold correlation co-efficient, as this would maximize the formation of densely connected sub-networks(2).

The resulting network can be subjected to clustering in order to find regulons(1)(2). There are different techniques for clustering large scale transcriptomic networks, such as feature-based clustering(K-Means), similarity matrix-based clustering(H cluster), and graph-based clustering(MCL(Markov clustering)(5)). Feng et al.(2) and Mentzen & Wurtele(1) used Markov clustering algorithm for clustering their co-expression network prepared from transcriptomic analysis, as they found it to be scalable to large graphs, and it yielded much better results when

compared to the other two clustering methods. Their evaluation was based on the determination of the best matches of over-representation of genes in GO (Gene Ontology) terms, and metabolic and regulatory pathways. It was concluded by them that MCL yielded better GS scores(global significance score) when compared to the other two clustering methods(1)(2).

Feng et al.(2) analysed a large human co-expression network formed by using transcriptomic data available in Array express(6) using the MetaOmGraph interface. High quality data from 18,637 Affymetrix chips encompassing over 500 experiments was used to form this co-expression network. Regulons formed by clustering this large transcriptomic network using Markov clustering(5) was analysed using over-representation of GO (Gene Ontology) terms and direct visualization of transcript levels(2). Similarly, Mentzen & Wurtele(1) created an Arabidopsis co-expression network by using 22,746 Affymetrix probes dataset derived from 963 micro-array chips from a wide variety of experiments using Array express(6) and MetaOmGraph(7). Markov clustering(MCL)(5) of the co-expression network resulted in 998 regulons and the significance of these regulons were evaluated by calculating the statistical over-representation of GO term and comparing them to randomly-generated sets of clusters(1). It was concluded in both cases that regulon analysis is statistically significant and it creates a framework for developing testable hypotheses about function of unknown genes or genes with no known physiological or developmental role. Hence, regulon analysis offers the potential to identify genes with unknown functionality, prevailing cellular processes and for associating genes which participate in the same biological processes(1)(2).

2.1.2 Existing web based tools for gene analysis

Gene expression data from a variety of experiments across different environmental, disease, and developmental stages, are currently publicly available for different species. Widely used public microarray and RNAsequence data repositories include ArrayExpress(6) and Gene Expression Omnibus(8). Substantial amounts of gene expression data are often generated by each transcriptomic experiment and it is often difficult for biologists to extract the information they seek. A number of software applications have been developed for biologists to query

large gene co-expression databases using a web browser interface. A few examples of such applications are Genevestigator(9), Arabidopsis Co-expression Tool(ACT)(10), KEGG(11)(12), MetNet(13), and GeneCat(14). Though these tools provide comparative gene analyses such as cis-element prediction, expression profiling, and co-expression analysis, there are currently no web tools which provide information about regulons generated by clustering transcriptomic networks.

RegulonIT is a software application which provides regulon, gene, and co-expression information. It is currently focussed on *Arabidopsis thaliana*, *Saccharomyces cerevisiae*, and *Homo sapiens* for very large transcriptomic datasets using a web interface. The datasets were prepared by Feng et al(2), Mentzen & Wurtele(1), and Chen, Xi(15) by using transcriptomic data from Array express using the MetaOmGraph interface.

2.2 Implementation

RegulonIT is an online application developed using the open source technologies: Java EE (Enterprise Edition), Struts (<http://struts.apache.org/>, version 1.3)(16) framework, Asynchronous JavaScript and XML (AJAX, <http://www.zammetti.com/articles/xhrstruts>)(17), JavaScript, Java Database Connectivity (JDBC), and Apache Axis(<http://ws.apache.org/axis/>)(18). The Apache web server is supported by a MySQL(version 5.0.77) database, which is available in the MetNet server, and a Tomcat(version 5.5) servlet container. The main idea behind using AJAX(17) is that re-building a web page for every user interaction is inefficient and should be avoided. When a form is submitted, AJAX helps retrieve results without the web page getting refreshed.

The performance of RegulonIT tool has been improved significantly by using client side scripting wherever possible. JavaScript has been used to achieve this, so that the business logic is processed in the client side, hence putting less load on the server. Also, in order to speed up user queries in the server side, database indexes have been created wherever possible in order to improve database retrieval time.

2.2.1 System Overview and Integration with External Databases

Figure 2.1 shows a schematic overview of the RegulonIT framework and its relationship with other databases. The features which include, search, sort, and filter are available in a form like layout where the user is prompted to enter an input. The form takes input using text boxes, drop down list boxes, check boxes or radio buttons depending on the functionality of the page. When user inputs a query, the request is sent to the server and a response is sent back to the user in the form of a table. Gene information like gene symbols, systematic names, GO (Gene Ontology) terms, and pathway information are retrieved from the RegulonIT database corresponding to the user query. The outcome of all search results are tables containing regulon, gene or co-expression data depending on the functionality of the page. During processing, results generated by RegulonIT are integrated with data from external websites. For example, in the case of *Arabidopsis thaliana*, the locus ids in the table generated are linked to TAIR (The Arabidopsis Information Resource)(19) in order to obtain more information about the gene function and characteristics. Similarly, systematic names for *Saccharomyces cerevisiae* are linked to the yeast genome(20) website and gene symbols for *Homo sapiens* are linked to gene cards(21) website. The application also allows the user to get pathway information from the KEGG(11)(12) database and the MetNet(13) database.

KEGG (Kyoto Encyclopedia of Genes and Genomes) is a database resource developed by Kanehisa Laboratories that integrates genomic, chemical, and systemic functional information for different species(11)(12). The RegulonIT tool integrates with the KEGG database for retrieving pathway information for genes. The KEGG integration has been implemented using the KEGG application programming interface (API) which consists of the SOAP/WSDL interface and the REST interface to the KEGG system. This allows searching biochemical pathways in processes in an easy manner. In order to use the KEGG API, the Apache Axis web services library has been imported and integrated into our project. Pathways from the MetNet database are also incorporated into the search results. MetNet is a publicly available software for analysis of genome-wide mRNA, protein, and metabolite profiling data(13). The MetNet integration is implemented using the MetNet application programming interface (API).

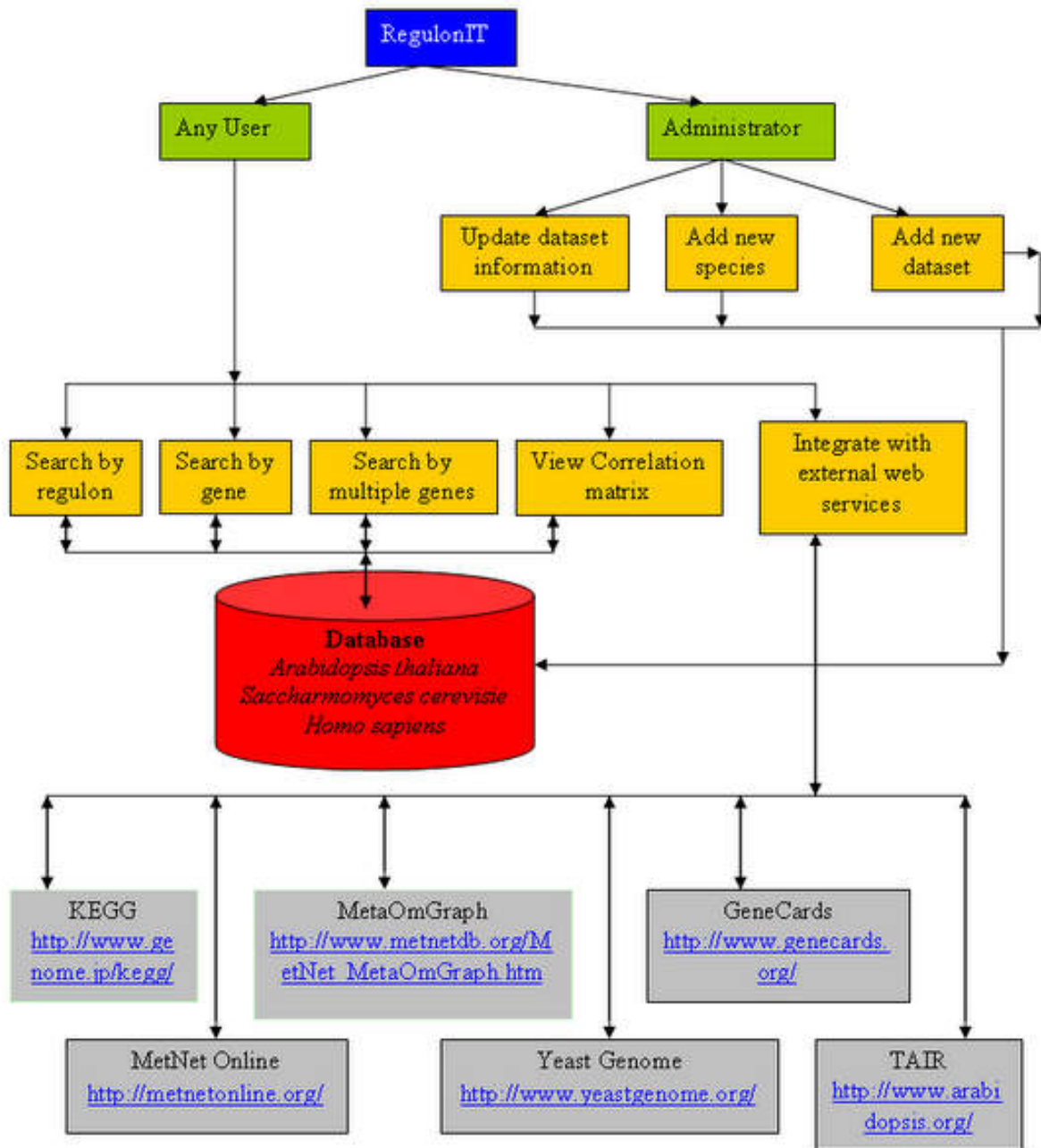


Figure 2.1 RegulonIT - System overview. The RegulonIT framework provides features like search by regulon, search by gene, search by multiple genes and viewing correlation matrix. It also provides integration with external web services like KEGG(11)(12), MetNet(13), TAIR(19), yeast genome(20), gene cards(21), and MetaOmGraph(7). The administrator of this tool will have the privilege to add new species and to add new datasets for existing species.

The MetNet API is a programming library that provides direct access to the MetNet database. The MetNet API is a JAR file which contains Java packages that has been used for retrieving pathway information from the MetNet database.

RegulonIT also allows the search results to be integrated with MetaOmGraph(7). The genes present in the table can be selected and exported to an xml file in a format that is compatible with MetaOmGraph. This file can be imported into MetaOmGraph and the accumulation levels of the genes can be viewed in a plot for different samples. This functionality has been implemented in the client side using Javascript and hence makes the process really fast. Javascript libraries from Downloadify(22) have been used to make it possible to save the file in the users local machine.

The RegulonIT tool has been developed using the Model-View-Controller(MVC) framework. MVC is a framework or a design pattern that is used for developing web applications by providing a clean separation of software architecture into three distinct elements.

1. Model: Model manages behaviour and business data of an application.
2. View: Views are used for displaying Model data in a form suitable for interaction. Views in our design contain HTML components, JavaScript, AJAX and Struts tags for displaying response retrieved from the server.
3. Controller: Controllers are for handling events and they act as an interface between the model and view components. The Controller receives the request from the browser (View), invokes a business operation and coordinates the view to return to the client.

Struts(16), a MVC web framework, is an open-source solution for creating Java web applications. This framework has been used for designing the RegulonIT tool as it provides a clean separation between the Model, View and Controller components. It provides a primary Controller component called the ActionServlet which handles requests from the View component and calls the corresponding business logic component. Struts also includes a set of custom tag

libraries for the View Component, which can be used for creating user interfaces that provide graceful interaction with the user.

2.2.2 Database design

Currently, the database is designed to provide information for three species: *Arabidopsis thaliana*, *Homo sapiens* and *Saccharomyces cerevisiae*. For a given species, new datasets can be added by an administrator. Each species has two tables for a given dataset which are:

- A genes table which contains gene information such as gene symbol, gene title, GO terms, etc.
- A pearsonmatrix table which contains correlation co-efficient for all pair of genes in the genes table.

For different datasets for a given species, the information in the genes table will remain the same except that a new column is added for regulon for each dataset. But, the pearsonmatrix information is different for different datasets. Hence a species will have one gene information table and many pearsonmatrix tables for different datasets.

In the tables shown in Figure 2.2, species can be *Arabidopsis thaliana*, *Saccharomyces cerevisiae* or *Homo sapiens*. Currently, for *Arabidopsis thaliana*, the database has three datasets and for *Homo sapiens* and *Saccharomyces cerevisiae*, the database has one dataset each. The *Arabidopsis thaliana* datasets were prepared by Mentzen & Wurtele, Feng et al.(2) and Chen(15) by using gene expression level data from MetaOmGraph. This expression data was converted into a co-expression network by choosing a Pearson correlation co-efficient of 0.7 and the resulting network was subjected to Markov clustering(MCL)(5) algorithm. The *Homo sapiens* dataset was prepared by Feng et al.(2) in a similar manner.

Currently, the datasets_information table contains dataset name and dataset description information for all five datasets. Each time a new organism or a new dataset is added, the datasets_information table gets updated automatically. The probeid column in the genes_species table acts as the primary key for the table. This column is referenced by columns in the

DATABASE SCHEMA

datasets_information table	
species	PK
dataset name	
dataset description	

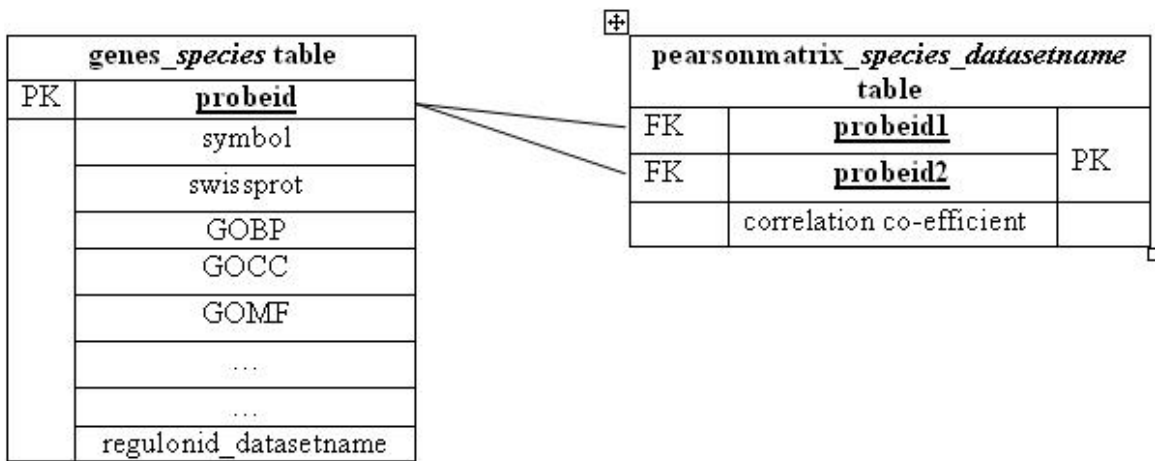


Figure 2.2 RegulonIT - Database schema. Species can be *Arabidopsis thaliana* , *Saccharomyces cerevisiae* or *Homo sapiens*. The probeid column in the genes_species table acts as the primary key for the table. This column is referenced by columns in the pearsonmatrix table.

pearsonmatrix table. Hence, there is a primary key, foreign key relationship between these columns in the two tables.

2.3 Results and discussion

The RegulonIT web application consists of a number of features which are used for searching and analysing information for *Arabidopsis thaliana*, *Saccharomyces erevisiae* and *Homo sapiens*. Most of these features work the same way for all 3 species, so the example of *Arabidopsis thaliana* and *Saccharromyces cerevisiae* have been used to explain how these features work.

2.3.1 Search by regulon

The search by regulon feature is used for searching regulon and gene information by regulon. It prompts the user to enter a regulon, select a correlation co-efficient, and select a dataset for viewing regulon information as shown in Figure 2.3. When the search page for *Arabidopsis thaliana* is opened, the dataset drop-down list box lists the datasets currently available in the RegulonIT database. Currently, we have regulon information for 3 different datasets for *Arabidopsis thaliana*. When additional datasets are added for a species by the administrator, the drop-down list box gets populated automatically with the new dataset, the next time the page is loaded. When a dataset is selected from the list, the form makes a request to the server, which fetches a detailed dataset description from the database and displays it just below the drop-down list box. This has been implemented using AJAX. The page also allows the user to select the gene attributes to be displayed once the ‘Search’ button is clicked. The attributes must be selected using a check box in order to be displayed. By default, all gene attributes are checked.

When the input is entered and the ‘Search’ button is clicked, the following validations are done in the client side using JavaScript before the request is sent to the server.

- Validate if an input has been entered.
- Validate if the input entered is a number

Regulon Presentation for *Arabidopsis thaliana*

Enter Regulon: [?](#)

Correlation Co-efficient:

Select Dataset:

Select columns to be displayed: [?](#)

ProbelD
 Gene Symbol
 Gene Title
 Description
 GO Biological Process
 GO Cellular Component
 GO Molecular Function
 Swiss Prot

Note: Correlation co-efficient used by biologists for clustering the gene network is 0.7

Figure 2.3 Search by regulon page for *Arabidopsis thaliana*. This page prompts the user to enter a regulon, choose a dataset, and view information about the entered regulon at the selected correlation.

- Validate if the number is greater than 0
- Validate if the number is an integer
- Validate if a dataset has been selected from the drop down list box.

If the input entered fails to meet any one of the conditions, then an alert box is displayed notifying the user of the error as shown in Figure 2.4. When a valid entry is entered, the search returns the following results:

- Information about the number of genes present in that regulon at the selected correlation co-efficient.

Figure 2.5 shows that regulon 21, has 56 genes present in it at a correlation co-efficient of 0.7 for the selected dataset.

- A table containing information about each gene in the regulon and the number of neighbours for each gene. The table shown in Figure 2.6 provides a detailed description of all 56 genes in regulon 21. The entry in the number of neighbours column in the table

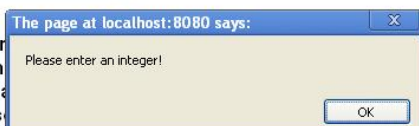
Regulon Presentation for *Arabidopsis thaliana*

Enter Regulon: [\[?\]](#)

Correlation Co-efficient:

Select Dataset:

Dataset Description: The Arabidopsis co-expression network was constructed by selecting gene-pairs with Pearson correlations greater than or equal to 0.7. Regulons were created from this co-expression network by MCL clustering algorithm. All methods and parameters were optimized by calculating the global significance score of regulons using gene ontology enrichment test. Please cite the relevant publications [Feng et. al., 2012; Chen, 2011]. Contact Yaping Feng @ ypfeng@iastate.edu with questions.



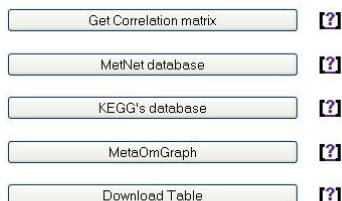
Wurtele, 2008]. Logarithm base 2 transformation was performed on all data. Then normally, the median absolute deviation (MAD) based scale normalization method was used. A correlation matrix was calculated from this dataset. When calculating the Pearson correlation matrix, positive values and negative values were not considered for both genes. The Arabidopsis co-expression network was constructed by selecting gene-pairs with Pearson correlations greater than or equal to 0.7. Regulons were created from this co-expression network by MCL clustering algorithm. All methods and parameters were optimized by calculating the global significance score of regulons using gene ontology enrichment test. Please cite the relevant publications [Feng et. al., 2012; Chen, 2011]. Contact Yaping Feng @ ypfeng@iastate.edu with questions.

Select columns to be displayed: [\[?\]](#)

- ProbeID
 Gene Symbol
 Gene Title
 Description
 GO Biological Process
 GO Cellular Component
 GO Molecular Function
 Swiss Prot

Note: Correlation co-efficient used by biologists for clustering the gene network is 0.7

Figure 2.4 Validation for search by regulon feature. When an invalid entry is entered, an error message is displayed.



Total number of genes in regulon at correlation co-efficient 0.7: 56

<input checked="" type="checkbox"/>	Gene Symbol	LocusID	SwissProt	Description	Pathway from METNET Database	Gene Title	GO Biological Process
<input checked="" type="checkbox"/>	TSO2	AT3G27060	Q9LSD0	ribonucleotide reductase small subunit, putative similar to RIBONUCLEOSIDE-DIPHOSPHATE	purine nucleotide metabolism (phosphotransfer and nucleotide modification)	TSO2 (TSO meaning ugly in Chinese); oxidoreductase/ ribonucleoside-diphosphate reductase/ transition metal ion binding	0006260 // DNA replication inferred from mutant phenotype // 0006260 // DNA replication // inferred from electronic annotation
<input checked="" type="checkbox"/>	AtAUR3	AT2G45490	O64629	putative protein kinase contains a protein kinase domain profile (PDOC00100)	No pathway information found	AtAUR3 (ATAURORA3); ATP binding / histone kinase(H3-S10 specific) / protein kinase	0006468 // protein acid phosphorylation inferred from sequence structural similarity // 0006468 // protein acid phosphorylation
			O80588	hypothetical protein predicted	No pathway information	FDF1 (FENDOSPERM)	0000226 // microtubule cytoskeleton organization

Figure 2.5 Regulon and gene Information for regulon 21. The search result shows that regulon 21 has 56 genes at a correlation of 0.7.

Total number of genes in regulon at correlation co-efficient 0.7: 56

Search Table							
<input checked="" type="checkbox"/>	Gene Symbol	LocusID	SwissProt	Description	Pathway from METNET Database	Gene Title	GO Biological P
<input checked="" type="checkbox"/>	TSO2	AT3G27060	Q9LSD0	ribonucleotide reductase small subunit, putative similar to RIBONUCLEOSIDE-DIPHOSPHATE	purine nucleotide metabolism (phosphotransfer and nucleotide modification)	TSO2 (TSO meaning ugly in Chinese); oxidoreductase/ ribonucleoside-diphosphate reductase/ transition metal ion binding	0006260 // DNA repl inferred from mi phenotype // 000 DNA replication // from electronic an
<input checked="" type="checkbox"/>	AtAUR3	AT2G45490	O64629	putative protein kinase contains a protein kinase domain profile (PDOC00100)	No pathway information found	AtAUR3 (ATAURORA3); ATP binding / histone kinase(H3-S10 specific) / protein kinase	0006468 // protein acid phosphoryl; inferred from sequ structural simila 0006468 // protein
<input checked="" type="checkbox"/>	EDE1	AT2G44190	O80588	hypothetical protein predicted by genscan	No pathway information found	EDE1 (ENDOSPERM DEFECTIVE 1); microtubule binding	0000226 // microt cytoskeleton organ inferred from mi phenotype // 000 endosperm develo
<input checked="" type="checkbox"/>	ORC2	AT2G37560	Q38899 // Q3E6W3	origin recognition complex protein identical to GB:U40269; supported by full-length cDNA:	No pathway information found	ORC2 (ORIGIN RECOGNITION COMPLEX SECOND LARGEST SUBUNIT 2); DNA replication origin binding /	0006260 // DNA repl inferred from seq structural similarity // DNA replication

Figure 2.6 Table containing detailed information about all the 56 genes in regulon 21 at a correlation of 0.7.

has a hyper-link on them, which when clicked displays a detailed description of all the neighbours.

- Additional search features are also displayed (Figure 2.10). These features can be used by selecting rows in the table thus generated and viewing more information. The first column of the table has check-boxes which are used for selecting the rows.

2.3.2 Search by gene

The search by gene feature allows the user to search for gene information by three different criteria for *S.cerevisiae* - systematic name, symbol and probeid. When an option is selected and the 'Submit' button is clicked, it displays more input boxes for providing input data. For example, when the systematic name option is selected and the 'Submit' button is clicked, the page displays a text box for entering the systematic name of the gene for which we want to view information and two drop-down list boxes; one for selecting the correlation co-efficient and the other one for selecting the dataset information as shown in Figure 2.7. The page also allows the user to select the gene attributes to be displayed when the 'Search' button is clicked.

Gene Presentation For *Saccharomyces cerevisiae*

Select Dataset:

Dataset Description: This correlation matrix and the regulons derived from it are the result of con transcriptomics data for the Affymetrix S98 genechip platform. Data was obtained from the Arrayf data from the GEO database and European studies), curated to remove duplicate and incomplete normalization, filtered for low expression, and replicate microarrays averaged. This resulted in 60 replicates) derived from 1598 microarrays. The correlation matrix was created using Pearsons pa regulons were created from the correlation matrix by MCL clustering. All methods and parameter: gene ontology enrichment for the final clusterings. Contact Jon Hurst at jnhurst@iastate.edu with information.

Select Search Criteria [?](#)

Systematic Name Symbol Probe ID

Enter Systematic Name:

Correlation Co-efficient:

Select columns to be displayed:

ProbeID Systematic Name Gene Symbol Gene Title

Figure 2.7 Search by gene page for *Saccharomyces erevisiae*(Yeast). This page prompts the user to select a dataset, enter a gene and view information about the entered gene at the selected correlation. In the case of *Saccharomyces cerevisiae*, the search could be performed by systematic name, gene symbol or probeid.

The attributes must be selected using a check box in order to be displayed. By default all gene attributes are checked.

When a valid systematic name is entered and the ‘Get Gene Information’ button is clicked, the page returns the following:

- A table containing detailed information about the gene entered. Figure 2.8 shows gene information when systematic name ‘YKL204W’ is entered.
- A table containing information about neighbours of the entered gene at the selected correlation co-efficient as shown in Figure 2.9. This table also contains the correlation co-efficient between the entered gene and all its neighbours at the selected correlation.
- Additional search features are also displayed (Figure 2.10). These features can be used by selecting rows in the table and viewing information. These search features are explained in detail in section 2.3.3.

Regulon to which gene belongs to:	22
Systematic Name:	YKL204W
ProbeID:	10762_at
Gene Symbol:	EAP1
SwissProt:	P36041
Gene Title:	eIF4E-associated protein competes with eIF4G for binding to eIF4E; inhibits cap-dependent translation; functions growthimplicated in the TOR signaling cascade
GO Biological Processes:	0006417 // regulation of translation // inferred from electronic annotation /// 0017148 // negative regulation of transl electronic annotation /// 0042493 // response to drug // inferred from mutant phenotype
GO Cellular Component:	0005737 // cytoplasm // inferred from electronic annotation /// 0005845 // mRNA cap binding complex // inferred from
GO Molecular Function:	0000166 // nucleotide binding // inferred from electronic annotation /// 0005515 // protein binding // inferred from ph; 0008190 // eukaryotic initiation factor 4E binding // inferred from physical interaction
At Correlation co-efficient 0.6 , Number of neighbours:	8

Figure 2.8 Table containing information about the gene with systematic name - 'YKL204W' at a correlation of 0.6. The table provides information like gene symbol, probeid, swissprot, GO terms, etc. It also displays the number of neighbours of the gene at the selected correlation, which in this case is 0.6.

<input checked="" type="checkbox"/>	Systematic Name	Regulon	Gene Symbol	Gene Title	Pathways from METNET Database	SwissProt	ProbeID	GO Biological P
<input checked="" type="checkbox"/>	YLR116W	22	MSL5	Component of the commitment complex which defines the first step in the splicing pathway; essential protein that interacts with	No Pathway Information found	Q12186	10235_at	0000398 // nuclear splicing via splicee inferred from ph interaction /// 000 mRNA process
<input checked="" type="checkbox"/>	YLR187W	55	SKG3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery cytoplasm	No Pathway Information found	Q06315	10168_at	---
<input checked="" type="checkbox"/>	YLR337C	22	VRP1	Proline-rich actin-associated protein involved in cytoskeletal organization and cytokinesis; related to mammalian Wiskott-Aldrich	No Pathway Information found	P37370 /// Q07229	10007_at	0006897 // endocy inferred from mi phenotype /// 000 actin filament organ inferred from ph
<input checked="" type="checkbox"/>	YMR047C	41	NUP116	Subunit of the Nup82 subcomplex of the nuclear pore complex; localized to both sides of the pore; contains a repetitive GLFG	No Pathway Information found	Q02630	9578_at	0006388 // tRNA sp endonucleolytic cl and ligation // inferi mutant phenoty 0006406 // mRNA
<input checked="" type="checkbox"/>	YNL278W	55	CAF120	Part of the evolutionarily-conserved CCR4-NOT transcriptional regulatory	No Pathway Information found	P53836	9161_at	0006350 // transcr inferred from elec annotation /// 000

Figure 2.9 Table containing information about the neighbours of gene - 'YKL204W'. This table provides detailed information about all the neighbours of the 'YKL204W' at a correlation of 0.6.

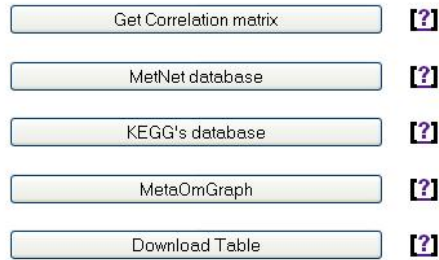


Figure 2.10 Additional search features once the results are generated. These features can be used by selecting the rows(genes) in the table returned by the search results.

2.3.3 Additional features from search results

The Search features available in this web application provide additional features once the results are generated and displayed in the form of a table. These features, as shown in Figure 2.5 and Figure 2.10, can be used by selecting the rows in the table using the check boxes available in each row and viewing information about the selected rows(genes).

These features are:

- View correlation matrix
- Integration with MetNet database
- Integration with KEGG database
- Integration with MetaOmGraph

2.3.3.1 View correlation matrix

The Correlation Matrix of ‘n’ genes, $X_1 \dots X_n$, is a ‘n*n’ matrix whose (i,j)th entry is $\text{Corr}(X_i, X_j)$ where $\text{Corr}(X_i, X_j)$ is the correlation co-efficient between genes, X_i and X_j . When the ‘Get Correlation Matrix’ button is clicked, it will first prompt the user to select the rows for which correlation matrix needs to be viewed. Once the rows are selected and the Submit button is clicked, correlation matrix for all pair of selected genes is displayed. Figure 2.11 shows the correlation matrix created by selecting all 8 neighbours of ‘YKL204W’ shown in Figure 2.9.

Correlation Matrix For *Saccharomyces cerevisiae*

Dataset: Scerevisiae_1point1

ProbeID		10007_at	10168_at	10235_at	4087_at	7924_at	8383_at	9161_at	9578_at
	Systematic Name	YLR337C	YLR187W	YLR116W	YIR006C	YPL190C	YOR181W	YNL278W	YMR047C
10007_at	YLR337C	1	0.68	0.7	0.79	0.59	0.73	0.62	0.55
10168_at	YLR187W	0.68	1	0.65	0.67	0.56	0.58	0.74	0.45
10235_at	YLR116W	0.7	0.65	1	0.66	0.45	0.66	0.54	0.46
4087_at	YIR006C	0.79	0.67	0.66	1	0.57	0.75	0.63	0.59
7924_at	YPL190C	0.59	0.56	0.45	0.57	1	0.45	0.52	0.41
8383_at	YOR181W	0.73	0.58	0.66	0.75	0.45	1	0.48	0.44
9161_at	YNL278W	0.62	0.74	0.54	0.63	0.52	0.48	1	0.45
9578_at	YMR047C	0.55	0.45	0.46	0.59	0.41	0.44	0.45	1

Figure 2.11 Correlation matrix for the selected genes. This correlation matrix is created by selecting all 8 neighbours of 'YKL204W' shown in Figure 2.9.

When the hyperlink on ProbeID in the correlation matrix table (Figure 2.11) is clicked, then the following results are displayed in a new page:

- Information about the gene selected. This table also provides the number of neighbours at the given correlation co-efficient.
- Table containing information about all the neighbours of the selected gene at a correlation co-efficient that was used for generating the correlation matrix previously.

The table also displays the correlation co-efficient between the selected Probe ID and its neighbours at that correlation co-efficient. The correlation co-efficient for viewing the number of neighbours can be changed by using the 'Change Correlation Co-efficient' drop down list box available just below the Gene Information table as shown in Figure 2.12.

2.3.3.2 Integration with MetNet database

The Search results in RegulonIT are designed to display pathway information from the MetNet(13) database using the MetNet API. The MetNet API consists of set of Java library

The Below Table Provides Information For YIR006C

Probe ID:	4087_at
Regulon to which gene belongs to:	22
Symbol:	PAN1
Gene title:	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p associates with actin patches on the cell cortex of poly(A) ribonuclease
SwissProt:	P32521
GO Biological Process:	0000147 // actin cortical patch assembly // inferred from mutant phenotype /// 0000910 // cytokinesis // inferred from endocytosis // inferred from mutant phenotype /// 0007120 // axial cellular bud site selection // inferred from mutant phenotype
GO Cellular Component:	0005634 // nucleus // inferred from direct assay /// 0005737 // cytoplasm // inferred from direct assay /// 0005737 // c3 annotation /// 0005856 // cytoskeleton // inferred from electronic annotation /// 0005886 // plasma membrane // inferred from electronic annotation /// 0010008 // endosome membrane // inferred from electronic annotation /// 0016020 // membrane // inferred from electronic annotation /// 0012222 // actin filament // inferred from direct assay
GO Molecular Function:	0003779 // actin binding // inferred from electronic annotation /// 0005609 // calcium ion binding // inferred from electronic annotation /// 0005609 // calcium ion binding // inferred from physical interaction
Number of neighbours at correlation 0.7 :	3

Change Co-relation Co-efficient:

Figure 2.12 Table generated when probeid ‘4087at’ is selected from Figure 2.11. The table provides detailed information about the gene selected and also displays the neighbours of the gene at the selected correlation.

files which are integrated into our project to pull out pathway information from the MetNet database.

As seen in Figure 2.13, our application pulls out pathway information for each row in the table. If the pathway information corresponding to a particular row is not found, ‘No pathway information found’ is displayed. If more than one pathway information is available, then they are displayed one after the other separated by a line. The pathways have a hyperlink on them which when clicked; display a more detailed description of the pathway from the MetNet online website as shown in Figure 2.14.

2.3.3.3 Integration with KEGG database

Currently, our web application has three search options available with KEGG(11)(12) as shown in Figure 2.15.

- Get Pathways - When the ‘Get Pathways’ radio button is clicked, it prompts the user to select the rows for which KEGG pathway information has to be displayed. When the rows are selected and the Submit button is clicked, it pulls out pathway information from

LocusID	SwissProt	Description	Pathway from METNET Database	Gene Title	GO Biological Process
AT5G24530	Q8LEJ4 // Q9FLV0	flavanone 3-hydroxylase-like protein ; supported by full-length cDNA: Ceres:149654.	Flavonoid (WYJ) flavonoid biosynthesis leucopelargonidin and	DMR6 (DOWNY MILDEW RESISTANT 6); oxidoreductase/oxidoreductase, acting on paired donors, with	0009617 // response to bacterium // inferred from genetic interaction /// 0009620 // response to fungus // inferred from
AT3G04720	P43082 // Q8H7F8	hevein-like protein precursor (PR-4) identical to hevein-like protein precursor GB:P43082 [Arabidopsis thaliana].	JA signaling	PR4 (PATHOGENESIS-RELATED 4); chitin binding	0006032 // chitin catabolic process // inferred from electronic annotation /// 0009615 // response to virus // inferred from expression
AT1G64280	B2BDI6 // P93002 // Q8L9W4	transcription factor inhibitor I kappa B, putative similar to GI:1916912 from [Arabidopsis thaliana]; supported by	JA signaling NPR1 mediated disease resistance	NPR1 (NONEXPRESSER OF PR GENES 1); protein binding / transcription activator	0006952 // defense response // inferred from electronic annotation /// 0008219 // cell death // inferred from genetic
AT2G26560	O48723 // Q8LDK8	similar to latex allergen from Hevea brasiliensis ; supported by full-length cDNA: Ceres:1999.	No pathway information found	PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	0006629 // lipid metabolic process // inferred from direct assay /// 0006629 // lipid metabolic process // inferred from electronic
	Q9C508 //	unknown protein	No pathway information	---	0006863 // purine transport //

Figure 2.13 MetNet pathway information. The search results displays the pathway information from the MetNet database for the genes present in the table. The pathways have hyperlinks on them, which when clicked, displays detailed information about the pathways in the MetNet online website.

MetNet Online

MetNet Home | [Browse](#) | [Search](#) | [Tools](#) | [My MetNet](#) |

Pathways | [Organelles](#) | [Interactions](#) | [Entities](#) ■Ara □Chl

Pathway details: **JA signaling** export functions:

[General info](#) | [Interaction details](#) | [Linked pathways](#) | [Protein-protein interactions](#)

Notes

Pathway was created on Thu Aug 7, 2008.
 Contributed by siva:
 Jasmonoyl-isoleucine (JA-Ile) promotes SCFCO11 interaction with JAZ transcriptional repressors, leading to their ubiquitination and degradation by the 26S proteasome. The MYC2 transcription factor is then free to regulate the expression of genes involved in jasmonate response. The JAR1 conjugating enzyme is localized in the cytosol, so JA-Ile might be synthesized there and translocated to the nucleus where MYC2 and JAZ are located. References:

Parts of this pathway occur in: ■ nucleus ■ cytosol ■ plastid ■ not assigned

Figure 2.14 MetNet pathway information from MetNet online website.

The screenshot shows a web interface with five buttons, each with a question mark icon to its right:

- Get Correlation matrix
- MetNet database
- KEGG's database
- MetaOmGraph
- Download Table

Below the buttons, there is a text prompt: "Please select an option for viewing data from KEGG database". Underneath this prompt are three radio button options:

- Get pathways
- Enter probeid and view pathway information
- Get Common pathway information

At the bottom, there is a text prompt: "Select row/rows in the table below and click submit" followed by a "Submit" button.

Figure 2.15 Different features available with KEGG database.

the KEGG database and displays the information in a new page(Figure 2.16). This page also contains a detailed description about the genes selected.

- Enter probeid and view Pathway information - Clicking on this option displays a textbox and prompts the user to enter the probeid for which KEGG pathway information has to be displayed. Once the probeid is entered and the 'Submit' button is clicked, the KEGG pathway information is retrieved and displayed in a new page.
- Get Common Pathways - This option is used for selecting a set of genes and displaying the pathway information that is common to these genes(Figure 2.17).

Figure 2.17 shows common pathways when rows containing locusids AT5G37510, AT5G08530 and AT3G12260 are selected for fetching the results.

2.3.3.4 Integration with MetaOmGraph

When the MetaOmGraph(7) button shown in Figure 2.10 is clicked, it displays two options:

- Regulon analysis
- Gene analysis

Locus ID	Symbol	RegulonID	Pathway Definition from KEGG's	Description	Swissprot	ProbelID	GO Biological Process	GO C
AT5G24530	DMR6	12	No pathway information found	flavanone 3-hydroxylase-like protein ; supported by full-length cDNA: Ceres:149654.	Q8LEJ4 /// Q9FLV0	249754_at	0009617 // response to bacterium // inferred from genetic interaction /// 0009620 // response to fungus // inferred from	---
AT4G39640	GGT1	12	Taurine and hypotaurine metabolism - Arabidopsis thaliana (thale cress)	putative gamma-glutamyltransferase gamma-glutamyltransferase, Arabidopsis thaliana, PIR2:S58286	B9DI67 /// Q39078 /// Q8VYW6	252906_at	0006751 // glutathione catabolic process // inferred from direct assay /// 0006979 // response to oxidative stress // inferred from direct assay	000950E // inferre 004804E // from dir
AT3G04720	PR4	12	No pathway information found	hevein-like protein precursor (PR-4) identical to hevein-like protein precursor GB:P43082 [Arabidopsis thaliana].	P43082 /// Q8H7F8	258791_at	0006032 // chitin catabolic process // inferred from electronic annotation /// 0009615 // response to virus // inferred from expression	001250E system electror
AT1G64280	NPR1	12	Plant hormone signal transduction - Arabidopsis thaliana (thale cress)	transcription factor inhibitor I kappa B, putative similar to GI:1916912 from [Arabidopsis thaliana]; supported by	B2BD16 /// P93002 /// Q8L9W4	259764_at	0006952 // defense response // inferred from electronic annotation /// 0008219 // cell death // inferred from genetic	000563E from dir cytopla: direct a:
			Nitrogen metabolism -	nitrate reductase, putative similar to nitrate reductase	C0Z2B5 /// P11035 ///		0006809 // nitric oxide biosynthetic process //	000577E from dir

Figure 2.16 Get KEGG Pathways for selected genes for *Arabidopsis thaliana*. This option prompts the user to select the genes for which KEGG pathway information has to be displayed. Once the genes are selected and the search button is clicked, the KEGG pathways are displayed in a new page as shown in the figure.

Kegg Pathway Information For Arabidopsis Thaliana

Locus ID	Common Pathways
AT5G37510	Oxidative phosphorylation - Arabidopsis thaliana (thale cress) Metabolic pathways - Arabidopsis thaliana (thale cress)
AT5G08530	
AT3G12260	

Figure 2.17 Get KEGG common pathways for *Arabidopsis thaliana*. This option allows the user to view KEGG pathways that are common to a set of genes. The above figure shows pathways that are common to locusids AT5G37510, AT5G08530 and AT3G12260.

```

- <Lists>
- <List name="Regulon 1">
  <id>253834_at</id>
  <id>253857_at</id>
  <id>257832_at</id>
  <id>261457_at</id>
  <id>245948_at</id>
  <id>246547_at</id>
</List>
- <List name="Regulon 54">
  <id>257611_at</id>
  <id>261144_s_at</id>
  <id>262505_at</id>
  <id>263256_at</id>
  <id>263703_at</id>
</List>
- <List name="Regulon 129">
  <id>245693_at</id>
</List>
- <List name="Regulon 178">
  <id>265481_at</id>
</List>
- <List name="Regulon 628">
  <id>249128_at</id>
</List>
</Lists>

```

Figure 2.18 Hierarchical representation of selected genes in XML file for Regulon Analysis. This option allows the user to analyze accumulation levels of genes, regulon-wise, in MetaOmGraph.

Selecting the ‘Regulon analysis’ option will first prompt the user to select the rows in the table which has to be exported to MetaOmGraph. It will also prompt the user to enter a file name to store this regulon and gene information in a xml file. Once the genes are selected and a file name is specified, the ‘Save To Disk’ has to be clicked. This will open a dialog box to specify the path where the xml file has to be saved. Figure 2.18 shows the hierarchy of the xml file for a select set of genes for regulon analysis. The genes selected are arranged according to the regulon to which they belong. Hence, this allows the user to analyze the accumulation levels of the selected genes, regulon-wise in MetaOmgraph. Once the xml file is saved in the local machine, it could be imported into MetaOmGraph by using the ‘Import Lists’ option available in the Project menu bar in MetaOmGraph. Once the xml file has been imported, the list of regulons shows up in the lists section in the left side of MetaOmGraph as shown in Figure 2.19.

Figure 2.20 shows a plot when regulon 1 is selected from the list and the ‘Plot’ option is used. The plot provides accumulation level information for all the genes in the list selected, in this case regulon 1, for different samples. Selecting the ‘Gene analysis’ option would put all

Lists	Locus ID	Gene Name	Pathways
Complete List	AT1G21065		
Regulon 1	AT3G26740		
Regulon 129	AT4G27800	PHOSPHATASE PPH1	
Regulon 178	AT4G27990		
Regulon 54	AT5G14970		
Regulon 628	AT5G19540		

Figure 2.19 Imported list from RegulonIT in MetaOmGraph. Once the xml file is imported into MetaOmGraph, it displays all the regulons in a list as shown in the figure above.

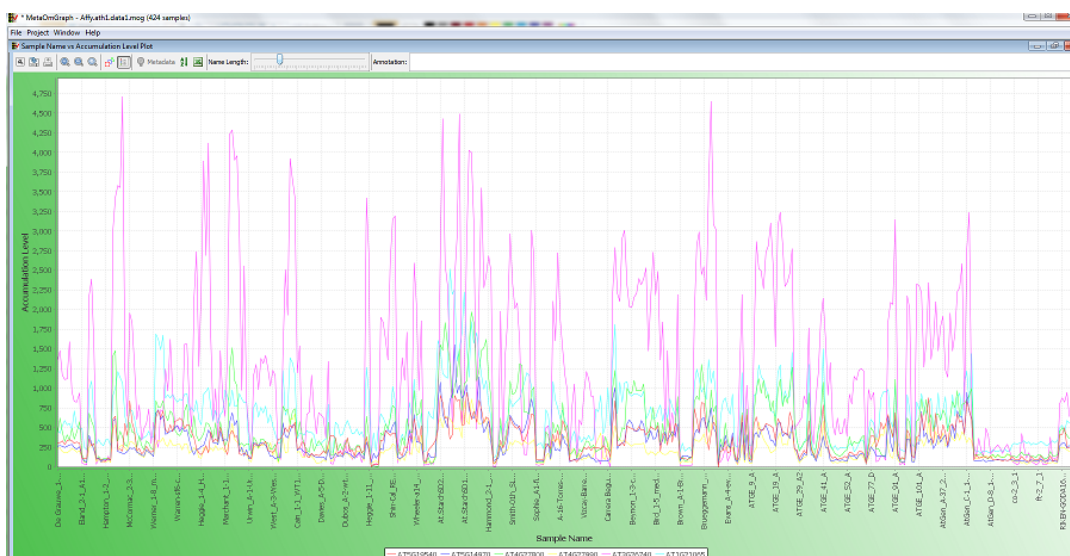


Figure 2.20 Plot in MetaOmGraph showing accumulation level of genes in regulon 1 for various samples.

the selected genes in a single list as shown in Figure 2.21, so that all the genes selected can be analysed in the same plot. This could then be imported into MetaOmGraph as discussed above.

2.3.4 Get correlation matrix from text area

This feature allows the user to enter a set of genes and view the correlation matrix between them. For *Saccharomyces cerevisiae*, there are three ways for viewing the correlation matrix as shown in Figure 2.22. We could either view by entering systematic names, Probe IDs or Symbols. Once the genes are entered in the text area, a dataset must be selected using the

```

- <Lists>
- <List name="All Selected Genes">
  <id>253834_at</id>
  <id>253857_at</id>
  <id>257832_at</id>
  <id>261457_at</id>
  <id>245948_at</id>
  <id>246547_at</id>
  <id>257611_at</id>
  <id>261144_s_at</id>
  <id>262505_at</id>
  <id>263256_at</id>
  <id>263703_at</id>
  <id>245693_at</id>
  <id>265481_at</id>
  <id>249128_at</id>
</List>
</Lists>

```

Figure 2.21 Hierarchical representation of selected genes in XML file for gene analysis. This creates a single list with all the selected genes.

drop down list box. When the ‘Submit’ button is clicked, the correlation matrix for the entered genes is retrieved and displayed (Figure 2.23). If ‘n’ genes are entered, then an ‘n*n’ matrix is displayed.

2.3.5 Search by multiple genes

This feature allows the user to enter more than one gene and view information. The form layout is somewhat similar to the ‘Get Correlation from Text area’ feature, where the genes to be analysed are entered in a text-area and the correlation co-efficient and the dataset are selected from the drop-down list box. When the dataset is selected from the drop down list box, a detailed description of the dataset is displayed just below the drop-down list box. When the ‘Submit’ button is clicked, the information about all the genes entered is retrieved from the database and is displayed in the form of a table. Detailed information about each of these genes can be viewed by clicking the hyperlink on the Probe ID column.

2.3.6 Search within table

So far, we have seen that most of the search results are displayed in the form of a table and some of these tables might contain a lot of rows that it might be difficult for the user to search for a particular entry in the table. In order to overcome this, we have a search feature which allows the user to enter a keyword and search the entire table for the entry. If the keyword is

Correlation Matrix For *Saccharomyces cerevisiae*

Select Search Criteria [?](#)

Systematic name
 Probe ID
 Symbol

YIL129C
 YIL153W
 YHR165C
 YGR097W
 YGL197W
 YDR432W

[?](#)

Select Dataset: List of datasets

Figure 2.22 Viewing correlation matrix from text area for *Saccharomyces erevisiae*. This feature prompts the user to enter the genes manually in the text area and view correlation matrix for all the entered genes.

Correlation Matrix For *Saccharomyces cerevisiae*

ProbeID		4227_at	4248_at	4370_at	4933_at	5228_at	6038_at	6039_g_at
	Systematic Name	YIL129C	YIL153W	YHR165C	YGR097W	YGL197W	YDR432W	YDR432W
4227_at	YIL129C	0	0.28	0.76	0.33	0.67	0.23	0.21
4248_at	YIL153W	0.28	0	0.31	0.34	0.32	0.42	0.49
4370_at	YHR165C	0.76	0.31	0	0.49	0.73	0.34	0.31
4933_at	YGR097W	0.33	0.34	0.49	0	0.59	0.4	0.44
5228_at	YGL197W	0.67	0.32	0.73	0.59	0	0.38	0.36
6038_at	YDR432W	0.23	0.42	0.34	0.4	0.38	0	0.72
6039_g_at	YDR432W	0.21	0.49	0.31	0.44	0.36	0.72	0

Figure 2.23 Correlation matrix table for the set of genes entered.

found, then the browser scrolls to that part of the page where the entry exists and highlights the entire row.

2.3.7 Sort

The sort feature is used to sort the data in the table. When a table needs to be sorted by a particular column, then the column header needs to be clicked once. When the header is clicked, the table gets sorted by ascending order of the column. When the column header is clicked again, the table gets sorted by descending order of the column. The sort feature is implemented by using the `sorttable.js`(23) library file.

2.3.8 Case Study 1 - Study of Regulon 48 in Human co-expression network prepared and clustered by Feng et al.(2)

RegulonIT tool was used for studying regulon 48 in the *Human* co-expression dataset prepared by Feng et al.(2). It can be seen from Figure 2.24 that the number of genes in regulon 48 is 9. When the Pearson correlation matrix is viewed for all the 9 genes, it could be seen from Figure 2.25 that 8 of the 9 genes are totally interconnected with each other. Further, the number of neighbours for each of these genes is 9 or 10. A closer look at each of the neighbours indicate that this regulon is isolated and has no interactions with other regulons as claimed by Feng et al. Figure 2.26 shows the Kegg(11)(12) pathway information for the 8 interconnected genes present in regulon 48. It could be seen that 7 of the 8 neighbours participate in the Mineral absorption pathway.

Feng et al.(2) analysis of Regulon 48 explains that, each of the genes encodes one of the eight metallothioneins. This is an isolated regulon, which means the genes present in this regulon are only connected to each other and there is no connection with any other genes in other regulons. It was concluded by Feng et al.(2) that regulon 48 is highly dense and contains all eight of the metallothionein (MT) antioxidant genes in the human genome.

Total number of genes in regulon at correlation co-efficient 0.7: 9

-
-
-
-
-

Search Table		Pathways	GO Biological Process	GO Cellular Component	GO Molecular Function	ProbeID	Number of neighbors
<input checked="" type="checkbox"/>	Gene Symbol	---	0006878 // cellular copper ion homeostasis // traceable author statement	---	0005515 // protein binding // inferred from physical interaction /// 0008270 // zinc ion binding // inferred from electronic annotation ///	212185_x_at	9
<input checked="" type="checkbox"/>	MT2A	---	0010038 // response to metal ion // traceable author statement	---	0005507 // copper ion binding // inferred from electronic annotation /// 0008270 // zinc ion binding // inferred from electronic annotation ///	208581_x_at	9
<input checked="" type="checkbox"/>	MT1X	---	---	---	---	---	---

Figure 2.24 Search results when Regulon 48 is used as the input query.

Correlation Matrix For *Homo sapiens*
Dataset: Human_regulons_1point1

ProbeID		204745_x_at	206461_x_at	208581_x_at	210524_x_at	211456_x_at	212185_x_at	212859_x_at	216336_x_at	217165_x_at
	Symbol	MT1G	MT1H	MT1X	DDX42	MT1P2	MT2A	MT1E	MT1M	MT1F
204745_x_at	MT1G	1	0.88	0.88	0.74	0.87	0.9	0.79	0.86	0.83
206461_x_at	MT1H	0.88	1	0.93	0.67	0.92	0.89	0.83	0.86	0.89
208581_x_at	MT1X	0.88	0.93	1	0.64	0.92	0.93	0.82	0.87	0.87
210524_x_at	DDX42	0.74	0.67	0.64	1	0.66	0.66	0.68	0.67	0.7
211456_x_at	MT1P2	0.87	0.92	0.92	0.66	1	0.88	0.81	0.86	0.85
212185_x_at	MT2A	0.9	0.89	0.93	0.66	0.88	1	0.78	0.86	0.82
212859_x_at	MT1E	0.79	0.83	0.82	0.68	0.81	0.78	1	0.87	0.85
216336_x_at	MT1M	0.86	0.86	0.87	0.67	0.86	0.86	0.87	1	0.83
217165_x_at	MT1F	0.83	0.89	0.87	0.7	0.85	0.82	0.85	0.83	1

Figure 2.25 Pearson correlation matrix for all 9 genes present in Regulon 48.

Kegg Pathway Information For *Homo sapiens*

Symbol ▾	KEGG Pathways	ChrLocation	GO Biological Process	GO Cellular Component	GO Molecular Function	Probe
MT1E	Mineral absorption - Homo sapiens (human)	chr16q13	---	0005737 // cytoplasm // non-traceable author statement	0005507 // copper ion binding // non-traceable author statement /// 0005507 // copper ion binding // inferred from electronic	212859_
MT1F	Mineral absorption - Homo sapiens (human)	chr16q13	---	0005737 // cytoplasm // non-traceable author statement	0005507 // copper ion binding // non-traceable author statement /// 0005507 // copper ion binding // inferred from electronic	217165_
MT1G	Mineral absorption - Homo sapiens (human)	chr16q13	---	---	0005507 // copper ion binding // inferred from electronic annotation /// 0005515 // protein binding // inferred from physical	204745_
MT1H	Mineral absorption - Homo sapiens (human)	chr16q13	---	---	0005507 // copper ion binding // inferred from electronic annotation /// 0005515 // protein binding // inferred from physical	206461_
MT1M	Mineral absorption - Homo sapiens (human)	chr16q13 /// chr1q43	---	0005737 // cytoplasm // non-traceable author statement	0005507 // copper ion binding // non-traceable author statement /// 0005507 // copper ion binding // inferred from electronic	216336_

Figure 2.26 Kegg Pathway information for all 8 important genes in Regulon 48.

2.3.9 Case Study 2 - Regulon inter-connectivity

The RegulonIT tool was used for looking up information about three genes, POU2AF1, CD79A and IGHM(Figure). It could be seen from the figure that POU2AF1 and CD79A belong to regulon 47 and IGHM belongs to regulon 10. A correlation matrix generated for these genes show that these genes are interconnected, which means regulon 47 and 10 are interconnected. Feng et al.(2) claim that Regulon 10 is almost entirely composed of immunoglobulins, and regulon 47 contains predominantly genes associated with immune signaling pathways, and this information could be used for developing testable hypothesis about the genes important in integration of immunoglobulin signaling and immune signaling(2).

2.4 Conclusions and future developments

The RegulonIT framework thus helps biologists for viewing regulon, gene and co-expression data in an user-friendly manner using a web interface. The application is available publicly and can be used by anyone with an internet connection and a web browser. The software tool has an user guide section which explains how to use the different features available with this

Search By Multiple Genes For *Homo sapiens*

Select Search Criteria

Probe ID
 Symbol

POU2AF1
 CD79A
 IGHM

Correlation Co-efficient:

Select Dataset:

Figure 2.27 Search by multiple genes feature used for looking up information about POU2AF1, CD79A and IGHM in the *Homo sapiens* dataset prepared by Feng et al.(2)

	Gene Symbol	RegulonID	ProbeID	GO Biological Process	GO Cellular Component	GO Molecular Function
	CD79A	47	205049_s_at	0006955 // immune response // inferred from electronic annotation /// 0007166 // cell surface receptor linked signal	0005771 // multivesicular body // inferred from sequence or structural similarity /// 0005771 // multivesicular body //	0004888 // transmembrane receptor activity // inferred from electronic annotation /// 0005515 // protein binding // inferred from sequence or
	POU2AF1	47	205267_at	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription; DNA-dependent // inferred	0005634 // nucleus // inferred from electronic annotation	0003677 // DNA binding // inferred from electronic annotation /// 0003712 // transcription cofactor activity // traceable author
	IGHM	10	209374_s_at	0006955 // immune response // non-traceable author statement	0005576 // extracellular region // inferred from electronic annotation /// 0005624 // membrane fraction // non-traceable	0003823 // antigen binding // traceable author statement /// 0003823 // antigen binding // inferred from electronic annotation

Figure 2.28 Gene information for POU2AF1, CD79A and IGHM. It could be seen that POU2AF1 and CD79A belong to regulon 47 and IGHM belongs to regulon 10.

Correlation Matrix For *Homo sapiens*

Dataset: Human_regulons_1point1

ProbeID		205049_s_at	205267_at	209374_s_at
	Symbol	CD79A	POU2AF1	IGHM
205049_s_at	CD79A	1	0.71	0.7
205267_at	POU2AF1	0.71	1	0.74
209374_s_at	IGHM	0.7	0.74	1

Figure 2.29 Pearson Correlation Matrix generated for all three genes, POU2AF1, CD79A and IGHM shows that Regulon 47 and Regulon 10 are interconnected.

application and helps the user to understand the tool better.

As with any software application, the RegulonIT application can be modified to include further enhancements. Some features suggested are:

- Capability to download tables generated as csv or text files.
- Integration with more external tools like Cytoscape, MetViz, etc.
- Adding micro-array data into the RegulonIT database and develop a feature that generates regulons on the fly.
- Adding more species data into the database.
- Developing a feature that enables the user to compare two or more regulons.

2.5 Availability and requirements

- Project name: RegulonIT

- Project home page: <http://metnetdb.org:9090/regulonit/>
- Operating system: Platform independent (web-based application)
- Programming language: Java
- Other requirements: A web browser.
- Any restrictions to use by non-academics: none

2.6 Abbreviations

TAIR, The Arabidopsis Information Resource; KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology; MCL, Markov clustering; ACT, Arabidopsis Co-expression Tool; AJAX, Asynchronous JavaScript and XML; JDBC, Java Database Connectivity; API, Application Programming Interface; MVC, Model-View-Controller; HTML, Hypertext Markup Language; URI, Uniform Resource Identifier.

2.7 Authors contributions

AB developed the RegulonIT web tool with constant guidance, support and advice from LM and EW. LM provided suggestions for choosing the resources to be used for developing the web based tool. EW helped in writing the manuscript by providing biological information. Biologists working in the Virtual Reality Application Center(VRAC) in the Iowa State University have also been helping by providing regulon, gene and co-expression data for all three species.

The next chapter explains the implementation in detail.

CHAPTER 3. ORGANIZATION AND IMPLEMENTATION

In this chapter, the details of the implementation are discussed. Java EE has been used extensively for developing this web application. Other notable technologies and API's used are the Struts 1.3(16), MySQL 5.0.77, Ajax (Asynchronous JavaScript and XML)(17), JavaScript, Java database connectivity(JDBC) and Cascaded style sheets(CSS).

3.1 Project organization

The project is organized based on the model-view-controller framework. It contains three main java packages

- Controller - The Controller package contains Action classes. These are basically Java classes which extend the Action class available in the Struts library. The execute() method of the Action class is overridden and the business logic is implemented in this method.
- DAO - DAO stands for Data Active Objects. This package contains Java classes that help connecting to the database and executing SQL queries.
- Model - The model package contains classes that are used for manipulating business data. These classes are Java Beans.

The struts-config.xml file and web.xml file are present in the WEB-INF folder and all the view files(JSPs) are stored in the /webapp folder of the project.

3.2 Struts overview

Figure 3.1 shows the flow pattern of the Struts MVC system architecture. JSP or Java Server Pages are compiled into Java servlets the first time a JSP page is requested. Tomcat 5.5

is a servlet container which provides the environment necessary for this translation, and servlets in the controller component are designed to handle the requests made by the view component from a web browser. Struts uses a special servlet called the `ActionServlet`, which is configured in the `web.xml` file to direct requests to the appropriate servlet in the controller component. The action servlet receives a forward request from the action and instructs Tomcat to send the request to the forward's URL. This architecture makes web applications much easier to design, create, and maintain.

The web application has a deployment descriptor file, `web.xml`, which describes the configuration of the web application. The configuration includes welcome pages, servlet mappings and parameters to servlets. The Struts `ActionServlet` is configured in such a way that it will handle all requests for a given mapping as shown in Figure 3.2.

The Struts configuration file, `struts-config.xml`, contains details as to how the model, view, and controller components are tied together. It associates paths with the controller components known as Action classes as shown in Figure 3.3. The mechanism by which Struts work is discussed below.

When the Struts `ActionServlet` receives an incoming request, it invokes the corresponding controller (Action) component configured in the `struts-config.xml` file. For each action, the resulting page (View) that should be displayed once the action is complete can also be configured. There could be more than one view as the result of an action. The Struts system using this configuration file forwards the response to the appropriate page once the business logic has been processed. The model part of the application is called from within the controller component. A Java Bean is associated with an action in the `struts-config.xml` file and is used for storing form data or display data. These beans are made visible to the controller component, using the `ActionForm` class available with Struts, and any JSP (view) page that is associated with that controller. The client submits the data from the web browser using POST/GET methods, and the Struts system populates the bean with this data before calling the controller component. The front end in our web application is developed using Java Server Pages (JSP) which uses

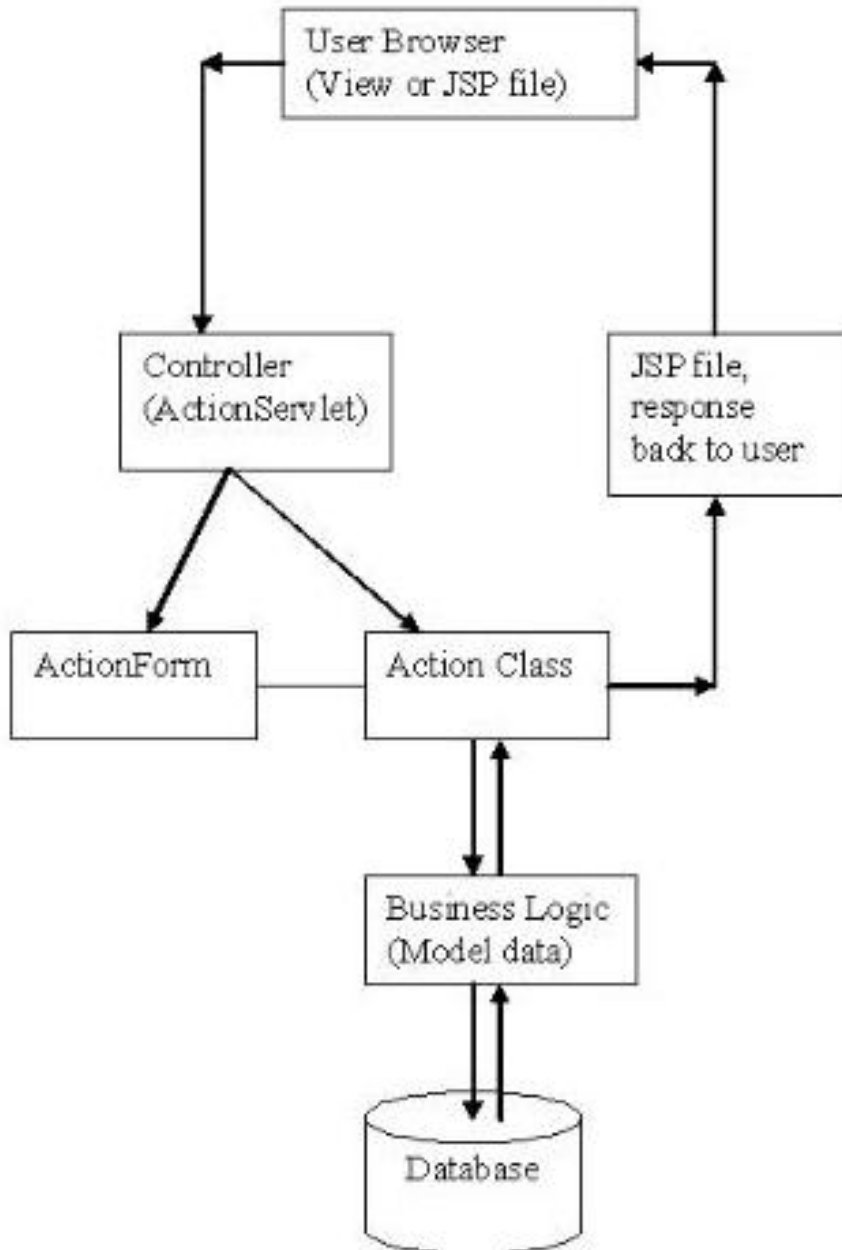


Figure 3.1 Flow pattern of the Struts MVC framework

```

<servlet>
  <servlet-name>action</servlet-name>
  <servlet-class>
    org.apache.struts.action.ActionServlet
  </servlet-class>
  <init-param>
    <param-name>config</param-name>
    <param-value>/WEB-INF/struts-config.xml</param-value>
  </init-param>
  <load-on-startup>1</load-on-startup>
</servlet>
<servlet-mapping>
  <servlet-name>action</servlet-name>
  <url-pattern>*.do</url-pattern>
</servlet-mapping>

```

Figure 3.2 web.xml

```

  <action path="/login"
    type="controller.loginauthenticationAction"
    name="loginauthenticationform">
    <forward name="success" path="/admincapabilities.jsp"/>
    <forward name="failure" path="/index.jsp"/>
  </action>

```

Figure 3.3 Example of action path configuration

the Struts tag libraries for developing a seamless presentation layer. The Struts tag libraries includes Struts-specific tags that help display dynamic data in our view.

3.3 Implementation

The following sections use the example of search by regulon feature in *Arabidopsis thaliana* to explain how the application has been implemented. JSP(Java Server Pages), HTML(Hyper Text Markup Language), JavaScript, AJAX (Asynchronous JavaScript and XML), CSS(Cascaded Style Sheets) have been used for delivering dynamic data.

3.3.1 Request View

The view component is basically a JSP file which contains text boxes, radio buttons, drop-down list boxes and check boxes for obtaining input from the user. The code in Figure 3.4 shows implementation of some of these input boxes.

This creates a text box with name ‘regulonid’ and a drop down list box with name ‘corelationcoeff’. The search by regulon JSP page when loaded for the first time also displays the list of datasets available for *Arabidopsis thaliana*. This is achieved by using AJAX and the ‘onload’ option available with the body tag.

The function `retrieveURL()` in Figure 3.5 takes in two parameters:

- The request query string which contains the action path information, and
- The ‘datasets’ tag which will be used for displaying the response once the request has been processed. The `retrieveURL()` function is implemented as a part of AJAX.

3.3.1.1 AJAX

Ajax stands for Asynchronous JavaScript + XML. The main idea behind AJAX is that re-building a web page for every user interaction is inefficient and should be avoided. In other terms, when a form is submitted, AJAX helps retrieving results without the web page getting refreshed. Frank Zammetti’s(17) article on XHR Struts has been used for implementing this.

```

<table cellpadding = "10">
  <tr>
    <td class="left">
      <b>Enter RegulonId:</b>
    </td>
    <td class="left">
      <input type="text" id="regid" name="regulonid" style="width:40px">
    </td>
  </tr>

  <tr>
    <td><b>Co-relation Co-efficient : </b></td>
    <td>
      <select name="corelationcoeff">
        <option value="0.7" >0.7</option>
        <option value="0.75" >0.75</option>
        <option value="0.8" >0.8</option>
        <option value="0.85" >0.85</option>
        <option value="0.9" >0.9</option>
        <option value="0.95" >0.95</option>
      </select>
    </td>
  </tr>
</table>

```

Figure 3.4 Example of request view component

```

<body onload="retrieveURL( 'getlistofdatabases.do?organism=arabidopsis ',
                           'databases ');" >

```

Figure 3.5 The retrieveURL Javascript function call from the body tag

Ajax is based on a component called XMLHttpRequest. The XMLHttpRequest is a client side component and must be instantiated via scripting in the JSP using JavaScript.

The basic idea of the code in Figure 3.6 is simple. When the retrieveURL() function is called, it creates an instance of the XMLHttpRequest object depending on the web browser, and then sends a request to the URL provided using the GET method. The third parameter in the req.open is used to specify whether the call be asynchronous or not. Setting the value to true makes it asynchronous. Once the req.send() statement is executed, the request is forwarded to the struts-config.xml file which decides which Action class needs to be called. Once the business logic is processed in the servlet (Action class), a response is sent back. One important line in the above code is the req.onreadystatechange = processStateChange(tag) line. This line of code is for setting up an event handler. When the state of the request changes, a response is sent back and the processStateChange() function will be called.

We then question the state of the XMLHttpRequest object and respond appropriately. Next, we check the HTTP response code that was received. If the response code received is any number other than 200, it will result in an error. In the example shown in Figure 3.6, when a complete response is returned from the servlet, and if it has an OK response, the text we received is inserted into an HTML element whose identity is 'datasetsdata', since the variable tag has 'datasets' as its value. Hence, a call is made to the server without the web page getting refreshed and the results are displayed on the same page. The asynchronous nature of AJAX helps the user in making more than one request to the server without waiting for response from a given request.

Once the user enters a regulon, selects a correlation co-efficient and selects a dataset from the populated list, the 'Search' button needs to be clicked. The functionality of the 'Search' button is implemented as shown in Figure 3.7.

The code in Figure 3.7 calls a JavaScript function get_checked_values() by passing information about the regulon, correlation co-efficient, and dataset. This function gets the gene attributes to be displayed, once we get the response, and sends the request to the server using the retrieveURL() function in AJAX. Once the request is sent, the business logic is called by the Controller component is explained in the section 3.3.2.

```

var req;
var which;

function retrieveURL(url,tag) {
    loadSubmit();
    if (window.XMLHttpRequest) { // Non-IE browsers
        req = new XMLHttpRequest();
        req.onreadystatechange = function () {
            processStateChange(tag);
        };
    }
    try {
        req.open("GET", url, true);
    } catch (e) {
        alert(e);
    }
    req.send(null);
} else if (window.ActiveXObject) { // IE
    req = new ActiveXObject("Microsoft.XMLHTTP");
    if (req) {
        req.onreadystatechange = function () {
            processStateChange(tag);
        };
        req.open("GET", url, true);
        req.send();
    }
}

function processStateChange(tag) {
    if (req.readyState == 4) { // Complete
        if (req.status == 200) { // OK response
            document.getElementById("progress").style.visibility = "hidden";
            document.getElementById(tag + 'data').innerHTML = req.responseText;
        } else {
            alert("Problem: " + req.statusText);
        }
    }
}

```

Figure 3.6 AJAX implementation

```
<input type="button" value="Search" onclick=
"get_checked_values('searchbyregulonarabidopsis.do?corel_val=' +
correlationcoeff.value + '&data_set=' + this.form.dataset.value ,
'genes', this.form, this.form.dataset.value);"/>
```

Figure 3.7 Functionality of the Search button

3.3.2 Controller

The Controller component forms the crux of our application. The controller component contains Action classes which process the business logic and sends back the response to the view component. For the search by regulon, using *Arabidopsis thaliana* as a specific example, the important segments in the code are explained in Figure 3.8.

The Java class 'searchbyregulonarabidopsisAction' extends the Action class available in the Struts library. The execute method of the Action class is overridden and the business logic is implemented in this method. The execute method defines four parameters:

- ActionMapping mapping: The ActionMapping class contains a method called findforward() which is used for forwarding the response to the view that needs to be displayed once the business logic has been executed.
- ActionForm inform: The ActionForm is the Java Bean with set() and get() properties that are used for storing and retrieving form values. These are usually input values from the JSP file which has been entered by the user.
- HttpServletRequest class is used for handling requests from the JSP and the HttpServletResponse is for handling responses once the Action class has completed execution of its logic.

The request.getParameter() method of the HttpServletRequest class is used for getting data from the request query string sent from the JSP. By using this method, information about the regulon, correlation and dataset information is obtained and a call is made to the


```

public class searchbyregulonarabidopsisAction extends Action {

public ActionForward execute(ActionMapping mapping, ActionForm inForm,
HttpServletRequest request, HttpServletResponse response) throws Exception {

String regulon;
regulon = request.getParameter("regulon_value");
...
...
ResultSet result1 = searchbyregulonarabidopsisDAO.getResultset(regulon,
                                                                corel, dataset);
ArrayList<arabidopsisForm> list = new ArrayList<arabidopsisForm>();
String AGI;
int count = 0

while (result1.next()) { // process results one row at a time
    ArrayList<arabidopsisForm> locusids = new ArrayList<arabidopsisForm>();
    count++;
    arabidopsisForm a1 = new arabidopsisForm();
    a1.setRegulonid(Integer.parseInt(regulon));
    a1.setDataset(dataset);
    a1.setProbeid(result1.getString(1));

    a1.setSymbol(result1.getString(2));
    ...
    ...
    a1.setAGI(AGI);
    Scanner scanner1 = new Scanner(AGI);
    scanner1.useDelimiter(";");

    while(scanner1.hasNext()) {
        arabidopsisForm a2 = new arabidopsisForm();
        String locusid;
        locusid = scanner1.next();
        a2.setAGI(locusid);
        locusids.add(a2);
    }
    ....
    ....
}
n1.setNowhenincreased(count);
request.setAttribute("list", list);
...
...
return mapping.findForward("success");

}
}

```

Figure 3.8 Example of a Controller class

searchbyregulonarabidopsisDAO class in the DAO(Data Access Objects) package for retrieving data from the database for the input provided by the user. The data thus retrieved from the database is stored using a ResultSet object and is iterated and stored in a list using the user defined arabidopsisForm class and the ArrayList collection which is available in the Java.Util library package. The arabidopsisForm class acts as the Model component for storing data. The data containing regulon and gene information for the input entered by the user is now present in the form of a list and is sent back to the view component using the request.setAttribute() method.

3.3.3 Model

The model package contains classes that are used for holding data retrieved from the database. As shown in Figure 3.9, the model class can have list attributes for storing data that have multiple values. For example, a gene can have more than one locus id. Hence when the response is sent back, there will be a list(list of locus ids) within another list(the master list with all the information retrieved from the database for the entered input).

3.3.4 DAO

As discussed in section 3.3.2, database connections are handled by a separate package called the DAO package.

Database connectivity is achieved using the JDBC (Java Database Connectivity) API. The configurations are made in the context.xml file, as shown in Figure 3.10, where we can declare the characteristics of the resource to be returned for JNDI lookups of resource-ref and resource-env-ref elements in the web application deployment descriptor. We must also define the needed resource parameters as attributes of the Resource element, to configure the object factory to be used.

The driverclass name, username, password and the database url are specified and connection is established using the InitialContext and DataSource objects in the DAO class as shown in Figure 3.11.

```

public class arabidopsisForm extends OrganismForm{

String swissprot;
String locusid;
ArrayList<arabidopsisForm> locusids;
...
...
public String getSwissprot() {
    return swissprot;
}
public void setSwissprot(String swissprot) {
    this.swissprot = swissprot;
}
public String getLocusid() {
    return locusid;
}
public void setLocusid(String locusid) {
    this.locusid = locusid;
}
public ArrayList<arabidopsisForm> getLocusids() {
    return locusids;
}
public void setLocusids(ArrayList<arabidopsisForm> locusids) {
    this.locusids = locusids;
}
...
...
}

```

Figure 3.9 Example of a Model class

```

<Resource name="jdbc/TestDB" auth="Container" type="javax.sql.DataSource"
    maxActive="1000" maxIdle="30" maxWait="10000"
    username="***" password="***" driverClassName="com.mysql.jdbc.Driver
    url="***"/>

```

Figure 3.10 Database configuration in context.xml file

```

InitialContext initContext = new InitialContext ();
DataSource ds = (DataSource)initContext.lookup("java:comp/env/jdbc/TestDB");
java.sql.Connection conn = ds.getConnection ();
Statement stm = conn.createStatement ();
ResultSet result1 = stm.executeQuery (sqlquery);

```

Figure 3.11 Establishing database connection using InitialContext and DataSource objects

The Statement class can be used for executing any SQL statements and the result set data thus obtained after data is retrieved is sent back to the Action class which in turn stores the result set as a list and sends the response back to the JSP.

3.3.5 Response view

Once the logic is processed by the Action class in the Controller package, the response is forwarded to the appropriate JSP using the findforward() method of the Controller class. This JSP contains Struts tags and HTML tags for reading the response and displaying the results in a table format. In most of the search features, the response is in the form of a list which contains genetic information for the input entered by the user. For ‘Search by Regulon for Arabisopsis thaliana’ feature, each element in this list is an instance of the arabidopsisForm model class.

The first three lines of the code in Figure 3.12 include three main tag libraries available with Struts - the bean, html and logic tag libraries. A detailed explanation of these tag libraries is given in the section 3.3.8. The logic:present tag in the code is used to check if a list with name ‘list’ has been sent from the servlet. If the list is present, it is iterated using the logic:iterate tag, and the bean:write tag is used to retrieve the value of each attribute stored as shown in the code. The HTML table tag is used for displaying the list in the form of a table. The sortable.js(23) JavaScript library file included within the script tags is used for sorting the table thus obtained and the style tag is used for creating cascaded style sheets for formatting the page. Also, the script tag contains JavaScript functions which will be executed from the client side i.e the web browser. The code in Figure 3.13 shows an example of a JavaScript

```

<%@ taglib uri="http://struts.apache.org/tags-bean" prefix="bean" %>
<%@ taglib uri="http://struts.apache.org/tags-html" prefix="html" %>
<%@ taglib uri="http://struts.apache.org/tags-logic" prefix="logic" %>

<html>
<head>
<style type="text/css">
div.locusid
{

width:100px;
height:100px;
overflow:auto;
}
...
...
<script src="sortable.js"></script>
<link rel="stylesheet" type="text/css" href="stylesheet.css"/>
<script type="text/JavaScript" src="jshashtable.js"></script>
<script>
...

...
<logic:present name="list">
<logic:iterate id="arabidopsisinfolist" name="list">
<tr>
<bean:define id="locusid" name="arabidopsisinfolist" property="AGI"/>
<bean:define id="regulonid" name="arabidopsisinfolist" property="regulonid"/:
<td align="center">
<div class="locusid">
<logic:iterate id="locusids" name="arabidopsisinfolist" property="locusids">
<bean:define id="locusid" name="locusids" property="AGI"/>
<br>
<b><a href=http://www.arabidopsis.org/servlets
      /TairObject?type=locus&name=<%=locusid %> /><b><%=locusid %></b>
<br>
</logic:iterate>
</div>
</td>
<logic:equal name="checkedvals" property="gomf_checked" value="true">
<td align="center">
<div class="auto">
<b><bean:write name="arabidopsisinfolist" property = "gomf" /></b>
</div>
</td>
</logic:equal>
...
...
</tr>
</logic:iterate>
</logic:present>

```

Figure 3.12 Example of a response view component

```

function iteratetable(id) {
searchid = id.replace(/^\s+/g, "");
searchid = searchid.replace(/\s+$/g, "");
var flag = 0;
try {
rows = document.getElementById
('regulontable').getElementsByName("TR");
for (var j = 1; j < rows.length; j++) {
cells = rows[j].getElementsByName("TD");
for (var i = 1; i < cells.length; i++) {
temp = cells[i].textContent;
temp = temp.replace(/^\s+/g, "");
temp = temp.replace(/\s+$/g, "");
if (temp.toUpperCase() == searchid.toUpperCase()){
ScrollToElement(cells[i]);
for (var k=0; k < cells.length; k++){
cells[k].style.backgroundColor = '#AAF';
}
flag = 1;
}
}
}
if (flag==0){
alert(" " + searchid + " " + "not found in table!");
}
}
catch (er) {
alert(er.description);
}
}

```

Figure 3.13 Example of a Javascript function

function which implements the ‘Search Within Table’ feature discussed earlier.

When the user enters a query and clicks the search button, the function in Figure 3.13 is called. The above code uses the HTML DOM(Document Object Model) for getting the table that needs to be searched. The HTML DOM defines a standard way for accessing and manipulating HTML documents. The `document.getElementById`.(‘regulontable’) first fetches the table which has ID as ‘regulontable’, and the `getElementsByName("TR")` method is then used for getting all the rows in the table. These rows are then iterated and for each row, the value entered by the user is checked in each column. If a match is found, then the browser scrolls to that part of the page where the match is found and highlights the entire row.

3.3.6 Getting MetNet pathways using MetNet API

The MetNet(13) API(application programming interface) is a programming library that provides direct access to the MetNet database. It offers flexible data retrieval methods for Java applications that use biological network information. The MetNet API is a JAR file which contains Java packages that can be used for pulling out genetic information from the MetNet


```

Entity ent = Entity.identify(locusid);
PathwayVector pv = ent.getPathways();
for (int i = 0; i < pv.size(); i++) {
System.out.println("Pathway id = " + pv.get(i).id + ",
                    name = " + pv.get(i).name);
}

```

Figure 3.14 Code for retrieving pathways from MetNet database

database. In our web application, we use the MetNet API primarily for retrieving pathway information. The MetNet database currently contains pathway information for Arabidopsis and *Saccharomyces cerevisiae*(yeast).

The code in Figure 3.14 gives a brief idea as to how pathway information is retrieved for Arabidopsis.

The identify() method in the above code is used for retrieving a entity object corresponding to a given locus id from the MetNet database. The entity object thus retrieved uses the getPathways() method for returning a collection of pathway objects. The PathwayVector Class in the MetNet API package is used for managing this collection of pathway objects. The PathwayVector class contains ‘id’ and ‘name’ attributes which provides a detailed description of the pathways retrieved. In order to use the MetNet API, the MySQL driver needs to be imported, but we don’t have to reference it in our source code.

3.3.7 Getting KEGG pathways using KEGG API

The KEGG(11)(12) API(application programming interface) consists of the SOAP/WSDL interface and the REST interface to the KEGG system. It allows searching biochemical pathways in processes. In order to use the KEGG API, the Apache Axis web services library has been imported into our project. This is because the class developed in KEGG API extend classes and implements interfaces developed in the Apache Axis library. Apache Axis is essentially a SOAP engine, a framework for constructing SOAP processors such as clients, servers

```
String [] pathways;
String KEGG_gene_id;
KEGGLocator locator = new KEGGLocator();
KEGGPortType serv = locator.getKEGGPort();
pathways = serv.get_pathways_by_genes(kegg_gene_id);
```

Figure 3.15 Code for retrieving pathways from KEGG database

and gateways. The API is open source and the current version of Axis is written in Java ((11) and ((12)).

The code in Figure 3.15 first creates an instance of KEGGLocator class and uses the getKEGGPort() method for getting the KEGG port. This method returns an instance of KEGGPortType class. The get_pathways_by_genes() method of this instance is used for retrieving pathway information for the entered gene.

3.3.8 Creating views using Struts tag

The application also uses Struts tag libraries in some pages for creating input boxes for getting input from the user. The below section uses the example of ‘View Correlation Matrix’ for Arabidopsis thaliana for explaining how these tags work. Three main tag libraries are available with Struts.

- html - This taglib contains tags used to create Struts input forms, as well as other tags generally useful in the creation of HTML-based user interfaces. Some of the important Struts tags available are html:text, html:radio, html:form, html:select, html:submit etc.

A Java Bean is used for storing the above form data so that it can be used by the controller layer. These Beans are automatically made visible to the controller components. The client submits the data from the web browser using POST/GET methods, and the Struts system updates that data in the Bean before calling the controller component. The Java Bean extends the Struts ActionForm class.


```

<html:form action="/getcorelationmatrixtxtareaarabidopsis">
<table cellpadding="20">
<tr>
<td>
<br><html:radio property="searchcriteria" value="locusid" /> locusid
</td>
...
...
<html:select property="dataset" onchange="fngetdatasetdescription(this.form,"
    <option value="default">Select Dataset</option>
    ...
    ...
</td>
<html:submit onclick="fnvalidate(form);" />
</td>
<td>
<html:reset />
</html:form>

```

Figure 3.16 Example of a view component created using struts tags

Figure 3.17 shows the Java Bean for the view component in Figure 3.16:

- bean - This tag library contains tags that help in accessing beans and their properties.
- logic - This tag library contains tags that are useful in implementing conditional processing of response from the controller and iterating over object collections for generation of output.

Once the request is sent to the servlet, the ActionForm(Java Bean) is populated, the business logic is processed by the Action class and the response is sent back to a JSP which is determined by the struts-config.xml file.

```
public class correlationinfoform extends ActionForm{

    String textareal;
    String searchcriteria;
    String dataset;

    public String getDataset() {
        return dataset;
    }

    public void setDataset(String dataset) {
        this.dataset = dataset;
    }

    public String getSearchcriteria() {
        return searchcriteria;
    }

    public void setSearchcriteria(String searchcriteria) {
        this.searchcriteria = searchcriteria;
    }

    public String getTextareal() {
        return textareal;
    }

    public void setTextareal(String textareal) {
        this.textareal = textareal;
    }
}
```

Figure 3.17 Example of an ActionForm

CHAPTER 4. GENERAL CONCLUSIONS

The RegulonIT framework thus provides an user friendly way for viewing regulon, gene and co-expression data for three species - *Arabidopsis thaliana*, *Saccharomyces cerevisiae*, and *Homo sapiens* using a web interface. It provides interactions with external websites and web services like TAIR, yeast genome, MetNet, KEGG, etc., for providing more genetic information. The tool also provides integration with MetaOmGraph for viewing accumulation levels of genes for different samples.

The tool has been developed using the Struts framework as it provides a clean separation between the model, view and controller components and hence allows easy maintenance. AJAX has been used so that pages are not refreshed each time a request is made. The web tool allows easy addition of new datasets by privileged users and hence makes it possible to maintain live data.

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