Customizable views on semantically integrated networks for systems biology

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Associate Editor: Olga Troyanskaya

ABSTRACT

Motivation: The rise of high-throughput technologies in the post-genomic era has led to the production of large amounts of biological data. Many of these datasets are freely available on the Internet. Making optimal use of these data is a significant challenge for bioinformaticians. Various strategies for integrating data have been proposed to address this challenge. One of the most promising approaches is the development of semantically rich integrated datasets. Although well suited to computational manipulation, such integrated datasets are typically too large and complex for easy visualization and interactive exploration.

Results: We have created an integrated dataset for *Saccharomyces cerevisiae* using the semantic data integration tool Ondex, and have developed a view-based visualization technique that allows for concise graphical representations of the integrated data. The technique was implemented in a plug-in for Cytoscape, called OndexView. We used OndexView to investigate telomere maintenance in *S. cerevisiae*.

Availability: The Ondex yeast dataset and the OndexView plug-in for Cytoscape are accessible at http://bsu.ncl.ac.uk/ondexview.

Supplementary information: Supplementary data is available at Bioinformatics online.

Received on August 27, 2010; revised on February 10, 2011; accepted on March 9, 2011

1 INTRODUCTION

1.1 Systems biology and integrative bioinformatics

Systems biology considers multiple aspects of an organism’s structure and function at the same time, using the plethora of data that is publicly available online. Biologists have access to heterogeneous data covering many different aspects of biology; 1230 entries are listed in the 2010 database issue of Nucleic Acids Research (http://nar.oxfordjournals.org/content/38/suppl_1). For model organisms such as *Saccharomyces cerevisiae*, the abundance of freely available data has long since exceeded the point at which it can be analysed manually.

Most data sources still exist in isolation, each with its own specialization and focus (Stein, 2002). In many cases, databases lack semantic links to each other, even when they are providing data about the same entities. This partitioning of knowledge is a particular problem for systems biology, hampering the examination of the emergent behaviours inherent in complex biological systems. The problem of using distributed, heterogeneous datasets is addressed by the subdiscipline of integrative bioinformatics. There are many different approaches to the integration and querying of large heterogeneous datasets. Early XML-based approaches (Achard et al., 2001) were soon replaced by more sophisticated methods. Federated approaches, such as the distributed annotation system (DAS) (Pilic et al., 2007) establish a central view on the data by translating each internal query into a set of external queries in order to retrieve the required data from the outside sources on the fly (Heimbigner and McLeod, 1985). Semantic web approaches, as endorsed by the Open Biological and Biomedical Ontologies foundry (OBO) (Smith et al., 2007) or as implemented in YeastHub (Cheung et al., 2005), establish a network of interlinked ontologies using a set of controlled vocabularies (Brinkley et al., 2006). Data warehousing approaches such as BioMART (Haidar et al., 2009) EcoCyc (Keseler et al., 2010) and SAMBA (Tanay et al., 2004), convert and incorporate data from their external sources into their own database schema and provide custom queries.

1.2 Ondex

Ondex is a graph-based data integration framework (Kohler et al., 2006), which takes a semantic warehousing approach. Links between entities in different datasets may be directly extracted from the available data sources, inferred as part of the integration, or generated by external tools, such as BLAST (Altschul et al., 1990). These data can subsequently be matched and interlinked with each other semantically. The result is a semantically enriched dataset, with which users can interact and also visualize.
Ondex incorporates data into a network of entities termed ‘concepts’, connected by ‘relations’, all of which can carry ‘attributes’. All concepts, relations and attributes have ‘types’, which are organized in a hierarchical fashion. For example, the concept type Protein is a subtype of Molecule, which is itself a subtype of Thing. This hierarchy means that every Protein concept is also a Molecule and a Thing. Similarly, the relation type catalyzes is a subtype of actively_participates_in. Therefore, every statement that p:Protein catalyzes r:Reaction means that p actively_participates_in r. Adding this type of information means that the computer stores not only data, but also its meaning, providing a ‘semantic representation’ of the data.

A special kind of attribute that all concepts in an Ondex graph have is the cross-reference (called ‘concept accession’ in Ondex). Concept accessions make it easy to connect concepts originating from different sources. For example, if an Ondex dataset contains two Gene concepts which have been imported from two different data sources, but which share the same concept accession, Ondex can connect these concepts with a new relation of type same_as, and can at a later time merge these concepts into a single concept. All concepts and relations also have attached provenance information stating their origin and any associated evidence codes.

The process of integrating data into this data structure is performed by the Ondex workflow engine, which employs a plugin architecture. Parsers, mapping methods and other plugins can be developed using an open API (Taubert et al., 2007) and can subsequently be used in workflows.

In this work, we describe a mechanism to collapse groups of concepts into a simpler, more easily visualized and conceptualized representation. We have implemented this mechanism as a plugin for Cytoscape, called OndexView, which facilitates the focused analysis of parts of a large, complex network. We demonstrate the value of this approach by applying it to an investigation into the systems biology of telomere maintenance in the baker’s yeast *S. cerevisiae*.

### 1.3 Telomere maintenance and BMH1/2

Telomeres are structures composed of the ends of eukaryotic chromosomes together with their capping nucleoprotein complexes. These structures appear to play a major role in the ageing process (Blasco, 2007; Cheung and Deng, 2008). Without the capping proteins, chromosome ends appear as double-stranded breaks to the cell’s DNA damage detection mechanism, triggering a checkpoint response and ultimately cell cycle arrest (Longhese, 2008; Sandell and Zakian, 1993). With each cell division, telomeres shorten (Longhese, 2008). When telomere length falls under a certain threshold, the checkpoint response is triggered. This mechanism appears to contribute to the establishment of a cell’s finite lifespan.

*Saccharomyces cerevisiae* is an excellent subject for studying telomere biology, because it is one of the simplest and most well-studied eukaryotic model organisms, and telomere biology is highly conserved across eukaryotes. In *S. cerevisiae*, an important component of the telomere maintenance mechanism is the protein Cdc13, which binds to the single-stranded DNA overhangs of telomeres. Cdc13 has two major functions: capping the telomeric DNA and recruiting telomerase (Garvik et al., 1995; Nugent et al., 1996), which is part of the telomere repair mechanism. *CDC13* is an essential gene, so it is difficult to characterize using knock-out mutants. However, there is a temperature-sensitive mutant called *cdc13-1*. This mutant has a wild-type phenotype below 26°C, but above this temperature telomeres become uncapped, the checkpoint response is induced and the cells stop dividing (Weinert and Hartwell, 1993).

Epistatic interactions between *cdc13-1* and every non-essential gene of the *S. cerevisiae* genome have been studied (Addinall et al., 2008) using a high-throughput synthetic genetic array (SGA) assay (Tong et al., 2001). Addinall and co-workers identified a large number of genes which appear to genetically interact with *cdc13-1*. The biological function of many of these genes is already understood, but the role of others requires further investigation.

A particularly challenging problem is the phenotype of the two paralogues BMH1 and BMH2. The deletion of the gene *BMH1* strongly suppresses the *cdc13-1* phenotype, while the deletion of its parologue *BMH2* suppresses *cdc13-1* rather weakly. *BMH1* and *BMH2* share 91.6% sequence identity. They both encode 14-3-3 proteins, a class of proteins which usually occur as dimers and which bind to phosphoproteins (Chaudhri, 2003). Members of the 14-3-3 family have a variety of different functions in eukaryotes, including directly modifying the functionality of their target proteins, mediating and controlling transport processes between the cytoplasm and different organelles and serving as scaffolds for interactions between different proteins (Tzivion et al., 2001). An important role for *BMH1* and *BMH2* in the regulation of carbohydrate metabolism has also been suggested (Bruckmann et al., 2007). It is not immediately obvious why *BMH1* and *BMH2* behave differently despite their close homology. Clearly, the difference in phenotype between two such closely homologous genes cannot be understood by studying the genes in isolation; a systems biology approach is essential.

In order to investigate this problem, we used Ondex to integrate five publicly available data sources as well as a homology dataset generated from BLAST results. We then enriched this data with semantic links between the concepts from the different data sources. In addition, we developed a novel, view-based visualization approach which we used to analyse this large, complex dataset. This analysis produced several testable hypotheses.

### 2 METHODS

#### 2.1 Data sources

We integrated six different data sources using Ondex. Genomics data, as well as the latest Gene Ontology (Ashburner et al., 2000) annotations, were obtained from the Saccharomyces Genome Database (SGD) (Cherry et al., 1997). A yeast regulatory network was acquired from Balaji et al. (2006). A curated model of the yeast metabolic network was sourced from Herrgard et al. (2008). A yeast protein–protein interaction (PPI) network and a network of known genetic interactions (GI) were taken from the BioGRID database (Stark et al., 2006). The BioGRID data includes the GIs reported by Addinall et al. (2008). Homology links between genes were created using BLAST (Altschul et al., 1990) with an 85% sequence identity threshold (Table 1). Further information regarding the data sources can be found in the Supplementary Material.

#### 2.2 Integration

The source datasets were integrated to form a combined Ondex knowledge network. A metadata model was designed for the knowledge network to capture the semantics of concept and relationship

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Table 1. Data sources used in this work

<table>
<thead>
<tr>
<th>Data</th>
<th>Source</th>
<th>Version/date</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genome</td>
<td>SGD</td>
<td>11/02/2010</td>
</tr>
<tr>
<td>GO annotations</td>
<td>SGD</td>
<td>11/02/2010</td>
</tr>
<tr>
<td>Interactome</td>
<td>BioGRID</td>
<td>v2.0.61</td>
</tr>
<tr>
<td>Regulatory network</td>
<td>Baliga et al. (2006)</td>
<td>NA</td>
</tr>
<tr>
<td>Metabolic network</td>
<td>Herrgard et al. (2008)</td>
<td>v1.0</td>
</tr>
<tr>
<td>Homology</td>
<td>BLAST (id. &gt; 85%)</td>
<td>NA</td>
</tr>
</tbody>
</table>

NA=not applicable.

Fig. 1. Simplified schematic of the data structure underlying the Ondex Saccharomyces knowledge network. Circles represent concept types, and lines represent relations between them.

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2.3 A novel visualization strategy

The graph produced by the integration is stored in the Ondex XML format OXL (Taubert et al., 2007) and can be browsed in Ondex. The resulting network is large and complex, and contains many types of concepts and relations. In order to present a more succinct and biologically focused view of the data, we developed a plugin for the network visualization tool Cytoscape (Shannon et al., 2003) called OndexView.

This new visualization allows the user to define ‘views’ on the data. A view focusses on one type of concept. All concepts of that type found in the knowledge network are visualized as network nodes. The user can query the knowledge network for associations between the concepts. These associations will be visualized as edges between the corresponding nodes. Querying for associations is accomplished by specifying a set of metadata motifs. The instances of these motifs found in the underlying knowledge network are then used to create corresponding associations in the view. Metadata motifs are alternating sequences of concept types and relation types that begin and end on the same concept type (Fig. 2E).

A modified depth-first search algorithm is used to extract motif instances from the underlying Ondex knowledge network. At each depth level, the algorithm checks whether the currently explored path matches the target motif. For example, a user interested in proteins and metabolic pathway generation considerably more efficient than the alternative of trawling through large databases of publications.

Using OndexView, we defined five motifs over Gene concepts covering genetic and physical interactions, homology, regulation and metabolic precedence (Table 2).

We created a view using all five motifs, querying for the immediate neighbourhood of BMH1, BMH2 and CDC13. We then laid out the view, separating all neighbouring genes into groups: Exclusive neighbours of BMH1, exclusive neighbours of BMH2, joint neighbours of BMH1 and BMH2 and others.
Fig. 2. Schema illustrating two examples for constructing associations based on metadata motifs. (A) The motif shown selects all paths from a polypeptide that is part of a transcription factor which regulates a gene that is transcribed to an mRNA which is translated into another polypeptide. (B) The motif from (A) is shown in context of the complete metadata structure. (C) A small example subnetwork to which the motif can be applied. Finding the motif (A) in the subnetwork, we identify three matching paths. Each element in these paths matches its corresponding element in the motif. (D) The view resulting from collapsing the paths identified in (C) according to motifs from (A) contains three edges; one for each matching path. (E) The motif selects all paths from a protein that modifies a process that produces a metabolite which is then consumed by another process back to another protein that modifies that process. Such a motif could be described as ‘precedence in a metabolic pathway’. (F) The motif from (E) is shown in context of the complete metadata structure. (G) A small example subnetwork to which the motif can be applied. Finding the motif (E) in the subnetwork, we identify two matching paths. Each element in these paths either matches or is a subtype of the corresponding element in the motif. (H) The views resulting from collapsing the paths identified in (G) according to motifs from (E) contains two edges; one for each matching path.
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3 RESULTS AND DISCUSSION

3.1 The Ondex Saccharomyces knowledge network

Using the Ondex data integration platform, we integrated five publicly available data sources covering various aspects of *S. cerevisiae* biology into a semantically enriched and interlinked knowledge network. The resulting knowledge network consists of a total of 240964 concepts of 59 different types, connected by 754391 relations of 28 types.

3.2 OndexView: a Cytoscape plugin

We implemented a new method for semantic simplification as the Cytoscape plugin OndexView, that uses views on the underlying data. Users can load integrated Ondex networks into OndexView and open views on them.

A user can invoke predefined views over the knowledge network or define custom views. A built-in motif editor is included in OndexView for this purpose. To apply a view, a concept type is selected from the knowledge network. The user then chooses one or more motifs for the selected concept type. OndexView extracts all associated associations according to the algorithm outlined in Section 2.3. The program then offers a query interface to the user, which can be used to focus on specific nodes (such as genes) or collections of nodes (such as pathways and complexes) and their neighbourhoods. Once the query has been processed, OndexView displays the selected view in the main Cytoscape window.

3.3 Telomere maintenance in *S. cerevisiae*

*BMIH1* and *BMIH2*, despite their 91.6% sequence identity, have very different interactions with the temperature-sensitive telomere uncapping mutant *cdc13-1*. Our analysis of the Ondex Saccharomyces knowledge network, conducted using OndexView, led to the formulation of several hypotheses to explain the different interaction profiles of *BMIH1* and *BMIH2*.

From the semantically collapsed graph, it is apparent that the neighbourhoods of *BMIH1* and *BMIH2* have only 23.5% of genes in common; *BMIH1* and *BMIH2* have completely separate sets of transcriptional regulators. This information is not readily apparent in the uncollapsed graph. Analysis of the node description fields reveals that 19.3% of the two genes’ combined neighbourhood are cell cycle-related genes, while 10.1% are glucose metabolism related genes.

Of the genes that physically interact with both *BMIH1* and *BMIH2*, 14.3% are histone related (Table 3).

<table>
<thead>
<tr>
<th>Association name</th>
<th>Motif</th>
</tr>
</thead>
<tbody>
<tr>
<td>homologous</td>
<td>Gene is homologue Gene</td>
</tr>
<tr>
<td>metabolic path</td>
<td>Gene encodes Peptide a_part_of Protein</td>
</tr>
<tr>
<td></td>
<td>participates_active_in Genes</td>
</tr>
<tr>
<td></td>
<td>Metabolite taken_by Process</td>
</tr>
<tr>
<td></td>
<td>has_active_participant Protein has_part Polypeptide encoded_by Gene</td>
</tr>
<tr>
<td></td>
<td>Polypeptide encoded by Gene</td>
</tr>
<tr>
<td></td>
<td>participates_active_in Physical_Interaction</td>
</tr>
<tr>
<td></td>
<td>has_passive_participant Polypeptide encoded_by Gene</td>
</tr>
<tr>
<td></td>
<td>Gene encodes Polypeptide is_part_of Transcription_Factor regulates Gene</td>
</tr>
<tr>
<td></td>
<td>Gene participates_active_in Genetic_Interaction has_passive_participant Gene</td>
</tr>
</tbody>
</table>

### Table 2. Motif definitions used in this work

### Table 3. Gene groups in the neighbourhood of *BMIH1* and *BMIH2* in the created view and their cardinalities

<table>
<thead>
<tr>
<th></th>
<th>Total</th>
<th>Cell cycle related</th>
<th>Glucose metabolism related</th>
<th>Histone related</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neigh. of <em>BMIH1</em></td>
<td>68</td>
<td>15 (22.1)</td>
<td>7 (10.3)</td>
<td>4 (5.9)</td>
</tr>
<tr>
<td>Neigh. of <em>BMIH2</em></td>
<td>79</td>
<td>15 (18.9)</td>
<td>8 (10.1)</td>
<td>4 (5.1)</td>
</tr>
<tr>
<td>Intersection of <em>BMIH1</em>/<em>BMIH2</em> neighbours</td>
<td>28</td>
<td>7 (25.0)</td>
<td>3 (10.7)</td>
<td>4 (14.3)</td>
</tr>
<tr>
<td>Union of <em>BMIH1</em>/<em>BMIH2</em> neighbours</td>
<td>119</td>
<td>23 (19.3)</td>
<td>12 (10.1)</td>
<td>4 (3.3)</td>
</tr>
</tbody>
</table>

1Over-represented with respect to the distribution of GO terms in the *S. cerevisiae* genome, hypergeometric test, P=0.00046.

2Over-represented with respect to the distribution of GO terms in the *S. cerevisiae* genome, hypergeometric test, P=0.0079.
interaction between Bmh2 and Rad53. However, they hypothesise that Bmh1 interacts with Rad53 in the same way that Bmh2 does.

Accepting Usui and Petrin’s assumption, a significant difference in protein abundance during the time of checkpoint induction could explain the different effects of BMH1 and BMH2 deletions. The collapsed network neighbourhood of BMH1 and BMH2 shows clearly that the two genes are regulated completely independently from one another. Furthermore, according to their description fields in the network, two of BMH1’s transcriptional regulators, ACE2 and SWI4, are known to be active during G1 phase (Andrews and Moore, 1992; McBride et al., 1999). This observation leads us to conjecture that BMH1 could be more strongly expressed than BMH2 during the G1 phase, resulting in a higher abundance of Bmh1 protein during and after G1 phase.

We hypothesize that due to its independent transcriptional regulation, BMH1’s products are present at higher levels than those of BMH2 at checkpoint time. Thus, deleting BMH1 would remove the majority of the Bmh1 and Bmh2 protein available as binding partners for Rad53, severely impairing the cell’s checkpoint response in the face of uncapped telomeres. Removing BMH2, in contrast, removes a smaller proportion of binding partners for Rad53, thus resulting in a milder suppression effect on cdc13-1.

The differential regulation hypothesis has been summarized in Figure 3A, by generating a neighbourhood graph of BMH1 and BMH2 and removing all nodes except for those mentioned in the above discussion.

Experimental validation of the differential regulation hypothesis could be performed in several ways. Expression profiling of BMH1 and BMH2 over the course of the cell cycle could be performed.

Consultation of pre-existing data has so far been inconclusive; a time course microarray performed by Spellman and colleagues showed BMH1 expression levels to be slightly higher than those of BMH2 throughout the the cell cycle and spiking 4-fold during G1 phase (Spellman et al., 1998) (Supplementary Fig. S2). However, due to the low resolution of the assay, the observed peak is represented by only one datapoint, rendering its significance rather doubtful.

Another possibility would be the examination of an ace2 swi4 Δ double mutant, which under the above hypothesis should replicate the bmh1Δ phenotype regarding suppression of cdc13-1.

3.5 Phosphorylation of Cdc13

A different hypothesis was formed after further examining the OndexView network neighbourhood of BMH1 and BMH2. The network shows a set of edges, indicating that Bmh1 and Bmh2 physically interact with Snf1, Snf4 and Gal83, which according to their node description fields, are members of the AMP-dependent kinase (AMPK) complex. Snf1 also interacts with Cdc13 and Stm1, another telomere-capping protein. The publication linked in the Ondex knowledge network reveals that this interaction is a phosphorylation, (Pucek et al., 2005).

Publications linked from the nodes reveal that the AMPK complex is a heterotrimer composed of the α-subunit Snf1 (the actual kinase), its activating γ-subunit Snf4 and a third component β-subunit that tethers Snf1 and Snf4 together. Sip1, Sip2 and Gal83 compete for the place of this third component (Jiang and Carlson, 1997). These three competing proteins have been shown to determine the AMPK’s substrate specificity and its cellular localization (Lin et al., 2003; Schmidt and McCartney, 2000). For example, the Gal83 variant of the AMPK complex has been shown to be able to enter the nucleus (Vincen et al., 2001).

In the network, two edges exist indicating that Bmh1 and Bmh2 both physically interact with Snf1 (Elbing et al., 2006). However, Bmh1 alone interacts with the γ-subunit Snf4 (Gavin et al., 2002), while Bmh2 alone interacts with the β-subunit Gal83 (Krogan et al., 2006).

The nature of these interactions is currently unknown, but 14-3-3 proteins have been reported to affect kinases in several different ways, including scaffolding and direct alteration of the target’s phosphorylation (Ptacek et al., 2005). If Bmh1/2 are involved in scaffolding for the formation of different AMPK variants, then the deletion of BMH1 and the subsequent over-representation of Bmh2 dimers could favour the formation of Gal83-AMPK variants which can enter the nucleus to phosphorylate Cdc13. We, therefore, hypothesize that the phosphorylation of Cdc13 could potentially affect its temperature sensitivity and thus the cdc13-1 phenotype.

The phosphorylation hypothesis has been summarized in Figure 3B, by generating a neighbourhood graph of BMH1 and BMH2 and removing all nodes except for those mentioned in the above discussion.

Experimental validation of the phosphorylation hypothesis is more difficult. An examination of the phenotype of gal83Δ mutants could offer further insight. If such a test would corroborate the importance of the AMPK complex for the observed phenotype, one could examine whether in vitro phosphorylation of Cdc13 by the AMPK is possible. However, without further evidence we have to consider the effect of a potential phosphorylation of Cdc13 on its temperature sensitivity in particular to be mere speculation.
3.6 Impact of noisy data
Like any other data integration approach, the Ondex *Saccharomyces* knowledge network is limited by the state of knowledge contained in its data sources. There are two main types of errors that affect the system. (i) Incorrect information from the databases, such as curator errors, will also be present in the integrated network, unless detectable by Ondex’s inconsistency checks as discussed in Section 2.2. For example, contradictions between data sources can be detected and rectified. (ii) Information that is missing from the source databases will also be missing in the integrated dataset. A particular problem in this respect is the lack of negative knowledge recording throughout the systems biology community. In many sources, it is not possible to decide if non-existence of a database entry is indicative of the subject being known not to exist or not being known to exist.

It is obvious that such problems also impact downstream analyses with OndexView. However, by enabling the user to review the evidence underlying the integrated data, she/he can be pointed to the original publications that can be consulted. For example, as described in Section 3.4, the publication linked from the physical interaction edge between Bmh2 and Rad53 clarified the circumstances around the non-existence of an edge between Bmh1 and Rad53. So it can be argued that performing visual analyses with OndexView on the Ondex *Saccharomyces* knowledge network also impacts on missing data, as it allows for clarifications and corrections.

3.7 Comparison to related works
While the Ondex *Saccharomyces* knowledge network in conjunction with OndexView’s semantic simplification method shows parallels to previous data integration approaches, there are a number of important differences. Like the work presented in this article, semantic web approaches, such as YeastHub (Cheung et al., 2005) store their integrated data in a machine-interpretable fashion, thus providing flexible platforms that can be adapted for various purposes. However, unlike OndexView, such systems require complex querying language constructs to access them. Data warehousing approaches such as SAMBA (Tanay et al., 2004) and EcoCyc (Keseler et al., 2010), on the other hand, are related to the presented work in that they collect the contents of heterogeneous data sources in one centralized repository. Unlike the Ondex *Saccharomyces* knowledge network, they offer web interfaces, which makes them very easy to query for standard use. However, they are based on less semantically rigorous data structures, rendering them less flexible. In summary, the Ondex *Saccharomyces* knowledge network combines aspects from both semantic web approaches and data warehousing approaches; featuring both their strengths, but also some of their weaknesses.

4 CONCLUSIONS
The data produced by high-throughput approaches has the potential to revolutionize our understanding of biology, but can do so only if the computational techniques necessary to visualize and analyse the data can scale with the amount of data generated. Data integration methods have proven to be a successful way to face this challenge. We have shown that a view-based approach can be a powerful tool to simplify the visualization of the complex knowledge networks generated by semantic data integration, without loss of the underlying information. The view-based approach provides concise visualizations tailored to providing only the information relevant to a particular investigation.

Biological phenomena such as the different phenotypes arising from deletion of BMH1 and BMH2 emerge from the interplay of several independent molecular biological networks. OndexView enables users to visualize not only these networks but also the ways in which they dovetail. This visualization serves as a starting point for the user, who can now easily explore genes, their various relationships and the underlying evidence, thus gathering inspirations facilitating the generation of testable hypotheses regarding the functions of these genes.

4.1 Outlook
There are a number of improvements that could be applied to OndexView and the presented knowledge network, as well as a number of ideas that build upon this work. The exploration of evidence trails behind the simplified edges in OndexView could be made more easily accessible. Rather than showing evidence in a textual representation in graph attributes, an option to visualize it graphically on demand would further increase the tool’s usefulness. However, due to the limitations of the Cytoscape API, which renders graph views immutable, such new features will more likely be included in a re-implementation of OndexView for Ondex’s own graph visualization frontend.

Furthermore, the Ondex *Saccharomyces* knowledge network could be enriched with probabilities on the connections between concepts, which could be inferred from the original data sources as well as the evidence coverage. Then, if more experience can be gathered on molecular pathways that potentially qualify for explaining observed epistasis effects, they could be generalized into a collection of semantic motifs. Instances of these motifs in the graph could be ranked according to their overall probability. The generation of such ranked lists could further assist biologists with the formation of hypotheses.

ACKNOWLEDGEMENTS
J.W. and M.P. created the Ondex yeast dataset and all required Ondex workflow modules not already present in the Ondex distribution; J.W. and A.W. designed the view-based visualization approach; J.W. implemented the OndexView plug-in for Cytoscape; J.W., E.H. and J.D. investigated BMH1/2 epistasis with OndexView and generated the presented hypotheses; J.W., S.J.C., P.L., J.H. and A.W. wrote the paper; S.J.C., P.L., D.W., D.L., J.H. and A.W. supervised the project. Furthermore, the authors would like to thank the Ondex development team and the Newcastle Integrative Bioinformatics writing group for their help.

Funding: The authors are pleased to acknowledge funding from the Biotechnology and Biological Sciences Research Council (BBSRC) Systems Approaches to Biological Research (SABR) initiative [Grant number BB/F006039/1].

Conflict of Interest: none declared.

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