Genome-Wide Discovery of Modulators of Transcriptional Interactions in Human B Lymphocytes

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Abstract. Transcriptional interactions in a cell are modulated by a variety of mechanisms that prevent their representation as pure pairwise interactions between a transcription factor and its target(s). These include, among others, transcription factor activation by phosphorylation and acetylation, formation of active complexes with one or more co-factors, and mRNA/protein degradation and stabilization processes.

This paper presents a first step towards the systematic, genome-wide computational inference of genes that modulate the interactions of specific transcription factors at the post-transcriptional level. The method uses a statistical test based on changes in the mutual information between a transcription factor and each of its candidate targets, conditional on the expression of a third gene. The approach was first validated on a synthetic network model, and then tested in the context of a mammalian cellular system. By analyzing 254 microarray expression profiles of normal and tumor related human B lymphocytes, we investigated the post transcriptional modulators of the MYC proto-oncogene, an important transcription factor involved in tumorigenesis. Our method discovered a set of 100 putative modulator genes, responsible for modulating 205 regulatory relationships between MYC and its targets. The set is significantly enriched in molecules with function consistent with their activities as modulators of cellular interactions, recapitulates established MYC regulation pathways, and provides a notable repertoire of novel regulators of MYC function. The approach has broad applicability and can be used to discover modulators of any other transcription factor, provided that adequate expression profile data are available.

1 Introduction

The reverse engineering of cellular networks in prokaryotes and lower eukaryotes [1, 2], as well as in more complex organisms, including mammals [3, 4, 5], is

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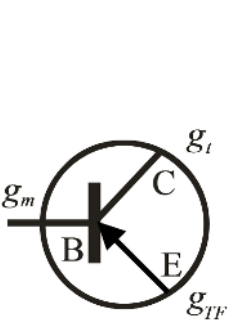
unraveling the remarkable complexity of cellular interaction networks. In particular, the analysis of targets of specific transcription factors (TF) reveals that target regulation can change substantially as a function of key modulator genes, including transcription co-factors and molecules capable of post-transcriptional modifications, such as phosphorylation, acetylation, and degradation. The yeast transcription factor STE12 is an obvious example, as it binds to distinct target genes depending on the co-binding of a second transcription factor, TEC1, as well as on the differential regulation by MAP kinases FUS3 and KSS1 [6]. Although the conditional, dynamic nature of cellular interactions was recently studied in yeast [7, 8, 9, 10], methods to identify a genome-wide repertoire of the modulators of a specific transcription factor are still lacking.

In this paper, we explore a particular type of "transistor like" logic, shown in Fig. 1a, where the ability of a transcription factor g_{TF} (emitter) to regulate a target gene g_t (collector) is modulated by a third gene g_m (base), which we shall call a modulator. Pairwise analysis of mRNA expression profiles will generally fail to reveal this complex picture because g_m and g_{TF} (e.g., a kinase and a transcription factor it activates) are generally statistically independent and because the correlation between the expression of g_{TF} and g_t is averaged over an



(a)

(b)

TF Interaction	I	I^-_{Ki}	I^+_{Ki}	ΔI_{Ki}	I^-_{CF}	I^+_{CF}	ΔI_{CF}
Ki	–	–	–	–	0.007	0.016	0.009
CF	–	0.001	0.018	0.008	–	–	–
G_1	0.732	0.542	0.579	0.037	0.552	0.548	0.004
G_2	0.064	0.079	0.093	0.014	0.007	0.378	0.371
G_3	0.097	0.007	0.351	0.344	0.071	0.042	0.029

(c)

Fig. 1. Synthetic network model of transistor-like regulatory logic. (a) Transistor model. (b) Schematic representation of the synthetic network. (c) Unconditional MI, conditional MI and conditional MI difference for the TF interactions conditioning on the expression level of the Ki and the CF; entries colored in red are determined to be statistically significant.

entire range of values of g_m and thus significantly reduced. However, we show that by conditioning on the expression of the modulator gene (e.g., an activating kinase), a statistically significant change in the $g_{TF} \leftrightarrow g_t$ correlation can be measured, thus directly identifying key post-transcriptional regulation mechanisms, including modifications by signaling molecules, co-factor binding, chromatin accessibility, modulation of protein degradation, etc. An important element of this analysis is that, while signaling proteins are conventionally viewed as constitutively expressed, rather than transcriptionally modulated, in practice their abundance within a cell population is subject to fluctuations (either functional or stochastic). Depending on the number of available microarray expression profiles and on the range of fluctuation, this may be sufficient to establish a $g_{TF} \leftrightarrow g_t$ statistical dependency, conditional on the availability of one or more signaling molecules.

We validated the approach on a simple synthetic network and then applied it to the identification of key modulators of MYC, an important TF involved in tumorigenesis of a variety of lymphomas. We identify a set of 100 putative modulators, which is significantly enriched in genes that play an obvious post-transcriptional or post-translational modulation role, including kinases, acyltransferases, transcription factors, ubiquitination and mRNA editing enzymes, etc. Overall, this paper introduces the first genome-wide computational approach to identify genes that modulate the interaction between a TF and its targets. We find that the method recapitulates a variety of known mechanisms of modulation of the selected TF and identifies new interesting targets for further biochemical validation.

2 Method

As discussed in [11, 12], the probability distribution of the expression state of an interaction network can be written as a product of functions of the individual genes, their pairs, and higher order combinations. Most reverse engineering techniques are either based on pairwise statistics [5, 11, 13], thus failing to reveal third and higher order interactions, or attempt to address the full dependency model [14], making the problem computationally untractable and under-sampled. Given these limitations, in this paper we address a much more modest task of identifying the "transistor-like" modulation of specific regulatory interaction, a specific type of third order interactions that is biologically important and computationally tractable in a mammalian context. Furthermore, given the relatively high availability of microarray expression profile data, we restrict our analysis to only genes that modulate transcriptional interactions, i.e., a TF regulating the expression of its target gene(s).

In our model, just like in an analog transistor where the voltage on the base modulates the current between the other terminals, the expression state of the modulator, g_m, controls the statistical dependence between g_{TF} and g_t, which may range from statistically independent to strongly correlated. If one chooses mutual information (MI) to measure the interaction strength (see [11] for the

rationale), then the monotonic dependence of $I(g_{TF}, g_t|g_m)$ on g_m, or lack thereof, can reveal respectively the presence or the absence of such a transistor-like interaction.

Analysis along the lines of [11] indicates that currently available expression profile sets are too small to reliably estimate $I(g_{TF}, g_t|g_m)$ as a function of g_m. To reduce the data requirements, one can discretize g_m into well sampled ranges g_m^i. Then, $|I(g_{TF}, g_t|g_m^{i_1}) - I(g_{TF}, g_t|g_m^{i_2})| > 0$ (at the desired statistical significance level) for any range pair (i_1, i_2) is a sufficient condition for the existence of the transistor logic, either direct (i.e., g_m is causally associated with the modulation of the TF targets) or indirect (i.e., g_m is co expressed with a true modulator gene). Below we present details of an algorithm that, given a TF, explores all other gene pairs (g_m, g_t) in the expression profile to identify the presence of the transistor logic between the three genes.

2.1 Selection of Candidate Modulator Genes

Given a expression profile dataset with N genes and an a-priori selected TF gene g_{TF}, an initial pool of candidate modulators g_m, $\{m\} \in 1, 2, \ldots, M$, is selected from the N genes according to two criteria: (a) each g_m must have sufficient expression range to determine statistical dependencies, (b) genes that are not statistically independent of g_{TF} (based on MI analysis) are excluded. The latter avoids reducing the dynamic range of g_{TF} due to conditioning on g_m, which would unnecessarily complicate the analysis of significance of the conditional MI change. It also removes genes that transcriptionally interact with g_{TF}, which can be easily detected by pair-wise co-expression analysis, and thus are not the focus of this work. We don't expect this condition to substantially increase the false negative rate. In fact, it is reasonable to expect that the expression of a post-transcriptional modulator of a TF function should be statistically independent of the TF's expression. For instance, this holds true for many known modulators of MYC function (including MAX, JNK, GSK, and NFκB).

Each candidate modulator g_m is then used to partition the expression profiles into two equal-sized, non-overlapping subsets, L_m^+ and L_m^-, in which g_m is respectively expressed at its highest (g_m^+) and lowest (g_m^-) levels. The conditional MI, $I^{\pm} = I(g_{TF}, g_t|g_m^{\pm})$, is then measured as $I(g_{TF}, g_t)$ on the subset $L^{\pm}$. Note that this partition is not intended to identify the over or under expression of the modulator, but rather to estimate g_m^i. Then, $|I(g_{TF}, g_t|g_m^+) - I(g_{TF}, g_t|g_m^-)| > 0$ for target genes using the two tails of the modulator's expression range. The size of $L_m^{\pm}$ is constrained by the minimal number of samples required to accurately measure MI, as is discussed in [11]. Mutual information is estimated using an efficient Gaussian kernel method on rank-transformed data, and the accuracy of the measurement is known [11].

2.2 Conditional Mutual Information Statistics

Given a triplet (g_m, g_{TF}, g_t), we define the conditional MI difference as:

$$\Delta I(g_{TF}, g_t|g_m) = |I^+ - I^-| = |I(g_{TF}, g_t|g_m^+) - I(g_{TF}, g_t|g_m^-)| \quad (1)$$

For simplicity, hereafter we use I for the unconditional MI (i.e., the MI across all samples) and ΔI for conditional MI difference. To assess the statistical significance of a ΔI value, we generate a null hypothesis by measuring its distribution across 10^4 distinct (g_{TF}, g_t) pairs with random conditions. That is, for each gene pair, the non-overlapping subsets $L_m^{\pm}$ used to measure $I^{\pm}$ and ΔI are generated at random rather than based on the expression of a candidate modulator gene (1000 ΔI from random sub-samples are generated for each gene pair). Since the statistics of ΔI should depend on I, we binned I into 100 equiprobable bins, resulting in 100 gene pairs and $10^5 \Delta I$ measurements per bin. Within each bin, we model the distribution of ΔI as an extended exponential, $p(\Delta I) = exp(-\alpha \Delta I^n + \beta)$, which allows us to extrapolate the probability of a given ΔI under this null hypothesis model. As shown in Fig.2, both the mean and the standard deviation of ΔI increase monotonically with I (as expected) and the extended exponentials produce an excellent fit for all bins. Specifically, for small I, the exponent of the fitted exponential distribution is $n \approx 1$. This is

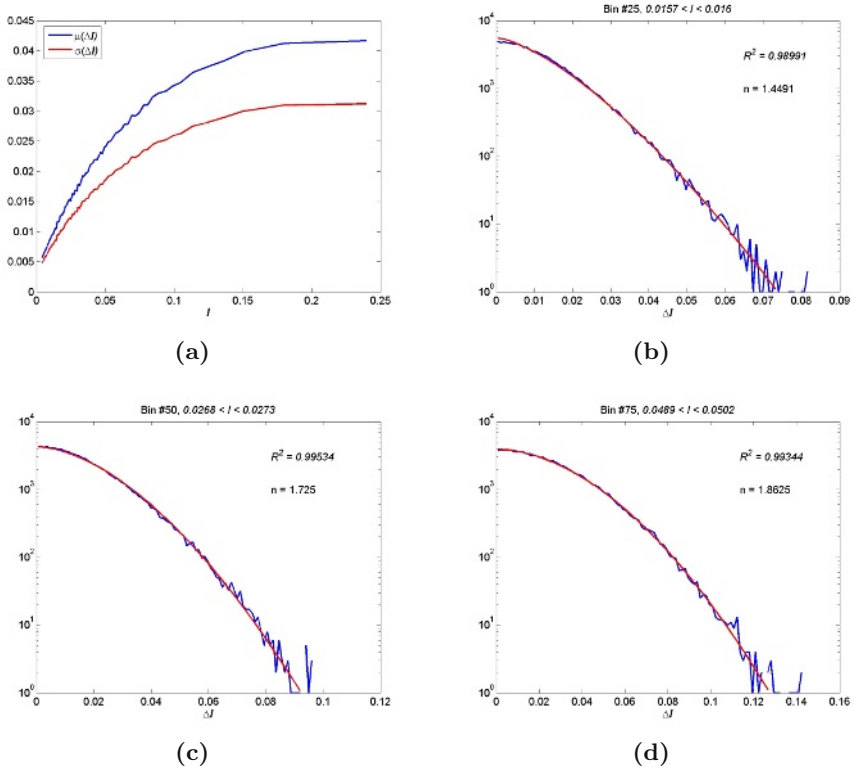


Fig. 2. Null distribution for the ΔI statistics. (a) Mean (μ) and standard deviation (σ) of the ΔI statistics in each bin as a function of I. (b) - (d), distribution of the ΔI statistics (blue curves) and the extended exponential function, $p(\Delta I) = exp(-\alpha \Delta I^n + \beta)$ (red curves), obtained by least square fitting in bin 25, 50 and 75; a goodness-of-fit measure, R^2, and the value of n are also shown for each bin.

because in this case both I^+ and I^- are close to zero and ΔI is dominated by the estimation error, which falls off exponentially [11]. For large I, the estimation error becomes smaller than the true mutual information difference between the two random sub-samples,hence $n \approx 2$ from the central limit theorem.

2.3 Interaction-Specific Modulator Discovery

Given a TF, g_{TF}, and a set of candidate modulators g_m selected as previously discussed, we compute $I(g_{TF}, g_t)$ and $\Delta I(g_{TF}, g_t|g_m)$ for all genes g_t in the expression profile such that $g_t \neq g_m$ and $g_t \neq g_{TF}$. Significance of each ΔI is then evaluated as a function of I, using the extended exponentials from our null hypothesis model. Gene pairs with a statistically significant p-value ($p < 0.05$), after Bonferroni correction for multiple hypothesis testing, are retained for further analysis.

Significant pairs are further pruned if the interaction between g_{TF} and g_t is inferred as an indirect one in both conditions $g_m^{\pm}$, based on the ARACNE [5, 11] analysis on the two subsets $L_m^{\pm}$. This is accomplished by using the Data Processing Inequality (DPI), a well-know property of MI introduced in [5, 11], which states that the interaction between g_{TF} and g_t is likely indirect (i.e. mediated

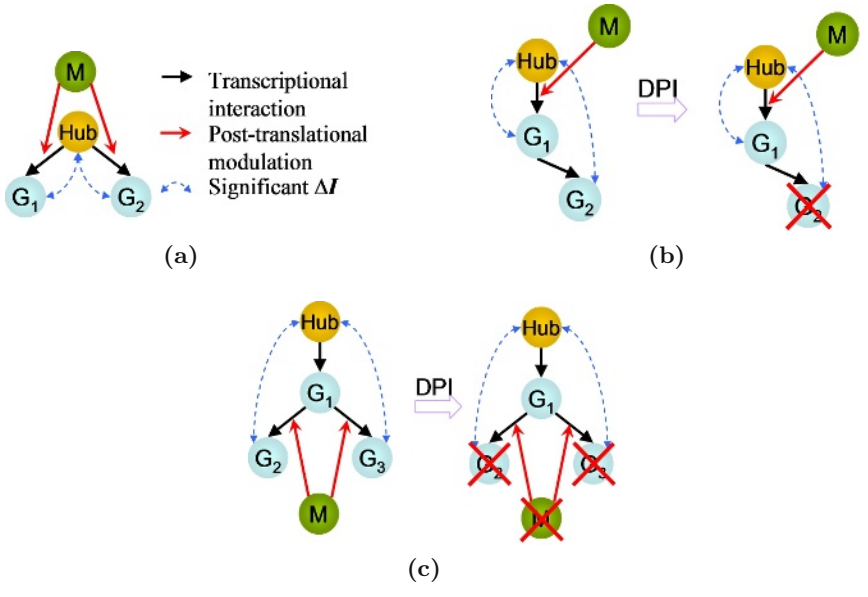


Fig. 3. Schematic diagram of the effect of DPI on eliminating indirect regulatory relationships. (a) Correct modulation model where the modulator (M) significantly changes the regulatory relationship between the TF (Hub) and its direct targets (G_1 and G_2). (b) Removal of indirect connections to the hub eliminates the detection of a significant ΔI on indirect targets. (c) Modulators that affect the downstream target of the TF hub, thus causing significant ΔI between the TF and its indirect neighbors, will be removed by applying DPI.

through a third gene g_x), if $I(g_{TF}, g_t) < min[I(g_{TF}, g_x), I(g_t, g_x)]$. This step eliminates some specific cases, illustrated in Fig. 3, where g_m can produce a significant ΔI even though it does not directly affect the $g_{TF} \leftrightarrow g_t$ interaction. Briefly, two cases will be addressed by the use of the DPI: (a) g_m affects the $g_{TF} \leftrightarrow g_x$ interaction instead of $g_{TF} \leftrightarrow g_t$ (Fig. 3b); and (b) g_m modulates g_x, therefore affecting the $g_x \leftrightarrow g_t$ interaction instead of the $g_{TF} \leftrightarrow g_t$. Thus g_m is not a modulator of the g_{TF} gene and should be removed (Fig. 3c). As discussed in [5, 11], the DPI was applied with a 15% tolerance to minimize the impact of potential MI estimation errors.

3 Results

3.1 Synthetic Model

We first tested our approach on a simple synthetic network (Fig. 1b) that explicitly models two post-translational modifications (activation by phosphorylation and by co-factor binding) that modulate the ability of a TF to affect its targets. The synthetic network includes a TF, a protein kinase (Ki) that phosphorylates the TF, a co-factor (CF) that can bind to TF forming a transcriptionally active complex, and three downstream targets of the TF's isoforms. The transcription activation/inhibition was modeled using Hill kinetics with exponential decay of mRNA molecules. Phosphorylation and cofactor binding were modeled using Michaelis Menten and mass-action kinetics respectively (see Supplementary Table 1 for kinetic equations).

A set of 250 synthetic expression profiles was generated from this model using Gepasi (ver 3.30) [15] by (a) randomly sampling the independent variables (concentration of mRNA for the TF, Ki, and CF) from a uniform distribution, so that they were statistical independent (b) simulating network dynamics until a steady state was reached, and (c) measuring the concentration of all mRNA species that were explicitly represented in the network (using a Gaussian experimental noise model with mean 0 and standard deviation equal to 10% of the mean concentration for each variable). Note that only the mRNA concentrations were used as inputs to our algorithm, even though all molecular species (including all proteins isoforms) were explicitly represented in the model. By conditioning on the expression of the Ki and CF, using the 40% of expression profiles with their most and least expressed values, our approach correctly identified the two and only two significant ΔI, associated with the pairs (CF, g_2) and (Ki, g_3), as shown in Fig. 1c.

3.2 Analysis of Human B Lymphocyte Data

We then used our method to identify a genome-wide repertoire of post-transcriptional modulators of the MYC proto-oncogene – a TF which represents a major hub in the B cell transcriptional network [5]. The analysis was performed on a collection of 254 gene expression profiles, representing 27 distinct cellular phenotypes derived from populations of normal and neoplastic human B

lymphocytes. The gene expression profiles were collected using the Affymetrix HG-U95A GeneChip®System (approximately 12,600 probes). Probes with absolute expression mean $\mu < 50$ and standard deviation $\sigma < 0.3\mu$, were considered non-informative and were excluded a-priori from the analysis, leaving 7907 genes.

We further selected 1117 candidate modulators with sufficient expression range ($\mu > 200$ and $\sigma > 0.5\mu$) that were statistically independent of MYC based on MI (significance was established as in [11]). The top 40% and bottom 40% of the expression profiles in which a candidate modulator g_m is expressed at its highest and lowest levels, respectively, were used to define the two conditional subsets $L_m^{\pm}$. The choice of the 40% threshold was specific to this dataset. It ensured that ≥ 100 samples were available within each conditional subset for estimating MI with a reasonable accuracy [11], while keeping the modulators' expression range within the two subsets as separated as possible.

The analysis inferred a repertoire of 100 genes, at a 5% statistical significance level (Bonferroni corrected), which are responsible for modulating 205 regulatory relationships between MYC and its 130 inferred targets in an interaction-specific fashion. See Supplementary Fig. 1 for a map of the modulators and the affected interactions. A complete list is available in the Supplementary Table 2.

3.3 Gene Ontology Enrichment Analysis

To analyze the biological significance of these putative modulator genes, we studied the enrichment of the Gene Ontology [16] Molecular Function categories among the 100 modulators compared to the initial list of 1117 candidate modulators. As shown in Table 1, the top enriched categories represent functions consistent with their activities as modulators of cellular interactions. In particular, putative modulators were enriched in kinases (PKN2, MAP4K4, BRD2, CSNK1D, HCK, LCK, TRIB2, BRD2 and MARCKS), acyltransferase (GGT1, SAT and TGM2) and transcriptional regulators (CUTL1, SSBP2, MEF2B, ID3, AF4, BHLHB2, CREM, E2F5, MAX, NR4A1, CBFA2T3, REL, FOS and NFKB2). This is in agreement with the established evidence that MYC is modulated

Table 1. Most enriched Gene Ontology Molecular Function categories for the inferred MYC modulators. False discovery rate (FDR) are calculated from Fisher's exact test and adjusted for multiple hypothesis testing. Only categories with at least 5 genes from the initial 1117 candidate modulators were used.

Gene Ontology Molecular Function Categories	Enrichment FDR
DNA binding	0.007
Transferase activity	0.010
Acyltransferase activity	0.010
Antioxidant activity	0.018
Phosphoric monoester hydrolase activity	0.026
Adenyl nucleotide binding	0.028
Transcription regulator activity	0.052
Protein serine/threonine kinase activity	0.066

through phosphorylation and acetylation events, affecting its protein stability [17, 18], and that MYC requires broadly distributed effector proteins to influence its genomic targets [19]. We also found that 4 of the 6 modulators with the largest number of affected targets (e.g. UBE2G1, HCK, USP6 and IFNGR1), are associated with non-target-specific functions (e.g. protein degradation, upstream signaling pathway components and receptor signaling molecules, etc). On the other hand, the 14 modulators that are transcription factors (and may thus be MYC co-factors) tend to be highly interaction-specific, affecting only 1-4 target genes (see Supplementary Fig. 1).

3.4 Literature Validation of Known MYC Modulators

Closer scrutiny, through literature review reveals that a number of the inferred modulators play a role in the post-transcriptional and post-translational modulation of MYC, either by direct physical interaction, or by modulating well-characterized pathways that are known to affect MYC function.

Among the list of putative modulators, we found two well known co-factors of MYC: MAX and MIZ-1. Numerous studies, [20] among many others, have shown that transcriptional activation by MYC occurs via dimerization with its partner MAX. Similarly, MIZ-1 has been shown to specifically interact with MYC through binding to its helix-loop-helix domain, which may be involved in gene repression by MYC [21]. Several protein kinases identified by our method are also notable: CSNK1D, a member of the Casein Kinase I gene family, is a reasonable MYC modulator since one of its related family member, Casein Kinase II, has been demonstrated to phosphorylate MYC and MAX, thus affecting the DNA-binding kinetics of their heterodimer [22, 23]. MYC is also know to be phosphorylated by JNK [24] and GSK [25], which affect the stability of its protein. Although both kinases were excluded from our initial candidate modulator set due to their insufficient expression range, our approach was able to identify some of their upstream signaling molecules, such as MAP4K4 and HCK. Both MAP4K4 and HCK are members of the BCR singling pathway that is known to control MYC activation and degradation [26]. In particular, MAP4K4 has been previously reported to specifically activate JNK [27].

MYC stability is also known to be regulated through ubiquitin-mediated proteolysis [28]. Two enzymes in this process, USP6 and UBE2G1, were identified as putative modulators of MYC. Although there is no biochemical evidence implicating these two proteins specifically, they serve as a reasonable starting point for biochemical validation. We also identified putative modulators that could potentially influence the MYC mRNA stability. One of them, APOBEC3B, is closely related to APOBEC1, which has been well characterized as a RNA-editing enzyme capable of binding MYC mRNA in the 3' untranslated region, thus increasing its stability [29]. While APOBEC1 was excluded from our analysis due to its insufficient expression range, the identification of its closely related family member, APOBEC3B, may suggest a similar mechanism. Another protein from this category, HNRPDL, encodes a heterogeneous nuclear ribonucleoprotein which interacts with mRNA and may have a role in

mRNA nuclear export. MYC stimulates gene expression in part at the level of chromatin, through its association with co-factors that affect the histone acetylation and DNA methylation. DNMT1, which encodes a DNA methyltransferase, was found in our putative modulator list. Current literature suggests that MYC may repress transcription through the recruitment of DNA methyltransferase as corepressor, which may in turn lead to hypoacetylated histones that are often associated with transcriptional silencing [30, 31].

Many other genes in our list of putative modulators of MYC also present relevant biological functionality, such as transcription factors FOS, CREM, REL and NFKB2, anti-apoptosis regulator BCL-2, to name but a few. Those for which functional relevance can not be established from the current literature likely belong to two groups: (a) novel bona fide MYC modulators requiring further biochemical validation and (b) genes that are co-expressed with a bona fide modulator, such as gene from the same biological pathway. A likely example of the latter case is NFKB2 and its inhibitor NFKBIA, which are both identified as modulators of MYC, while having substantially correlated expression profiles (Pearson correlation 0.55).

Table 2. Promoter analysis of the MYC target genes affected by TF-modulators. Binding signatures of 8 of the 14 TFs in the putative modulator list were obtained through TRANSFAC. Promoter sequences of the target genes (2Kb upstream and 2Kb downstream of the transcription initiation site) were retrieved from the UCSC Golden Path database [33] and masked for repetitive elements. Statistical significance is assessed by considering a null score distribution computed from random sequences using an order-2 Markov model learned from the actual promoter sequences, where P_{BS} is calculated as the probability of finding at least one binding site per 1Kb sequence under the null hypothesis. We used a significance threshold of 0.05; findings below this threshold are shown in red.

Modulator	Binding Signature	MYC targets	P_{BS}
CUTL1		NP	0.032
CREM		PRKDC	0.041
BHLHB2		TLE4 MLL IL4R	0.030 0.039 0.140
MEF2B		KLF12 CR2 CYBB	0.391 0.326 0.045
FOS		ZNF259	0.049
REL		KEL	0.125
E2F5		IL4R	0.870
NFKB2		FOXK2	0.041

3.5 Transcription Factors Co-binding Analysis

For the putative modulators annotated as TF, one potential mechanism of modulation is as MYC co-factors. We thus searched for the binding signatures of both MYC and the modulator-TF within the promoter region of the genes whose interaction with MYC appeared to be modulated by the TF. Of the 14 TFs in our putative modulator list, 8 have credibly identified DNA binding signatures from TRANSFAC [32] (represented as position-specific scoring matrix). These TFs affect 12 MYC interactions with 11 target genes. Additionally, 4 of the 5 target genes whose expressions are positively correlated with MYC present at least one E-Box in their promoter region ($p < 4.03 \times 10^{-4}$)[1] . As is shown in Table 2, of the 12 instances of statistically significant modulator target pairs, 7 target genes harbor at least one high specificity TF binding signature ($P_{BS} < 0.05$) in their promoter region. The overall p-value associated with this set of events is $p < 0.0025$ (from the binomial background model). This strongly supports the hypothesis that these TFs are target specific co-factors of MYC.

4 Conclusion and Discussion

Cellular interactions can be neither represented as a static relationship nor modeled as pure pairwise processes. The two issues are deeply interlinked as higher order interactions are responsible for the rewiring of the cellular network in a context dependent fashion. For transcriptional interactions, one can imagine a transistor-like model, in which the ability of a TF to activate or repress the expression of its target genes is modulated, possibly in a target-specific way, by one or more signaling proteins or co-factors. Such post-transcriptional and post-translational conditional interactions are necessary to create complex rather than purely reactive cellular behavior and should be abundant in biological systems. Unfortunately, most post-translational interactions (e.g. phosphorylation or complex formation) do not affect the mRNA concentration of the associated proteins. As a result, they are invisible to naïve co-expression analysis methods. However, proteins that are involved in post-translational regulation may be themselves transcriptionally regulated. At steady state, the concentration of such post-translationally modified proteins and complexes can then be expressed as a function of some mRNA expressions, albeit in a non-obvious, conditional fashion. With this in mind, we show that conditional analysis of pairwise statistical dependencies between mRNAs can effectively reveal a variety of transient interactions, as well as their post-transcriptional and post-translational regulations.

In this paper, we restrict our search to genes that affect the ability of a given TF to transcriptionally activate or repress its target(s). While the identification of the targets of a transcription factor is a rather transited area, the identification

[1] MYC is known to transcriptional activate its targets through binding to E-box elements. Repression by MYC occurs via a distinct mechanism, not involving E-boxes, which is not yet well characterized.

of upstream modulators is essentially unaddressed at the computational level, especially in a TF-target interaction specific way. Experimentally, it constitutes an extremely complex endeavor that is not yet amenable to high-throughput approaches. For instance, while hundreds of MYC targets are known, only a handful of genes have been identified that are capable of modifying MYC's ability to activate or repress its targets. Even fewer of these are target specific.

We show that such modulator genes can be accurately and efficiently identified from a set of candidates using a conditional MI difference metric. One novelty of our approach is that it requires no a-priori selection of the modulator genes based on certain functional criteria: the candidate modulators include all genes on the microarray that have sufficient dynamic range and no significant MI with the TF gene. The first requirement can be actually lifted without affecting the method other than making it more computationally intensive and requiring more stringent statistical tests (as the number of tested hypotheses would obviously increases). This is because conditioning on a gene with an expression range comparable to the noise is equivalent to random sub-sampling of the expression profiles, an event that will be filtered out by our statistical test.

Another critical element of our method is the phenotypic heterogeneity of the expression profiles. This ensures that no sufficiently large subset of the expression profiles can be obtained without sampling from a large number of distinct phenotypes, including both normal and malignant cells. In fact, the average number of distinct cellular phenotypes in any subset of gene expression profiles used in the analysis is about 20, with no subset containing fewer than 13. Thus, the modulators identified in this paper are not associated with a specific cellular phenotype.

To derive a null model for estimating the significance of individual conditional mutual information differences, ΔI, we investigated the statistics of ΔI as a function of the unconditional mutual information I. Other models, such as dependence of ΔI on I^+ or I^-, were also investigated, but they proved to be less informative. It is possible that a more accurate null model may be learned by studying the variation of ΔI as a function of both I and either I^+ or I^-. For example, this may answer questions such as: given measured values of I and I^-, what is the probability of seeing a specific difference in ΔI? While this may provide finer-grained estimates of the statistical significance, this also would dramatically increases the number of Monte Carlo samples necessary for achieving a reasonable numerical precision, which would prohibit the actual deployment of the strategy.

Method limitations follow broadly into three categories: (a) The computational deconvolution of molecular interaction is still manifestly inaccurate. This has obvious effects on the discovery of interaction-specific modulators, i.e. we may identify modulators of "functional" rather than physical interactions. (b) The method cannot dissect modulators that are constitutively expressed (housekeeping genes) and activated only at the post-translational level (e.g., the p53 tumor suppressor gene), nor modulators that are expressed at very low concentrations. However, in both cases a gene upstream of the most direct modulator

may be identified in its place. For instance, JNK is a known modulator of MYC activity, which is weakly expressed in human B cells and, therefore it is not even included in the initial candidate modulator list. However, MAP4K4, which is upstream of JNK in the signaling cascade, is identified as a MYC modulator in its place. (c) The method cannot disambiguate true modulators from those co-expressed with them.

Techniques to deal with all these drawbacks are currently being investigated. However, we believe that, even in its current state, our approach presents a substantial advancement in the field of reverse engineering of complex cellular networks.

5 Supplementary Material

Supplementary Materials are available at:
`http://www.dbmi.columbia.edu/~kaw7002/recomb06/supplement.html`.

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