Novel Method for the Prediction of Drug–Drug Interactions Based on Gene Expression Profiles

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Abstract. The accurate prediction of new interactions between drugs is important for avoiding unknown (severe or mild) adverse reactions to drug combinations. The development of effective *in silico* methods for evaluating drug interactions based on gene expression data requires an understanding of how various drugs alter gene expression. Current computational methods for the prediction of drug–drug interactions (DDIs) utilize data for known DDIs to predict unknown interactions. However, these methods are limited in the absence of known DDIs for prediction. To improve the interpretation of DDIs, a recent study has demonstrated strong non-linear (i.e., dose-dependent) effects of DDIs. In this study, we present a new unsupervised learning approach involving tensor decomposition (TD)-based unsupervised feature extraction (FE) in 3D. We utilize our approach to reanalayze available gene expression profiles for *Saccharomyces cerevisiae*. We found that non-linearity is possible, even for single drugs. Thus, non-linear dose dependence cannot always be attribted to

DDIs. Our analysis provides a basis for the design of effective methods for evaluating DDIs.

Keywords: Unsupervised learning, Tensor decomposition, *In silico* drug discovery, drug–drug interactions, Gene expression

1 Introduction

Although *in silico* methods are thought to be effective strategies for improving the long, expensive process of drug discovery, *in silico* drug discovery is, at best, still under development [2-4]. In addition to the two main approaches for drug discovery, i.e., ligand-based drug discovery [5-7] and structure-based drug discovery [8-10], interest in gene expression profile-based drug discovery [11] has recently increased. For this process, it is important to understand how drug treatments alter gene expression profiles. However, this is a complex issue owing to the huge number of gene expression alterations resulting from each treatment. The alterations are often non-linear, with non-monotonic dose-dependent effects. This non-linearity often prevents the selection of effective drugs, since it is difficult to determine if expression levels of individual genes are up- or downregulated by particular drug treatments.

In drug discovery, analyses of drug–drug interactions (DDIs) are aimed at the prevention or reduction of possible reactions caused by therapeutic drug combinations [12-18]. Several machine-learning approaches have been proposed to accurately predict interactions between drugs. For example, Yan et al. [19] proposed a learning approach called DDIGIP, which utilizes a regularized least square classifier coupled with a Gaussian interaction profile (GIP) kernel on known DDI profiles to predict new DDIs;

the performance of this approach was supported by 5-fold (and 10-fold) experimental cross-validation. Rohani et al. [20] proposed a learning approach utilizing a neural network in which concatenated pairs of drugs are used as inputs according to a calculated integrated similarity matrix to predict unknown interactions. Experimental results have demonstrated that the proposed approach performs better than other baselines. Other learning approaches have also been proposed to predict new DDIs [12, 21-27].

However, the above-mentioned methods are not capable of predicting unknown interactions if data for known DDIs are not available. Hence, Lukačišin and Bollenbach [1] evaluated how DDIs affect gene expression profiles in a combinatorial manner; they found that DDIs can exhibit convex relationships with gene expression profiles. Our main contributions are summarized as follows. (1) We provide a method for the reliable interpretation of the effects of interactions between drugs on gene expression data; in particular, we propose a new unsupervised method involving tensor decomposition (TD)-based unsupervised feature extraction (FE) [28] and apply this approach to datasets used in [1]. (2) We demonstrate that our TD-based unsupervised FE can replicate the findings of Lukačišin and Bollenbach [1] based on a principal component analysis (PCA) [29]. (3) Using the newly proposed TD-based unsupervised FE method, we show that convex dose dependence can appear in single drug treatments. Thus, our analysis improves our general understanding of DDIs in [1], especially when considering multi-drug effects. (4) As our analysis provides detailed insight into interactions between drugs in the context of gene expression [30], it has practical implications for improving performance when designing computational methods to accurately predict interactions between drugs.

2 Materials and Methods

Fig. 1 shows a flowchart of the analyses performed in this study.

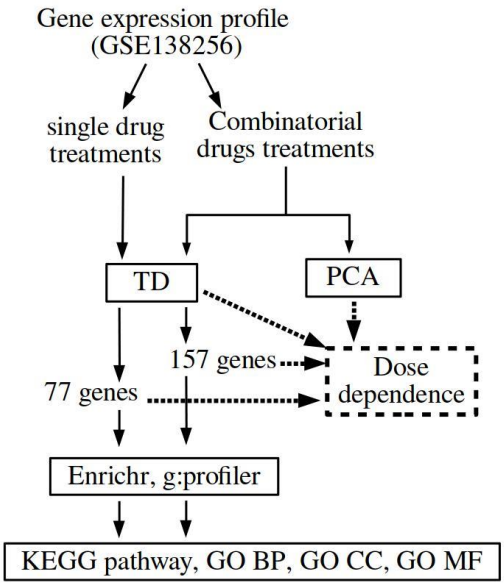

Fig. 1. Flowchart of analyses performed in this study.

2.1 Gene expression profiles

Gene expression profiles were downloaded from Gene Expression Omnibus (GEO) [31] with GEO ID GSE138256. The processed file named "GSE138256_GeneExpression.csv.gz" was used. The file "GSE138256_SampleConditionsAndOrdering.csv.gz" was also downloaded for the purpose of sample annotations. These dataset sets were composed of gene expression profiles of *Saccharomyces cerevisiae* treated with individual drugs or pairs of the following four drugs: myriocin, cycloheximide, LiCl, and rapamycin. When *S. cerevisiae*

was treated with pairs of drugs, the combinatorial dose was carefully tuned to ensure the same growth rate, to the greatest extent possible.

Table 1. Number of doses tested for drug combinations.

	Myriocin	Rapamycin	LiCl
Cycloheximide	22	20	19
LiCl	27	18	
Rapamycin	16		

Table 2. Number of doses tested for individual drugs. Numbers in parentheses indicate unique doses.

drug	Number of samples
Myriocin	25 (14)
Cycloheximide	23 (11)
LiCl	28 (14)
Rapamycin	30 (14)

2.2 PCA

PCA was applied to individual pairs of drugs. For the *i*th gene expression level and *j*th dose, $x_{ij} \in \mathbb{R}^{N \times M}$, where *N* is total number of genes (i.e., 6717) and *M* is total number of combinatorial doses for each pair of drugs (**Table 1**). x_{ij} is normalized as $\sum_i x_{ij} = 0$

and $\sum_i x_{ij}^2 = N$. PCA was applied to x_{ij} such that PC loadings and PC scores were attributed to samples and genes, respectively. Lowess smoothing was applied to PC loadings to reduce noise signals using the `lowess` command implemented in R [32].

2.3 TD-based unsupervised FE

TD-based unsupervised FE was applied to gene expression profiles. Gene expression profiles were formatted as a tensor, $x_{ijk} \in \mathbb{R}^{N \times 16 \times 6}$, representing the expression of the *i*th gene and *j*th combinatorial dose of the *k*th pair of drugs. Since the number of combinatorial doses varied among pairs, the minimum number of combinatorial doses, 16, was employed. When more combinatorial doses were tested for specific pairs of drugs, some measurements were discarded, attempting to maintain equal intervals between doses. x_{ijk} was normalized as $\sum_i x_{ijk} = 0$ and $\sum_i x_{ijk}^2 = N$. Higher order singular value decomposition (HOSVD) [28] was applied to x_{ijk} to obtain the following:

$$x_{ijk} = \sum_{l_1 l_2 l_3} G(l_1 l_2 l_3) u_{l_1 j} u_{l_2 k} u_{l_3 i}$$

where $G(l_1 l_2 l_3) \in \mathbb{R}^{N \times 16 \times 6}$ is a core tensor, and $u_{l_1 j} \in \mathbb{R}^{16 \times 16}$, $u_{l_2 k} \in \mathbb{R}^{6 \times 6}$, and $u_{l_3 i} \in \mathbb{R}^{N \times N}$ are the singular value vectors defined as the column vectors of orthogonal matrices. $u_{l_1 j}$ is attributed to the *j*th dose, $u_{l_2 k}$ is attributed to the *k*th pair of drugs, and $u_{l_3 i}$ is attributed to the *i*th gene. Lowess smoothing was also applied to singular value vectors to reduce noise using the `lowess` command implemented in R.

To select $u_{l_3 i}$ for gene selection in subsequent analyses, it was first necessary to determine which $u_{l_1 j}$ an $u_{l_2 k}$ are biologically meaningful. After identifying such $l_1$and l_2, it is necessary to identify the l_3 associated with $G(l_1 l_2 l_3)$ with the largest absolute

values given fixed $l_1$and l_2. With the selected l_3, P-values, P_i, were obtained for the ith gene as follows:

$$P_i = P_{\chi^2}\left[> \sum\left(\frac{u_{l_3 i}}{\sigma_{l_3}}\right)^2\right]$$

where $P_{\chi^2}[> x]$ is the cumulative probability of the χ^2 distribution with an argument larger than x. The summation is taken over l_3s to compute P-values. P_i was corrected with the BH criterion [28] and genes with $P < 0.01$ were selected.

Gene expression levels in response to a single dose (**Table 2**) were also formatted as a three-mode tensor, $x_{ijk} \in \mathbb{R}^{N \times 14 \times 4}$, which represents the ith gene expression level for the jth dose of the kth drug. Since the number of unique doses was 14, excluding cycloheximide, the total number of doses for cycloheximide was also set to 14 and two replicates were included for three doses. The same procedure employed for the analysis of combinatorial drug treatments was repeated and genes were selected.

2.4 Enrichment analysis

The gene symbols of selected genes were uploaded to YeastEnrichr[1], a yeast version of Enricher [33], prepared for humans, as well as to g:profiler [34].

3 Results

We first applied PCA to gene expression levels, x_{ij}, attributed to individual pairs of drug treatments to attempt to reproduce previous observations [1]. In the previous study [1], the first PC loading takes constant values, independent of dose, while the second

[1] https://amp.pharm.mssm.edu/YeastEnrichr/

and the third PC loadings exhibit linear and convex dose-dependence, regardless of pairs of drugs. In our analysis, the first PC also took constant values, regardless of the drug combination (not shown). However, the second and third PC loadings behaved slightly differently (**Fig. 2**). For the combination of cycloheximide and LiCl, although the second and the third PC loadings behaved as expected, the fourth PC loading also showed concave or convex dose-dependence. Since the fourth PC loadings were not discussed in the original paper, it is possible that the same paper was recovered in the original analysis but was not reported. Nevertheless, for the combination of LiCl and rapamycin, the second PC loadings did not have linear dependence but instead showed stepwise dependence, which was not reported in the original study. Additionally, for the remaining four combinatorial cases, the second and third PCs did not always have linear and concave or convex dose-dependence, respectively.

It is possible that the disagreement between the present study (in which the third PC did not always have linear and concave or convex dependence on dose, respectively) and the original study could be explained by insufficient pre-processing of gene expression profiles. To evaluate this possibility, we applied HOSVD to the tensor, x_{ijk}, generated from combinatorial drug treatments (**Fig. 3**). It is obvious that u_{1j} takes constant values independent of dose density, u_{2j} has linear dependence on dose density, and u_{3j} has concave or convex dependence on dose density, as observed in the original study [1]. This suggests the superiority of TD-based unsupervised FE to identify essential features, regardless preprocessing.

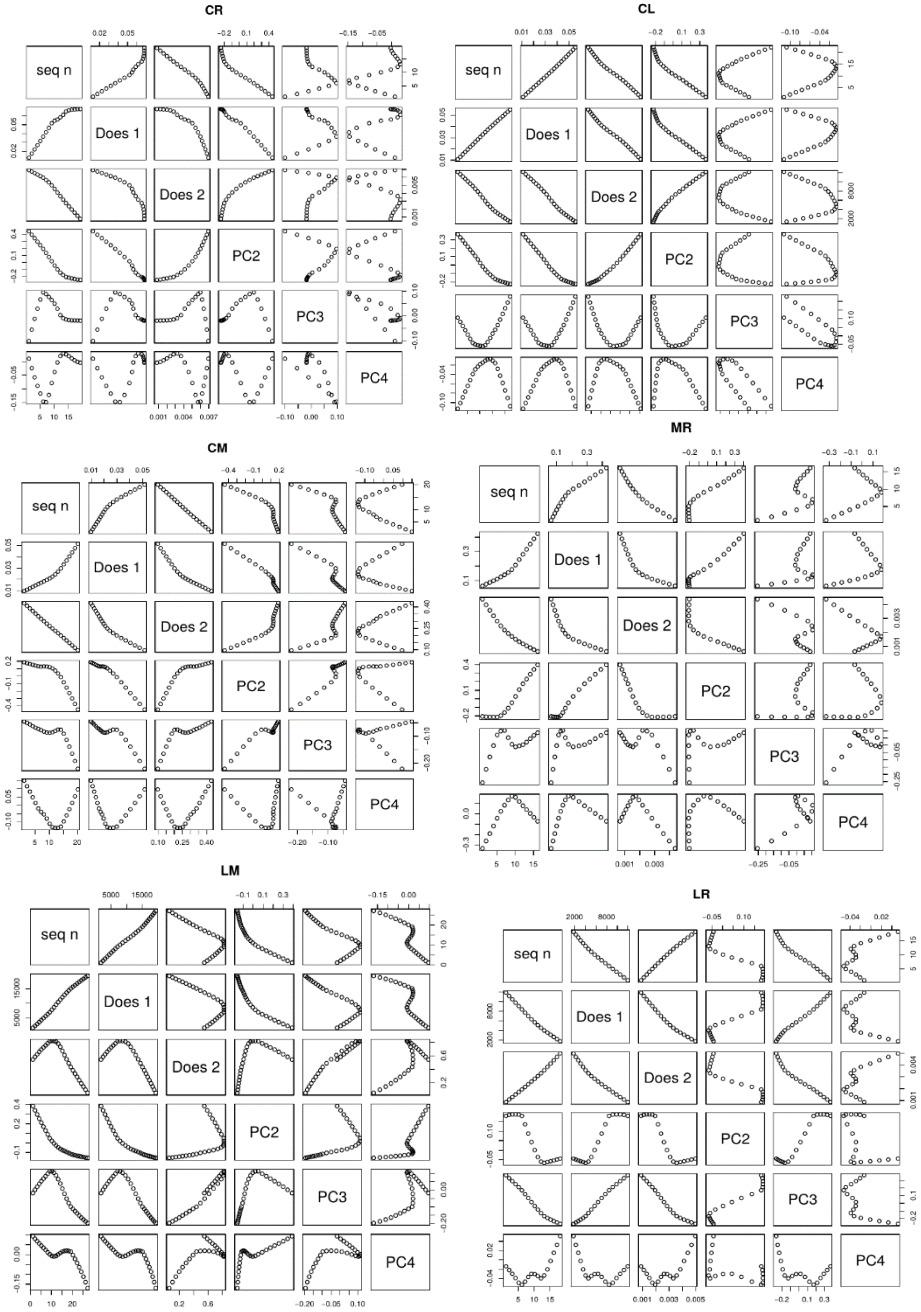
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Fig. 2. Scatter plots of j, dose densities of the first and second drug, and the second to fourth PC loadings. All values are Lowess smoothed. Two letters above each panel show the combinations of drugs: M: Myriocin C: Cycloheximide, L: LiCl, R: Rapamycin

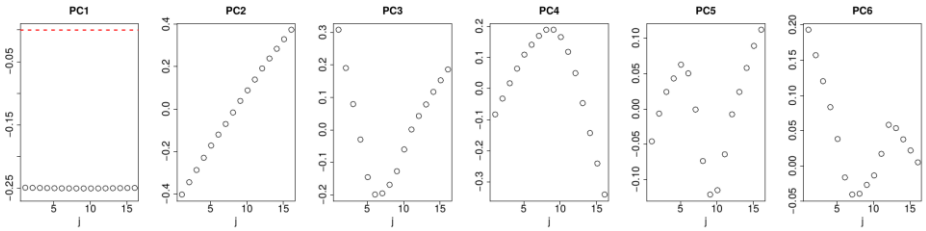
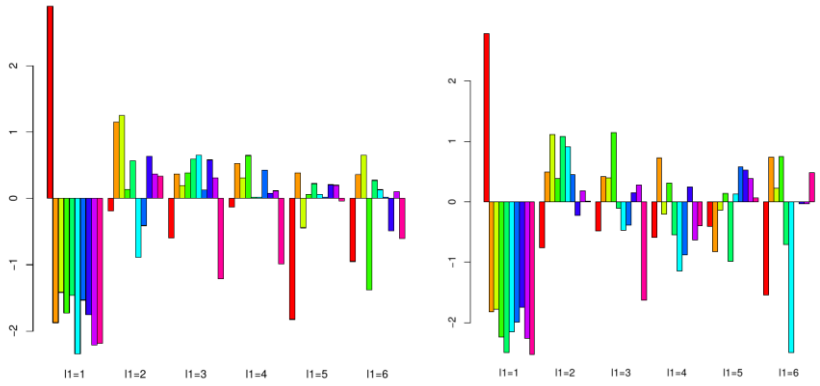


Fig. 3. Lowess-smoothed $u_{l_1 j}$, $1 \leq l_1 \leq 6$ for combinatorial drug treatments.

One might notice that u_{4j} is also concave or convex and u_{5j} and u_{6j} have more complex shapes (S-letter shaped). To see if these shapes are artifacts or reflect individual gene expression profiles, we focused on genes whose expression levels are likely coincident with these concave and convex shapes. Since we noticed that u_{1k} had constant values over six combinatorial treatments, we searched for $G(l_{1,}1, l_3)$ with the largest contribution to l_1=3,4 and relatively small contributions to l_1=1,2, which are associated with constant or linear dependence (**Fig. 4**A). It is obvious that $G(l_{1,}1,1)$ had the largest contribution to l_1=1, i.e., a constant (or dose density-independent) profile, while $G(l_{1,}1,2)$ and $G(l_{1,}1,3)$ had the largest contribution to l_1=2, i.e., linearly dependent on dose density. Thus, to identify $u_{l_3 i}$ associated with profiles other than constant or linear profiles, we employed $4 \leq l_3 \leq 6$ for gene selection. Based on P-values and correction as described in the Materials and Methods, we selected 157 genes (**Table 3**).



(A) (B)

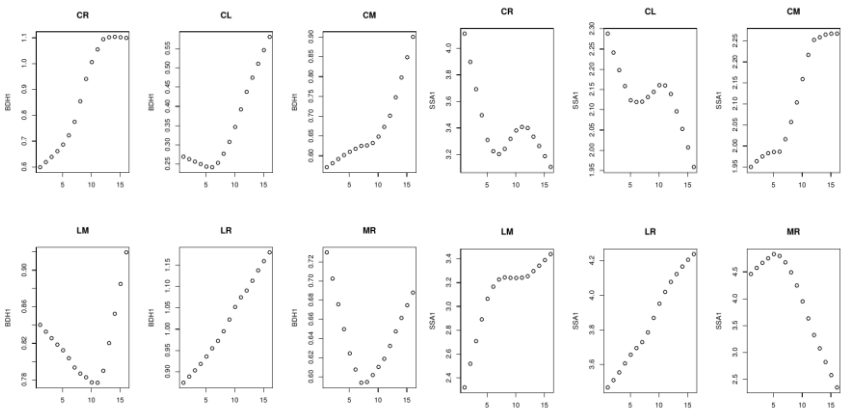
Fig. 4. Common logarithmic absolute values of $G(l_1, 1, l_3)$ for combinatorial (A) or single (B) drug treatments. For each l_1, $G(l_1, 1, l_3)$ values are aligned from left to right in increasing order of l_3 . The same colors correspond to the same l_3.

Table 3. List of 157 genes selected by TD-based unsupervised FE toward combinatorial drugs treatments. These genes are associated with concave or convex dose dependence, since they are expected to be associated with u_{3j} and u_{4j} (**Fig. 3**).

BDH1 GCV3 CDC19 YAL037C-B SSA1 ADE1 YBL005W-B TIP1 HSP26 YBR116C TKL2 TEF2 DUR1 GLK1 HIS4 AGP1 PGK1 YCR013C HSP30 RPL35A RPL41A RPL41B TPI1 FMP16 YDR154C CPR1 HSP42 YDR210C-D HSP78 YDR261C-D HXT7 HXT6 HXT3 RPS17B EMI2 YDR524W-C YRF1-1 DLD3 GLC3 GCN4 TIR1 RGI1 YER067C-A YER138C YRF1-2 ACT1 HSP12 GSY1 RPL29 YFR032C-B YFR052C-A HXK1 ADE5 YGL102C OLE1 LEU1 YGR027W-A YGR038C-B NQM1 CTT1 TPO2 TDH3 ADE3 ENO1 BGL2 YRF1-3 YHL050C YHR052W-A CUP1-1 YHR054W-A CUP1-2 HXT4 RPL42B ENO2

YHR219W RPL39 BUD19 RPS21B YJL133C-A TDH1 TDH2 OPI3 SOD1 BAT2 GPM1 CWP2 CWP1 FBA1 UGP1 YLL066C UBI4 HSP104 SSA2 YLR035C-A PDC1 SHM2 RPL22A BUD28 AHP1 CCW12 YLR154W-A YLR154W-B YLR154W-F YLR154C-G YLR157C-B YLR162W RRT15 RPS31 CBF5 NOP56 YLR198C YLR227W-B YEF3 RPL38 ADE13 YRF1-4 YRF1-5 YML133C DAK1 YML039W TSA1 GLO1 YMR045C YMR046W-A PGM2 ADE17 ALD3 SIP18 HSC82 YRF1-6 DBP2 LEU4 POR1 YNL054W-B RPL25 ADH1 RPS30B WTM1 RPS12 GDH1 FIT3 YRF1-8 YRF1-7 HSP82 SSE1 YPR002C-A GLN1 RPL43A OPI11 TEF1 RPS23B YPR137C-B ASN1 YPR158C-D YPR158C-C GPH1 YPR204W

To see if the 157 genes selected in this analyses were associated with concave, convex, or the more complicated S-shaped pattern, we plotted Lowess-smoothed expression profiles of two representative genes, *BDH1* and *SSA1*, as shown in **Fig. 5** (note that gene expression profiles of other genes are available as supplementary materials). Gene expression profiles have distinct dose dependence for drug combinations, although concave, convex, and S-shaped profiles were observed. Thus, the profiles shown in **Fig. 3** were not artifacts but reflected the expression patterns of individual genes. TD-based unsupervised FE not only generated singular value vectors that represent constant, linear, concave, or convex dependence on dose density but also characterizes more complicated (S-letter shaped) profiles for individual genes. Thus, it is a very useful strategy for analyzing gene expression profiles obtained under distinct conditions in an integrated manner.



(A) (B)

Fig. 5. Lowess-smoothed gene expression profiles for *BDH1* (A) and *SSA1* (B). Two letters above each panel show the combinations of drugs: M: Myriocin C: Cycloheximide, L: LiCl, R: Rapamycin

Next, we validated the selected genes by evaluating their biological functions. We uploaded 157 genes to YeastEnrichr and found enrichment for numerous biological functions. In particularly, we detected 23 significant biological terms in the KEGG pathway analysis (see 10 top ranked terms in **Table 4**), 91 terms in the GO Biological Process (BP) category (see 10 top ranked terms in **Table 5**), 22 terms in the GO Cellular Component (CC) category (see 10 top ranked terms in

Table 6), and 35 terms in the GO Molecular Function (BF) category (see 10 top ranked terms in **Table 7**). Thus, the selected genes had key biological functions. To confirm the observed enrichment, we also analyzed the genes using g:profiler. Although we obtained fewer significantly enriched terms, there were 219 biological terms, including KEGG pathways and GO BP, MF, and CC terms (lists of individual biological terms obtained using YeastEnrichr and g:profiler are available as supplementary materials). Thus, the biological significance of the selected genes is not database-dependent, supporting the robustness and reliability of the analysis.

Table 4. Ten top-ranked KEGG 2019 terms for 157 genes selected by TD-based unsupervised FE when combinatorial drug treatments were employed.

Term	Overlap	P-value	Adjusted P-value
Glycolysis / Gluconeogenesis	17/54	2.47E-23	1.14E-21
Starch and sucrose metabolism	9/39	1.56E-11	2.39E-10
Ribosome	16/170	3.81E-13	8.76E-12
Fructose and mannose metabolism	6/21	1.05E-08	1.20E-07
Methane metabolism	6/25	3.33E-08	3.06E-07
Galactose metabolism	5/22	6.61E-07	5.07E-06
Amino sugar and nucleotide sugar metabolism	5/30	3.40E-06	2.23E-05
Protein processing in endoplasmic reticulum	7/88	5.99E-06	3.44E-05
Longevity regulating pathway	5/36	8.66E-06	4.43E-05
Valine, leucine and isoleucine biosynthesis	3/12	9.91E-05	3.26E-04

Table 5. Ten top-ranked GO biological process (BP) 2018 terms for 157 genes selected by TD-based unsupervised FE when combinatorial drug treatments were employed.

Term	Overlap	P-value	Adjusted P-value

glycolytic process (GO:0006096)	13/20	1.92E-23	3.06E-21
ATP generation from ADP (GO:0006757)	13/20	1.92E-23	3.06E-21
nicotinamide nucleotide metabolic process (GO:0046496)	13/24	6.00E-22	6.38E-20
pyruvate metabolic process (GO:0006090)	14/33	1.35E-21	1.07E-19
carbohydrate catabolic process (GO:0016052)	13/28	8.77E-21	5.59E-19
glucose metabolic process (GO:0006006)	13/32	7.92E-20	4.21E-18
gluconeogenesis (GO:0006094)	9/16	9.80E-16	3.91E-14
hexose biosynthetic process (GO:0019319)	9/16	9.80E-16	3.91E-14
cytoplasmic translation (GO:0002181)	16/162	1.79E-13	6.35E-12
translation (GO:0006412)	20/297	2.22E-13	7.07E-12

Table 6. Ten top-ranked GO cellular component (CC) 2018 terms for 157 genes selected by TD-based unsupervised FE when combinatorial drug treatments were employed.

Term	Overlap	P-value	Adjusted P-value
cytosolic part (GO:0044445)	20/204	1.64E-16	5.64E-15
cytosol (GO:0005829)	32/676	1.82E-16	5.64E-15
retrotransposon nucleocapsid (GO:0000943)	15/91	4.40E-16	9.10E-15
nucleus (GO:0005634)	44/1599	7.80E-14	1.21E-12
cytosolic ribosome (GO:0022626)	17/185	1.00E-13	1.25E-12
mitochondrion (GO:0005739)	33/1063	8.36E-12	8.64E-11
fungal-type cell wall (GO:0009277)	12/132	5.56E-10	4.93E-09
cytosolic large ribosomal subunit (GO:0022625)	10/101	6.94E-09	5.38E-08
large ribosomal subunit (GO:0015934)	10/104	9.24E-09	6.36E-08
cytosolic small ribosomal subunit (GO:0022627)	6/71	2.00E-05	1.24E-04

Table 7. Ten top-ranked GO molecular function (MF) 2018 terms for 157 genes selected by TD-based unsupervised FE when combinatorial drug treatments were employed.

Term	Over-lap	P-value	Adjusted P-value
helicase activity (GO:0004386)	12/39	1.16E-16	1.30E-14
RNA-directed DNA polymerase activity (GO:0003964)	12/48	1.95E-15	1.09E-13
DNA-directed DNA polymerase activity (GO:0003887)	12/59	2.91E-14	1.09E-12
DNA polymerase activity (GO:0034061)	12/61	4.47E-14	1.25E-12
nuclease activity (GO:0004518)	12/64	8.27E-14	1.85E-12
ribonuclease activity (GO:0004540)	12/66	1.22E-13	2.28E-12
RNA binding (GO:0003723)	24/477	4.39E-13	7.02E-12
DNA helicase activity (GO:0003678)	8/35	2.37E-10	3.32E-09
purine ribonucleoside triphosphate binding (GO:0035639)	7/78	2.66E-06	3.31E-05
nucleoside-triphosphatase activity (GO:0017111)	10/195	3.33E-06	3.74E-05

4 Discussion and Conclusion

To analyze and interpret the effects of drug interactions on gene expression, we propose a new unsupervised method, a TD-based unsupervised FE in 3D, and applied it to gene expression profiles of *S. cerevisiae* treated with single or combinatorial drugs. Because

strong non-linear dependence was observed for both treatments (single and combined), our analysis demonstrates that these effects are unlikely to reflect DDIs.

In this study, we partially reproduced the original observations [1] by PCA; however, TD-based unsupervised FE allowed us to obtain the same results in a more robust and reliable manner. Based on our findings, the expression levels of some genes exhibit non-linear dependence on the dose density. However, non-linear dependence on the dose density was also observed for treatment with single drugs (see Additional file 2[35]). Thus, it is not clear whether the concave or convex dependence on dose can be explained by DDIs. To further evaluate the ability of individual drugs to result in non-linear dose dependence, we applied the newly developed TD-based unsupervised FE to the alternative tensor, x_{ijk}, generated from gene expression profiles of *S. cerevisiae* treated with single drugs (see Materials and Methods). **Fig. 6** shows the Lowess-smoothed $u_{l_1 j}$, $1 \leq l_1 \leq 6$ for single drug treatments. Contrary to our expectation, non-linearity was substantially greater than that shown in **Fig. 3** based on combinatorial treatments. Linear dependence was minimal and an S-letter shaped pattern was observed prior to concave or convex patterns. To determine if the strong non-linearity is associated with individual gene expression profiles, we selected genes associated with singular value vectors that exhibit non-linearity, shown in **Fig. 6**. We initially noticed that u_{1k} has constant values over four single drug treatments, as in the case of combinatorial drug treatments (not shown). Thus we need to find $G(l_1, 1, l_3)$ with the largest contribution to $3 \leq l_1 \leq 6$ and relatively small contributions to l_1=1,2, indicating constant or linear dependence (**Fig. 6**).

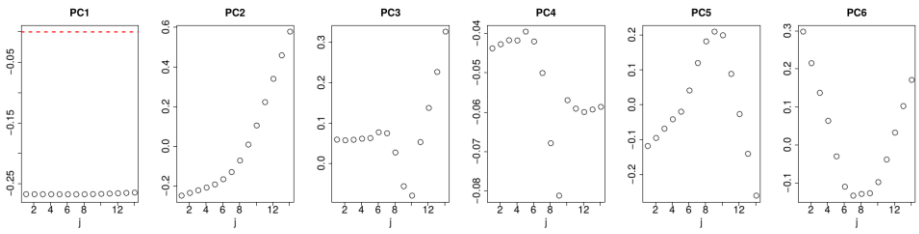
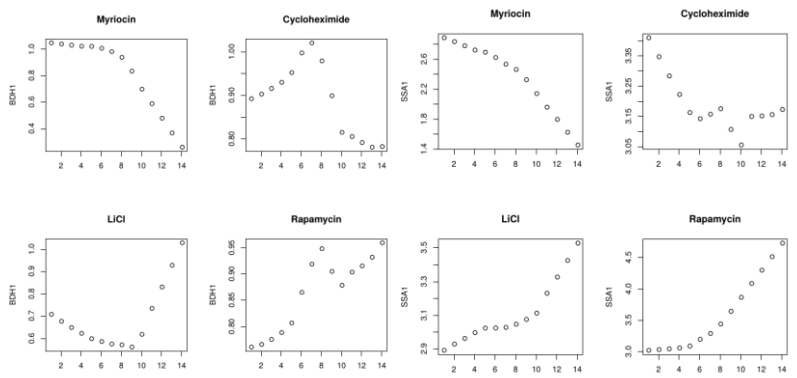


Fig. 6. Lowess-smoothed $u_{l_1 j}$, $1 \leq l_1 \leq 6$ for single drug treatments.

Observed patterns (**Fig. 4**B) exhibited greater non-linearity than those shown in **Fig. 4**A for combinatorial treatments. When drugs were treated in combinatorial manner, $G(1,1,1)$ has the largest absolute values among $G(1,1,l_3)$; this means that constant profiles are associated the first singular value vector, u_{1i}. $\mathrm{G}(2,1,2)$ and $\mathrm{G}(2,1,3)$ had the largest absolute values among $G(2,1,l_3)$, indicating that linear profiles are associated with the second singular value vector, u_{2i}, as well as the third singular value vector, u_{3i}. Nevertheless, in **Fig. 4**B, although $G(1,1,1)$ had the largest absolute values among $G(1,1,l_3)$s, $G(2,1,l_3)$, $2 \leq l_3 \leq 6$, had substantial contributions, indicating that there is no clear separation between genes whose expression profiles are associated with dose dependence represented by u_{2i}, which are most likely linear profiles, and those with dose dependence represented by u_{3i} to u_{6i}, likely representing non-linear profiles, i.e., concave, convex, and S-letter shaped profiles. Thus, to select genes with strong non-linear dependence on dose, we selected l_3=4, since $G(3,1,4)$ had the largest absolute values among $G(3,1,l_3)$ and ultimately identified 77 significant genes (**Table 8**).

Table 8. List of 77 genes selected by TD-based unsupervised FE toward single drugs. These genes likely exhibit concave or convex dose dependence, since they are expected to be associated with u_{3j} (**Fig. 6**)

BDH1 SSA1 YAR009C RPS8A YBL005W-B YBR012W-B HSP26 RPS6B GLK1 PGK1 YCR013C YCR018C-A TPI1 HSP42 YDR261C-D YDR316W-B HXT7 HXT6 EMI2 OM45 CYC7 GLC3 RGI1 YER067C-A YER138C YER160C HSP12 YFR052C-A HXK1 PNC1 STF2 YGR038C-B CTT1 YGR161C-D TDH3 ENO1 YHR052W-A CUP1-1 YHR054W-A CUP1-2 RTC3 HXT4 YHR214C-B TDH1 TDH2 SOD1 YKL153W GPM1 FBA1 UGP1 HSP104 YLR035C-A CCW12 YLR157C-B TFS1 YLR227W-B YEF3 TMA10 YML045W YML039W YMR045C PGM2 ALD3 YMR173W-A YNL284C-B RPS3 YNL054W-B YNR034W-A ADH1 RPS12 YPL257W-B HSP82 RPS6A YPR137C-B YPR158W-B YPR158C-D GPH1



(A) (B)

Fig. 7. Lowess-smoothed gene expression profiles of *BDH1* (A) and *SSA1* (B).

Fig. 7 shows Lowess-smoothed gene expression profiles of two representative genes whose expression levels are also shown in **Fig. 5** with respect to combinatorial drug treatments (expression profiles of other genes are available as supplementary materials). Non-linearity of dose dependence is not clearly reduced. Accordingly, the strong non-linearity of dose dependence observed for combinatorial drug treatments may not reflect DDIs but rather the nonlinearity on the dose dependence of the expression of individual genes (as shown in **Fig. 8**, showing extensive overlap of selected genes for single and combinatorial drug treatments). In conclusion, in our comparison of gene expression profiles between single and combinatorial drug treatments, we did not obtain clear evidence that the strong non-linearity between gene expression levels and dose can be directly attributed to DDIs.

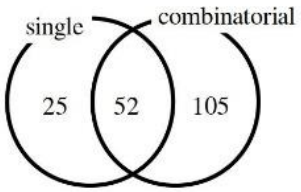


Fig. 8. Venn diagram of genes selected for combinatorial and single drug treatments.

We further evaluated the biological significance of the 77 genes selected for treatment with single drugs. We identified a number of significant (adjusted *P*-values less than 0.05) KEGG pathways (**Table 9**) and GO terms in the BP (**Table 10**), CC (**Table 11**), and MF categories (**Table 12**). Thus, the selected genes were biologically relevant.

Table 9. Ten top-ranked KEGG 2019 terms for 77 genes selected by TD-based unsupervised FE when single drug treatments were employed.

Term	Overlap	P-value	Adjusted P-value
Glycolysis / Gluconeogenesis	14/54	1.30E-22	3.76E-21
Starch and sucrose metabolism	7/39	1.32E-10	1.92E-09
Fructose and mannose metabolism	5/21	1.44E-08	1.34E-07
Galactose metabolism	5/22	1.85E-08	1.34E-07
Amino sugar and nucleotide sugar metabolism	5/30	9.80E-08	5.68E-07
Longevity regulating pathway	5/36	2.55E-07	1.23E-06
Methane metabolism	3/25	1.19E-04	4.92E-04
Protein processing in endoplasmic reticulum	4/88	3.71E-04	1.34E-03
Ribosome	5/170	5.04E-04	1.63E-03
Tyrosine metabolism	2/14	1.29E-03	3.75E-03

Table 10. Ten top-ranked GO BP 2018 terms for 77 genes selected by TD-based unsupervised FE when single drug treatments were employed.

Term	Overlap	P-value	Adjusted P-value
glycolytic process (GO:0006096)	11/20	2.13E-22	1.69E-20

ATP generation from ADP (GO:0006757)	11/20	2.13E-22	1.69E-20
nicotinamide nucleotide metabolic process (GO:0046496)	11/24	3.13E-21	1.65E-19
carbohydrate catabolic process (GO:0016052)	11/28	2.66E-20	1.05E-18
glucose metabolic process (GO:0006006)	11/32	1.58E-19	5.00E-18
pyruvate metabolic process (GO:0006090)	11/33	2.36E-19	6.23E-18
gluconeogenesis (GO:0006094)	8/16	4.17E-16	8.23E-15
hexose biosynthetic process (GO:0019319)	8/16	4.17E-16	8.23E-15
glucose import (GO:0046323)	5/33	1.62E-07	2.84E-06
glucose transport (GO:0015758)	5/34	1.89E-07	2.99E-06

Table 11. Ten top-ranked GO CC 2018 terms for 77 genes selected by TD-based unsupervised FE when single drug treatments were employed.

Term	Overlap	P-value	Adjusted P-value
retrotransposon nucleocapsid (GO:0000943)	22/91	1.62E-34	6.30E-33

nucleus (GO:0005634)	34/1599	9.70E-18	1.89E-16
cytosol (GO:0005829)	17/676	5.94E-10	7.73E-09
cytosolic part (GO:0044445)	8/204	1.18E-06	1.15E-05
cytosolic small ribosomal subunit (GO:0022627)	5/71	7.92E-06	6.18E-05
mitochondrion (GO:0005739)	15/1063	1.10E-05	7.12E-05
small ribosomal subunit (GO:0015935)	5/79	1.34E-05	7.45E-05
cytosolic ribosome (GO:0022626)	6/185	7.94E-05	3.87E-04
fungal-type cell wall (GO:0009277)	5/132	1.57E-04	6.79E-04
chaperonin-containing T-complex (GO:0005832)	2/12	9.42E-04	3.67E-03

Table 12. Ten top-ranked GO MF 2018 terms for 77 genes selected by TD-based unsupervised FE when single drug treatments were employed.

Term	Overlap	P-value	Adjusted P-value
RNA-directed DNA polymerase activity (GO:0003964)	21/48	2.04E-39	1.04E-37
DNA-directed DNA polymerase activity (GO:0003887)	21/59	4.61E-37	1.18E-35
DNA polymerase activity (GO:0034061)	21/61	1.08E-36	1.83E-35

nuclease activity (GO:0004518)	21/64	3.60E-36	4.60E-35
ribonuclease activity (GO:0004540)	21/66	7.77E-36	7.92E-35
RNA binding (GO:0003723)	25/477	5.41E-22	4.60E-21
glucokinase activity (GO:0004340)	3/6	1.09E-06	5.55E-06
hexokinase activity (GO:0004396)	3/6	1.09E-06	5.55E-06
mannokinase activity (GO:0019158)	3/6	1.09E-06	5.55E-06
fructokinase activity (GO:0008865)	3/6	1.09E-06	5.55E-06

We confirmed the observed patterns of enrichment using g:profiler. In this analysis, we detected fewer significantly enriched terms overall but still observed enrichment for various KEGG pathways and GO terms. Thus, the biological significance of the selected genes did not depend on the database and the analyses were robust and reliable (lists of individual biological terms obtained using YeastEnrichr and g:profiler are available as supplementary materials).

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