Identification of Candidate Drugs for Heart Failure using Tensor Decomposition-Based Unsupervised Feature Extraction Applied to Integrated Analysis of Gene Expression between Heart Failure and Drug Matrix Datasets

Y-h. Taguchi

Department of Physics, Chuo University, Tokyo 112-8551, Japan
tag@granular.com

Abstract. Identifying drug target genes in gene expression profiles is not straightforward. Because a drug targets not mRNAs but proteins, mRNA expression of drug target genes is not always altered. In addition, the interaction between a drug and protein can be context dependent; this means that simple drug incubation experiments on cell lines do not always reflect the real situation during active disease. In this paper, I apply tensor decomposition-based unsupervised feature extraction to the integrated analysis of gene expression between heart failure and the Drug Matrix dataset where comprehensive data on gene expression during various drug treatments of rats were reported. I found that this strategy, in a fully unsupervised manner, enables us to identify a combined set of genes and compounds, for which various associations with heart failure were reported.
Keywords: Tensor decomposition·Drug discovery·Heart diseases

1 Introduction

In silico drug discovery is an important task because experimental identification/verification of therapeutic compounds is a time-consuming and expensive process. There are two major trends of *in silico* drug discovery: the ligand-based approach and structure-based approach. The former is very straightforward; new drug candidates are identified based upon the similarity with known drugs no matter how the similarity is evaluated. Although it is a powerful method, there are some drawbacks; if there are no known drugs for target proteins, then there is no way to find new drug candidates. Even if there are many known drugs for the target protein, it is hopeless to find compounds that are effective but without any similarity with known drugs. The second, structure-based approach, can address these weaknesses. It can identify new therapeutic compounds even without the information about known drugs. Of course, there are some drawbacks in this strategy, too. If the target protein structure is not known, it must be predicted prior to the drug discovery process. Even if the target protein's structure is known, because we need to numerically verify the binding affinity between the ligand

adfa, p. 1, 2011.

compound and target protein, which also requires a large amount of computational resources, structure-based *in silico* drug discovery is still far from easy to perform. In addition, prediction accuracy of protein structure and of ligand-binding structure is not very high at all. Thus, it would be helpful to have an additional/alternative strategy for *in silico* drug discovery.

Recently, an alternative approach was proposed that is aimed at finding drug candidates computationally using gene expression profiles of cell lines treated with compounds. This third approach is not straightforward at all. First of all, because compounds target not mRNAs but proteins, mRNA expression of drug target proteins is not always affected. Therefore, direct identification of a drug target protein in gene expression data cannot be done. Second, gene expression alteration caused by treatment with a compound may be context dependent; in other words, in a cell line, the gene expression difference caused by incubation with a compound may differ from that in diseases. To compensate these difficulties, the gene expression signature strategy was developed. In this approach, gene expression alteration profiles caused by treatment of a cell line with various drug candidates are compared with those of known drugs. If the profiles are similar, then new drug candidates are expected to function similarly to known drugs. Although this third strategy is a useful one, if there are no known drugs for the target disease, this approach cannot function at all as in the case of ligand-based approaches.

In this paper, I propose a strategy that can infer drug candidates from drug treatment-associated gene expression profiles without the information about known compounds for diseases. In this strategy, I employ the tensor decomposition (TD)-based unsupervised feature extraction (FE) approach, which is an extension of the recently proposed principal component analysis (PCA)-based unsupervised FE; PCA-based unsupervised FE successfully solved various bioinformatic problems [1–19]. In this TD-based strategy, tensors were generated using a mathematical product of a gene expression profile of drug-treated cell lines and of a gene expression profile of a disease. Then, pairs of compounds and genes are identified whose mRNA expression alteration is associated with drug-treated cell lines and is coincident with such alteration during disease progression. Biological evaluation of the identified genes and compounds based upon past studies turned out to be promising.

2 Materials and Methods

2.1 Mathematics of TD

In this subsection, I briefly discuss what the TD is and how I apply TD to the present problem. Suppose an m-mode tensor $x_{j_1 \cdots j_{m-1} i}$ represents gene expression of the ith gene under the j_k (k=1,...,m-1, j_k=1,…,N_k) conditions, examples of which are diseases, patients, tissues, and time points. Then, TD is defined as

$$x_{j_1 \cdots j_{m-1} i} = \sum_{l_1 \cdots l_m}^{N_1 \cdots N_m} G(l_1 \cdots l_m) x_{l_m i} \prod_{k=1}^{m-1} x_{l_k j_k} \quad (1)$$

where $G(l_1 \cdots l_m)$ is a core tensor and $x_{l_m i}$ and $x_{l_k j_k}$ are singular value matrices that are supposed to be orthogonal to one another. Because $G(l_1 \cdots l_m)$ is assumed to be as large

as $x_{j_1 \cdots j_{m-1} i}$, it is obviously an overcomplete problem; thus, there are no unique solutions. To solve TD uniquely, I specifically employed the higher-order singular value decomposition [20] (HOSVD) algorithm that tries to attain TD such that smaller number of core tensors and singular value vectors can represent $x_{j_1 \cdots j_{m-1} i}$ as much as possible.

2.2 Tensor Generation for Integrated Analysis

It is quite common when there is a set of gene expression profiles of human cell lines or model animals treated with various compounds at multiple dose densities. For example, Drug Matrix[1] and LINCS [21] are good examples, although the former comprises only temporal gene expression after drug treatments. Nonetheless, it is not easy to infer a drug's action on diseases by means of only these gene expression profiles; some kind of integrated analysis with disease gene expression profiles is required, but it is not so straightforward. Candidate drugs should satisfy these conditions:

- Gene expression in these profiles must significantly decrease or increase with the increasing dose density of compounds.
- Gene expression alteration caused by drug treatment must be significantly coincident with that associated with disease progression.

How these two independent significance values can be evaluated is unclear. For example, we can have two sets of significant gene expression alterations of the *i*th gene, $\{\Delta x_i\}$, caused by drug treatment and those of the *i*'th gene, $\{\Delta x'_{i'}\}$, during disease progression, respectively. First, we need to test whether the two sets of genes are significantly overlapping. Next, when there is a significant overlap, we have to determine whether these two gene expression alteration profiles correlate significantly. Furthermore, because the analysis is usually conducted among multiple compounds, all the significance evaluation must be corrected based upon a multiple comparison criterion. It is obviously a complicated and not a promising strategy.

Nevertheless, if we can have gene expression profiles expressed via a tensor, $x_{j_1 \cdots j_{m-1} i}$, where j_k (k=1,...,m-1) corresponds to drug candidates, dose density, and disease progression, we can easily evaluate a candidate drug using TD, eq. (1). If there are $x_{l_k j_k}$ values that represent significant dependence upon dose densities and disease progression, genes' and compounds' singular value vectors that share core tensor G with larger absolute values with these $x_{l_k j_k}$s can be used for the selection of genes as well as compounds as follows.

Suppose $\{l_k\}$ is a set of indices of genes' or compounds' singular value vectors that are associated with significant dose density dependence as well as disease progression dependence. Genes and compounds can be identified as being associated with significant singular value vector components. For this purpose, P-values are attributed to each ith gene/j_kth compound assuming a χ^2 distribution,

[1] https://ntp.niehs.nih.gov/drugmatrix/index.html

$$P_i = P_{\chi^2}[> \sum_{\{l_m\}} \left(\frac{x_{l_m i}}{\sigma_{l_m}}\right)^2] \text{ or } P_{j_k} = P_{\chi^2}[> \sum_{\{l_k\}} \left(\frac{x_{l_k j_k}}{\sigma_{l_k}}\right)^2] \quad (2)$$

where $P_{\chi^2}[> x]$ is the cumulative probability that the argument is greater than x assuming the χ^2 distribution and σ_{l_m} and σ_{l_k} are standard deviations. After adjusting *P*-values using the Benjamini–Hochberg (BH) criterion [22], genes and compounds that have significant P-values, e.g., less than 0.01, are selected as those contributing to the specified singular value vectors. Nevertheless, because such a tensor can be obtained only when drug treatment is performed on patients, this strategy is useless; if we can test drug efficiency directly on patients, then there is no need for *in silico* drug discovery. To overcome this discrepancy, I replace $x_{j_1 \cdots j_{m-1} i}$ with a product, $x_{j_1 \cdots j_{m'} i} \cdot x_{j_1 \cdots j_{m"} i}$, where $x_{j_1 \cdots j_{m'-1} i}$ is gene expression for the drug treatment of cell lines/model animals, while $x_{j_1 \cdots j_{m"-1} i}$ is gene expression for the patients ($m - 1 = m' + m"$). Because these two can be obtained independently, we can test any kind of combinations of drug treatments and diseases even after all measurements were performed.

2.3 Gene Expression Profiles

Gene expression profiles for drug treatments of rats were retrieved from Drug Matrix under the gene expression omnibus (GEO) ID GSE59905, while heart failure human gene expression was taken from GEO ID 57345. For both datasets, expression files of genes, GSE57345-GPL11532_series_matrix.txt.gz, GSE59905-GPL5426_series_matrix.txt.gz, and GSE59905-GPL5425_series_matrix.txt.gz were directly downloaded from the series matrix.

2.4 Various Servers for Enrichment Analysis

To Enrichr [23] and TargetMine [24], 274 gene symbols were uploaded. For TargetMine, human was assumed as an organism under study, and the BH criterion was used for *P*-value correction.

2.5 Statistical Analysis

All the statistical analyses were performed within the R software. HOSVD was carried out using the `hosvd` function in the rTensor package.

3 Results

3.1 TD-based Unsupervised FE Was Applied to a Combined Tensor

From gene expression profiles of the rat left ventricle (LV) treated with 218 drugs, we selected four time points (1/4, 1, 3, and 5 days after treatment). Although these do not directly represent drug dose dependence, time course observations can be replaced with dose dependence, because drug dose density is expected to monotonically decrease with time. On the other hand, human heart gene expression profiles are composed of 82

idiopathic dilated cardiomyopathy patients, 95 ischemic patients, and 136 healthy controls, respectively. Among them, 3937 genes sharing gene symbols between human and rat were considered. Then, the generated tensor is

$$x_{j_1 j_2 j_3 i} = x_{j_1 j_2 i} \cdot x_{j_3 i} \ , 1 \le j_1 \le 218, 1 \le j_2 \le 4, 1 \le j_3 \le 313, 1 \le \mathrm{i} \le 3937 \quad (3)$$

which represents the products of gene expression of the *i*th gene of LV treated with $j_1$compound at the j_2th time point after the drug treatment and gene expression of the j_3th human heart, respectively. HOSVD was applied to $x_{j_1 j_2 j_3 i}$ and core tensor $G(l_1 l_2 l_3 l_4), 1 \le l_1 \le 218, 1 \le l_2 \le 4, 1 \le l_3 \le 313, 1 \le l_4 \le 3937$, compound singular value matrix $x_{l_1 j_1}$, time point singular value matrix, $x_{l_2 j_2}$, human sample singular value matrix, $x_{l_3 j_3}$, and gene singular value matrix, $x_{l_4 i}$, were obtained. Prior to selection of genes and compounds, we need to know which time points singular value vector represents time dependence and which human sample singular value vector represents the distinction between patients and healthy controls (Fig. 1). As for time point singular value vectors, I decided to use the 2nd singular value vector because it has the strongest correlation with days. It also represents reasonable time development. After drug treatment, gene expression gradually increases because it takes awhile for a drug treatment to have an effect. Then, after it has a peak on day 1, a monotonic decrease follows. On the other hand, for human sample singular value vectors, the 2nd and 3rd ones were selected because they have a clear distinction between patients and healthy controls.

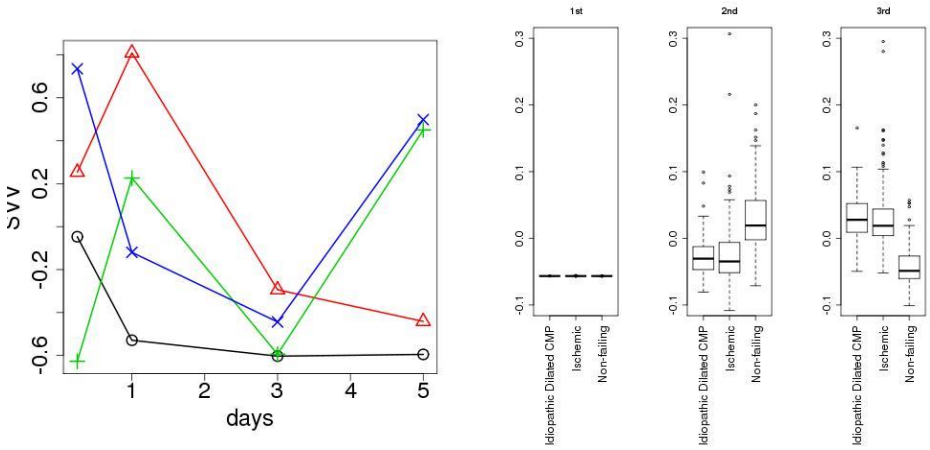

Fig. 1. Left: Time points' singular value vectors. Black circle: 1st, red triangle: 2nd, green cross: 3rd, and blue cross: 4th singular value vectors, respectively. Pearson's correlation coefficients toward days are -0.72, -0.82, 0.51, and -0.09, respectively. **Right**: A box plot of human sample singular value vectors. From left to right, the 1st, 2nd, and 3rd singular value vectors are shown.

Next, I tried to identify gene singular value vectors and compound singular value vectors associated with core tensor $\mathrm{G}(l_1 l_2 l_3 l_4), l_2 = 2, 2 \le l_3 \le 3$ that have larger absolute values (Table 1). One can see that the 2nd singular value vector of compounds is always associated with top 20 core tensors. The selection of gene singular value vectors

is not so trivial. First of all, generally low-ranked gene singular value vectors are listed. This means that gene expression associated with disease progression is not a majority. This is a common situation because the disease usually affects only a limited number of genes. Then, tentatively, I decided to select top 10 gene singular value vectors, 21st, 25th, 27th, 28th, 33rd, 36th, 37th, 38th, 41st, and 42nd singular value vectors of genes. Using these singular value vectors, *P* values were attributed to genes and compounds. The attributed *P* values were adjusted by the BH criterion. Then, 281 probes and 0 compounds associated with adjusted *P* values less than 0.01 were selected. Because no compounds pass our criteria, I sought another way to select compounds. Fig. 2 shows the histogram of the 2nd singular value vectors of compounds. There are obviously some outliers. Then, tentatively, I selected 43 compounds having the absolute 2nd singular value vector components larger than 0.1.

3.2 Biological Evaluation of the Selected Compounds and Genes

To see if we can successfully identify biologically relevant compounds and genes, we evaluated these selected genes and compounds. At first, a literature search was performed on the 43 drugs. Then, some heart failure-related studies were identified for most of the 43 drugs (Table 2). This means that biologically relevant drugs were likely to be identified successfully. As for the genes identified, 274 genes associated with the identified 281 probes are shown in Table 3.

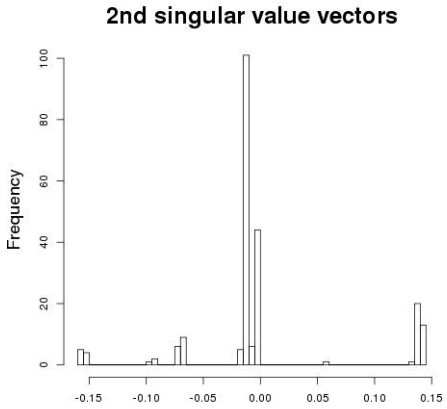

Fig. 2. A histogram of 2nd singular value vectors of compounds.

Table 1. $G(l_1 l_2 l_3 l_4), l_2 = 2, 2 \le l_3 \le 3$, in the order of larger absolute values of *G*

l_1	l_3	l_4	G	l_1	l_3	l_4	G
2	2	27	66.2	2	3	40	-25.5
2	3	38	-43.7	2	2	29	25.2
2	2	33	40.6	2	2	31	-22.6
2	2	28	-40.2	2	3	39	21.8
2	3	41	38.2	2	2	32	20.7
2	3	37	-31.6	2	3	33	-19.7
2	2	21	28.5	2	2	26	-19.5
2	3	36	-26.8	2	2	11	-18.2
2	3	42	-26.2	2	2	18	-17.3
2	2	25	-26.2	2	3	31	15.4

Table 2. Literature search performed on 43 drugs identified by TD-based unsupervised FE. Numbers are Pubmed IDs (https://www.ncbi.nlm.nih.gov/pubmed/) that report the relation to heart failure.

Amitriptyline [27994924]	Atropine [24279866]	Baclofen [27682809]	Bezafibrate [26957517]	Caffeine [25944789]

Calcitriol [27209698]	Chlorambucil [8164221]	Cimetidine [18656805]	Citalopram [25326372]	Clemastine [16288909]
Clonazepam [15699937]	Cyclophosphamide [24467219]	D-Tubocurarine Chloride [14839919]	Dexamethasone [25923220]	Dexchlor-pheniramine [---]
Digitoxin [27082032]	Diphenhydramine [22158278]	Doxazosin [26515144]	Ebastine [21410688]	Fenofibrate [26497978]
Fluphenazine [23395964]	Gabapentin [19195912]	Ifosfamide [14586140]	Iproniazid [13688979]	Lacidipine [23911888]
Loratadine [21880544]	Nevirapine [15526045]	Nimodipine [17191657]	Nitrendipine [22750214]	Ofloxacin [21559378]
Oxymetazoline [22855901]	Paroxetine [26216863]	Phenacemide [---]	Phenytoin [24172819]	Rosiglitazone [21666037]
Sparteine [4408029]	Stavudine [---]	Valsartan [26992459]	Vecuronium Bromide [---]	Venlafaxine [23301719]
Vinblastine [25537132]	Vincristine [---]	Zidovudine [25838291]		

Table 3. The 274 genes associated with 281 probes identified by TD-based unsupervised FE.

Atp6v1h Smad4 Tfam Ramp2 Vdac2 Sfrp4 Accn3 Pdxk Ccnl1 Kcnk3 Pdk4Nfe2l2 Nexn Ccl2 Lphn3 P2rx3 Odz2 Mpp3 Kcnt1 Gapdh Ncoa2 Pacsin2 Slpi Tnfaip6 Prelp Ppp2r2d Sharpin Slc38a2 Col5a1 Steap3 Ppp1r14a Bves Nsf Sox18 Ndfip1 Yme1l1 Gosr1 Nf1 Fndc5 Pold4 Wbp4 Immt Sdhd Dlc1 Itga6 Eif2s2 Bmpr1a Abcb10 Mknk2 Kpna1 Bag3 F8 Lrp1 Vezt Aqp4 Pdcl3 Schip1 Gbe1 Synj1 Map2k4 Laptm4b Psmd12 Mtus1 Ddit4l Mlycd Ppm1b Mterf Ing4 Vsnl1 Rhoa Ltbp4 Dhrs1 Txndc12 Tnfrsf12a Itm2c Samm50 B4galt7 Fbl Chchd4 Pdrg1 Pycr2 Rplp1 Rps20 Bzw1 Fos Cybb Sccpdh Smpd1 Kcmf1 Gna12 Nedd4l Bpgm Akap1 Actr1b Msn Dnajc5 Lcp1 Agpat1 Tarbp2 Git2 Usp14 Nfatc4 Rxrg Uqcrc2 Actn1 Ndufs2 Rps18 Slc40a1 Chdh Rela Ciapin1 Fbxo22 mrpl9 Ppp1r14c Btbd9 Obscn Cmklr1 Fyttd1 Sirt5 Flt1 Grwd1 Hrc Trpc4ap Dcps Idh3a Tmem30a Fut8 Pi4k2a Cdh23 Eif4a1 C1qa Gpx3 Slc25a4 Fgf9 Psmc1 Rbm10 Nr0b2 Acsl1 A2m Alas1 Suclg1 Acads Atp5a1 Ccnd2 Csnk2b Psmb4 Canx Cd36 Pggt1b Pde4b Npr3 Hspa5 Nr3c1 Apob Got2 Actg2 Nr3c2 Egfr Ldha Adcy3 Cryab Man2c1 Il6r Slc6a1 Adra1b Ednra Tnfrsf1a Atf3 Mapk6 Agrn Rab15 Ywhae Arf4 Pdia4 Ppara Il6st Adrb2 Egr1 Got1 Myc Myl2 Mme Spin2b Stat3 Slc2a4 Apod Dpp4 Mapk10 Azgp1 Ephx1 Htr4 Mgp Spp1 Adora3 Eef2k Hmgb1 Nes Ptgds Slc5a1 Ywhah Cd74 Aoc3 Atp1b1 Itpr3 Ak3 Lcat Pccb Ppm1a Ppp2ca Sod1 Glul Ghr Kcnj8 Areg Cd63 Ctf1 Tnni3 Rps6 Serpinh1 Uchl1 Btg2 Mapk9 Tpm1 Vtn Hapln1 Mgat3 Ca3 Tpsab1 Anxa2 Ccr1 Junb Gnb3 Stx7 Gnb2l1 Il1rl1 Fstl1 Gatm Pdk2 Ces1 Fabp5 Csda Txnip Lss Acvr1c Scn2b Mfn2 Mxd3 Ptger2 Mvd Gucy1a3 Ppif Mapk14 Gnb1 Ttn Acta1 Gstp1 Hmbs C3 Vim Cebpg Amhr2 Idh3g Csrp3 Acox3 Cyb5b Cast

To evaluate biological reliability of these 274 genes, they were uploaded to various enrichment servers. When they were uploaded to TargetMine, top five tissue enrichment results were related to the heart (Table 4). Top four significant disease enrichment results represent heart failure (Table 5). When they were uploaded to Enrichr, top three OMIM disease enrichment results were related to heart failure (Table 6). Two out of top three MGI Mammalian Phenotype Level 3 enrichment results were also related to heart failure (Table 7). Thus, our identification of genes was also successful.

Table 4. Top five significant tissue enrichment results of TargetMine.

Tissue	p-Value	Matches
left ventricular apex samples	1.880e-37	101
heart atrium	1.357e-36	155
heart	8.637e-36	153
ventricular myocardium	4.306e-35	95
atrial myocardium	1.716e-34	98

Table 5. Top four disease enrichment results of TargetMine.

Disease	p-Value	Matches
Myocardial Ischemia	1.546e-7	22
Infarction, Middle Cerebral Artery	6.072e-6	9
Reperfusion Injury	9.567e-5	13
Cardiomyopathies	1.448e-4	13

Table 6. Top three significant OMIM Disease enrichment results of Enrichr.

Name	Overlap	P-value	Adjusted p-value
cardiomyopathy, hypertrophic	5/17	2.516E-05	9.814E-05
cardiomyopathy	5/42	2.615E-04	5.099E-03
cardiomyopathy, dilated	4/33	1.031E-03	1.341E-02

Table 7. Top three significant MGI Mammalian Phenotype Level 3 enrichment results of Enrichr.

Term	Overlap	P-value	Adjusted P-value
MP0001544_abnormal_cardiovascular_system_physiology	54/1130	5.133E-016	3.233E-014
MP0002106_abnormal_muscle_physiology	35/671	1.171E-011	1.844E-010
MP0002127_abnormal_cardiovascular_system_morphology	50/1223	2.818E-012	5.919E-011

Enrichr also outputted many epigenetic feature enrichment results. Top most significant ENCODE TF-ChiP-seq 2015 is POLR2A_heart_mm9; POLR2A is a transcription factor (TF) reported to be a stable reference gene for gene expression alteration in gene expression studies on rodent and human heart failure [25]. This finding suggested that *POLR2A* is constantly expressive in heart failure, which is coincident with our analysis. Top most significant TF-LOF Expression result from GEO is yy1_227711985_skeletal_muscle_lof_mouse_gpl8321_gse39009_up. YY1 is a TF reported to play critical roles in cardiac morphogenesis [26]. The top most significant ENCODE Histone Modifications 2015 result is H3K36me3_myocyte_mm9; H3K36me3 was reported to play

a crucial role in cardiomyocyte differentiation [27]. These TFs as well as histone modifications identified by our strategy can be possible drug targets.

4 Conclusions

In this paper, I introduced a new strategy that integrates disease (heart failure) gene expression profiles with drug treatment-related tissue gene expression profiles. The identified genes as well as compounds have been widely reported to be related to heart failure. Thus, this strategy turned out to be useful for *in silico* drug discovery.

References

1. Kinoshita, R., Iwadate, M., Umeyama, H., Taguchi, Y.H.: Genes associated with genotype-specific DNA methylation in squamous cell carcinoma as candidate drug targets. BMC Syst Biol. 8 Suppl 1, S4 (2014).
2. Taguchi, Y., Iwadate, M., Umeyama, H., Murakami, Y., Okamoto, A.: Heuristic principal component analysis-aased unsupervised feature extraction and its application to bioinformatics. In: Wang, B., Li, R., and Perrizo, W. (eds.) Big Data Analytics in Bioinformatics and Healthcare. pp. 138–162 (2015).
3. Murakami, Y., Kubo, S., Tamori, A., Itami, S., Kawamura, E., Iwaisako, K., Ikeda, K., Kawada, N., Ochiya, T., Taguchi, Y.H.: Comprehensive analysis of transcriptome and metabolome analysis in Intrahepatic Cholangiocarcinoma and Hepatocellular Carcinoma. Sci Rep. 5, 16294 (2015).
4. Taguchi, Y.-H., Iwadate, M., Umeyama, H.: Heuristic principal component analysis-based unsupervised feature extraction and its application to gene expression analysis of amyotrophic lateral sclerosis data sets. 2015 IEEE Conf. Comput. Intell. Bioinforma. Comput. Biol. (2015).
5. Umeyama, H., Iwadate, M., Taguchi, Y.: TINAGL1 and B3GALNT1 are potential therapy target genes to suppress metastasis in non-small cell lung cancer. BMC Genomics. 15, S2 (2014).
6. Murakami, Y., Kubo, S., Tamori, A., Itami, S., Kawamura, E., Iwaisako, K., Ikeda, K., Kawada, N., Ochiya, T., Taguchi, Y.-H.: Comprehensive analysis of transcriptome and metabolome analysis in Intrahepatic Cholangiocarcinoma and Hepatocellular Carcinoma. Sci. Rep. 5, 16294 (2015).
7. Taguchi, Y., Murakami, Y.: Principal component analysis based feature extraction approach to identify circulating microRNA biomarkers. PLoS One. (2013).
8. Taguchi, Y.-H., Murakami, Y.: Universal disease biomarker: can a fixed set of blood microRNAs diagnose multiple diseases? BMC Res. Notes. 7, 581 (2014).
9. Murakami, Y., Tanahashi, T., Okada, R., Toyoda, H., Kumada, T., Enomoto, M., Tamori, A., Kawada, N., Taguchi, Y.H., Azuma, T.: Comparison of hepatocellular carcinoma miRNA expression profiling as evaluated by next generation sequencing and microarray. PLoS One. 9, (2014).

10. Taguchi, Y. -h., Iwadate, M., Umeyama, H.: Principal component analysis-based unsupervised feature extraction applied to in silico drug discovery for posttraumatic stress disorder-mediated heart disease. BMC Bioinformatics. 16, 139 (2015).
11. Y-h. Taguchi: Identification of More Feasible MicroRNA–mRNA Interactions within Multiple Cancers Using Principal Component Analysis Based Unsupervised Feature Extraction. Int. J. Mol. Sci. 17, E696 (2016).
12. Taguchi, Y.-H., Iwadate, M., Umeyama, H.: Heuristic principal component analysis-based unsupervised feature extraction and its application to gene expression analysis of amyotrophic lateral sclerosis data sets. In: Computational Intelligence in Bioinformatics and Computational Biology (CIBCB), 2015 IEEE Conference on. pp. 1–10 (2015).
13. Taguchi, Y.-H.: Principal component analysis based unsupervised feature extraction applied to publicly available gene expression profiles provides new insights into the mechanisms of action of histone deacetylase inhibitors. NEPIG. (2016).
14. Taguchi, Y.-H., Iwadate, M., Umeyama, H.: SFRP1 is a possible candidate for epigenetic therapy in non-small cell lung cancer. BMC Med. Genomics. 9, (2016).
15. Taguchi, Y.-H.: microRNA-mRNA interaction identification in Wilms tumor using principalcomponent analysis based unsupervised feature extraction. In: 2016 IEEE 16th International Conference on Bioinformatics and Bioengineering (BIBE). pp. 71–78 (2016).
16. Taguchi, Y.-H.: Principal component analysis based unsupervised feature extraction applied to budding yeast temporally periodic gene expression. BioData Min. 9, 22 (2016).
17. Murakami, Y., Toyoda, H., Tanahashi, T., others: Comprehensive miRNA expression analysis in peripheral blood can diagnose liver disease. PLoS One. 7, e48366 (2012).
18. Ishida, S., Umeyama, H., Iwadate, M., Taguchi, Y.H.: Bioinformatic Screening of Autoimmune Disease Genes and Protein Structure Prediction with FAMS for Drug Discovery. Protein Pept. Lett. 21, 828–839 (2014).
19. Taguchi, Y.-H.: Principal Components Analysis Based Unsupervised Feature Extraction Applied to Gene Expression Analysis of Blood from Dengue Haemorrhagic Fever Patients. Sci. Rep. 7, 44016 (2017).
20. De Lathauwer, L., De Moor, B., Vandewalle, J.: A Multilinear Singular Value Decomposition. SIAM J. Matrix Anal. Appl. 21, 1253–1278 (2000).
21. Duan, Q., Reid, S.P., Clark, N.R., Wang, Z., Fernandez, N.F., Rouillard, A.D., Readhead, B., Tritsch, S.R., Hodos, R., Hafner, M., Niepel, M., Sorger, P.K., Dudley, J.T., Bavari, S., Panchal, R.G., Ma'ayan, A.: L1000CDS2: LINCS L1000 characteristic direction signatures search engine. npj Syst. Biol. Appl. 2, 16015 (2016).
22. Benjamini, Y., Hochberg, Y.: {C}ontrolling the false discovery rate: a practical and powerful approach to multiple testing. J. R. Stat. Soc. B57, 289–300 (1995).
23. Kuleshov, M. V., Jones, M.R., Rouillard, A.D., Fernandez, N.F., Duan, Q., Wang, Z., Koplev, S., Jenkins, S.L., Jagodnik, K.M., Lachmann, A., McDermott, M.G., Monteiro, C.D., Gundersen, G.W., Ma'ayan, A.: Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. Nucleic Acids Res. 44, W90–W97 (2016).

24. Chen, Y.-A., Tripathi, L.P., Mizuguchi, K.: TargetMine, an Integrated Data Warehouse for Candidate Gene Prioritisation and Target Discovery. PLoS One. 6, e17844 (2011).
25. Brattelid, T., Winer, L.H., Levy, F.O., Liestøl, K., Sejersted, O.M., Andersson, K.B.: Reference gene alternatives to Gapdh in rodent and human heart failure gene expression studies. BMC Mol. Biol. 11, 22 (2010).
26. Beketaev, I., Zhang, Y., Kim, E.Y., Yu, W., Qian, L., Wang, J.: Critical role of YY1 in cardiac morphogenesis. Dev. Dyn. 244, 669–680 (2015).
27. Cattaneo, P., Kunderfranco, P., Greco, C., Guffanti, A., Stirparo, G.G., Rusconi, F., Rizzi, R., Di Pasquale, E., Locatelli, S.L., Latronico, M.V.G., Bearzi, C., Papait, R., Condorelli, G.: DOT1L-mediated H3K79me2 modification critically regulates gene expression during cardiomyocyte differentiation. Cell Death Differ. 23, 555–64 (2016).