Genome analysis

Graphical data mining of cancer mechanisms with SEMA

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Abstract

Motivation: An important goal of cancer genomics initiatives is to provide the research community with the resources for the unbiased query of cancer mechanisms. Several excellent web platforms have been developed to enable the visual analyses of molecular alterations in cancers from these datasets. However, there are few tools to allow the researchers to mine these resources for mechanisms of cancer processes and their functional interactions in an intuitive unbiased manner.

Results: To address this need, we developed SEMA, a web platform for building and testing of models of cancer mechanisms from large multidimensional cancer genomics datasets. Unlike the existing tools for the analyses and query of these resources, SEMA is explicitly designed to enable exploratory and confirmatory analyses of complex cancer mechanisms through a suite of intuitive visual and statistical functionalities. Here, we present a case study of the functional mechanisms of TP53-mediated tumor suppression in various cancers, using SEMA, and identify its role in the regulation of cell cycle progression, DNA repair and signal transduction in different cancers.

SEMA is a first-in-its-class web application designed to allow visual data mining and hypothesis testing from the multidimensional cancer datasets. The web application, an extensive tutorial and several video screencasts with case studies are freely available for academic use at https://sema.research.cchmc.org/.

Availability and implementation: SEMA is freely available at https://sema.research.cchmc.org. The web site also contains a detailed Tutorial (also in Supplementary Information), and a link to the YouTube channel for video screencasts of analyses, including the analyses presented here. The Shiny and JavaScript source codes have been deposited to GitHub: https://github.com/msolmazm/sema.

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

The collection of large genomics datasets from clinical and population studies provide an unprecedented opportunity to query the molecular underpinnings of disease mechanisms. The raw and processed data from these projects have been made easily accessible to the bioinformatics community through the data portals, and tools have been developed to ease the process of acquiring and assembly of these datasets for computational analyses (Birger et al., 2017;
of the data, including as clustered heatmaps, and of the statistical results are also implemented.

2 Implementation

2.1 Interface design
The app, after launching from the home page, consists of a graph area and a plot area (Fig. 1). Users input variables into the graph, and draw links between them to formulate causal relationships to be tested. Importantly, there are no restrictions on the complexity of the graph, and users can formulate multi-component, multi-level (e.g. A causes B causes C) or even cyclic relationships. Currently, SEMA features mRNA, miRNA, protein (RPPA), somatic mutations (from whole-exome sequencing), germline variations (from whole-exome sequencing), somatic copy number variations (CNV) and clinical data from 26 cancer types (i.e. those that have >100 samples) in TCGA (Supplementary Table S1), and mRNA, somatic mutations, copy number variation and clinical data from 5 cancers in Therapeutically Applicable Research to Generate Effective Treatment (TARGET) consortium. In addition, we have included some pre-computed tumor characteristics from the PanCan immune Atlas analyses of TCGA data (Thorsson et al., 2018), which includes tumor neo-antigen burden, lymphocyte infiltration, T-cell receptor richness and evenness, among many other useful metrics.

Users form hypotheses to be tested by drawing appropriate links between the variables on the graph. The variables on the graph can be visualized individually or collectively as a clustered heatmap. In addition, users can visualize pair-wise distribution of linked nodes, e.g. a box plot of the mRNA expression of a gene stratified by copy number variations in another. After the model is evaluated by SEM, users can also compare the individual statistical parameters of the links between cancer types (see Supplementary Information).

The model is statistically evaluated after the user clicks ‘Evaluate’. Statistical evaluation of the model is conducted by structural equation modeling (SEM) tool implemented in the R package lavaan (Rosseel, 2012). The fit statistics for the whole model can be visualized in the Model Parameters Table, while the fit statistics for the individual relationships are overlaid on the respective links on the graph and both color- and thickness-coded. Users can do comparative analyses of the fit results between cancers in the plot area (see Supplementary Information). Although there is no consensus in the field on which measures or what respective cutoffs to choose for an acceptable model fit, the general guidelines are that the comparative fit indices, e.g. Tucker-Lewis Index (TLI), should be high (e.g. TLI > 0.9–0.95), while absolute fit measures, e.g. Standardized Root Mean Square Residual (SRMR), should be low (e.g. <0.1) (Hu and Bentler, 1999). Since the chi-squared test for SEM is overly sensitive to the sample size, this test (and the associated p-value) is usually not taken into consideration when dealing with large sample sizes, and is therefore not included in the parameter table.

2.2 Exploratory analyses: variable selection
In the cases when a priori information on the gene/molecule of interest is limiting, or when a researcher simply would like to engage in an unbiased study, it is useful to do exploratory analyses. To aid in such exploratory analyses, we have compiled an extensive database of pre-computed all-against-all correlations of all the data types in TCGA (~300 billion correlations), which the user can tap into to select the best variables to include in a model. For example, a user can identify, in an unbiased manner, the somatic mutations and copy number variations that affect cell cycle progression and overall
survival in glioblastomas, include these variables in the model, and perform further analyses to obtain an optimal model to explain the regulation of cell cycle progression in these cancers (see the Tutorial in Supplementary Information, and below for a demonstration of this feature).

2.3 Factor analyses
In addition to the molecular and clinical variables, users can also devise latent constructs, or factors, which are not measured in the datasets, but can be deduced based on the data. For example, tumor immune infiltration, a very important phenomenon in cancers, is not reported in the data, but can be deduced based on collective mRNA expression patterns of some key marker genes. Similarly, mitotic index of tumors, differentiation (or stemness) status, etc. are some of the examples that could be depicted as factors in SEM, and analyzed with relation to molecular and clinical data. A demonstration of analyses of a complex model with factors can be found in the tutorial videos at the SEMA web site.

2.4 Variable manipulation
We have also implemented functionalities for custom creation of variables: binarization and grouping. It may desirable for users to categorize a numeric variable for more intuitive analyses and visualizations. For example, copy number variations (CNV) are numerically encoded data, which may be more intuitive to analyze as categorical variables (e.g. ‘Diploid’ and ‘Copy Gain’), in which case the variable could be binarized. It may also be useful to analyze some variables as a group, rather than individually. For example, one may wish to analyze the collective effect of the Ras/MAPK pathway mutations on MEK phosphorylation and survival in cancers. In this case, the individual variables (e.g. somatic mutations in NF1, KRAS, NRAS and BRAF) will be grouped under a new variable (e.g. Ras_MAPK) where the categories (e.g. ‘WT’ and ‘Mutant’) can be defined by the user (e.g. ‘WT’ if none of the individual genes are mutated, and ‘Mutant’ if any of the genes are mutated). The use of these functionalities allows for fine-grained analyses of functional associations in cancers, such as answering the question: what is the effect of TP53/CDKN2A double mutations on cell cycle progression compared to individual mutations? A video on the web site demonstrates the use of this functionality in a case study.

SEMA was developed in R Shiny and JavaScript. The code files have been deposited to GitHub (https://github.com/msolmazm/sema). For SEM analyses, the sem function in the R package lavaan is used. The graph part of SEMA uses the commercial package yFiles for HTML, which is why any potential developers wishing to improve upon or modify SEMA code will have to obtain their copy of this library to run SEMA locally.

3 Results and discussion
As a show-case of integrated pan-cancer analyses in SEMA, we have analyzed the effect of TP53 mutations (TP53.Mut) on clinical outcome, and the potential mechanisms of its action across human cancers. Mutations in TP53 are very common in human cancers, with the highest rates observed in Esophageal (ESCA), lung squamous (LUSC) and ovarian (OV) cancers (Fig. 2A). As expected, TP53.Mut also correlated with poor outcome in several cancers (HNSC, KICH, KIRC, KIRP, LAML, LIHC, THYM and UCEC), though it correlated with better outcome in glioblastomas (GBM) and low-grade gliomas (LGG) (Fig. 2B–C). A quick analysis of global correlates of TP53.Mut in GBM and LGG reveals that the correlation of TP53.Mut with better outcome in GBM and LGG is largely due to
the confounding effect of IDH1 mutations in these cancers, which significantly co-occurs with TP53.Mut (Supplementary Fig. S1A). Controlling for IDH1 mutations in this model shows that TP53.Mut does not have a significant correlation with survival in these cancers (Supplementary Fig. S1B).

The results in Supplementary Figure S1 showcase the effect that confounding factors can have on the interpretation of a hypothesis (model) in the large genomic datasets. As with most statistical modeling tools, users should be careful to avoid some common pitfalls associated with the interpretation of such correlations. SEM is essentially a hypothesis testing tool (i.e. it is for confirmatory analyses), and is sensitive to the misspecification of the proposed associations between variables. Thus, the goodness-of-fit indices or the strength of associations of individual links in a model only reflect how well the model fits the data, and do not necessarily imply that the hypothesis is biologically correct. In the analysis of the effects of TP53 mutations above, this is illustrated by the frequent co-occurrence, or mutual exclusivity, of the oncogenic events in cancers, which may have confounding effects on their correlations with other molecular and clinical parameters (e.g. co-occurrence of TP53.Mut with IDH1 mutations in GBM and LGG, Supplementary Fig. S1). Therefore, the researchers are strongly encouraged to try different versions of their hypotheses by employing the exploratory analyses like described above and below, with the inclusion and exclusion of additional suspected players, and testing the model fit across different datasets, to ensure robustness of the results and prevent overfitting.

Next, we asked how TP53.Mut leads to poor outcome in HNSC, KICH, KIRC, KIRP, LAML, LIHC, THYM and UCEC. First, we tested the best-characterized function of p53: the regulation of cell cycle. To model cell cycle regulation, we designed a latent factor (CellCycle.Factor) that was defined by the mRNA expression of CCNB1, PCNA and MKI67, three well-established markers of active proliferation. As expected, TP53.Mut had a positive effect on CellCycle.Factor in most cancers (Fig. 2D–E); and CellCycle.Factor in turn was also associated with worse survival in many cancers (Fig. 2F). Importantly, including CellCycle.Factor in the model reduced the direct effect of TP53.Mut on the clinical outcome in KICH, KIRC and KIRP and LIHC (Supplementary Fig. S2), indicating that the main effect of TP53.Mut on clinical outcome in these cancers was through promoting the cell cycle progression.

Since the inclusion of CellCycle.Factor in other cancers where TP53.Mut has a significant effect on clinical outcome (i.e. UCEC, THYM, LAML and HNSC) did not lessen the direct effect of TP53.Mut on the clinical outcome, the role of TP53.Mut in these cancers might be due to its role in other pro-tumorigenic processes. To find out the genes whose regulation mediates the effect of TP53.Mut on the outcome, we performed an exploratory analysis of global correlates of TP53.Mut in each cancer. Interestingly, in UCEC, one of the highest correlates with both TP53.Mut and overall survival was the mRNA (from RNAseq) and protein (from RPPA) expression of ESR1, the estrogen receptor. TP53.Mut was significantly negatively associated with ESR1 (Supplementary Fig. S3A–B), suggesting that TP53.Mut may be mutually exclusive with the hormone receptor status in the endometrial carcinomas. Importantly, including ESR1 mRNA expression in the model completely abolished the direct effect of TP53.Mut on the overall survival (Supplementary Fig. S3C), suggesting that the effect of TP53.Mut on the overall survival in UCEC was due to its mutual exclusivity with...
ESR1 expression, which predicts significantly better survival in UCEC (Supplementary Fig. S3C–D).

A similar analysis in THYM revealed POLH mRNA expression as the highest correlate of TP53.Mut (Fig. 3A). POLH codes for DNA polymerase η (eta), which is involved in DNA repair and hypermutation during immunoglobulin class switch recombination, and is a known target of p53 (Fischer, 2017). Accordingly, it is frequently suppressed in TP53-mutant cancers (Fig. 3B). The inclusion of POLH in the model also abrogated the direct effect of TP53.Mut on survival (Fig. 3A), likewise suggesting that POLH is one of the most important targets of TP53.Mut in THYM, and shows the indispensable tumor suppressor role of POLH in thymomas.

In Acute Myeloid Leukemia (LAML), there were no significant correlates among frequent somatic mutations. Then, we looked at the copy number variations that correlated with both TP53.Mut and overall survival, and identified TRIM36 as the top candidate, along with many other genes. TRIM36 is on chromosome 5, which is frequently lost (monosomy 5) in myeloid neoplasms, including AML (Le Beau, 1992). Importantly, TP53.Mut significantly co-occurs with the loss of TRIM36 in LAML (Fig. 4A). Controlling for TRIM36 loss reduces the effect of TP53.Mut on overall survival in LAML, although not completely (p-value of effect of TP53.Mut on overall survival after controlling for TRIM36 loss = 0.017), suggesting that TP53.Mut has significant effect on overall survival independent of its co-occurrence with chromosome 5 loss. To identify this effect, we examined the mRNA expression correlates of TP53.Mut and overall survival. To eliminate any confounding effect of TRIM36 copy number changes, we also included TRIM36 copy number variations in this analysis. We looked for gene mRNAs that positively correlated with both TP53.Mut and overall survival, but did not significantly correlate with TRIM36 loss. The top 2 genes identified in this manner were FHL2 and CSF1. An analysis of the effect of TP53.Mut on FHL2 expression across cancers showed that it is not frequently associated with TP53.Mut (not shown), suggesting that it might not be a direct TP53.Mut target. However, CSF1 expression was significantly upregulated in TP53.Mut-dependent manner in 6 cancers (Fig. 4B), suggesting that CSF1 may be a direct target of TP53.Mut in many cancers, including LAML (Fig. 4C), as also reported previously (Fischer, 2017). Importantly, including CSF1 mRNA expression in the model significantly reduced the effect of TP53.Mut on overall survival (Fig. 4D), suggesting that the regulation of CSF1 expression by TP53.Mut contributes to its pro-tumorigenic effect in LAML. It is worth noting that CSF1-CSF1R signaling has a well-established oncogenic role in LAML (Edwards et al., 2019), and our analysis here links somatic mutations in TP53 to the activation of this pathway in several cancers. All of the analyses presented here were performed using only SEMA functionalities.

4 Conclusion
SEMA is a web application to test simple and complex hypotheses in the form of graphs using the powerful SEM approach. By allowing the inclusion of different data types (e.g. protein, RNA, mutations, clinical survival) in a single path model, SEMA provides a platform for integrative analyses of multidimensional data. Unlike other platforms, such as cBioPortal and UCSC Xena, where the focus is on enabling the analyses and visualizations of individual molecular aberrations in cancers, SEMA is focused on enabling the mining of complex relationships between molecular aberrations. Users can engage in confirmatory analyses, or perform exploratory analyses, through the use of a suite of intuitive visual and statistical tools. SEMA is the only available tool that can be used for this type of analyses. Although it currently only features TCGA and TARGET datasets, we will expand the database to include more multi-dimensional datasets in the near future. As with any computational tool, the broader and deeper functionalities in SEMA will require a learning curve on the part of the users, especially those who are new to statistical modeling and related concepts. To facilitate the familiarization of researchers with the use of functionalities in SEMA, the tutorial on the web (and Supplementary Information) demonstrates steps for hypothesis building and testing using basic path models and factor analyses in SEMA. In addition, we have built a YouTube channel for SEMA, featuring screencasts of various analyses in SEMA, including for the analyses presented above. The YouTube channel will be continuously updated with new videos of analyses, demonstrations of newly introduced functionalities, and the analyses submitted by the user community.

5 Requirements
Web browser compatibility: SEMA has been tested to run on Chrome, Firefox and Safari. SEMA is not compatible with the Internet Explorer and Edge.
Programming language: SEMA was written in Shiny and JavaScript.
License: GPL 3.0.

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Fig. 4. Decoding the effect of TP53.Mut in LAML. (A) Stacked barplot showing the co-occurrence of TP53.Mut with TRIM36 loss (i.e. chromosome 5 monosomy/shallow loss). (B) The z-scores of the effect of TP53.Mut on CSF1mRNA expression in 26 adult cancers. (C) Heatmap of the indicated variates in LAML patients. The values in the rows were scaled. Somatic mutations are white when wild-type, and light red when mutated. For copy number variations, white indicates no change, pink: gain, red: amplification, light blue: shallow loss and deep blue: deep loss. RNA expressions are z-transformed according to the color key. (D) Model of the effect of TP53.Mut on overall survival after including the mediating effects of TRIM36.GISTIC and CSF1.RNA. The overlaid numbers are the P-values for LAML. All the figure panels were produced in SEMA.