

Sparse Tangibles: Collaborative Exploration of Gene Networks using Active Tangibles and Interactive Tabletops

Ahmed Sabbir Arif¹, Roozbeh Manshaei¹, Sean Delong¹, Brien East¹, Matthew Kyan³, Ali Mazalek^{1,2}

Synaesthetic Media Laboratory

Electrical Engineering & Computer Science³

Ryerson University¹

Georgia Institute of

York University

Toronto, Ontario

Technology²

Toronto, Ontario

Canada

Atlanta, GA, USA

Canada

{asarif, roozbeh.manshaei, sean.delong, beast, mazalek}@ryerson.ca, mkyan@cse.yorku.ca

ABSTRACT

We present Sparse Tangibles, a tabletop and active tangible-based framework to support cross-platform, collaborative gene network exploration using a Web interface. It uses smartwatches as active tangibles to allow query construction on- and off-the-table. We expand their interaction vocabulary using inertial sensors and a custom case. We also introduce a new metric for measuring the “confidence level” of protein and genetic interactions. Three expert biologists evaluated the system and found it fun, useful, easy to use, and ideal for collaborative explorations.

Author Keywords

Systems biology; biomedical engineering; sparse network; visualization; tabletop; active tangibles; participatory design.

ACM Classification Keywords

H.5.2 Information Interfaces and Presentation (e.g., HCI): User Interfaces—input devices and strategies, interaction styles, user-centered design; I.6.7 Simulation and Modeling: Simulation Support Systems—environments.

INTRODUCTION

Gene network exploration is an integral part of uncovering the secrets and structure of genetic pathways. Biologists explore gene networks to find the genetic differences and structural evolution among divergent organisms, and to identify the structural limitations on the possible paths of evolution. Because gene interaction structure is sparse, the structural features of a gene interaction network are often generalizable across different organisms. As a result, gene exploration often points towards “probable” interactions, which results in new discoveries.

Currently there is no efficient gene interaction network exploration interface available. Most present systems either

fail to work with big data sets or fail to provide the support for custom query construction. Most of these solutions are also system-dependent (that is, do not work with all operating systems), require the installation of proprietary software, or demand high processing power. Furthermore, almost all present solutions are desktop-based, which hinders collaborative exploration and generally limits the users to smaller screens.

We formed an interdisciplinary team of six to address these issues. Apart from two HCI researchers and an engineer, the group consists of three expert biomedical/signal processing engineers, whom we identify as potential users of the system. Therefore, and to fully utilize their expertise, we adopted an iterative design process where all design decisions were evaluated and analyzed by the team members, and interactions were redesigned until every member found them satisfactory.

Here, we present the final design of a novel tabletop-active tangible-based framework that supports cross-platform and collaborative gene network exploration using Web interfaces. The intention was not only to design and develop an easy to use gene network exploration interface but also to provide the biology community with a flexible framework that can be used to add new visualizations and features. The intention was also to encourage collaborative exploration and support non-experts who are coming into an expert domain.

The contribution of our work is threefold. First, we discuss the design and development of a new approach for visualizing and manipulating gene networks that can aid in conceptual understanding in both learning and discovery contexts. Second, we demonstrate how smartwatches can be used as active tangibles on tabletops. We allow users to construct custom queries using smartwatches by expanding their interaction vocabulary using the inertial sensors and a custom case. Finally, we introduce a new method for measuring the confidence level of protein and genetic interactions, based on the total number of articles confirming the interactions and the impact factor of the venues that published the articles.

THE EXPLORATION OF GENE INTERACTIONS

Gene interactions in different organisms provide an insight into functional and structural connections among genes and

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their produced proteins [11, 22]. The expression of a gene can be either self-regulating or influenced by a collaboration between itself and other expressing genes.

Recently, uncovering the networks of gene interactions (i.e. regulatory relationships between genes) has become a systematic and large-scale phenomenon [9]. Yet, the task of analyzing gene interactions is challenging due to the large number of genes, which increases the search space for possible interactions. In addition, the complexity and scale of such networks, either known or inferred, renders the task of surveying functional attributes and understanding biological processes within model organisms a challenge in and of itself.

The area of network science has addressed this issue by defining gene networks as a set of nodes (e.g. genes or their produced proteins) and edges forming linkages between them (e.g. interactions). This simplification makes it easier for practitioners to extract local and global structural features and provides a better understanding of the processes driving the growth and response of living organisms [1].

An interaction could be either *physical* or *genetic*. A physical interaction refers to the experience where a direct physical association between two gene products (proteins) has been identified, while a genetic interaction is identified when the effect of mutating one gene is reflected by the perturbation in another gene [2]. Interactions can also be classified as *inhibitory* and *excitatory*. In an excitatory interaction, the expression of one gene increases/decreases the expression of another gene, while in inhibitory interaction, an increase in the expression of a gene decreases the expression of another gene [14]. Every gene in a regulatory network has one or more activator or inhibitor genes. Thus, to understand the structure of a gene interaction network, practitioners usually explore the network to discover the activators and inhibitors of the genes involved.

The knowledge of gene interactions also plays an important role in uncovering the structure of genetic pathways. It assists researchers and practitioners to better understand the path of evolution, including the genetic differences and structural evolution among divergent organisms [15]. It also assists them to identify the structural limitations on the possible paths of evolution. Besides, as gene interaction structure is sparse, the number of actual interactions is far less than the maximum number of possible interactions [10]. Therefore, the structural features of a gene interaction network are often generalizable across different organisms, which also highlights the importance of exploring gene networks.

RELATED WORK

In this section, we provide a brief survey of the existing work in the area.

Biological Data Visualization

With the increasing importance of and access to large data sets by diverse prospective users, several multi-touch and tangible interfaces have been created to support interaction

with and understanding of biological concepts and data. For example, Schkolne et al. [17] developed an immersive tangible interface for designing DNA components, and SynFlo exploits tangible interaction in combination with a tabletop to introduce synthetic biology concepts to non-experts [25]. Neither system, however, focuses on search or comparison of large data sets. The G-nome Surfer is a tabletop multi-touch application for collaborative exploration of genomic databases [18]. However, its expressivity is limited, as it does not allow users to define and set query operators directly.

Some projects have aimed at the visualization of biological pathways using traditional GUIs. VisANT [6], a Web-based system, provides a framework for visualizing and analyzing different types of networks of biological interactions and associations, while Cytoscape supports the visualization and integration of molecular interaction networks and biological pathways [19]. NAViGaTOR [3] is a software package for visualizing and analyzing protein-protein interaction networks. It can query in two interaction databases and display networks in both 2D and 3D. Likewise, EINVis supports the visualization and exploration of the interaction networks [24], but can only work with smaller networks. GeneMANIA, in contrast, can find genes that are related to a set of input genes using a very large set of functional association data [23]. None of these packages, however, support collaborative exploration.

Our system, in contrast, not only allows users access to large data sets but also supports collaborative exploration of the data. It also enables users to define and set query operators.

Query Construction using Tangibles

Numerous tangible interface systems have explored the use of tangibles for constructing queries. Facet-Streams [7], for example, allows users to construct expressive queries using passive tangibles on a tabletop display surface. Although, this system can simplify the construction of complex queries, it has some limitations, including physical clutter, separation of query formulation from the browsing of results, and a lack of persistency for query parameters.

Some systems have also explored the use of active tangibles for constructing queries. An early example, Navigational Blocks [3], is a tangible interface that employs electronically augmented blocks to query a database. Each block represents one query parameter and its six faces represent possible values. In this case, the number of blocks and their fixed values limit the search space to a predefined number of queries. Another system, DataTiles [16], uses transparent RFID-tagged tiles on a horizontal display surface to manipulate digital information. Each tile represents specific information or control structures, and the placement of tiles on the surface can trigger computational functions, such as submitting a query or launching an application. While the system provides an expressive physical language, the interaction is constrained to a horizontal surface on which the tiles must be placed within predefined grid cells.

Tangible Query Interfaces (TQI) [20] introduced two kinds of active tangible interfaces for query formulation: *parameter wheels* for fixed query parameters, and *parameter bars* that can be dynamically assigned to various parameters. In both cases, the tangibles can represent either discrete or continuous values, and are manipulated and interpreted within physical constraints, such as racks. Although, this configuration affords expressive query construction, it limits the portability of the tangibles, as well as the possibilities for collaboration.

Unlike most query interfaces, Stackables [8] explores the use of active tangibles that enable vertical stacking. Each tangible represents a query parameter and multiple tangibles can be stacked to express a query consisting of logical AND or NOT. Results are visualized on an adjacent display screen. In this system, the interaction with the tangibles is limited to using its sliders and button. Sifteo Cubes¹, on the other hand, can detect shaking, flipping, tilting, neighboring, and tapping, but do not provide the support for multi-touch. A more recent project used smartphones as active tangibles on a tabletop display, allowing users to query for the common files on smartphones when they are in close proximity [13]. However, similar to Facet-Streams [7] and the TQI [20], the tangibles must be on the table to perform the queries.

By contrast, the active tangibles proposed in this paper can support all the actions stated above, as well as multi-touch, in both on- and off-the-table scenarios.

Recent work by Valdes et al. [21] investigated the use of gestural interaction with active tangibles for manipulating large data sets. They studied user expectations of a hybrid tangible and gestural language engaging this space. Based on the results, they provided a vocabulary of user-defined gestures for interaction with active tangibles. We used this as a guideline to design the interactions for our system.

SPARSE TANGIBLES

Sparse Tangibles allows users to explore gene and protein networks on an interactive tabletop using active tangibles. It supports both on- and off-the-table interactions. On-the-table interactions utilize multi-touch and the position of the active tangibles on the tabletop. Off-the-table interactions utilize multi-touch on the active tangibles and also actions such as stacking and shaking by utilizing both inertial and custom sensors.

A User Scenario

Let us assume a user wants to visualize a network of all interactions involving the gene *YDR194C* with agreement scores² above 0.5 in organism *Escherichia coli*. Towards that, first, she picks up an active tangible, selects the *Gene* option, and chooses *YDR194C* from the alphabetic list by performing vertical swipe gestures. Then, she places the active tangible on the table to see all organisms and networks

that include *YDR194C* in a doughnut chart and force-directed graphs, correspondingly. She uses the active tangible as a dial to scan through the organisms in the doughnut chart and selects *Escherichia coli* by tapping on the screen. This filters the data and displays only the network for *Escherichia coli* containing *YDR194C*. The user then picks up another active tangible, selects the *Agreement Score* option, and then picks the score 0.5 using a slider. The active tangible displays the selected score on the screen. She, then, places it on top of the active tangible for *YDR194C-Escherichia coli*. This queries the network with the selected threshold and refreshes the chart and the graph to highlight only the interactions that yield an agreement score of 0.5 or above by graying out the other connections. The 0.5 agreement score yields too few results, so the user decides to change the agreement score from 0.5 to 0.3. To do this, she simply adjusts the slider on the agreement score tangible, which updates the highlighted interactions. She is satisfied with the results and decides to save this search by bumping the selected agreement score into the below tangible for *YDR194C-Escherichia coli*. Next, she removes the top agreement score tangible, shakes it once to clear its contents, and continues to perform additional operations, such as using to select another organism or gene.

BASIC INTERACTIONS AND VISUALIZATIONS

Sparse Tangibles allows practitioners to explore all verified physical and genetic interactions based on *an organism* or *a gene*, using a linear navigation approach. Thus, to explore a network within a particular organism, first, users have to select the organism from a list to see all existing networks, and then pick the one they are interested in. Likewise, to explore a network involving a particular gene, they first have to select the gene from a list, which will display all networks involving that gene (across all organisms), and then select the network they want to explore. Here, we discuss these basic interactions and visualizations.



Figure 1. Active tangible interactions: (a) users swipe to select from three parameters, organism, gene, and agreement score, (b) users select a parameter by tapping, which displays a list of organisms, genes, or a slider to pick an agreement score.

Step 1: Navigation Initiation

Once users decide whether they want to explore gene and protein interactions based on an organism or a gene, they

interaction. The *agreement score* is a way of further restricting our attention to only those interactions that have reasonable consensus amongst the research community.

¹ Sifteo Cubes: <https://www.sifteo.com>

² The database under query contains the combined consensus of many researchers as to the likely existence of a particular gene-gene

have to *initiate* the navigation for that particular parameter using the active tangibles. The start screen of the tangibles requests the users to *Swipe to continue* and allows them to select from three available parameters: *gene*, *organism*, and *agreement score*, by performing vertical swipe gestures. A *down* gesture moves the parameters forward and an *up* gesture moves them backward. See Figure 1 (a). The *organism* and *gene* parameters allow users to initiate the navigation from an organism or a gene. The *agreement score* then filters the data according to the degree to which publications confirm the existence of a particular interaction. When navigating to the intended parameter, users can select it by tapping on the screen, which will update the screen with an alphabetic list of all available organisms or genes. See Figure 1 (b).

Users can then navigate to a particular organism or gene by performing vertical swipes. The list displays all organisms by their scientific names. We considered using symbols instead of names, but decided against it to avoid confusion, as there are no commonly accepted symbols available. Once an organism or gene is selected, users can either continue navigating further on the tangible screen or can place it on the table to visualize the current data.

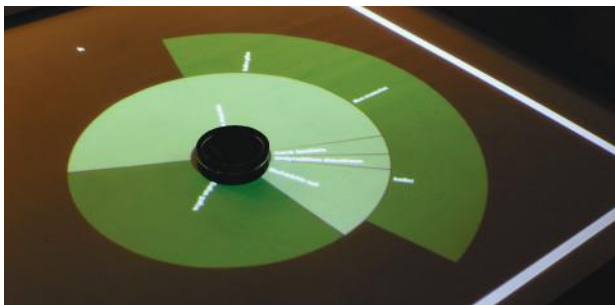


Figure 2. When an active tangible is placed on the table after selecting the *organism* or *gene* parameter, the system displays all available networks involving that organism or gene, respectively, in a doughnut chart. The outer slice is a magnifier. When users point the tangible towards a zone like a dial, the system magnifies the respective slices for better visualization.

If an organism is selected, and the tangible is placed on the table, the system displays all available networks of that organism on the table in a doughnut chart surrounding the active tangible. See Figure 2. In the chart, the labels signify the most active gene or protein in a network (i.e. the hub). We used the hubs to name the networks, due to the absence of a commonly accepted naming convention. The arc length of a slice and its central angle and area are proportional to the *density* of the networks, which we determine based on the total number of genes and proteins in a network. The system assigns each slice with a random shade of green and displays the labels inside the doughnut in white. We picked this style after testing several alternatives, where this yielded the best usability results. We also decided to make the doughnut chart translucent so that it does not occlude the contents behind, if any. See Figure 4. The system also displays all networks in force-directed graphs around the

chart. These graphs use a physical simulation of charged particles and springs, placing the most common interactions (based on the literature) in closer proximity. See Figure 3. The labels signify the scientific names of the genes and orbit around the corresponding target node at a fixed distance. They repel each other to avoid overlaps and orient themselves to the outside of clusters. Similar to the chart, the system assigns each network with a random color, but displays the labels in black to distinguish the genes from the networks.

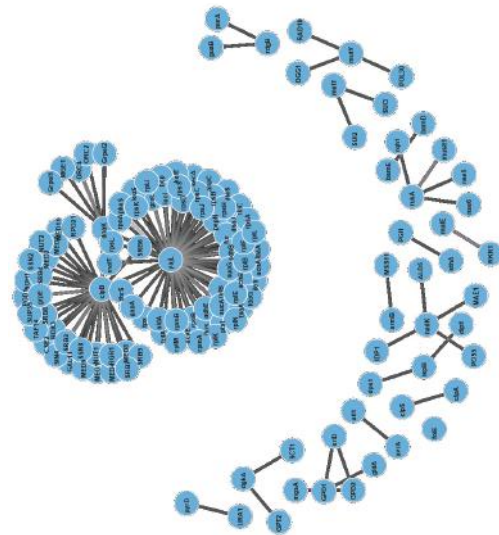


Figure 3. A screenshot of the visualization for gene networks within organism *Escherichia coli* in force-directed graphs.

Likewise, when an active tangible is placed on the tabletop after selecting a gene, the system displays all available organisms containing that particular gene on the tabletop in a translucent doughnut chart surrounding the tangible. The system also displays all networks in force-directed graphs.

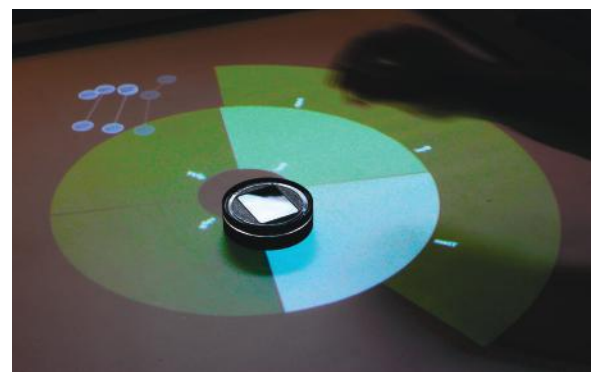


Figure 4. Gene network visualization in doughnut chart and force-directed graphs.

We assign each active tangible with a unique ID, thus the users can select multiple networks using multiple tangibles and compare them on the tabletop. Both the chart and the graphs follow their associated active tangibles as they are moved around the tabletop. The chart disappears when the tangibles are lifted from the table and reappears when placed again on the table. To free an active tangible from its

assigned organism or gene, users have to shake the device once, which will bring back the initial state to allow the selection of a new parameter.

Step 2: Network Selection

Users can select a network either on- or off-the-table. To select a network autonomously, first, they have to navigate to the intended network on the active tangible by swiping and then they have to tap on the screen. If a mistake was made, users can either go one step backward by performing a left swipe or reinitiate navigation by shaking the active tangible. Making selections off-the-table allows users to quickly bind several active tangibles to different parameters. The tangibles can be placed on the tabletop at any time to visualize the associated data.

On-the-table, users can use the active tangible as a dial to focus on a particular zone of the chart, representing a group of networks or organisms. When the active tangible points towards a zone, the system magnifies the respective slices for better visualization (Figure 2). This is because, complex organisms often contain hundreds of networks; also, very common genes are often prevalent in thousands of organisms, which makes it difficult to read the labels, as they become too small. When magnified, the users can select the network or organism of interest either by tapping on the corresponding slice or on the active tangible. Once selected, the system removes all networks and displays, leaving only the one picked by the users or the one present in the selected organism. The system also updates the doughnut chart accordingly. Similar to the previous step, users can correct their mistakes either by swiping on the tangible or by restarting the session by shaking it.



Figure 5. A user selecting an agreement score on an active tangible using the slider.

QUERY CONSTRUCTION

The Sparse Tangibles is intended to allow expressive query construction using active tangibles. To construct a query, users have to select different parameters on different active tangibles, where each tangible represents a query parameter, and then stack them to express a query consisting of logical AND. Almost all existing tangible-based query interfaces are limited to using physical buttons and sliders, while some support shaking, flipping, tilting, neighboring, or limited touch interactions, such as taps. Most techniques also require the tangibles to be on the tabletop to construct queries. As a result, all of them are either inflexible in terms of usability, or fail to support autonomous query construction. Sparse Tangibles address these issues by detecting stacking, shaking,

flipping, tilting, neighboring, and tapping, as well as multi-touch gestures.

Agreement Score Calculation

Sparse Tangibles is intended to allow practitioners to filter the data based on different criteria. However, our current implementation only supports filtering the data by *agreement score*, which is a normalized score of the number of times an interaction was confirmed in the literature and the impact factor of the venues where they were published. We calculate this for each interaction by adding the impact factors of all publications confirming that interaction and then normalizing the scores by dividing it with the highest impact score. Thus, the agreement score for each interaction ranges from 0 to 1. We use the following equation to calculate the actual agreement score for an interaction i .

$$Agreement_Score_i = \sum_{p=1}^n (impact_p) \quad (1)$$

We then normalize the actual score by dividing it with the highest impact score in the network. Here, n signifies the total number of publications reporting interaction i , p signifies a publication, $impact_p$ signifies the impact factor of the venue where p was published.

We hope that this metric will provide the researchers with a “confidence level” for each interaction. Currently, the only way to acquire a sense of this is by going through different genetic databases that report different interactions. Typically, due to the absence of a metric, validation of an interaction often depends on whether or not the investigator finds enough evidence of that interaction in the literature and subjectively deems the results reported in the publications reliable. The agreement score offers a less tedious, and more objective alternative.

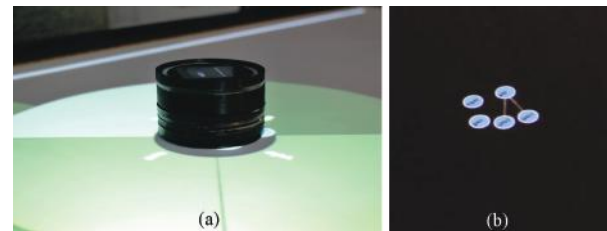


Figure 6. Query construction: (a) two active tangibles are stacked to construct a query, in this case, an agreement score threshold, (b) this filters the data for the selected agreement score and updates the visualization by graying out all interactions/edges below that threshold.

Selecting an Agreement Score

To select an agreement score, users have to pick up a free tangible and select the *Agreement Score* parameter from the start screen. This will display a slider on the touchscreen. See Figure 5. They then can select any value from 0 to 1 as the threshold for the agreement scores. Once selected, users can place the agreement score tangible on top of another tangible representing a network. See Figure 6 (a). This filters the data for the selected agreement score and updates the visualization by greying out all interactions (i.e. the edges of the force-directed graph) below that threshold. See Figure 6 (b). At

this point, users can double-tap on the top (agreement score) tangible in the stack to *bump* the selected threshold filter down into the network tangible below it to create a compound query. Users can remove the bumped filter by shaking the tangible, the same way they remove a tangible that is bound to a gene or organism. If the filter has not been bumped, they can simply pick up the top agreement score tangible to remove the filter.

TECHNICAL IMPLEMENTATION

We used HTML5 and JavaScript to implement the system. We decided on a Web-based solution (instead of native) for several reasons. First, almost all current devices provide support for HTML5/JavaScript, which makes our system as platform independent as possible. Second, it is relatively easier to distribute and update Web applications. It does not require users to install/reinstall a new/updated software, but only to refresh their Web browser. Third, there are numerous open source JavaScript libraries available on the Internet, which makes developing with JavaScript substantially easier. Finally, this keeps our option open to provide the research community with an online tool to create their own filters in the future.

Active Tangible Interactions and Visualization

We used LG G Watches as active tangibles. These devices run on the Android Wear OS and come with 41.91 mm IPS LCD displays (37.9 × 46.5 × 9.95 mm, 63 g), 4 GB internal storage, 512 MB RAM, and 9 Axis sensors. We 3D printed custom cases for each smartwatch to accommodate queries through stacking. These cases augment spring-loaded pins and targets on the top and the bottom, which allows them to communicate with each other when stacked. The on-board micro-controllers allow them to communicate with the interactive table. The cases also include arrays of LEDs surrounding the frames. Although the current version does not use the LEDs, this could be used to provide the users with additional visual feedback in a future version. We filed off the strap holders to fit the smartwatches into the cases. Each case is 7.5 cm in diameter, 2.4 cm in height, and weighs about 112 g with the smartwatch. See Figure 7.

We decided to use smartwatches as active tangibles for the following reasons. First, they run on the Android Wear OS that supports HTML5/JavaScript. This not only allows cross device communications via browsers, but also allows users to use other touchscreen devices (i.e. smartphones) as active tangibles. Second, they support multi-touch, which allows the use of gestures, such as swipe and pinch. Third, they include inertial sensors, including accelerometer, compass, and gyroscope. This allowed us to provide the support for in-air actions, such as shaking. Finally, most smartwatches come with a Micro USB port and support Bluetooth 4.0, which can be utilized to provide the support for stacking.

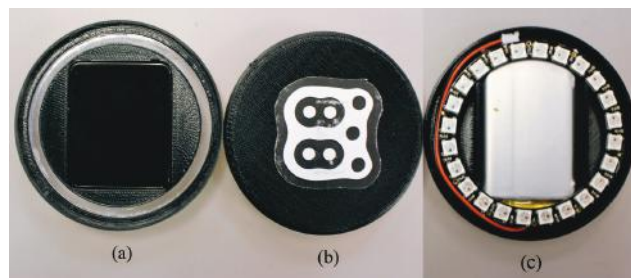


Figure 7. Smartwatches augmented with custom cases: (a) the front, (b) the back, with a reacTIVision fiducial marker, and (c) the inside, illustrates an array of LEDs, a battery, and a partial view of the microcontroller.

We implemented the smartwatch interface with HTML5 and JavaScript. We also used jQuery Mobile³ to provide the support for touchscreens. We picked jQuery Mobile instead of other alternatives, such as Hammer.js⁴, because it is more robust and optimizes the interface for smaller devices. To track the active tangibles on the tabletop and to distinguish between them we attached unique reacTIVision [12] fiducial markers onto each case. Illustrated in Figure 7 (b). We used Socket.IO⁵ to communicate with the table. Socket.IO is a JavaScript library that allows real-time bidirectional event-based communication via Web browsers. When an event, i.e. a tap or swipe, occurs in an active tangible, it broadcasts a message containing all necessary information for the table to listen. We decided to develop our own client-server model instead of Tuio.js, as it allows us to broadcast custom events.

Tabletop Interaction and Visualization

We used a custom Diffused Surface Illumination (DSI) table for Sparse Tangibles. It was 124 × 90 × 94 cm in dimension, with 110 × 78.5 cm active touch area. It ran on Windows 7 Professional at 1280 × 800 pixel resolution. We implemented the tabletop interface with HTML5/JavaScript that attempts to provide users with a better interaction experience by combining the most powerful visualization components, computer vision framework, and communication protocol with a data-driven approach to DOM (Document Object Model) manipulation. Towards that, we used jQuery⁶ to traverse and manipulate the DOM and JSON⁷ to store the gene interaction data. For data visualization, we used the D3.js⁸ JavaScript library. We used the Community Core Vision (CCV)⁹ engine to track the reacTIVision fiducial markers [12] attached onto the tangibles and also for multi-touch. However, to transmit the abstract description of surface, such as touch events and the states of the active tangibles, we used Tuio.js¹⁰ that pushes OSC/TUIO messages [12] to the Web browser.

Database Communication

Our system collects the protein/genetic interaction data from the Biological General Repository for Interaction Datasets

³ jQuery Mobile: <https://jquerymobile.com>

⁴ Hammer.js: <http://hammerjs.github.io>

⁵ Socket.IO: <http://socket.io>

⁶ jQuery: <https://jquery.com>

⁷ JSON: <http://json.org>

⁸ Data-Driven Documents: <http://d3js.org>

⁹ Community Core Vision Engine: <http://ccv.nuigroup.com>

¹⁰ Tuio.js: <http://fe9lix.github.io/Tuio.js>

(BioGRID)¹¹. This public database archives genetic/protein interaction data from model organisms and humans in the CSV (Comma Separated Values) format. Our system pulls all data from the database and converts them into optimized JSON files. The system also calculates and records the total number of networks in organisms and the agreement scores for each interaction. These operations are performed on the server using a .NET application. We used this database instead of alternatives such as IRefWeb¹² and GEMMA¹³, because BioGRID is arguably the most complete database. It holds over 770,000 interactions selected from both high-throughput datasets and individual focused studies, derived from over 54,000 publications in the primary literature [5].

EXPERT FEEDBACK

We invited three expert biologists to our lab to informally evaluate the system. They all work at a renowned research facility and have a master's degree in a related area. Two of them were female and one was male. Their age ranged from 28-30 years. They all arrived together. Upon arrival, we demonstrated the system, allowed them to interact with it, and then asked them to comment on various aspects of the system. The session lasted for about an hour. They were compensated for their time with a Cineplex movie pass.

They all found the system fun, useful, and easy to use. They also liked the visualization, but wanted more information on the tabletop, such as gene sequences, antibodies, etc. They also wanted the support for additional gestures on the screen. One of them particularly, wanted to drag and stretch the graphs using multi-touch. Two of them thought displaying the networks in 3D could be useful, while the other was not too sure about that. They all suggested using different colors to distinguish between the genes and proteins.

Similarly, they all liked the query construction feature, but wanted more filters. When asked whether or not they would create their own filters, if we make the system available, they all responded that they would. They informed us that researchers work on unique aspects of gene networks, thus finding a tool that fits their needs is difficult, if not impossible. Having a tool that allows them to visualize data by creating their own filters would greatly help their research.

All of them thought the system may encourage collaboration and causal exploration. However, they were split on whether the system will make them more productive or not. One of them thought it might, while the others disagreed. Similarly, one of them could see him/herself using the system at work, one was unsure, while the other could not. Nevertheless, the system triggered their curiosity. They all wanted to know more about it, and requested us to keep them informed on the progress.

FUTURE WORK

Based on our own experience as HCI researchers and domain experts, as well as on the feedback received from the

informal expert review, we discuss our future plans for Sparse Tangibles.

Additional Filters and Modeling/Simulation

In the future, we intend to support more query parameters to allow users to filter the data by the most common interaction (i.e. hubs), common patterns, etc. We will also provide an online tool that will allow the users to create their own filters. Furthermore, we intend to expand our system for modeling and simulation.

Keyword Search

Currently the system allows users to select networks using linear navigation. While this approach may be easier and more beneficial to non-experts (e.g. who do not know the scientific names of all organisms and genes), experts may find it time consuming. Thus, in the future, we would like to provide the support for keyword search in the database. This will allow users to skip the linear steps and jump directly to the data they want to work with. We excluded this feature from the prototype because virtual keyboards augmented with word prediction and auto correction often mistakenly correct a correctly inputted keyword, causing more errors. For the same reason, we did not allow users to rename organisms, genes, or networks, as naming these incorrectly can create erroneous rationales in the database. Thus, we are developing a custom keyboard that uses a biology-friendly corpus to suggest probable names and auto correct the misspelled ones.

Query Construction

Currently, the system allows users to construct queries by stacking the active tangibles. In the future, we will expand this feature to support logical AND, OR, and NOT. This will allow users to query and compare multiple organisms, such as finding the common genes in two different organisms. This could be attained without the need for a separate tangible for logical operators. For example, when a tangible is placed on top of another, the screen of the top tangible could show a "menu" of logical relationships for the users to select from. Another possibility is to assign the tangibles with a default parameter, and then allow users to change it, if necessary. The menu could be contextual, so that which relationship is selected by default would depend on which two parameters are stacked, as well as the available options for logical relationships.



Figure 8. The LEDs in the active tangibles.

Additional Visual Feedback

We intend to use the LEDs in the active tangibles to provide the users with additional visual feedback. For example, the

¹¹ BioGRID: <http://thebiogrid.org>

¹² IRefWeb: <http://wodaklab.org/iRefWeb>

¹³ GEMMA: <http://www.chibi.ubc.ca/Gemma>

LEDs can glow in different colors and brightness relative to the density of the networks, the total number of interactions in organisms, or the agreement scores. We have tested the tangibles with LEDs (see Figure 8), but have not investigated the feature fully.

CONCLUSION

In this paper, we demonstrated a novel tabletop and active tangible-based framework that supports cross-platform and collaborative gene network exploration using Web interfaces. We elaborated on the design and development of our approach and introduced a new metric for measuring the “confidence level” of protein and genetic interactions. In an informal evaluation session, three expert biologists found the system fun, useful, easy to use, and ideal for collaboration.

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REFERENCES

1. Albert-László Barabási. 2015. *Network Science*. Cambridge University. Retrieved July 21, 2015 from <http://www.barabasi.com/networksciencebook>
2. Andreas Beyer, Sourav Bandyopadhyay, and Trey Ideker. 2007. Integrating physical and genetic maps: From genomes to interaction networks. *Nature Reviews Genetics* 8, 9: 699-710.
3. Kevin R. Brown, David Otasek, Muhammad Ali, Michael J. McGuffin, Wing Xie, Baiju Devani, Ian Lawson van Toch, and Igor Jurisica. 2009. NAViGaTOR: network analysis, visualization and graphing Toronto. *Bioinformatics* 25, 24: 3327-3329.
4. Ken Camarata, Ellen Yi-Luen Do, Brian R. Johnson, and Mark D. Gross. 2002. Navigational blocks: navigating information space with tangible media. In *Proceedings of the 7th international conference on Intelligent user interfaces (IUI '02)*. ACM, New York, NY, USA, 31-38.
5. Andrew Chatr-aryamontri, Bobby-Joe Breitkreutz, Rose Oughtred, Lorrie Boucher, Sven Heinicke, Daici Chen, Chris Stark, Ashton Breitkreutz, Nadine Kolas, Lara O'Donnell, Teresa Regul, Julie Nixon, Lindsay Ramage, Andrew Winter, Adnane Sellam, Christie Chang, Jodi Hirschman, Chandra Theesfeld, Jennifer Rust, Michael S. Livstone, Kara Dolinski, and Mike Tyers. 2014. The BioGRID interaction database: 2015 update. *Nucleic Acids Research*: gku1204.
6. Zhenjun Hu, Joe Mellor, Jie Wu, Takuji Yamada, Dustin Holloway, and Charles DeLisi. 2005. VisANT: data-integrating visual framework for biological networks and modules. *Nucleic Acids Research* 33, 2: W352-W357.
7. Hans-Christian Jetter, Jens Gerken, Michael Zöllner, Harald Reiterer, and Natasa Milic-Frayling. 2011. Materializing the query with facet-streams: a hybrid surface for collaborative search on tabletops. In *Proceedings of the SIGCHI Conference on Human Factors in Computing Systems (CHI '11)*. ACM, New York, NY, USA, 3013-3022.
8. Stefanie Klum, Petra Isenberg, Ricardo Langner, Jean-Daniel Fekete, and Raimund Dachsel. 2012. Stackables: combining tangibles for faceted browsing. In *Proceedings of the International Working Conference on Advanced Visual Interfaces (AVI '12)*, Genny Tortora, Stefano Levialdi, and Maurizio Tucci (Eds.). ACM, New York, NY, USA, 241-248.
9. Christina Laufer, Bernd Fischer, Wolfgang Huber, and Michael Boutros. 2014. Measuring genetic interactions in human cells by RNAi and imaging. *Nature Protocols* 9, 10: 2341-2353.
10. Robert D. Leclerc. 2008. Survival of the sparsest: robust gene networks are parsimonious. *Molecular Systems Biology* 4, 1: 213.
11. Ben Lehner. 2011. Molecular mechanisms of epistasis within and between genes. *Trends in Genetics* 27, 8: 323-331.
12. Martin Kaltenbrunner and Ross Bencina. 2007. reacTIVision: a computer-vision framework for table-based tangible interaction. In *Proceedings of the 1st international conference on Tangible and embedded interaction (TEI '07)*. ACM, New York, NY, USA, 69-74.
13. Ali Mazalek and Ahmed Sabbir Arif. 2014. Mobile-based tangible interaction techniques for shared displays. In *Proceedings of the 16th international conference on Human-computer interaction with mobile devices & services (MobileHCI '14)*. ACM, New York, NY, USA, 561-562.
14. Vishal R. Patel, K. Eckel-Mahan, P. Sassone-Corsi, and P. Baldi. 2014. How pervasive are circadian oscillations? *Trends in Cell Biology* 24, 6: 329-331.
15. Patrick C. Phillips. 2008. Epistasis—the essential role of gene interactions in the structure and evolution of genetic systems. *Nature Reviews Genetics* 9, 11: 855-867.
16. Jun Rekimoto, Brygg Ullmer, and Haruo Oba. 2001. DataTiles: a modular platform for mixed physical and graphical interactions. In *Proceedings of the SIGCHI Conference on Human Factors in Computing Systems (CHI '01)*. ACM, New York, NY, USA, 269-276.
17. Steven Schkolne, Hiroshi Ishii, and Peter Schroder. 2004. Immersive Design of DNA Molecules with a Tangible Interface. In *Proceedings of the conference on Visualization '04 (VIS '04)*. IEEE Computer Society, Washington, DC, USA, 227-234.
18. Orit Shaer, Megan Strait, Consuelo Valdes, Heidi Wang, Taili Feng, Michael Lintz, Michelle Ferreira, Casey Grote, Kelsey Tempel, and Sirui Liu. 2012. The design, development, and deployment of a tabletop interface for collaborative exploration of genomic

- data. *International Journal of Human-Computer Studies* 70, 10: 746-764.
19. Paul Shannon, Andrew Markiel, Owen Ozier, Nitin S. Baliga, Jonathan T. Wang, Daniel Ramage, Nada Amin, Benno Schwikowski, and Trey Ideker. 2003. Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Research* 13, 11: 2498-2504.
 20. Brygg Ullmer, Hiroshi Ishii, and Robert J. K. Jacob. 2003. Tangible query interfaces: physically constrained tokens for manipulating database queries. In *Proceedings of the International Conference on Human-Computer Interaction (INTERACT '03)*, Vol. 3. IOS, Amsterdam, the Netherlands, 279-286.
 21. Consuelo Valdes, Diana Eastman, Casey Grote, Shantanu Thatte, Orit Shaer, Ali Mazalek, Brygg Ullmer, and Miriam K. Konkel. 2014. Exploring the design space of gestural interaction with active tokens through user-defined gestures. In *Proceedings of the SIGCHI Conference on Human Factors in Computing Systems (CHI '14)*. ACM, New York, NY, USA, 4107-4116.
 22. Kristel Van Steen. Travelling the world of gene-gene interactions. 2011. *Briefings in bioinformatics*: bbr012.
 23. David Warde-Farley, Sylva L. Donaldson, Ovi Comes, Khalid Zuberi, Rashad Badrawi, Pauline Chao, Max Franz, Chris Grouios, Farzana Kazi, Christian Tannus Lopes, Anson Maitland, Sara Mostafavi, Jason Montojo, Quentin Shao, George Wright, Gary D. Bader, and Quaid Morris. 2010. The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. *Nucleic Acids Research* 38, 2: W214-W220.
 24. Yubao Wu, Xiaofeng Zhu, Jian Chen, and Xiang Zhang. 2013. EINVis: a visualization tool for analyzing and exploring genetic interactions in large-scale association studies. *Genetic Epidemiology* 37, 7: 675-685.
 25. Wendy Xu, Kimberly Chang, Nicole Francisco, Consuelo Valdes, Robert Kincaid, and Orit Shaer. 2013. From wet lab bench to tangible virtual experiment: SynFlo. In *Proceedings of the 7th International Conference on Tangible, Embedded and Embodied Interaction (TEI '13)*. ACM, New York, NY, USA, 399-400.