# G-nome Surfer: a Tabletop Interface for Collaborative Exploration of Genomic Visualization

Orit Shaer
Wellesley College

Megan Strait
Tufts University

Consuelo Valdes
Wellesley College

Taili Feng
Wellesley College

Mikey Lintz
Olin College

Heidi Wang
Wellesley College

## ABSTRACT

We present G-nome Surfer, a multi-user, multi-touch table for collaborative exploration of genomic information. G-nome Surfer has been developed for a population of scientists who frequently meet in small groups for data exploration. To scaffold hypothesis forming, G-nome Surfer allows users to compare, annotate, share, and relate heterogeneous data including genome visualizations, publications, gene expression, and BLAST results. Evaluation of G-nome Surfer shows that it reduces workload and improves performance compared to state-of-the-art tools.

**Index Terms:** H.5.2 [Information Interfaces and Presentations]: User Interfaces;

## 1 INTRODUCTION

The increasing availability of large, tabletop, high resolution displays opens the design of computer interfaces that mediate co-located collaboration by allowing multiple users to simultaneously touch and manipulate data. In tabletop interaction, actions are visible across users, and multiple points of entry are available. Digital objects are rendered to look and behave like they operate under virtual laws of physics while tangible represenations are often incorporated into the interaction as well. Both tangible and digital objects are directly manipulated using touch and gestures that draw upon users' understanding of naive physics principles [1]. The horizontal surface affords spatial data collection and problem-solving strategies, which can reduce cognitive workload [5]

Motivated by the promise of tabletops to facilitate intuitive interaction with digital information and by the need to develop bioinformatics tools that support collaboration and high-level reasoning [2], we developed G-nome Surfer, a tabletop interface for collaborative exploration of genomics. While earlier prototypes of G-nome Surfer limited to the visualization of eukaryotic genomes were presented at the ACM CHI conference [3, 4], here we present a new version of G-nome Surfer that visualizes prokaryotic genomes. The design of G-nome Surfer is a result of an iterative user-centered design process in which we collaborated with domain scientists. Following, we describe G-nome Surfer's implementation, interaction techniques, and visualizations.

## 2 G-NOME SURFER

### 2.1 Implementation

G-nome Surfer is implemented on top of the Microsoft Surface platform using C# and the Microsoft Surface SDK[1]. It utilizes a local database of FASTA and GenBank files. For real-time sequence comparison and analysis we use the NCBI BLAST+ tools suite. The system also draws information in real-time from PubMed[2] and Entrez Gene. The navigation wheel of prokaryotic genomes is created off-line using GView[3] and stored locally.

Figure 1: G-nome Surfer 2.0: comparing gene ontology and expression data of different mouse genes.

### 2.2 Navigating Genomes and Retrieving Sequences

G-nome Surfer supports navigation of both eukaryotic and prokaryotic genomic maps at multiple zoom levels. To access a map, a user selects an organism and then specifices a chromosome, range, or gene name. The view is then updated to display a portion of the chromosome with the specified gene in the center of a horizontal chromosome track (see Figure 2).

For prokaryotes, a circular representation of the chromosome is displayed as a wheel beneath the chromosome track to give users an overview of its structure (see Figure 3). Users can pan through the chromosome track by flick gestures. Prokaryotic navigation also supports coarse traversal of the chromosome through the spinning of the chromosome wheel. Continuous visual feedback maintains users' sense of location.

Gene sequences are accessed by tapping a gene. The sequences are displayed in separate windows, which users overlay to align. When two sequences "snap" together, a new window opens with a matrix where the two sequences are represented as rows so that bases appear in successive columns and discrepancies are highlighted. For eukaryotes, when a user taps on a gene, its structure in terms of exons and introns is displayed in a structure track below the chromosome (see Figure 2). Sequences of individual exons can be accessed as well. These sequences are tethered to their source and support the same interactions as gene sequences.

### 2.3 Heterogeneous Information Upon Request

G-nome Surfer enables scientists to access and relate heterogeneous information. By holding a finger on a gene the gene star-shaped context menu appears, allowing the user to choose between ontology, publications, and gene expression information (available only for eukaryotic genomes). Ontology displays a summary of information from the Entrez Gene database. Publications displays titles

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[1] http://www.microsoft.com/surface/en/us/default.aspx

[2] http://www.ncbi.nlm.nih.gov/pubmed/

[3] https://www.gview.ca/

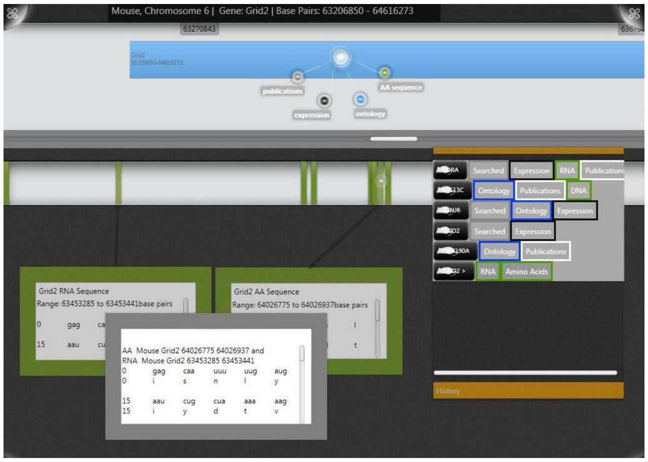

Figure 2: G-nome Surfer 2.0: pairwise alignment of RNA and protein sequences of mouse exons (left). Workflow visualization (right) displays a history of interactions.

and abstracts of publications related to a particular gene from the PubMed database.

The gene expression visualization displays an image of an organism with several regions highlighted across the body. When a region is tapped, an additional panel slides out from the right side of the window, showing a detailed list of tissues related to that area. The expression information is coded using a monochromatic scheme (see Figure 1). In an earlier version, this visualization used a red-green color scheme however, we found that this color scheme often confuses users and results in numerous mistakes. Users can move, orient, resize, and spatially arrange each piece of information upon the surface (see Figures 1, 2 and 3).

## 2.4 BLAST

When a tangible BLAST tool is placed upon a particular sequence a semi-transparent layer covers the surface and a context menu is presented. The user then selects one or more target sequences to invoke a BLAST. Figure 4 shows our visualization of BLAST results. Each rectangle represents a result, and its opacity represents similarity score - the more opaque, the higher the score. Results are organized as a cascade so results with higher scores are displayed closer to the user. To view detailed information about a result, a user taps the rectangle so that both information box and context of alignment to the original sequence appear.

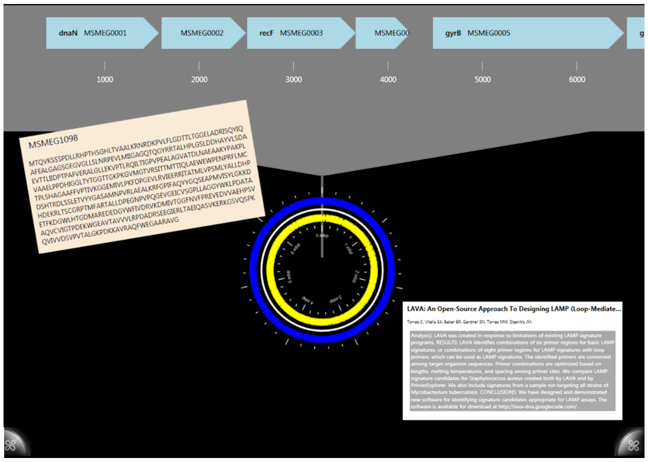

Figure 3: G-nome Surfer: browsing the Mycobacterium smegmatis genome (MC 155 strain).

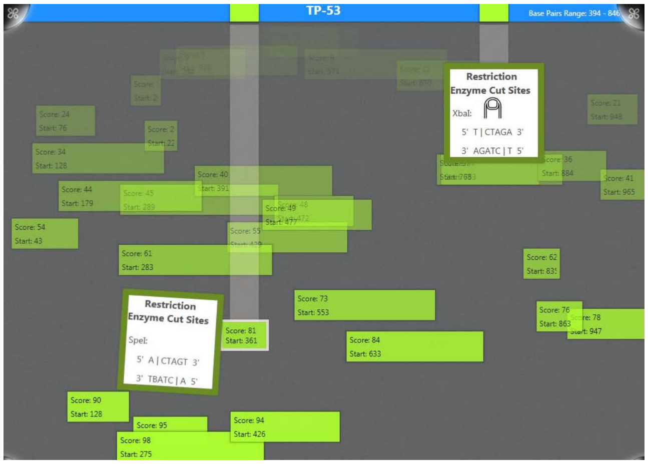

Figure 4: G-nome Surfer 2.0: displaying BLAST results of the human TP53 gene compared against the Mus musculus genome.

## 2.5 Workflow

The workflow visualization records and displays all interactions performed in G-nome Surfer (see Figure 2). Docked at the upper right corner, it can be accessed with a simple drag. Actions are organized by gene and displayed as color-coded blocks.

## 3 SUMMARY

We evaluated G-nome Surfers usabiility and usefullness iteratively with over 60 users [3, 4]. Findings indicate that G-nome Surfer supports high-level reasoning, reduces syntactic mental workload, and improves students performance. We plan to deploy G-nome Surfer in both educational and research settings.

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