

# G-nome Surfer: Supporting Collaborative Learning of Genomic Concepts through Tabletop interaction

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**Abstract:** G-nome Surfer is a tabletop user interface for genomic exploration. We designed G-nome Surfer to facilitate collaborative, fluid, and immediate interaction with large amounts of heterogeneous genomic information as well as to lower the threshold for using advanced bioinformatics tools. Based on the properties of tabletop interaction we expect G-nome Surfer to support collaborative inquiry-based learning of genomic concepts. We plan to evaluate G-nome Surfer in educational setting by integrating it to an undergraduate level Neuroscience genomics laboratory. In this paper we describe the current prototype of G-nome Surfer and our plans for future research.

## Introduction

Advances in genomic technologies have led to an explosive growth in the quantity and quality of biological information available. The ability to simultaneously collect detailed information about the structure and activity of multiple genes has fundamentally changed the way molecular biology research is conducted. The need to analyze such large and complex data sets has driven a change in the tools used in biological research and instruction: next to having a pipette and a pen, a web browser is currently the most widespread tool available for biologists as it provides access to powerful computational and statistical tools. However, existing web-based genomic tools have high threshold: they require both a broad domain knowledge and extensive training. In addition, these tools show severe limitations in terms of persistence, usability, and support of high-level reasoning (Bolchini et al. 2009, Mirel 2009, Veretnik et al. 2008).

Through a preliminary study of molecular and computational biologists (Shaer et al. 2010), we observed that to develop insights biologists gather a wealth of heterogeneous data from genomic databases and leverage a diverse set of bioinformatics tools. However, using current bioinformatics tools biologists often experience difficulties interpreting, comparing, annotating, sharing, and relating this vast amount of biological information. We further observed that such interactions are critical for learning new biological concepts and for forming scientific hypotheses. Motivated by these observations and by the potential held by tabletop interfaces for enhancing collaborative learning and research activities, our research seeks to investigate how tabletop reality-based interaction (Jacob et al. 2008) could enhance collaborative exploration of genomic information.

## The G-nome Surfer System

We thereby created G-nome Surfer (shaer et al. 2010), a tabletop interface for genomic exploration. Based on findings from our user study we designed G-nome Surfer to meet four design goals: 1) facilitating collaborative, immediate and fluid interaction with large amounts of heterogeneous genomic information, 2) lowering the threshold for using advanced bioinformatics tools, 3) reducing mental workload associated with accessing and manipulating genomic information, and 4) improving current information workflow processes in genomic research.

G-nome Surfer supports the following information tasks: searching the literature for what is known about a gene, a condition or a biological function; locating a gene on a genome, verifying its structure and neighboring genes; retrieving genomic nucleotide or protein sequences; searching for similarity between sequences (using the Basic Local Alignment Search Tool); and annotating genomic information. Figure 1 presents users interacting with the results of a genomic similarity search. Figure 2 shows the comparison and annotation of genomic sequences.

The design of G-nome Surfer draws on users' existing knowledge and skills to provide a tabletop reality-based interface (Jacob et al. 2008). Specifically, G-nome Surfer uses naive physics metaphors such as inertia, transparency, and mass in the layout of chromosomes and genes and in the representation of similarity search results. The interface also leverages users' spatial skills, allowing them to spatially organize information upon the surface to express relationships between multiple forms of evidence. The system leverages social skills and cues by providing multiple points of entry (through multiple forms of evidence that can be simultaneously manipulated), and by making modes visible to all users through the use of physical objects.

G-nome Surfer is implemented in C# using the Microsoft Surface platform and SDK. It draws genomic information from various databases including UCSC, Pub Med, and Entrez Gene and utilizes the NCBI local Basic Local Alignment Search Tool.

To validate the design of G-nome Surfer we conducted a first-use study with 16 participants that worked in pairs on a task that mirrors real world research scenario and requires the development of surface biological insights (Shaer et al. 2010). The results show that the system supports the five information tasks we described and sets a relatively low threshold for using bioinformatics tools. The study also demonstrate that G-nome Surfer provides a collaborative, immediate and fluid interaction with heterogeneous genomic information. However, an additional investigation is required to evaluate whether and how G-nome Surfer facilitates inquiry-based learning as well as reduces the mental workload associated with accessing and manipulating genomic information.



Figure 1, interacting with BLAST results.

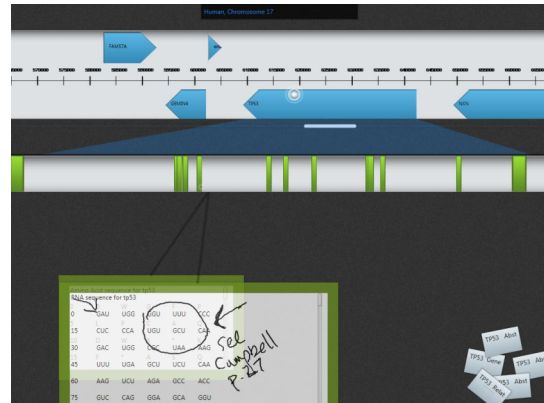


Figure 2, comparing and annotating genomic sequences.

## Future Work

Following the development of G-nome Surfer, we plan to evaluate it in three settings. First, to further evaluate G-nome Surfer's strengths and limitations in comparison to current state-of-the-art GUI based tools and to collaborative GUI, we intend to conduct a between-subjects *comparative study*. Second, to identify and quantify the benefits of G-nome Surface for collaborative inquiry-based learning, we plan to evaluate it in a *course setting*: during Fall 2010, and Fall 2011, students in an intermediate Neuroscience course at Wellesley College will use G-nome Surfer in a sequence of five genomic labs. Each lab is 3.5 hours long and includes up to 12 students. In labs, students work in teams to discover the molecular basis of a motor mutation in mice. In previous semesters students used a variety of web based genomic databases and bioinformatics tools to accomplish this goal. The learning goals of this labs sequence were previously thoroughly assessed by the instructors (Paul and Quinan 2009) thus, we plan to use findings from previous semesters as benchmark while applying the same evaluation to assess students' learning in the semesters where G-nome Surfer is used. In addition, we plan to apply methods such as observations, video analysis, and interviews to understand how G-nome Surfer facilitates learning. Finally, to evaluate the value of the proposed system to improving the workflow of collaborative genomic research, we intend to deploy the proposed system in a *research lab* at Wellesley College and conduct a longitudinal evaluation 'in the wild'.

## References

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