

University at Buffalo *The State University of New York*

Advancing Bioinformatics and Life Sciences Research with Sencha's Ext JS Framework



CUSTOMER SUCCESS STORY



The Sencha Ext JS framework enables a bioinformatics research lab at SUNY, Buffalo, to develop a public database that advances research on DNA sequence and gene regulation

Professor Marc Halfon and his team of researchers at the Jacobs School of Medicine and Biomedical Sciences, State University of New York at Buffalo, have done some phenomenal work in the area of bioinformatics. His laboratory conducts research on genetics and gene expression—investigating the mechanisms that control the fate of cells during their development. Most of his research is done using the common fruit fly (technically referred to as *Drosophila melanogaster*), a mainstay of genetic research for over a century. The conclusions and outcomes of his experiments on the small fruit flies are expected to apply directly to gene regulation in both other insects and in mammals, including humans. Professor Halfon's lab is heavily involved in curating, annotating, and validating information (often known as "biocuration" in research terms) through the development and maintenance of a comprehensive and growing public database called <u>REDfly.</u>



"It really made sense for us to use available components instead of writing our own... Ext JS components allowed us to create and deploy a robust user-interface with the desired performance"

Andrew Bruno, **Project Manager for REDFly**, University at Buffalo⁻

The majority of work done at Marc Halfon's research lab is populated into the REDfly database and currently contains over 40K records (and growing) of experimentally validated information on DNA sequences that regulate genes, patterns of gene expression, and more. Life scientists from all around the globe involved in genetic research on insect models mine the data from this repository and in turn use that to advance their research. "Scientists typically using this database will come in and search for certain criteria, such as a piece of DNA sequence and a bunch of attributes. The data tells them what the sequence does and how it ties into the organism—information that can be used to run computational analysis or to inform other experiments," said Halfon. This repository is the first, one-of-a-kind, single searchable database, containing over 30 years of experimental determination and is an important resource for the bioinformatics life sciences community.

Building REDfly Web App with Ext JS

The REDfly web app, built with the Ext JS framework, has the ability to efficiently mine multiple thousands of entries and display the queried data with incredible speed and accuracy. The web app's front-end UI is built with the Ext JS components and the back end in PhP/MySQL.

"The Grid and Forms are the backbone of the front-end UI," said Halfon.

The search results can be displayed with tabbed windows while the app also provides the ability to further drill down into each piece of queried data. The Ext JS 'Form' component is used for inputting data into the database. A biocurator working with Professor Halfon assists with reading scientific literature, sifting through and extracting the right data from these papers and entering it into the database.

"The Ext JS form component has a big use in our lab. The app's form components have various elements to them—such as validated inputs, free form text, lookups to other online resources to populate from and such," said Halfon.



The Grid and Forms are the backbone of the front-end UI,"

Dr. Marc Halfon, **Professor**, University at Buffalo

Figure: REDFly app built using Ext JS Framework and Components

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When Halfon's team started curating this database, they had a single software developer architecting and building the app. The database first started as a web page but quickly moved to a more functional web interface. "We had so much data, so having a clean look and feel was important. The bigger requirement was handling our searches efficiently, especially since users were uploading or querying large and disparate data feeds," said Halfon. Designing and writing the entire software stack to build the web app in-house wasn't really a practical option for his team given the time, number of resources, and large overhead related to app security and maintenance. "It really made sense for us to use available components instead of writing our own JavaScript code—and Ext JS components allowed us to create and deploy a robust user-interface with the desired performance," said Andrew Bruno, Project Manager for REDFly at the University at Buffalo's Center for Computational Research.

The Path Forward with Ext JS

Halfon's team hopes to refresh the web app's UI by enhancing the layout, input search elements, and overall app performance by utilizing some of the new features and capabilities that come with the latest Ext JS version. His team plans on upgrading the app with a more modern mobile interface. "We are excited to enhance the web interface even further as the database continues to grow over the coming years," Bruno said.



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Dr. Marc Halfon, **Professor**, University at Buffalo



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The fact that Sencha plays a small but important role in the genetic research at Professor Halfon's lab at the University at Buffalo along with helping advance the entire bioinformatics and life sciences community is truly rewarding!

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