

# Bringing Web 2.0 to the UCSC Genome Browser

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<http://hgwdev.cse.ucsc.edu/~larrym/presentations/genecats.ppt>

# Apologies

- Sorry for using the phrase “Web 2.0”.

A short history of Uls...

# 1800s



- Slow
- Didn't work

Charles Babbage's Difference Engine

# 1940s



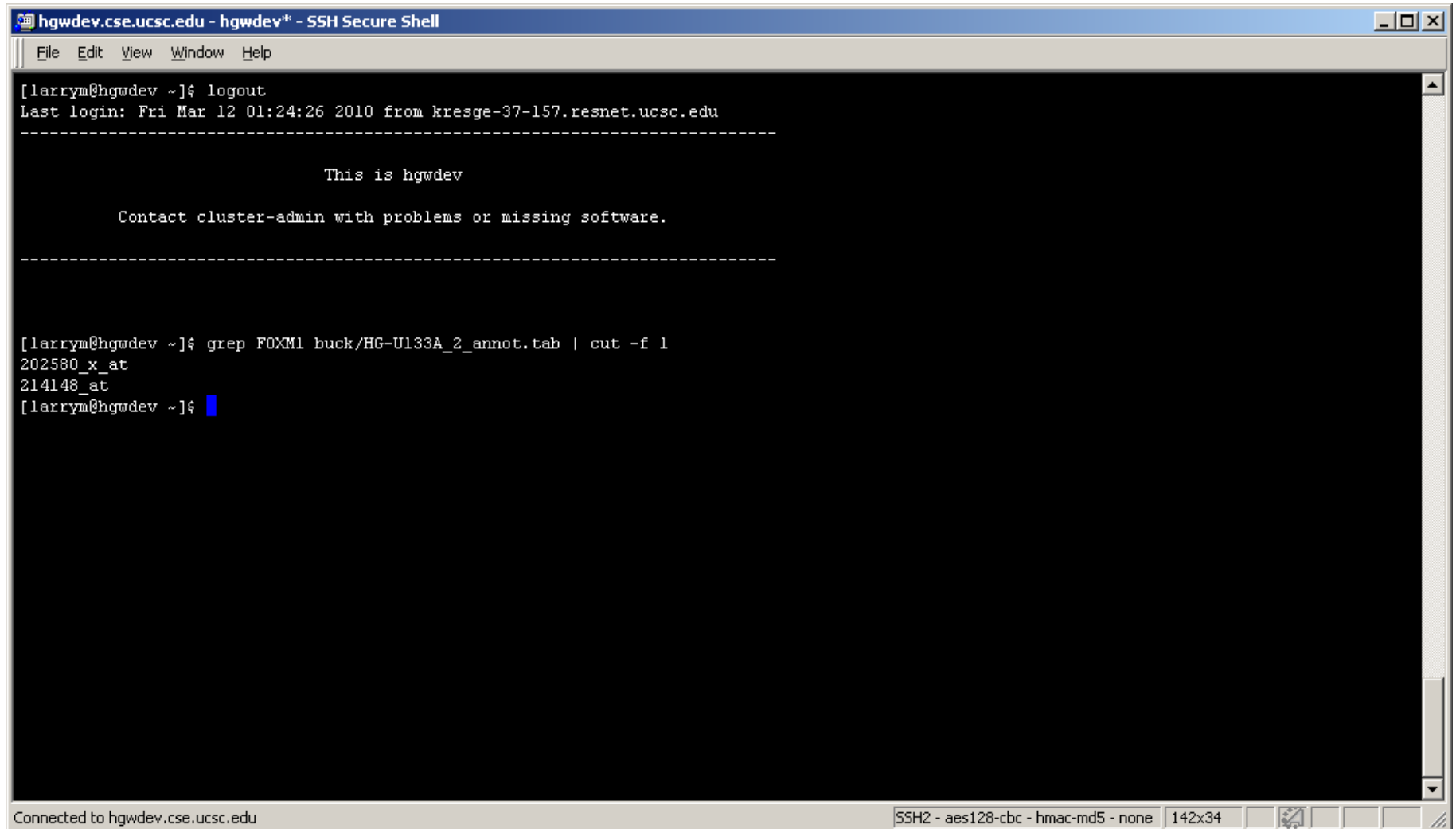
ENIAC

# 1960s



IBM 360 Series 2A/753x

# 1970



The image shows a screenshot of an SSH terminal window. The window title is "hgwdev.cse.ucsc.edu - hgwdev\* - SSH Secure Shell". The terminal content is as follows:

```
[larrym@hgwdev ~]$ logout
Last login: Fri Mar 12 01:24:26 2010 from kresge-37-157.resnet.ucsc.edu
-----

                This is hgwdev

        Contact cluster-admin with problems or missing software.

-----

[larrym@hgwdev ~]$ grep FOXM1 buck/HG-U133A_2_annot.tab | cut -f 1
202580_x_at
214148_at
[larrym@hgwdev ~]$
```

At the bottom of the terminal window, the status bar shows "Connected to hgwdev.cse.ucsc.edu" on the left and "SSH2 - aes128-cbc - hmac-md5 - none 142x34" on the right.

Unix shell

# 1972

```
04/06/07                PATENT ENQUIRY SYSTEM                18:55:35
                                                                PAEN02MA

Enter the required key : █ _____ ( ? - Help )

Key may be : - Application Id      (nnnnn/yy),
              - Patent Number     (nnnnnn),
              - Provisional Number (Pxnnnn),
              - PCT Number         (PCT/ccyy/nnnnn),
              - W.I.P.O. Number   (wOyy/nnnnn),
              - Search Name        (xxxxxxxxxxxxxxxxxxxx) for company name, or
                                   (surname;given names ) for personal name

Enter Comment          : _____

Print Details : N
Print Location : EM Number : 1_

Optional: You can restrict Search Name results to those applications
          filed since __ / __ / __ OR filed in the Year __

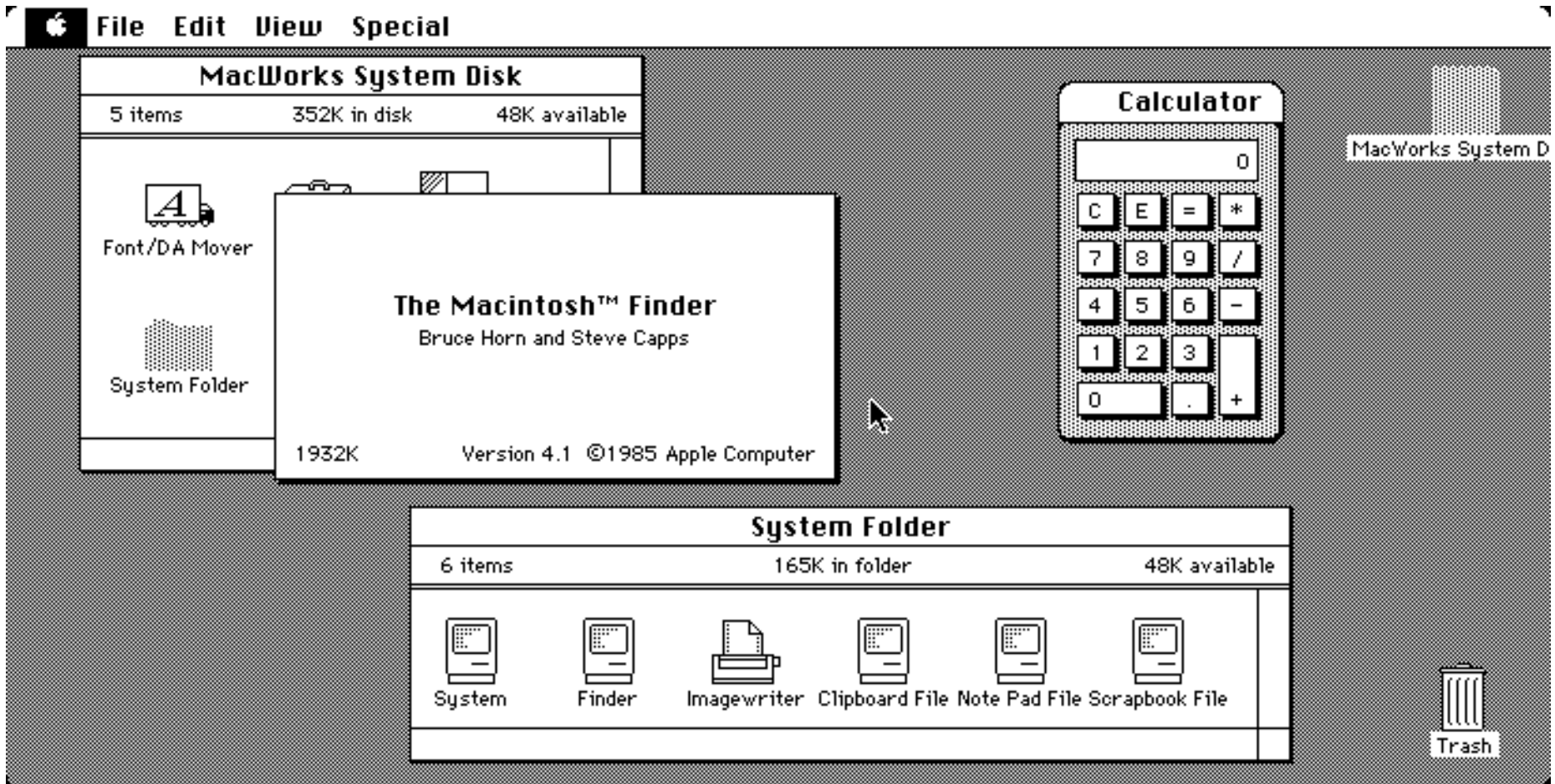
WARNING: Print via Internet access using email only
PAEN02CA V4.0 ( 1.1.1 ) XGUEST Command _____
```

IBM 3270 Terminal



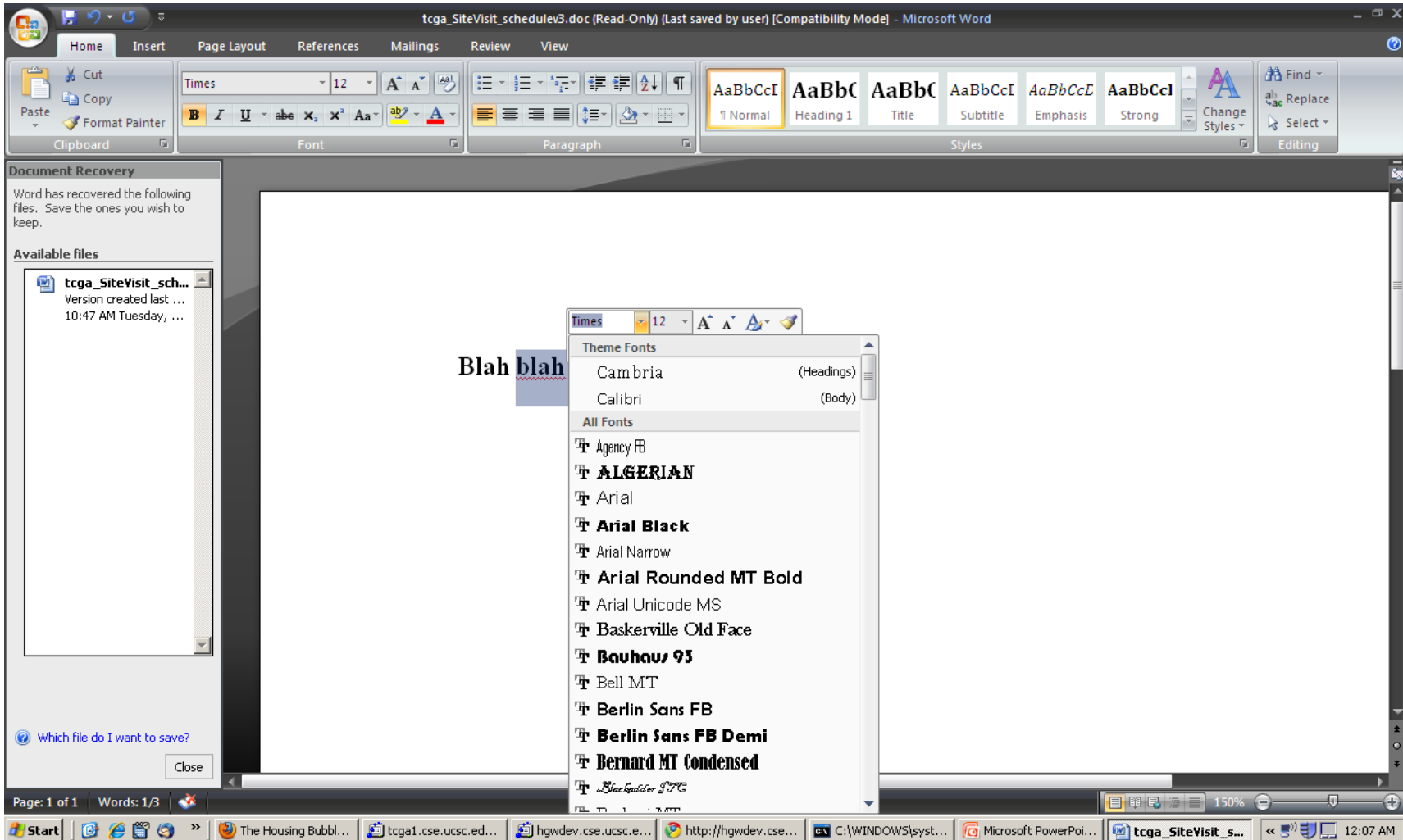


# 1984

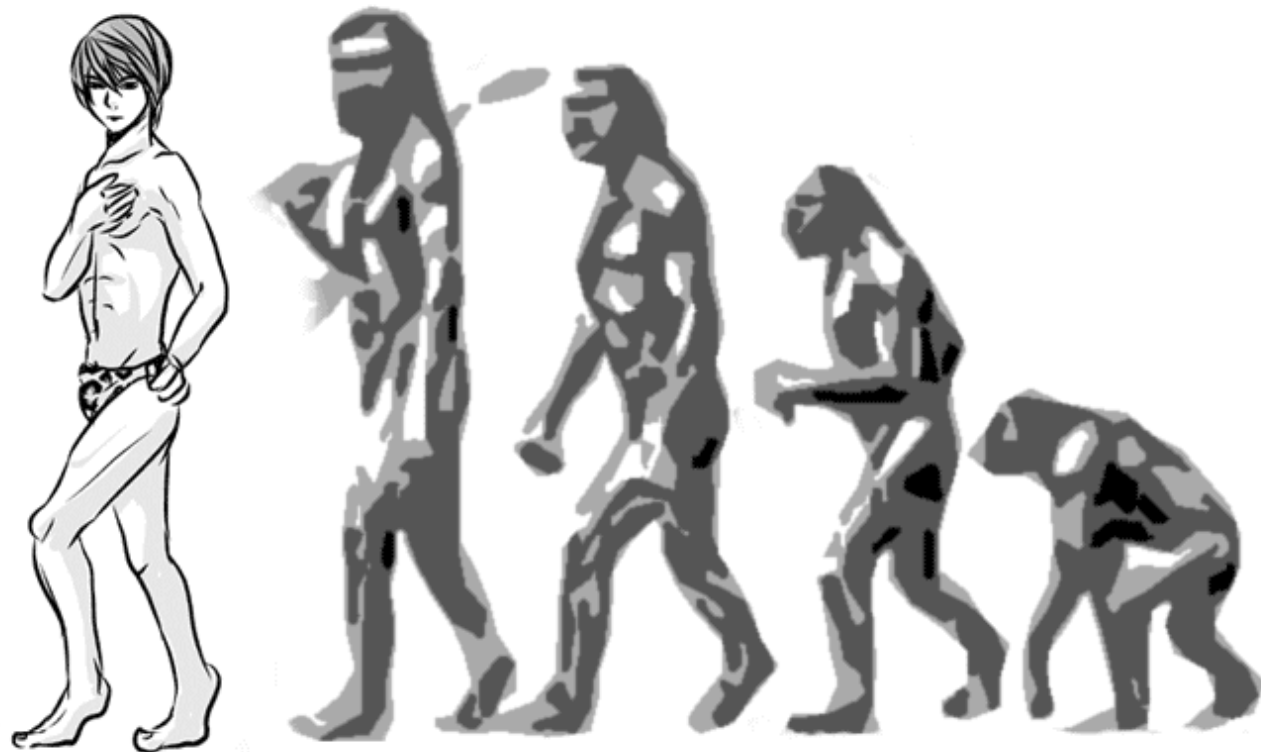


MacOS


# 1994



進化



# 1995



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# HTML is Lame

- Very primitive UI elements
- No dialogs
- Click and wait UI:
  - **Every** user action requires round trip to the server **and** redrawing the whole page
- Javascript very poorly supported until early/mid 2000s, so there was little that developers could do, other than using Flash or Java (which require plugins and are poorly integrated with the browser).

# 2007

The screenshot displays the UCSC Genome Browser interface for the TP53 gene region on human chromosome 17. The browser window title is "Human chr17:7,520,197-7,520,197". The address bar shows the URL: <http://genome.ucsc.edu/cgi-bin/hgTracks?hgsid=153960339&clade=mammal&org=Human&db=hg18&position=chr17:7,520,197-7,520,197&pix=800&Submit>. The navigation bar includes links for Home, Genomes, Blat, Tables, Gene Sorter, PCR, DNA, Convert, Ensembl, NCBI, PDF/PS, Session, and Help. The main heading is "UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly". Below the heading are navigation controls for moving (move) and zooming (zoom in, zoom out) the view. The position/search field contains "chr17:7,520,197-7,520,197". A chromosome map shows the location of the gene on chromosome 17. The main track displays various genomic features: Scale (0 bases), chr17: (p13.1), UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics (TP53), RefSeq Genes, Human mRNAs, Spliced ESTs, Mammal Cons (Vertebrate Multiz Alignment & Conservation (44 Species), Placental Mammal Basewise Conservation by PhyloP), Multiz Alignments of 44 Vertebrates (listing species like Human, Rhesus, Tarsier, Mouse, Dog, Elephant, Opossum, Platypus, Chicken, Lizard, X\_tropicalis, Stickleback), Simple Nucleotide Polymorphisms (dbSNP build 136) (rs1042522), and SNP Genotyping Arrays (Affy SNP 6.0, Affy SNP 6.0 SV, Illumina 1M-Duo, Illumina Cyto-12, Illumina 660K-0).

# 2008

- Donna encouraged Tim and I to start using Javascript to improve the UI:
  - Open/Close of track groups without doing a page refresh
  - Subtrack setting widget in hgTrackUi
- Zack and Steve used jQuery to do the Cancer Browser UI
  - I saw Steve's demo and started using jQuery in the GB



# What is “Web 2.0”?

- web 1.0 == IBM 3270 with colors
- web 2.0 == client-server with a really hard to program client

Mark Diekhans

# What is “Web 2.0”?

- Javascript to improve UI
- AJAX: Client side code interacts with the server without explicit user action
- Web Services: JSON based API

# What is JSON?

- Javascript **S**erialized **O**bject **N**otation
- Serialized Javascript objects
- Supported types:
  - Scalar (string, number or boolean)
  - Array
  - Hash
- De facto standard used by Javascript programs to fetch data from servers

# JSON vs. XML



vs.

`<?xml?>`

# JSON

```
{
  "firstName": "John",
  "lastName": "Smith",
  "age": 25,
  "address":
  {
    "streetAddress": "21 2nd Street",
    "city": "New York",
    "state": "NY",
    "postalCode": "10021"
  },
  "phoneNumber":
  [
    { "type": "home", "number": "212 555-1234" },
    { "type": "fax", "number": "646 555-4567" }
  ]
}
```

# XML

```
<Person>  
  <firstName>John</firstName>  
  <lastName>Smith</lastName>  
  <age>25</age>  
  <address>  
    <streetAddress>21 2nd Street</streetAddress>  
    <city>New York</city>  
    <state>NY</state>  
    <postalCode>10021</postalCode>  
  </address>  
  <phoneNumber type="home">212 555-1234</phoneNumber>  
  <phoneNumber type="fax">646 555-4567</phoneNumber>  
</Person>
```

# JSON

- Pros
  - Parsing is built into javascript implementations
  - Maps better to data structures
  - More succinct (no closing tags)
  - Easier to read
  - Much simpler syntax
  - Only one way to do it
- Cons
  - Less powerful (e.g. can't embed binary data)
  - No built in schemas

# JBrowse JSON example

```
{
  "headers":["start","end","strand","id"],
  "histBinBases":1000,
  "featureCount": 2462,
  "featureNCList":
  [
    [28734,16400072,
     {"path":"data/tracks/chr1/CpGIslands//lazyfeatures-0.json","state":"lazy"},
     null,null],
    [16464375,43251082,
     {"path":"data/tracks/chr1/CpGIslands//lazyfeatures-493.json","state":"lazy"},
     null,null],
    ...
  ],
  "key":"CpG Islands",
  "histogram":[0,0,0, ... ],
  "className":"basic",
  "clientConfig":{"featureCss":"background-color: #0D0;
    height: 8px","histCss":"background-color: #3D3"},
  "rangeMap":[],
  "label":"CpGIslands",
  "type":"FeatureTrack",
  "sublistIndex":4
}
```

**<http://jbrowse.org/ucsc/hg19/data/tracks/chr1/CpGIslands/trackData.json>**



# jQuery: Javascript Library

- Hides most cross-browser differences
- Lots of built in functionality (ajax etc.)
- Very active user community (hundreds of user contributed UI widgets)
- Lots of books and online resources
- Hopefully will become the de-facto UI toolbox for web browsers (analogous to Mac Toolbox, Windows GDI and X Windows API).
- jQuery UI library supports modal dialogs

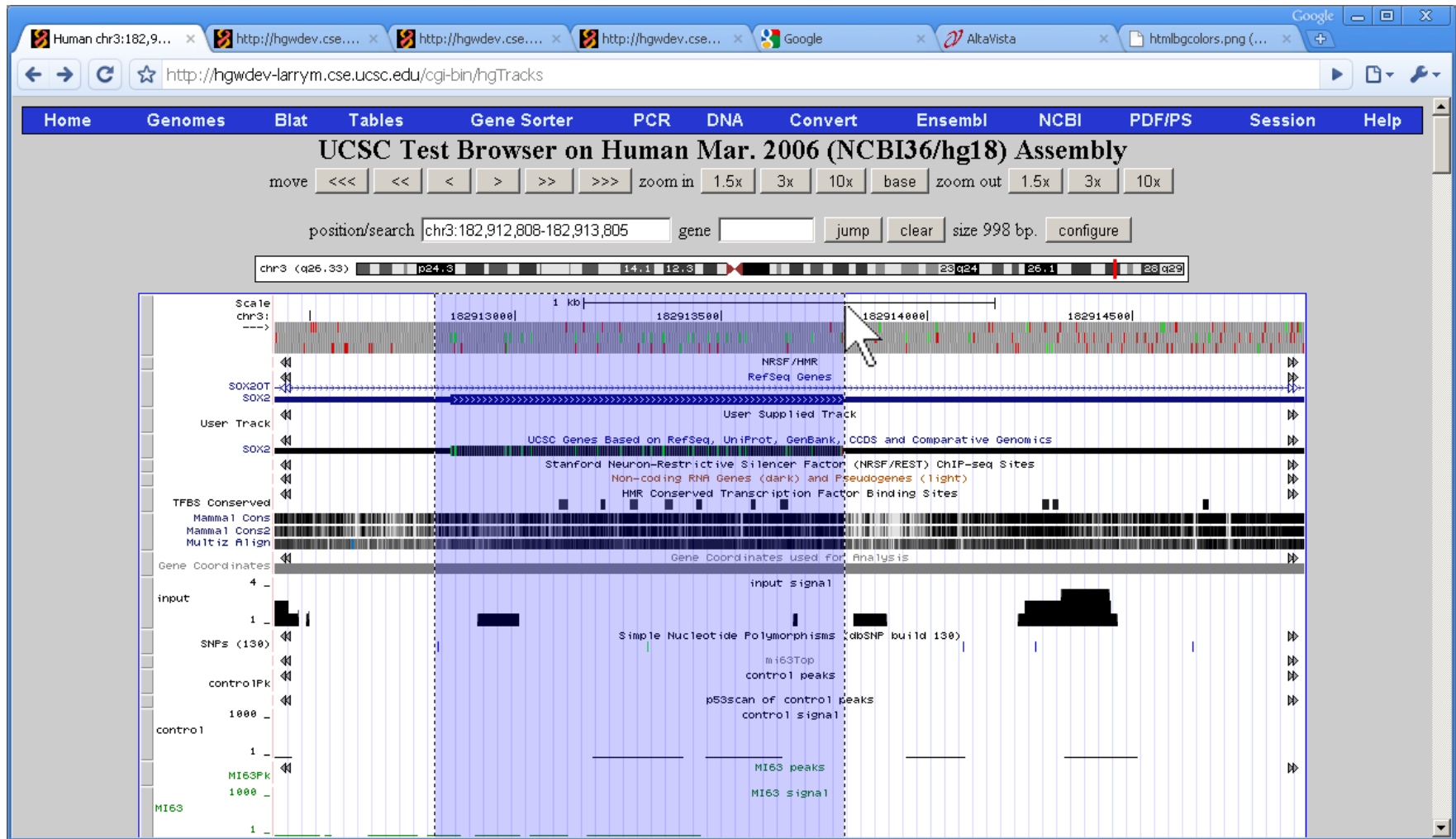
# jQuery (cont.)

- Powerful DOM element selector syntax:

```
$( "map[name!=ideoMap] " ).each (function (index)
    {
        parseMap (this, false);
    });
```

This code snippet applies the `parseMap` function to each map element whose name is not “ideoMap”.

# Drag and Select



# Drag and Select

- Hiram suggested this to me
- Ideal application of Javascript: simple, valuable UI addition that **has** to be implemented on the client side
- Issues:
  - Track Image is very crowded, so currently you have to select at the top of the image
  - We have had a least one serious browser issue: a bug in Chrome/Safari that we couldn't work around; bug was fixed relatively quickly because a genome browser user complained to the AppleWebKit team

# Gene Search Box

Human chr3:182,912,805-... x

http://hgwddev-larrym.cse.ucsc.edu/cgi-bin/hgTracks?hgid=1845142&clade=mammal&org=Human&db=hg18&position=chr3:182,912,805-182,913,822&hgt.s

Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl NCBI PDF/PS Session Help

### UCSC Test Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr3:182,912,805-182,913,822 gene HOX jump clear size 1,018 bp. configure

chr3 (q26.33) p24.3 14.1 12.9 23q24 25.1 28q29

Scale chr3: 500 bases | 182912900 | 182913000 | 182913100 | 182913200 | 182913400 | 182913500 | 182913600 | 182913700 | 182913800

SOX2OT  
SOX2

User Track  
SOX2

UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics  
Stanford Neuron-Restrictive Silencer Factor (NRSF/REST) ChIP-seq Sites  
Non-coding RNA Genes (dark) and Pseudogenes (light)  
HMR Conserved Transcription Factor Binding Sites

TFBS Conserved  
Mammal Cons  
Mammal Cons2  
Multiz Align

Gene Coordinates used for Analysis

input  
input signal

SNPs (130)  
Simple Nucleotide Polymorphisms (dbSNP build 130)

control IFk  
control peaks  
mi63Top  
p53scan of control peaks  
control signal

control  
MI63Pik  
MI63 peaks  
MI63 signal

# Gene Search Box

- Inspired by me getting tired of searching for “TP53” 20 times a day
- Dent Earl suggested the google suggest-style interface
- Fast Uptake showed that it was self explanatory (~10k uses/day within a week)

# JSON/RPC

- Gene search box is a classic AJAX application
  - As user types, client side Javascript code sends prefix to server, which responds with a list of genes
  - Server side code is very fast (simple select on an indexed field in knownGenes/refGene tables)
  - Avoids search page, so it eliminates a whole web page refresh
  - Self explanatory functionality
  - Client/Server interaction is via a JSON interface
- Interaction b/n client and server is essentially an asynchronous RPC
  - `char **getGeneList(char *prefix)`

# Example of a JSON RPC

position/search  gene

position/search  gene  jum

- HOXA1
- HOXA10
- HOXA11
- HOXA11AS
- HOXA13
- HOXA2
- HOXA3

**Client Side**

```
http://hgwdev-larrym.cse... x +
http://hgwdev-larrym.cse.ucsc.edu/cgi-bin/hgSuggest?db=hg18&prefix=HOX

[
  {"value": "HOXA1", "id": "chr7:27099139-27102150"},
  {"value": "HOXA10", "id": "chr7:27176735-27180480"},
  {"value": "HOXA11", "id": "chr7:27187301-27191360"},
  {"value": "HOXA11AS", "id": "chr7:27191552-27195437"},
  {"value": "HOXA13", "id": "chr7:27203024-27206250"},
  {"value": "HOXA2", "id": "chr7:27106498-27108919"},
  {"value": "HOXA3", "id": "chr7:27112334-27120141"},
  {"value": "HOXA4", "id": "chr7:27134651-27136924"},
  {"value": "HOXA5", "id": "chr7:27147521-27149812"},
  {"value": "HOXA6", "id": "chr7:27151641-27153893"},
  {"value": "HOXA7", "id": "chr7:27159863-27162821"},
  {"value": "HOXA9", "id": "chr7:27168582-27171674"},
  {"value": "HOXB1", "id": "chr17:43961806-43963271"},
  {"value": "HOXB13", "id": "chr17:44157125-44161110"},
  {"value": "HOXB2", "id": "chr17:43975018-43977392"},
  {"value": "HOXB3", "id": "chr17:43981231-44006809"},
  {"value": "HOXB4", "id": "chr17:44007868-44010742"},
  {"value": "HOXB5", "id": "chr17:44023618-44026102"},
  {"value": "HOXB6", "id": "chr17:44028098-44037333"},
  {"value": "HOXB7", "id": "chr17:44039594-44043382"},
  {"value": "HOXB8", "id": "chr17:44044707-44047300"}
]
```

**Server Side**



```
hgwdev.cse.ucsc.edu - hgwdev - SSH Secure Shell
File Edit View Window Help

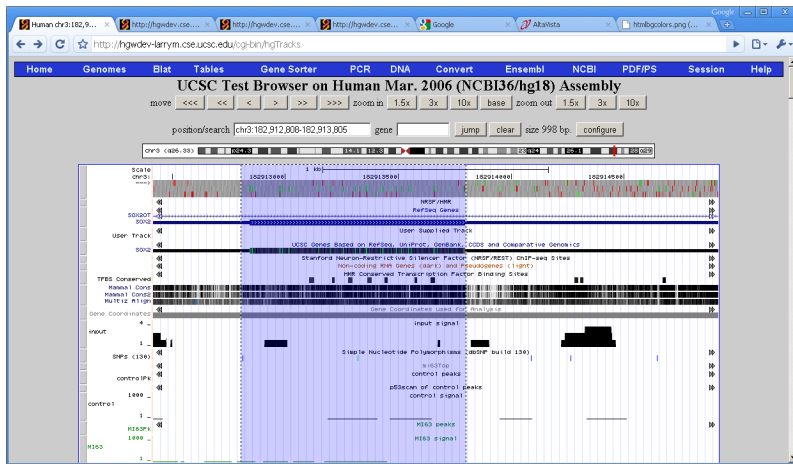
// requires utils.js

var suggestCache;

function ajaxGet(getDb, cache)
{
  // Returns jquery.autocomplete.js ajax_get function object
  // getDb should be a function which returns the relevant assembly (e.g. "hg18")
  // cache is an optional object used as a hash to cache responses from the server.
  suggestCache = cache;
  return function (key, cont) {
    if(suggestCache == null || suggestCache[key] == null)
    {
      $.ajax({
        url: "../cgi-bin/hgSuggest",
        data: "db=" + getDb() + "&prefix=" + key,
        // dataType: "json", // XXXX this doesn't work under IE, so we retrieve as text and do an eval to force to an object.
        trueSuccess: handleSuggest,
        success: catchErrorOrDispatch,
        error: function (request, status, errorThrown) {
          if (typeof console != "undefined") {
            console.dir(request);
            console.log(status);
          }
          var msg = "ajax call failed";
          if(status != "error")
            msg = msg + "; error: " + status;
          showWarning(msg + "; statusText: " + request.statusText + "; responseText: " + request.responseText);
        },
        key: key,
        cont: cont
      });
    } else {
  }
}

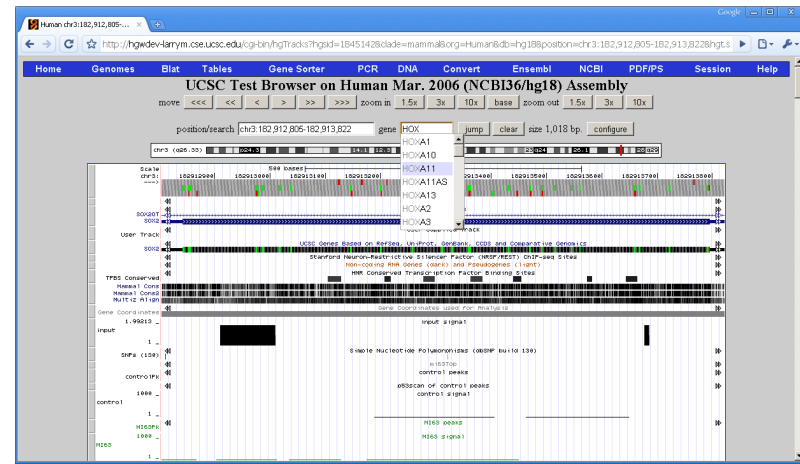
-:---F1 :/cluster/home/larrym/kent/src/hg/js/autocomplete.js 11:16PM 1.10 [(JavaScript-IDE CVS-1.3 Abbrev)]--L17-- 4%-----
0* tcsh

Connected to hgwdev.cse.ucsc.edu SSH2 - aes128-cbc - hmac-md5 - none 160x36
```



## Client Side only

No network I/O, so not susceptible to network latency



## AJAX

Susceptible to network latency, which limits utility for more interactive functionality

# Alternative Gene Search Box Implementation (ala jBrowse)

- Could pre-compute lookup lists for all assemblies and store them as static JSON files (~ 1 meg each)
- Client retrieves assembly specific lookup file when page is loading (cached after first time)
- Client side code does the lookup synchronously
- Pros
  - No delay on client side
  - Removes CGI hits, so less overhead on server
- Cons
  - Client side code is more complex
  - More complex build environment

# Pure AJAX App

- All of the UI is constructed and run on the client side; there are no HTML form submissions; e.g. the cancer browser, modern email apps (gmail, yahoo, zimbra)
- Pros
  - Usually yields a better UI
  - Forces separation between UI code and data, so it's easier to plugin a different UI (e.g. iPad/android)
  - Easier to pull in 3<sup>rd</sup> party data
- Cons
  - GB already has a lot of server side UI code
  - History is complicated (no more back button; this may actually be a good thing)
  - Javascript may cause performance issues (e.g. if you try to render on the client side)

# Cancer Browser

UCSC Cancer Genomics Heatmaps - Mozilla Firefox

File Edit View History Bookmarks Tools Help

ucsc.edu https://genome-cancer.soe.ucsc.edu/hgHeatmap/

Human chr... W IBM 3270 - ... http://x=FOX .each() - jQ... Mocha\_w32... UCSC ...

0.874  
-0.874

chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8 chr9 10 11 12 13 14 15 16 17 18 19 20 chrX Y

sampletype  
batch  
chemotherapy  
gender  
histologicaltype  
testdimensions  
itcomesuccess  
tumorgrade  
tumorstage  
vitalstatus

### Feature Settings

#### Select Features

Select Features to Show

- sampletype
- batch
- chemotherapy
- gender
- histologicaltype

[Update Features](#)

#### Subgrouping

**chemotherapy**

**Group 1**

No  
Yes  
Undefined

**Group 2**

No  
Yes  
Undefined

[Add Subgrouping](#)

#### Current Subgroups

**CHEMOTHERAPY**

**Group 1** No **Group 2** Yes

[Group 1](#) [Group 2](#)

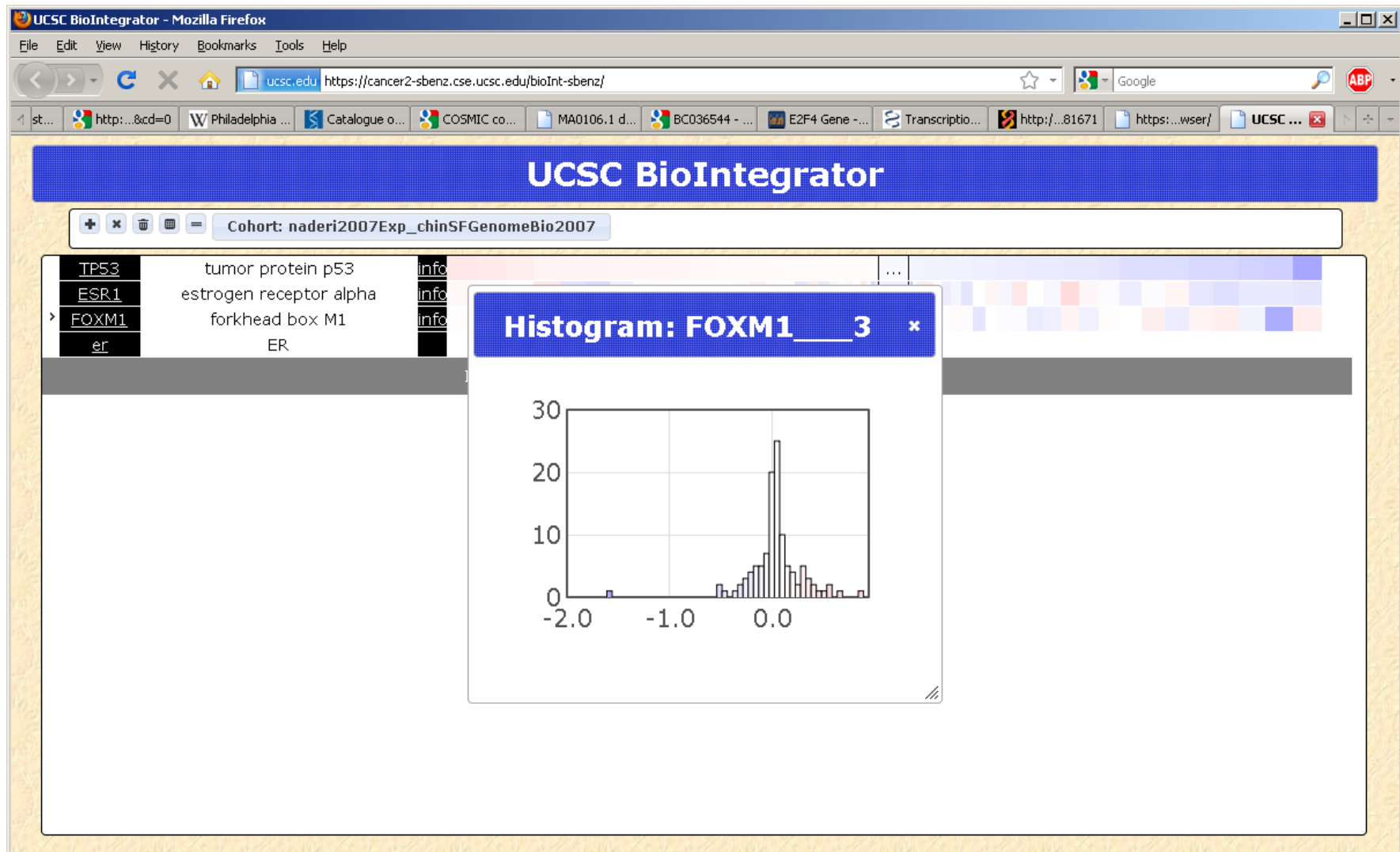
[Jump to hgMicroscope](#)

#### Statistic

Wilcoxon Benjamini-Hochberg (FDR)

[Generate Statistics](#)

# BioIntegrator



# Coming Attractions

- Track settings dialog
- Context menu for track items
- Track search
- Drag panning
- Drag reorder of tracks



# Track Search

Human chrhttp://hgdev-larrym.cse.ucsc.edu/cgi-bin/hgTracksX:151073054-151383976 - UCSC Genome Browser v233 - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://hgdev-larrym.cse.ucsc.edu/cgi-bin/hgTracks

Zimbra: Inbox Human corti... Source Cod... UCSC - Cam... MyUCSC Lo... W Difference e... Huma... W IBM 3270 - ... http...x=FOX .each() - jQ... Mocha\_W32...

Home Genomes Genome Browser Blat Tables Gene Sor FAQ Help

### Track Search (prototype!)

Search Advanced Search

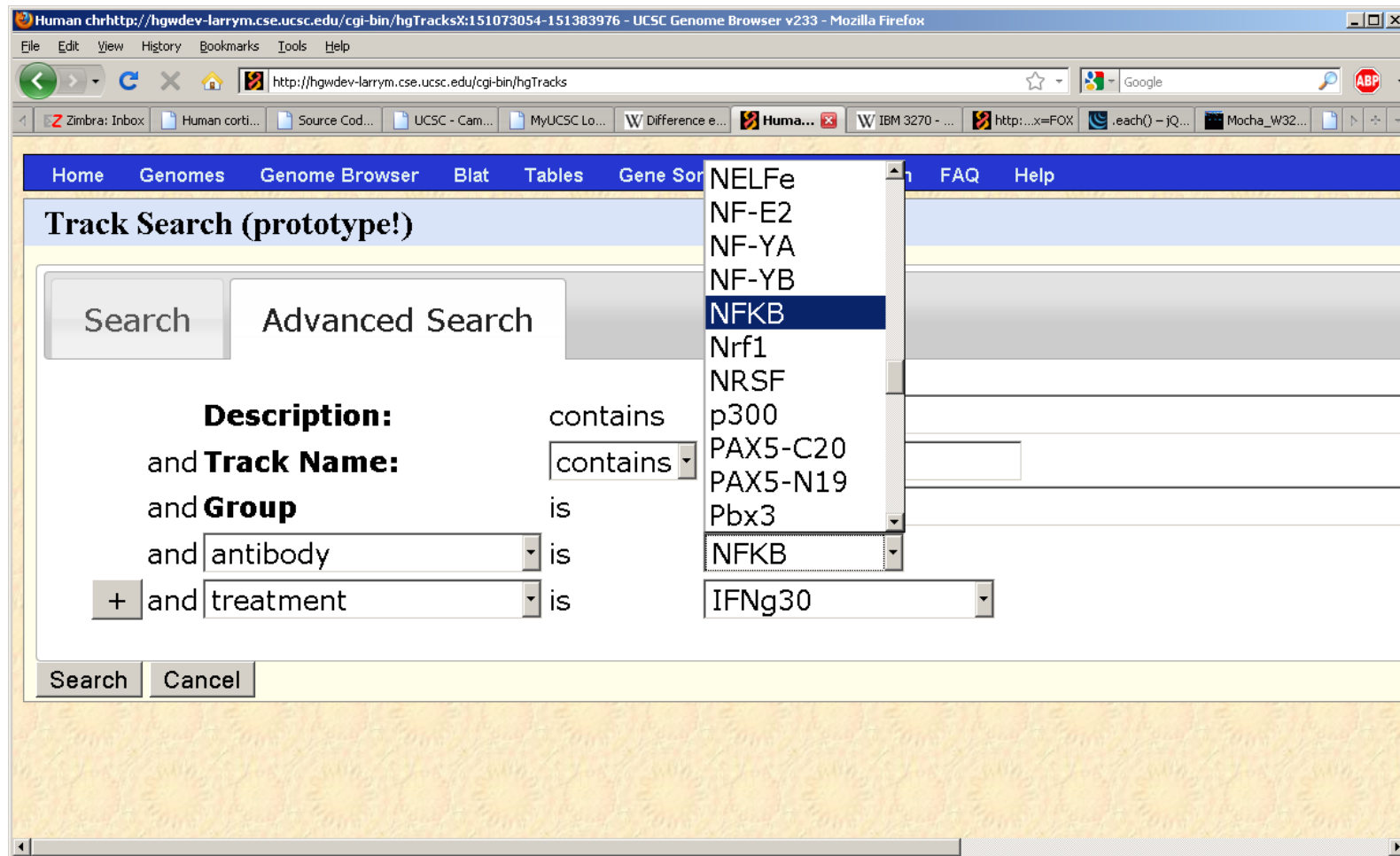
**Description:** contains  
and **Track Name:** contains  
and **Group** is  
and cell is  
+ and lab is

Search Cancel

- HRE
- HRPEpiC
- HSMM
- HSMMtube
- HUVEC
- Jurkat
- K562
- K562b
- LHSR
- LNCaP
- MCF-7**
- MCF-7
- HudsonAlpha



# Track Search



AJAX is used to change select box when user chooses a different metadata field

# Context Menus

The screenshot displays the UCSC Test Browser interface for Human chromosome 3 (hg18 assembly). The browser window title is "Human chr3:182,912,416-...". The URL is "http://hgwdev-larrym.cse.ucsc.edu/cgi-bin/hgTracks?hgt.dummyEnterButton.x=0&hgt.dummyEnterButton.y=0&hgsid=1901762&clade=mammal&org=Human". The page title is "UCSC Test Browser on Human Mar. 2006 (NCBI36/hg18) Assembly".

The interface includes navigation buttons (Home, Genomes, Blat, Tables, Gene Sorter, PCR, DNA, Convert, Ensembl, NCBI, PDF/PS, Session, Help) and a search bar with the position "chr3:182,912,416-182,914,917" and gene name "SOX2". The size of the region is 2,502 bp.

The main track shows the SOX2 gene structure. A context menu is open over the SOX2 track, listing the following options:

- hide
- dense
- squish
- pack
- full ✓
- Zoom to SOX2
- Get DNA for SOX2
- Open details page in new window

The SOX2 track is currently set to "full" view. Other tracks visible include NRSF/HMR, User Supplied Track, input signal, Mammal Cons, Multiz Align, Mammal Cons2, Gene Coordinates, RefSeq Genes, Nucleotide Polymorphisms (dbSNP build 130), m163Top, control peaks, p53scan of control peaks, control signal, MI63 peaks, MI63 signal, p53scan of mi63 peaks, siRNA peaks, and siRNA signal.

# Track Settings Dialog

The screenshot shows the UCSC Test Browser interface with the 'input Track Settings' dialog box open. The browser window title is 'Human chr3:182,912,416-...' and the URL is 'http://hgwdev-larrym.cse.ucsc.edu/cgi-bin/hgTracks?hgt.dummyEnterButton.x=0&hgt.dummyEnterButton.y=0&hgsid=1901762&clade=mammal&org=Human'. The browser's navigation bar includes links for Home, Genomes, Blat, Tables, Gene Sorter, PCR, DNA, Convert, Ensembl, NCBI, PDF/PS, Session, and Help. The main content area displays the 'UCSC Test Browser on Human Mar. 2006 (NCBI36/hg18) Assembly' with navigation controls for moving and zooming. The 'input Track Settings' dialog box is titled 'input Track Settings' and contains the following settings:

- input signal**
- Display mode:
- Type of graph:
- Track height:  pixels (range: 11 to 128)
- Vertical viewing range: min:  max:  (range: 1 to 1000)
- Data view scaling:  Always include zero:
- Transform function: Transform data points by:
- Windowing function:  Smoothing window:  pixels
- Draw y indicator lines: at y = 0.0:  at y =
- [Graph configuration help](#)
- [View table schema](#)
- Data last updated: 2009-07-21

The background interface shows a track browser with various tracks including 'User Track', 'SOX2', 'input', 'Mamma1 Cons', 'MULTI2 Align', 'Mamma1 Cons2', 'Gene Coordinates', 'SOX2OT', 'SOX2', 'SNPs (130)', 'contro1Pk', 'contro1', 'MI63Pk', 'MI63', 'siRNAPk', and 'siRNA'. The 'input' track is currently selected and displays a bar graph. The 'p53scan of mi63 peaks' track is also visible, showing 'siRNA peaks' and 'siRNA signal'.

# hgApi

- Experimental JSON API interface
  - getTrackList (used by steve's experimental integrated CB/GB tool)
  - getMetaData (used by track search)

The screenshot shows a Mozilla Firefox browser window with the address bar containing the URL: <http://hgwdev-larrym.cse.ucsc.edu/cgi-bin/hgApi?db=hg18&cmd=trackList>. The browser's address bar also shows a search engine (Google) and a search icon. The browser's menu bar includes File, Edit, View, History, Bookmarks, Tools, and Help. The browser's toolbar includes a back button, a forward button, a refresh button, a home button, and a search icon. The browser's tabs bar shows several open tabs, including "st...", "http://...&cd=0", "W Philadelphia...", "Catalogue o...", "COSMIC co...", "MA0106.1 d...", "BC036544 - ...", "E2F4 Gene -...", "Transcriptio...", "https://wser/", "UCSC BioInt...", and "htt...ist". The browser's main content area displays a JSON array of track information:

```
[
  {
    "track": "cytoBandIdeo",
    "shortLabel": "Chromosome Band (Ideogram)",
    "longLabel": "Chromosome Bands Localized by FISH Mapping Clones (for Ideogram)",
    "group": "Mapping and Sequencing Tracks"
  },
  {
    "track": "benzGenes",
    "shortLabel": "Gene Coordinates",
    "longLabel": "Gene Coordinates used for Analysis",
    "group": "Experimental Tracks"
  },
  {
    "track": "benzInput",
    "shortLabel": "input",
    "longLabel": "input signal",
    "group": "Experimental Tracks"
  },
  {
    "track": "mi63Top",
    "shortLabel": "mi63Top",
    "longLabel": "mi63Top",
    "group": "Experimental Tracks"
  },
  {
    "track": "encodeMsaTbaDec07",
    "shortLabel": "36-Way TBA",
    "longLabel": "TBA Alignments and Conservation of 36 Vertebrates in the ENCODE Regions",
    "group": "Pilot ENCODE Comparative Genomics and Variation",
    "subtracks": [
      {
        "track": "encodeMsaTbaDec07Viewcons",
```

<http://hgwdev-larrym.cse.ucsc.edu/cgi-bin/hgApi?db=hg18&cmd=trackList>

# Future Directions

- Richer JSON RPC interface? (For our own client side apps and perhaps 3<sup>rd</sup> parties as well):
  - getTrackList
  - getTrackImages
  - getTrackDetails
- Requires refactoring of some of our code so it can output either html or json

# Pitfalls

- You can end up DOS'ing yourself (DOS == Denial of Service)
  - Tooltips in very dense track map
- Too much usage and/or too sophisticated an interface can burden your servers; e.g. Gene Suggest for “A” in hg18 yields a list 163kb long.
- Very dependent on Javascript, so your apps can break spectacularly with new browser releases

# Pitfalls (cont.)

- hgTracks startup time is slow; large overhead from loading tracks (100-200 milliseconds)
  - A robust JSON based API would require something faster, perhaps something embedded in the web server (e.g. mod\_perl) or a dedicated process listening on another port (e.g. node.js).
  - This issue can be mitigated by using pre-computed static JSON files



# Pitfalls (cont.)

- If you make your APIs public and third-parties start to use them, then you can't arbitrarily change them (i.e. public APIs have development, support, testing and staging overhead).
  - JSON APIs should be easier to change than binary ones (e.g. adding hash keys shouldn't break existing code)

# Pitfalls (cont.)

- You have to test on all supported browsers:

| Browser           | January, 2010 | June, 2010   |
|-------------------|---------------|--------------|
| Internet Explorer | <b>39.7%</b>  | <b>40.6%</b> |
| IE8               | 13.1%         | 15.9%        |
| IE7               | 15.9%         | 15.8%        |
| IE6               | 10.5%         | 8.5%         |
| FireFox           | <b>37.4%</b>  | <b>36.2%</b> |
| Safari            | <b>12.7%</b>  | <b>10.2%</b> |
| Chrome            | <b>4.3%</b>   | <b>5.5%</b>  |

GB stats from awstats

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