

So, we have our map ...

...Now, we want to see how it  
looks compared to someone  
else's maps.

## CMap

- First developed for Gramene, now is part of the GMOD project.
- CMap is the map visualization and comparison tool for Gramene and GrainGenes, among other sites.
- It can display genetic and physical data.

CMap is the standard tool for map visualization in several web sites

## Gel Retrieval and Comparative Mapping (GRCM)

- Developed at the Cereal Research Centre, Canada. It is not publicly available but wheat-CAP participants can freely use it.
- Oriented to display genetic maps.
- More user-friendly than CMap, can be installed on a PC. However, current version does not work with IE 7, and some tools are not available in Firefox

Since GRCM runs in a normal PC, one can use it to analyze maps before submission

## map comparison tools compared

	<b>CMap</b>	<b>GRCM</b>
Easy to install ?	It takes a system administrator to install on a Unix / Linux server	Easier than CMap, but still difficult. Besides, it requires other programs: mySQL, SVG viewer, Java, and Tomcat
Operating system	Unix / Linux	Unix / Linux / Windows
Web accessible?	Yes	Yes
Types of information	Can handle different types of information: loci position, markers, QTLs, sequences, ESTs.	More oriented to genetic maps: loci, markers, QTLs. Images of gels with marker bands.
Easy of use?	Basic use is easy. Advanced users can configure and customize the display	Yes

## a few words about installing GRCM

**Before you install the visualization application itself you need to install:**

SVG Viewer. A plug-in for IE to display SVG graphics.  
<http://www.adobe.com/svg/viewer/install/main.html>

Java JDK 1.5. Be careful, this not the latest version.  
[http://java.sun.com/javase/downloads/index\\_jdk5.jsp](http://java.sun.com/javase/downloads/index_jdk5.jsp)

MySQL community server 5.0. A database server.  
<http://dev.mysql.com/downloads/mysql/5.0.html#downloads>

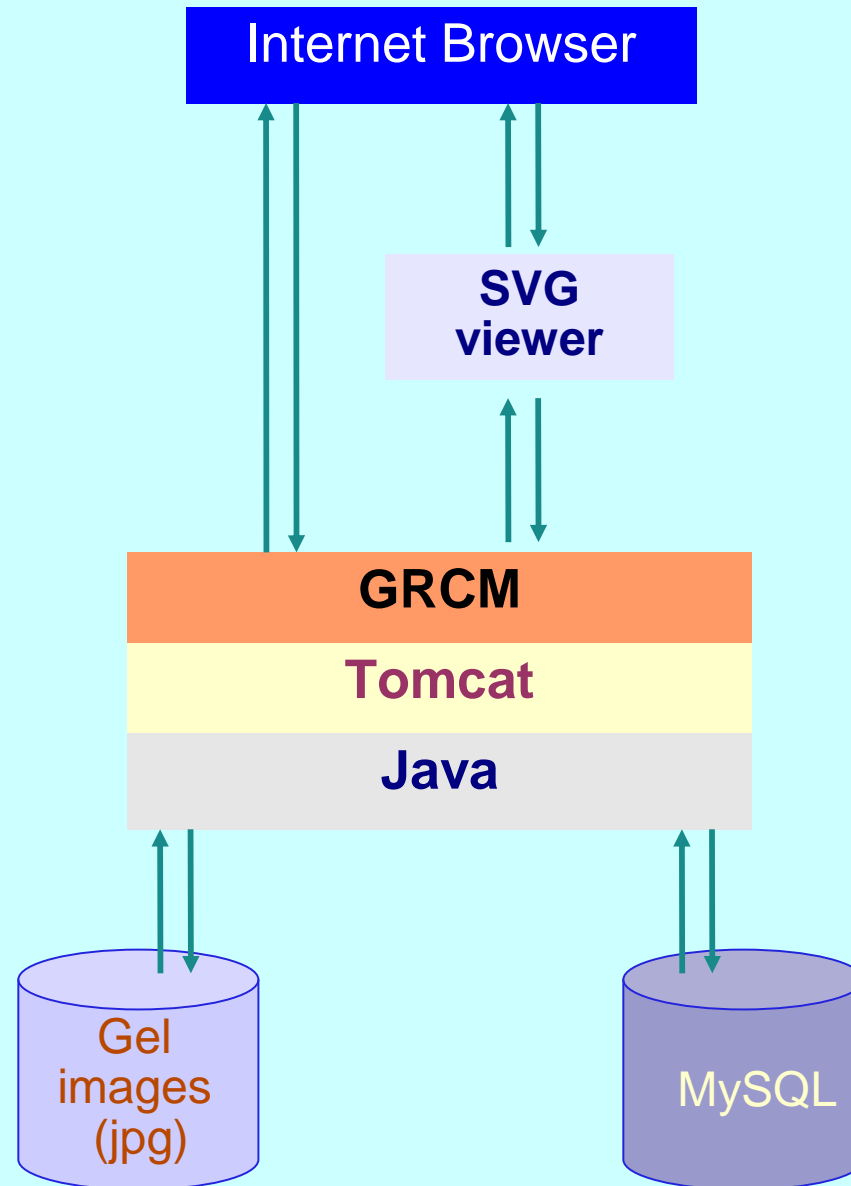
Tomcat 5.0.28. Be careful, this is not the latest version. Tomcat is a server for running Java based programs.  
<http://tomcat.apache.org/download-55.cgi#5.0.28>

**Don't give up!**

If you could install the software, configuring the program is relatively easy. Follow the Instructions in the setup guide

# Tools for map comparison and visualization

## Why so many complications ?



# Tools for map comparison and visualization

## Using and administering SGRM. User interface

[http://localhost:8080/gel\\_retrieval/gel.jsp](http://localhost:8080/gel_retrieval/gel.jsp)

select the map

choose markers

select chromosomes

Map    Comp

Source: WGRF

Map: ConV3

Marker/QTL Search

Marker  QTL

View    Clear

Delimit By Marker

all  
barc  
cfa  
cfd

Delimit    Accent

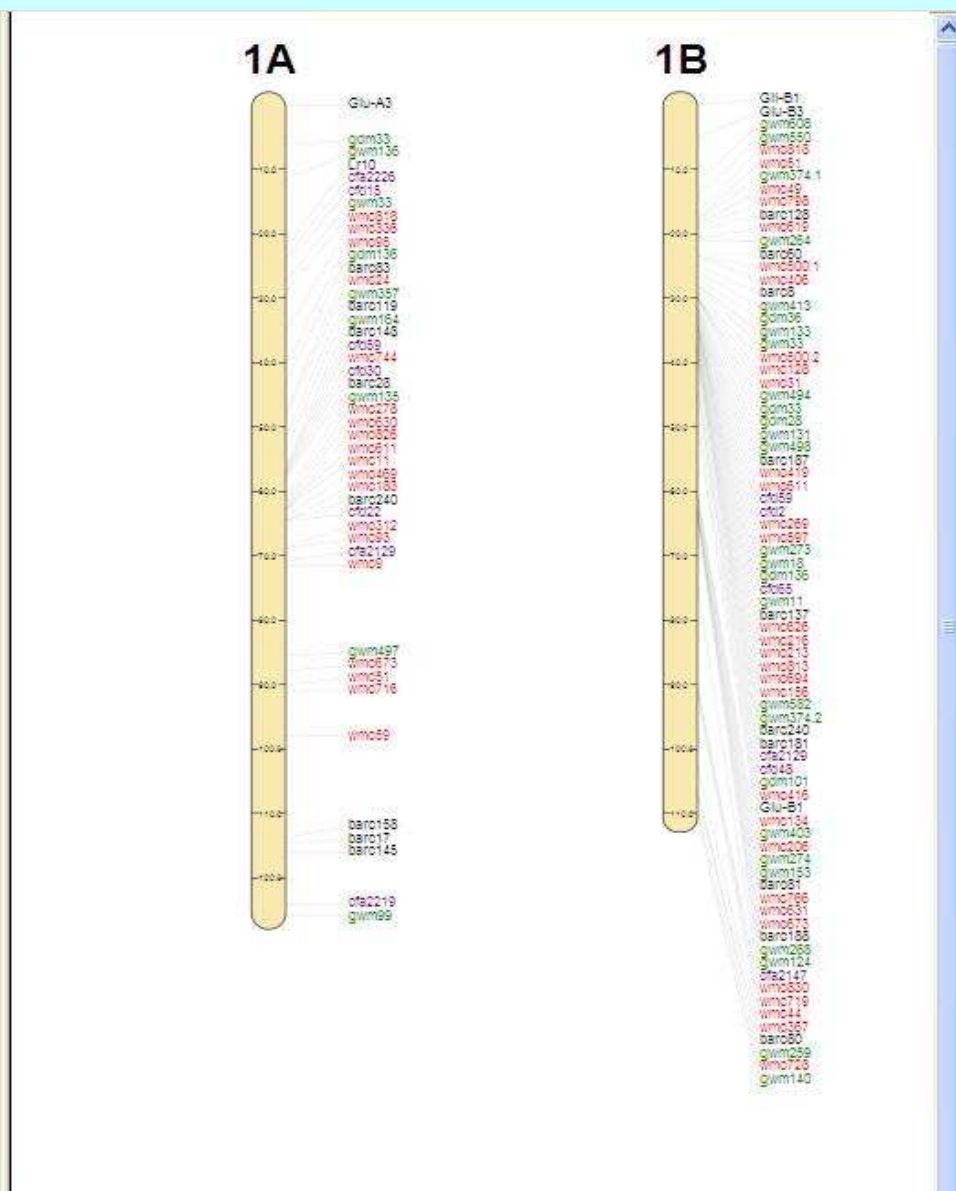
Display QTLs

Chromosomes

<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	1A 1B 1D	
<input type="checkbox"/>	2A 2B 2D	
<input type="checkbox"/>	3A 3B 3D	
<input checked="" type="checkbox"/>	4A 4B 4D	
<input type="checkbox"/>	5A 5B 5D	
<input type="checkbox"/>	6A 6B 6D	
<input type="checkbox"/>	7A 7B 7D	

Clear Map Display

Clear Thumbnails



Gel Images

gwm133\_scr24.jpg

after selecting a marker on the map, you can see a gel image for that marker

## Using and administering SGRM. Administrator interface

[http://localhost:8080/gel\\_retrieval/admin/UpdateWGRFDB.html](http://localhost:8080/gel_retrieval/admin/UpdateWGRFDB.html)

### WGRF Database Administration

Using the following links you can modify the data stored in a WGRF database. Please be very careful doing this as the changes you make are immediate and permanent.

1. [Add a new map](#)
2. [Remove a map](#)
3. [Replace an existing map](#)
4. [Create a new marker class](#)
5. [Create a new QTL class](#)
6. [Add QTLs to a map](#)
7. [Associate Markers and Images](#)
8. [Add alleles sizes for markers](#)

file format  
for creating  
maps

	A	B	C	D	E	F
1	marker_name	marker_type	marker_class	chromosome	marker_coordinate	keywords
2	cfd69	<a href="#">ssr</a>	<a href="#">cfd</a>	7D	144.8	<a href="#">cfd</a>
3	wmc364	<a href="#">ssr</a>	<a href="#">wmc</a>	7D	142.8	<a href="#">wmc</a>
4	gwm37	<a href="#">ssr</a>	<a href="#">gwm</a>	7D	140.9	<a href="#">gwm</a>
5	gwm48	<a href="#">ssr</a>	<a href="#">gwm</a>	7D	135.9	<a href="#">gwm</a>
6	barc53	<a href="#">ssr</a>	<a href="#">barc</a>	7D	129.9	<a href="#">barc</a>
7	wmc824	<a href="#">ssr</a>	<a href="#">wmc</a>	7D	124.2	<a href="#">wmc</a>
8	barc111	<a href="#">ssr</a>	<a href="#">barc</a>	7D	114.8	<a href="#">barc</a>
9	wmc671	<a href="#">ssr</a>	<a href="#">wmc</a>	7D	114.5	<a href="#">wmc</a>
10	cfd25	<a href="#">ssr</a>	<a href="#">cfd</a>	7D	110.7	<a href="#">cfd</a>
11	gdm67	<a href="#">ssr</a>	<a href="#">gdm</a>	7D	106.9	<a href="#">gdm</a>
12	wmc94	<a href="#">ssr</a>	<a href="#">wmc</a>	7D	101.7	<a href="#">wmc</a>
13	barc172	<a href="#">ssr</a>	<a href="#">barc</a>	7D	98.8	<a href="#">barc</a>
14						
15						

## Using and administering SGRM. Administrator interface

To have features in your mapped colored according to classes you need to use these two options

### Add New QTL Class

The purpose of the QTL class is to give a colour to the display of QTL information against a genetic map. You can only add a QTL class to an existing genetic map.

Datasource	<input type="text" value="WGRF"/>
Genetic Map	<input type="text" value="ConV3"/>
QTL Class Name	<input type="text"/>
QTL Colour	<input type="text"/>
Password	<input type="text"/>

### Create New Marker Class

The purpose of the marker class is to give a colour to a group of markers. For example, all markers that belong to the wmc marker class are to be coloured red. Marker classes are also used to delimit and accent groups in the gel retrieval application.

Datasource	<input type="text" value="WGRF"/>
Genetic Map	<input type="text" value="ConV3"/>
Class Name	<input type="text"/>
Colour	<input type="text"/>
Password	<input type="text"/>



## Using and administering SGRM. Administrator interface

To assign a QTL to a map more information is required:

### Add New QTLs

This page allows you add QTLs to a genetic map. Unlike traditional QTL positioning which is given in cM, the display of QTLs in the application require that the bounding markers be specified.

The file to upload has to be in a very specific format. The best way to create this file is to enter the information into an Excel spreadsheet and save the spread sheet in text format as a tab-delimited file and contain no empty fields. The file should have a column header and must contain the following information (in the indicated order).

1. QTL name
2. Chromosome
3. Start marker
4. End marker
5. Parent1
6. Parent2
7. Population type
8. Population size
9. # Environment tested
10. # Environment detected
11. Replicated
12. Significance
13. Coeff of determination
14. Allele with Pos. Trait Effect
15. Allele with substitution effect
16. Description
17. Publication
18. QTL class (used for assigning a colour on the display)
19. Keywords (comma separated list of terms to search by)

Datasource

Genetic Map

QTL File

Delete existing QTLs

Password

## Need help?

You can contact me at [masoria@ucdavis.edu](mailto:masoria@ucdavis.edu)

I can assist you to install the software using a conference tool

## No way, too lazy to do a full install...

There is a copy of the software installed on a GrainGenes server. Its use is restricted to wheat-CAP users.

url: <http://XXXX>

user: xxxxxx

password: xxxxx

Prepare your map data according to the instructions in the setup guide, and e-mail me your file.