

Viewing DAS tracks with Dalliance

Thomas A. Down
thomas@biodalliance.org

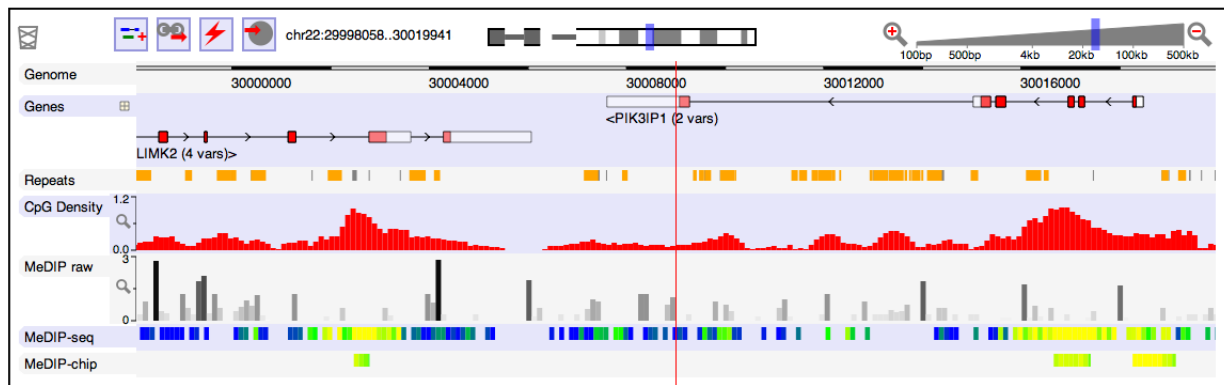
Dalliance is a genome viewer and exploration tool that runs within your web browser. This tutorial covers the basics of navigating around the genome, then shows how you can use DAS to add your own data to the browser.

Getting started

Dalliance works in most modern web browsers, including Google Chrome, Mozilla Firefox, and Apple Safari. Microsoft Internet Explorer doesn't work at the moment, but this may change with the imminent release of IE9. If you are using a training room machine, start Firefox now. If you're using your own machine and everything is up-to-date, then try any non-Microsoft browser.

To start Dalliance, just navigate to <http://www.biodalliance.org/human/ncbi36/>. Unless you're on a very slow connection, the browser should start up and display data within about five seconds, and should look something like this:

Human NCBI36



Powered by [Dalliance](#) 0.6.0-pre6

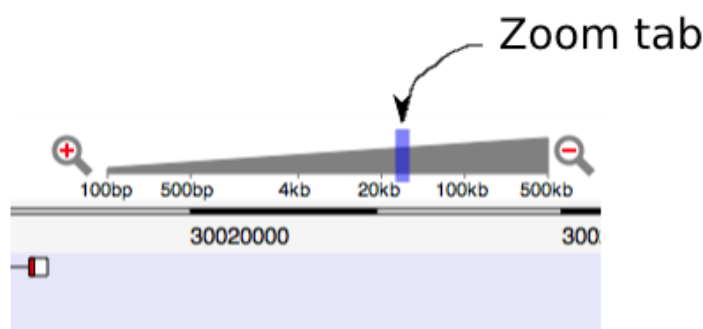
If there's a problem, ask one of the trainers now. Otherwise, try mousing around the browser area, and compare the display with any genome-browsing software you might previously have used.

At the top of the browser, you'll see a toolbar (many of the buttons will be explained later), some indicators of your genomic location, and a slider to control zoom level. The rest of the viewport should be a familiar genome display. Click on the tabs down the left hand side if you want an explanation of the data shown in the various tracks.

Getting browsing

The simplest way to move the display is to point in the main browser area and drag left or right, much like the navigation in popular mapping applications. However, there are a couple of alternatives: if your input device supports left-right panning gestures (for instance, the two-finger sweep on recent Apple trackpads, or scroll-balls on some mice), these allow you to smoothly scroll the Dalliace display. Alternatively, you can use the ← and → keys on your keyboard (combine with SHIFT if you want to scroll faster). **NB.** key shortcuts like ← and → will only work while the mouse pointer is within the browser area.

To zoom in and out, tap the + or - keys on your keyboard (again, if this doesn't work, make sure your mouse is pointing in the Dalliace viewport). Alternatively, you can drag the tab of the zoom slider:

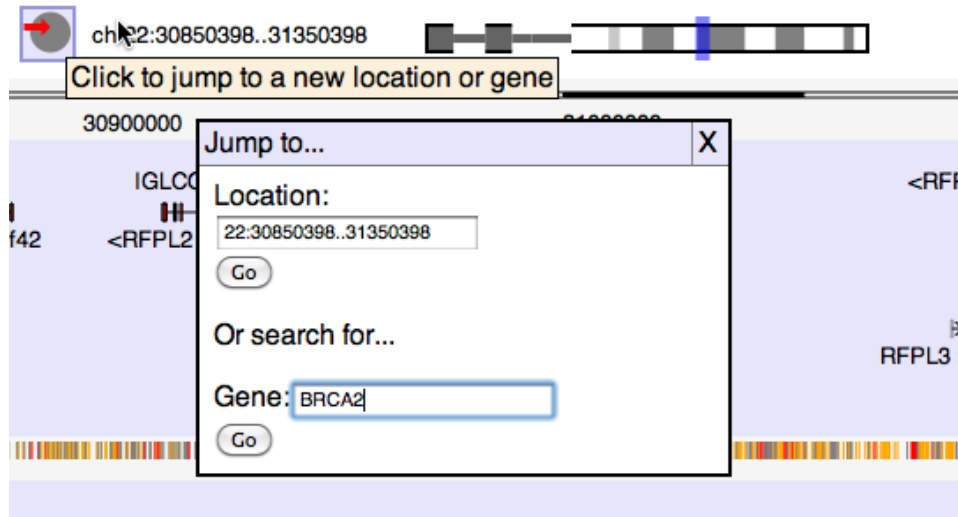


You can also zoom right in by tapping the space bar. In this case, the ‘Genome’ track – which previously just showed a ruler – should expand to show the actual genome sequence. Tap space again to return to your previous zoom level.

As you zoom and scroll, Dalliace tries to load data in the background. If you scroll rapidly, you might be able to ‘get ahead’ of the browser though, in which case you’ll see cross-hatched areas where missing data should go. Just wait a moment and your browser should catch up!

All the data you can see – including standard tracks like genes and repeats – has been loaded *via* the DAS protocol. If you know how to set up a DAS server, you should be able to easily set up a Dalliace browser for a new genome.

If you want to navigate to a completely different part of the genome, click on the *locator* section of the toolbar:



You can either type in coordinates for a feature of interest, or enter a search string to find a named feature (in the example above, the familial breast cancer gene “BRCA2”). There are a few limitations to search at the moment (in particular, it’s case sensitive – so if you are browsing the mouse genome you’ll have to search for “Brca2” instead!) but is useful nevertheless. Improving the search capabilities of DAS-based viewers is an area under further development.

Finally, you’ll notice that some tracks have additional controls in their name-tabs, *e.g.*



Experiment to see what these do.

Adding data

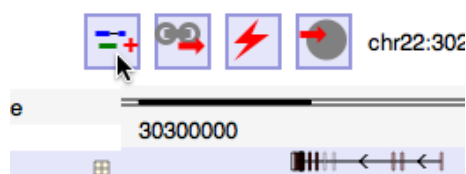
As a DAS client, it is easy to add new data to Dalliance. The only requirements are that you're running a DAS/1.5 or DAS/1.6 server which supports Cross Origin Resource Sharing (CORS). The details of CORS will be discussed in the Dalliance talk on day 2 of the workshop, but for now, suffice to say that all the major DAS middleware now supports CORS, and thus any new DAS source you set up is likely to be okay.

For this tutorial, we'll assume you've already set up an easyDAS source for your data. You should know the URI for your source, for instance:

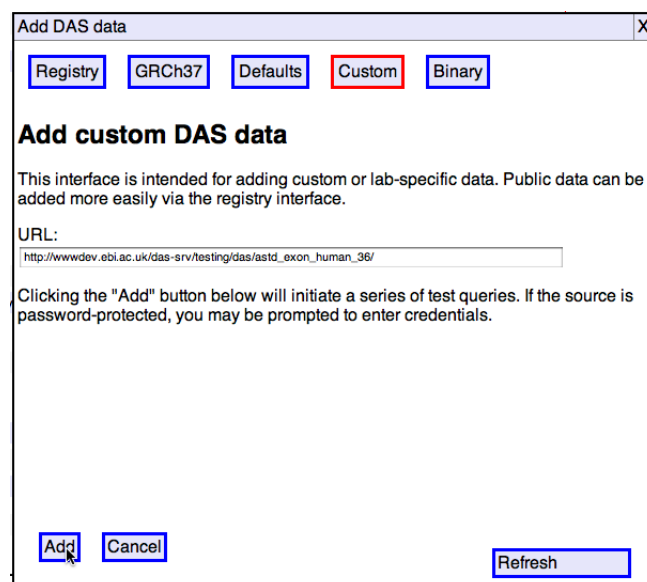
`http://www.ebi.ac.uk/das-srv/easydas/bernat/das/familiar_cancer_genes`

Hint: the penultimate component of a DAS URI will almost always be /das/. The final component is the data-source name (DSN) within that DAS server installation.

To add data to Dalliance, click the 'add track' button:



You'll see several options for adding data from the DAS registry, but in this case click over to the 'Custom' tab, where you will have the opportunity to enter your DAS URI:



When you click 'Add', Dalliance will issue a series of test queries to the DAS server. If these succeed, you'll see something like this:

Add DAS data

Registry GRCh37 Defaults **Custom** Binary

Add custom DAS data: step 2

Label:

Coordinate system:

(Based on server response, probably doesn't need changing.)

Quantitative: ☐

(Based on server response, probably doesn't need changing.)

At this point, you'll have the option to rename your new track, if you wish. If the server fully implements the current DAS/1.6 protocol, Dalliace should be able to determine the correct coordinate system automatically (and re-map features if necessary). For older DAS server software, you may have to enter the coordinate system manually (in which case you'll see a warning message). Finally click 'Add' again, and your new track should appear at the bottom of the browser view.

Customizing your view

You can re-order tracks – for instance, to more easily see coincidences between two tracks of interested – by dragging and dropping the track-name tabs. You'll see a red bar marking the point where the track will go when you drop it.

Similarly, you can delete a track completely by dragging it to the waste-bin in the top-left corner of the display. There are a few limitations here: you're not currently allowed to delete the "Genome" track, for example. But any normal track you've added can be removed this way.

If you get tracks too badly mixed up, or delete something important, just click the red lightning bolt to reset the browser to a default state.

Explore!

With your new data added to the Dalliance browser, why not try navigating around, or exploring some of the other data sets that are available through Dalliance's registry browser.

One of the advantages of integrating different types of data in a genome viewer is the possibility of finding coincidences between different data types. If you think you see an interesting coincidence, double-click on one of the features to center it underneath the red guideline, which should make it easier to check. If need be, you can then zoom in: features under the guideline will always remain centered when you zoom. Try using the zoom-toggle facility (tap SPACE) to switch between 'browsing' and 'inspecting' perspectives on your data.

If you find something exciting, there's an 'Export' button in the toolbar which allows you to export the current display in a choice of either SVG or PDF formats.

Dalliance is a relatively new program, and remains under very active development. We'd love to hear your experiences, or ideas about new ways you'd like to visualize your data. Thomas Down (Dalliance lead developer) will be at the DAS workshop on all three days, or just drop us a line:

- <http://www.biodalliance.org/>
- thomas@biodalliance.org
- [@biodalliance](#) on Twitter