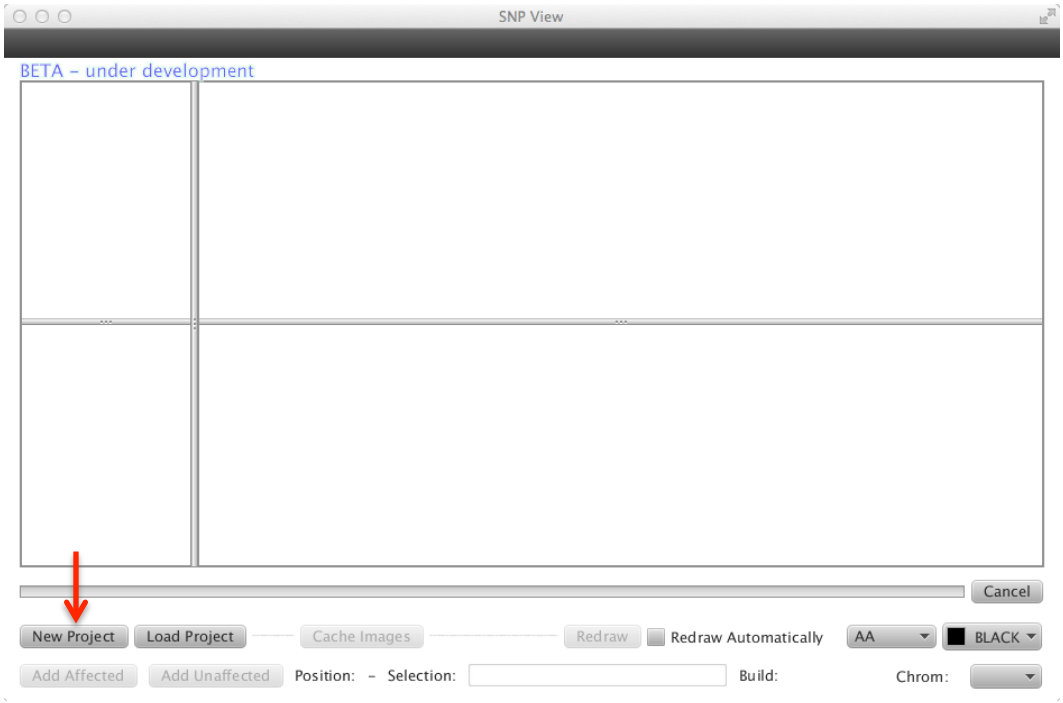
SNP Viewer Beta

Instructions

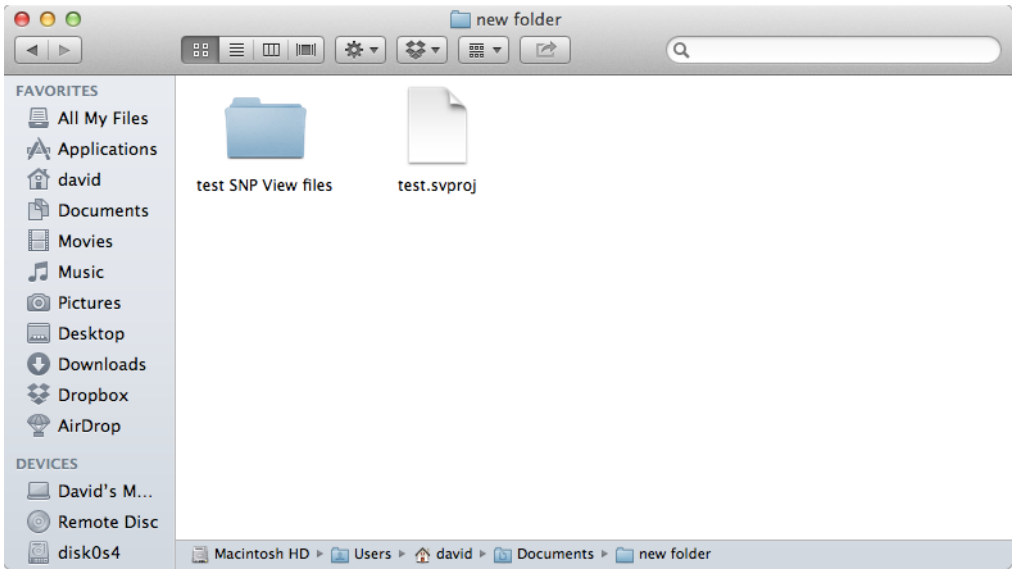
SNP viewer aims to be a simple, easy-to use program that enables the viewing and analysis of Affymetrix SNP chip data for autozygosity mapping.

Upon launching the program you should be created with a screen looking like the picture below.

Getting Started:



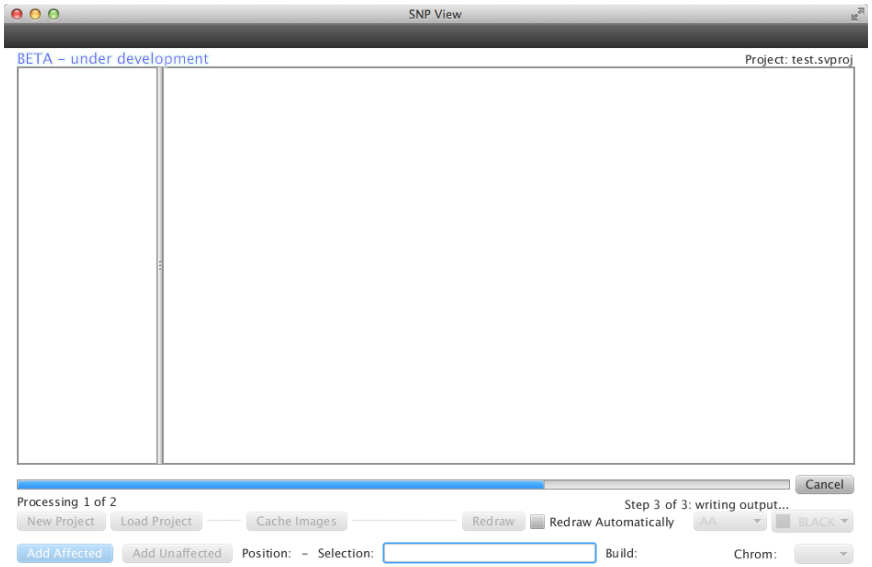
Click the "New Project" button or choose "New Project" from the "File" menu to start a new project. You will be prompted to create a new project file which will consist of your chosen name for the project with an ".svproj" extension. A folder containing important files required for the project will also be created with as shown below:



Any changes to your project will be recorded in the project file automatically. You do not need to save your project manually.

If you have a saved project this can be loaded using the "Load Project" button or File menu option instead.

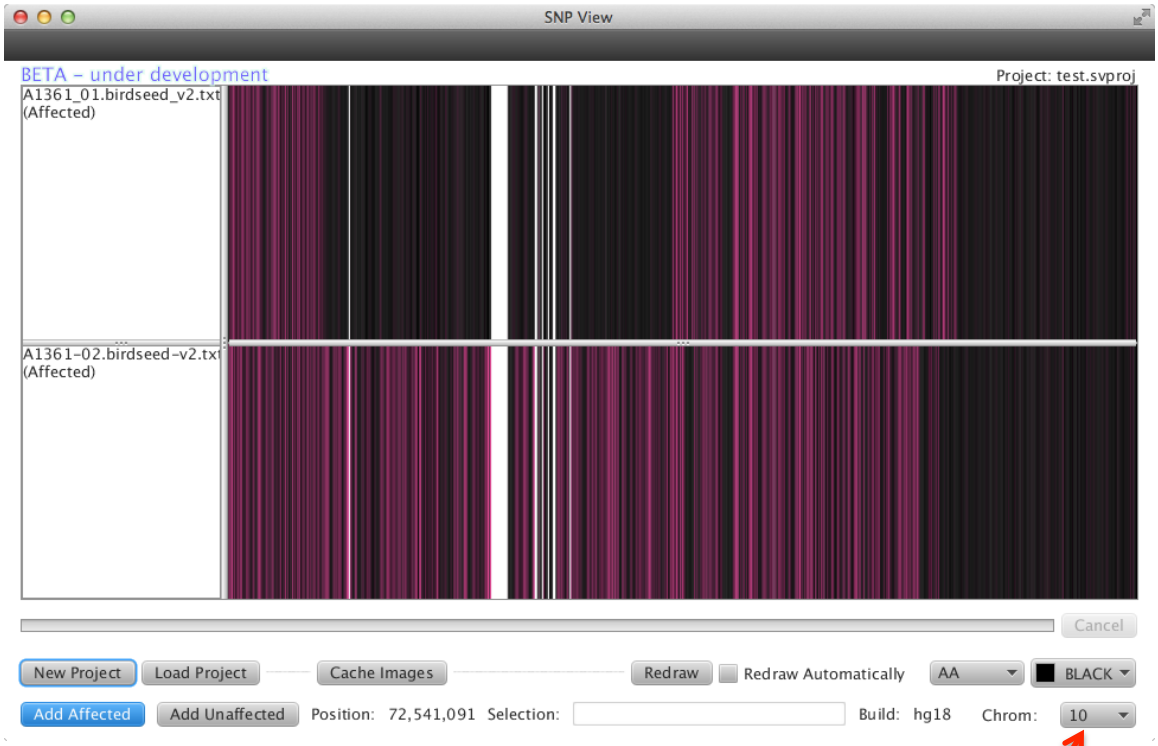
Upon starting a project use the "Add Affected" or "Add Unaffected" buttons to add samples to your project. You will be presented with a file chooser dialog from which you can select one or more birdseed files to add to your project.



The program will process birdseed files from the Affymetrix genotyping console directly as long as they contain the "Call Code" field. There is

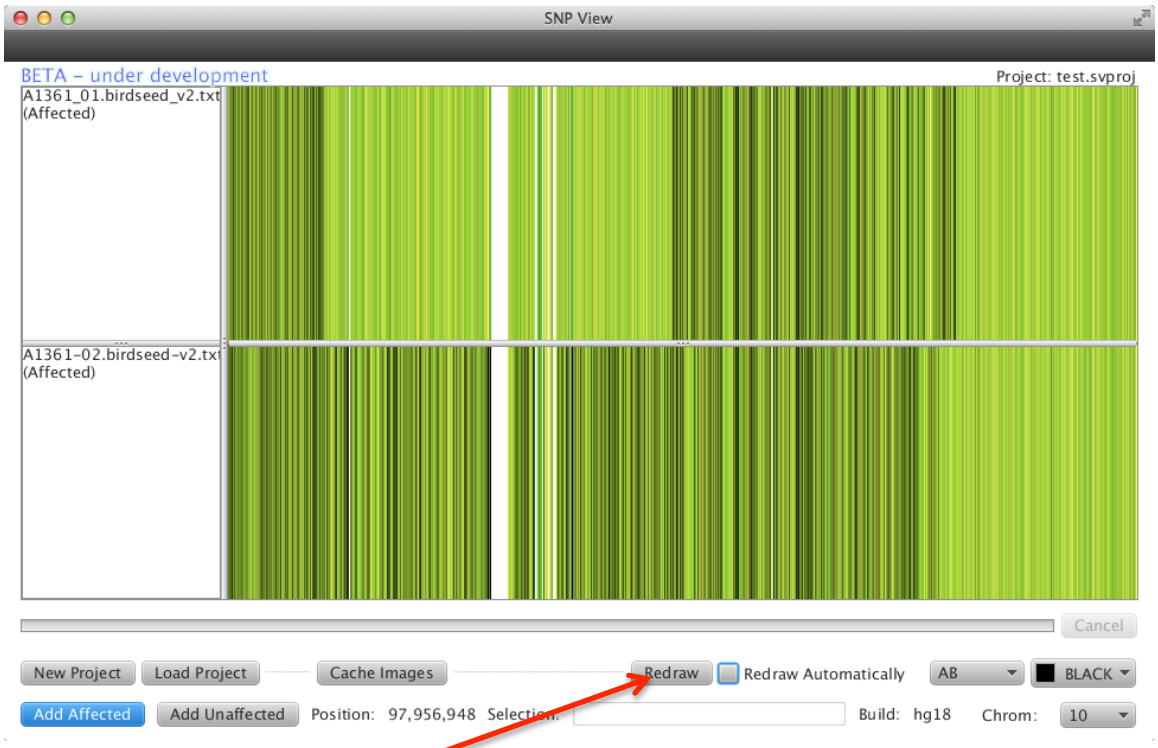
no need to use an accessory program to adjust these files.

Display and Colours



SNP Viewer displays one chromosome at a time. The chromosome can be changed using the dropdown box at the bottom-right of the window. The default colour-scheme displays "AA" calls in black, "BB" calls in dark grey and "AB" calls in pink. In this manner homozygous regions can be identified as dark areas with very little or no pink while haplotypes can be crudely compared between samples by comparing the black/grey striping for each file.

You may change the colour using the dropdown menus towards the bottom-right of the window – the picture below shows an example with heterozygous calls coloured in black while homozygous calls are coloured green or yellow:



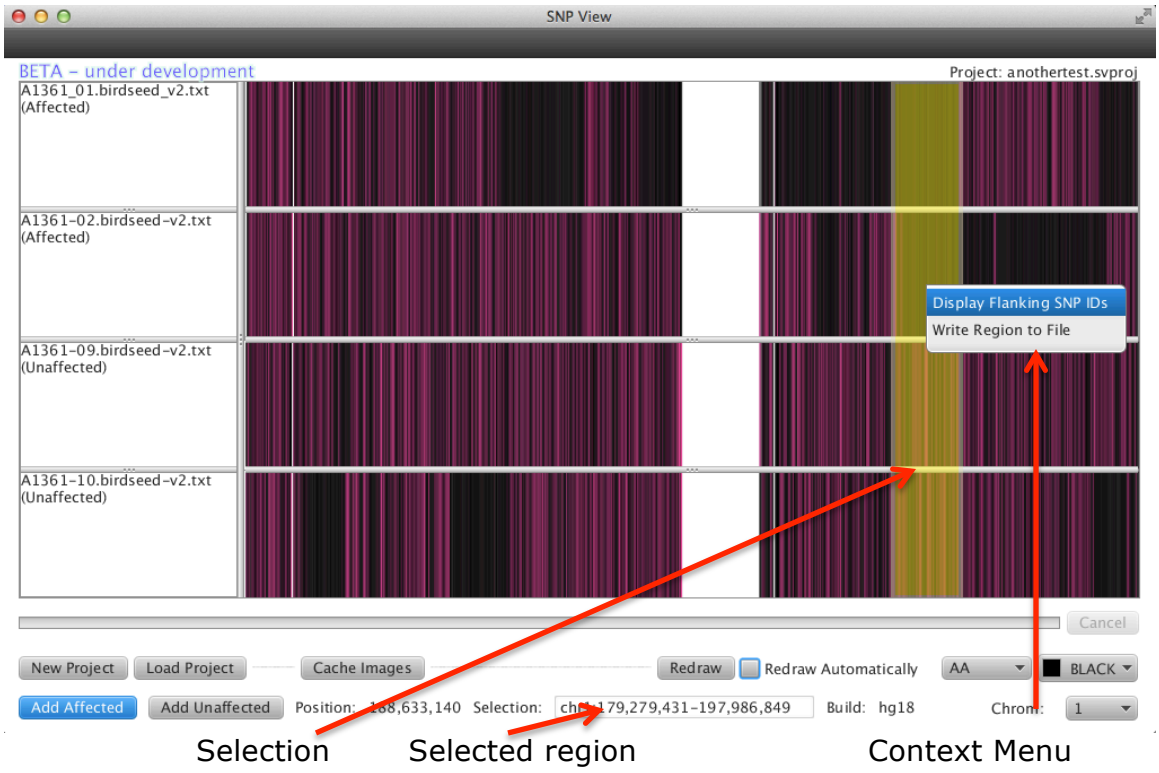
Click the "Redraw" button to display your new colour-scheme or switch to a new chromosome. If the "Redraw Automatically" checkbox is ticked the chromosome images will be redrawn automatically any time a new colour is chosen.

Selecting Regions

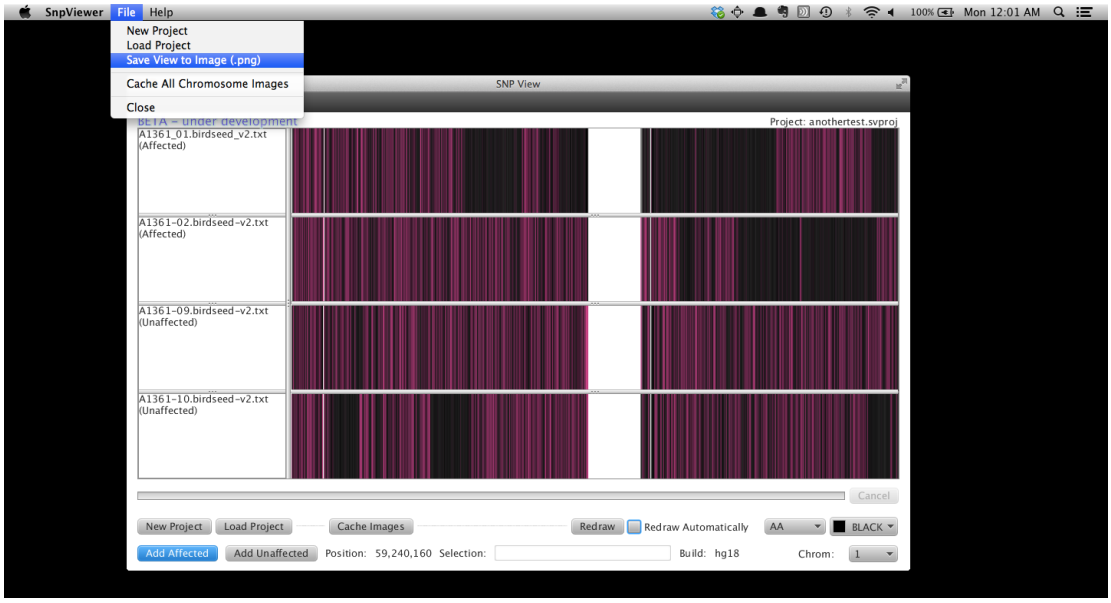
Moving the mouse cursor across the chromosome image will display the corresponding coordinate next to the "Position" label at the bottom of the window. You can select a region for interrogation by holding your mouse button and dragging across the region of interest. A highlighting box will show the region selected and the corresponding start and end coordinates will be displayed in the "Selection" text box at the bottom centre of the window.

Furthermore, you can right-click the selected area and choose to either display the coordinates and rsIDs of the flanking SNPs or to write the region to a '.csv' file ('csv' files

can be opened with Excel or similar programs in order to examine the region in detail).



You may also save the images as displayed on screen be either right-clicking anywhere on the chromosome image or using the “File” menu option “Save View to Image”.



Drawing and Caching Chromosome Images

By default, each time you change the chromosome viewed the program will draw the genotypes for each file and cache the generated images for quick access for future views. You can use the "Redraw" button to force the program to regenerate the image for a chromosome if, for example, you've increased the size of the window a lot and the cached images look fuzzy. If you tick the "Redraw Automatically" checkbox images will always be redrawn fresh.

Because caching images can save time when flicking between chromosomes you can use the "Cache Images" button or file menu option to cause the program to cache images for all samples and chromosomes for quick access. Because this process takes a few minutes you might want to set this running while you go do something else. Once done you can quickly look at different chromosomes without having to wait for the program to draw the images.

Please note: if you change genotype colour-schemes any cached images will be lost.

Features still to add:

Auto-detect regions: At present selecting "Affected" or "Unaffected" samples has little effect but to ensure that "Unaffected" samples are at the bottom of the view. In future an option to automatically detect homozygous regions will use Affected and Unaffected samples to identify regions shared in Affected samples but absent in Unaffected samples.

Zoom region: In addition to displaying flanking SNPs and writing regions to .csv files, a third option to display a zoomed view of a selected region should be added.

Remove sample from project: A simple option to remove samples from a project should be added, although not considered urgent until the "Auto-detect" feature is working.

Output native Excel (.xlsx) format: Rather than outputting .csv files, native .xlsx format files could be written with automatic colour-formatting of genotype calls.

Integration with Gene Retriever-like functions: While copying and pasting regions identified by this program into Gene Retriever is trivial, an option to perform similar search and annotations from Snp Viewer could be a useful feature.

Integrated help: Really the help menu should do something helpful, but for now there is this document.

An icon: Anyone with a bright idea for an icon feel free to suggest something.

Feedback etc.

Any ideas for features are most welcome. Please don't hesitate to report any bugs with the program – this is the only way these things can get fixed!

This software is unpublished and currently in beta – if you find it useful and intend to publish any images/data generated by Snp Viewer I would be very grateful if you could let me know.

Snp Viewer is written in its entirety by David Parry (d.a.parry@leeds.ac.uk) at the cost of many hours and possibly the author's sanity. The aim was to create a user-friendly program that would be useful for homozygosity mapping and run on Mac OS X, Linux and Windows. It is the author's intention to open-source the project once the code is in a complete and tidy-enough state.