FROG-kb: Forensic Resource/Reference on Genetics–knowledge base

http://frog.med.yale.edu/

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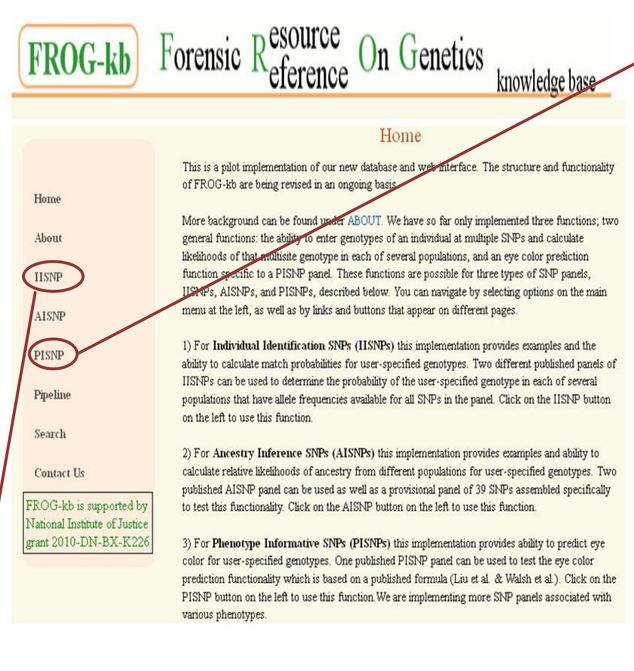
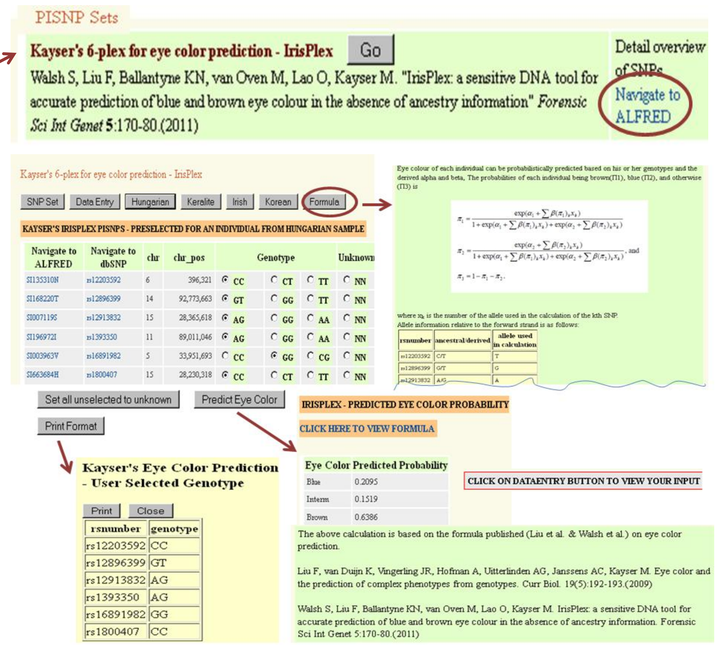
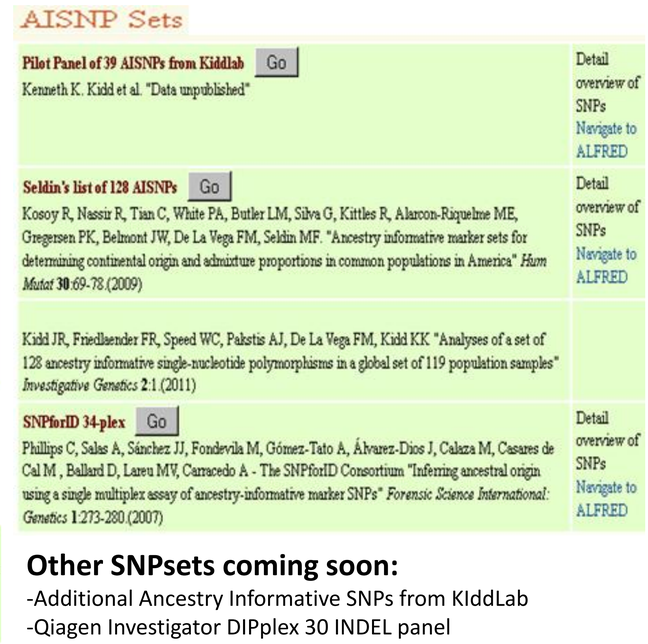
This work is supported by National Institute of Justice Grant : 2010-DN-BX-K226

Overview

FROG-kb (http://frog.med.yale.edu) is an open access web application that is useful for teaching and research relevant to forensics and can serve as a tool facilitating forensic practice. The underlying data for FROG-kb are provided by the already extensively used and referenced ALlele FREquency Database, ALFRED (http://alfred.med.yale.edu). In addition to displaying data in an organized manner, computational tools that use the underlying allele frequencies with user-provided data are implemented in FROG-kb. These tools are organized by the different published SNP/marker panels available. This web tool currently has implemented general functions for two types of SNP panels, individual identification and ancestry inference, and a prediction function specific to a phenotype informative panel for eye color.







Other SNPsets coming soon:

-Additional Ancestry Informative SNPs from KIddLab

-Qiagen Investigator DIPplex 30 INDEL panel

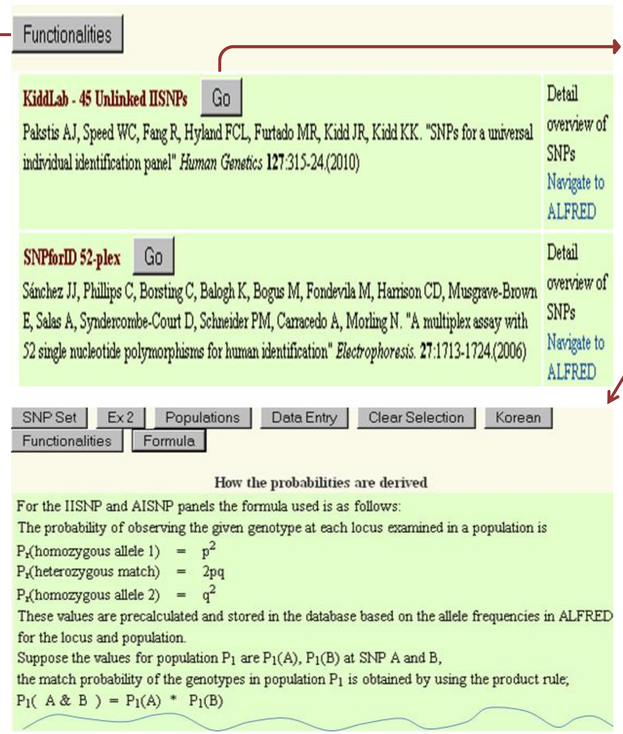
IISNP functionality

For each IISNP panels listed below there are several elements. Associated with each of the panel listings is a **Detailed Overview of SNPs** link into ALFRED precisely for a more detailed overview of the panel. That link opens the SNP Set page within ALFRED into a new browser window. The SNP Set module in ALFRED has multiple options, including the ability to see for each SNP a pie chart on Google Maps of frequencies for all populations with data.

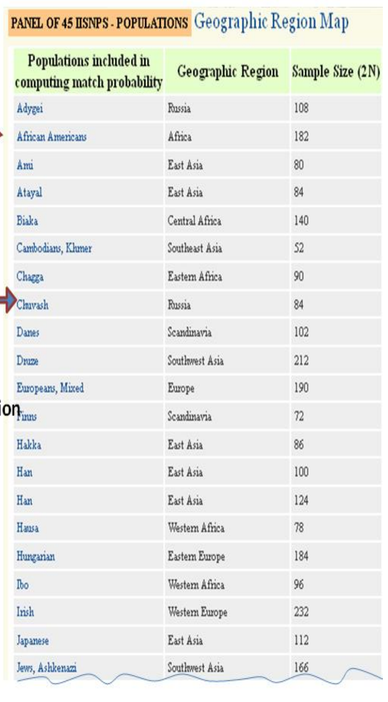
After clicking on the **GO** button to enter an IISNP Set, several options are possible. Each has a link to the list of the SNPs in the panel. Within that **SNP Set** list each rs number is an active link to the dbSNP record for that SNP. The **Populations** button provides the list of populations for which comparable calculations can be made. This is the set of populations for which all SNPs in the set have allele frequency data. Note, within the **SNP Set** in ALFRED additional populations may have data for some, but not all populations; those populations are not included in the calculations. Each population name in this SNP Set list within FROG is an active link to information on the population stored within ALFRED; that page will open in a new browser window. Example options are also accessible using **Ex 1** or similar buttons. These are screen shots to provide examples, but seem to load slowly—we are working on that.

More important is **Data Entry** that opens the ability to specify an individual multi-site genotype and then calculate the probability of that genotype in each of the populations. The genotype is entered by simply clicking on the radio button for the genotype at each SNP. Note, it is not necessary to click on the "NN" for missing data. At the bottom of the list are three buttons: **Set all unselected to unknown**, **Print Format** and **Compile** The **Print Format** will generate a condensed version of the input data that can be printed as a permanent record of the input data. The **Compile** will initiate calculation and display the results. If there are SNPs with no selection, a warning will be sent and the option exists to examine which SNPs have no entry and to either enter a genotype or use the **Set all unselected to unknown** to fill those with "NN". Afterward, it is necessary to click on **Compile** again.

There are also buttons with **population names** for example **Pima Mexican**, **Korean** that will open a pre-entered data entry page for one individual from the specified population. Those should be tried before experimenting by entering a new genotype profile of an unknown or a forensic case.



Link to Population page in ALFRED



Data input and output screen for IISNPs