KinVis: Package Documentation

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Introduction To KinVis

`KinVis` is a visual analytic tool for analyzing and visualizing kinship in Genome Wide Association Studies (GWAS).

`KinVis` is entirely built in R and Shiny, and provides users with a way of importing GWAS data, and then visualizing kinship on inter- and intra-population levels.

This is an early version of `KinVis` (version 1.0.0), and we are aware of a number of bugs, as well as possible improvements that can be made to improve functionality and usability. We will be working on these over the coming 1-2 months.

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The Application

`KinVis` is a Shiny application, and therefore consists of two main files - `server.R` and `ui.R` - as well as a numerous helper functions.

Manual Download

To set up the application, download the package, unpack the download, and run `install("KinVis")` from the parent directory of the package. Please note that `KinVis` requires several external packages, and these may have to be downloaded and installed as part of the installation process.

To attach the package, run `library(KinVis)`. This should add the package to the search path, and allowing it to be run.

To run the application, please run `runKinVis("DataPath")`, where `"DataPath"` is the absolute path to the folder from which the user will be loading the data. Within the application, the user will be prompted to navigate once again to this folder, where the user can select the relevant populations to import.

Once the command to run the application has been executed, it may take a few seconds to attach the required packages. After this, the application will load.

Using install_github()

Alternatively, users may download the package using the `install_github()` command, available through Hadley Wickham's `devtools` package (download `devtools` by running `install.packages("devtools")`. To do this, simply run:

`install_github("arun96/KinVisPackage", subdir="KinVis")`

This will download the package from Github, as well as any necessary packages. Once this is completed, attach the package by running `library(KinVis)`.

Users may then run the package as specified in the section above.

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Overview of Functionality

File Inputs and Ouputs

`KinVis` allows users to input three types of files, based on the process that users want to use.

Note: Download functionality only works when KinVis is run in a browser, and not the RStudio Viewer. The Viewer does not have this functionality implemented. However, file uploads should work in both the viewer and in a browser.

Visualization

`KinVis` provides numerous visualizations, depending on the type of data being viewed, and the process being used to visualize the data.

In the Populations tab, `KinVis` displays three types of charts - MDS Plots, Bar Plots and Box Plots. An MDS plot is displayed for all the six processes, a bar plot is generated for indep and pairwise, and a box plots is generated for indep.hIBS and pairwise.hIBS.

In the Individuals tab, the application displays a much wider range of charts. For the indep and pairwise processes, a population bar graph, heat map, and individuals bar graph is displayed. For the indep.hBN and pairwise.hBN processes, a dendrogram is displayed (with options for the user to select the clustering method, cut, and group). No individual graphs are displayed for the indep.hIBS or pairwise.hIBDS processes.

Input Data

Currently, users must specify the location of their data when loading the application. This is so that `KinVis` can read both the populations data (from the imported population), but also the individuals' data (within a selected population).

Therefore, users must use the `runKinVis()` function described above, and pass in the absolute path to their data folder.

Note: We are hoping to resolve this in the next version of KinVis, so that users no longer need to pass in the location to the data folder.

Groups

At the bottom of both the Populations and Individuals tabs, `KinVis` allows users to create groups using selected data. Within the application, groups can be created, named or deleted.

These groups can then be visualized (clicking on a group will select the populations/individuals within that group, and visualize them), or downloaded (into a simple `.csv` format).

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Other Functionality

In addition to the functionality above, `KinVis` also allows users to do the following:

1. Users are able to save their workspaces, so that they can continue their work later.

2. In addition to being able to load files, users are also able to load workspaces.

3. At the bottom of both tabs, users are able to take notes, which are saved and can be exported with the saved workspaces.

4. Users are able to export many of the visualizations as images. This is due to our usage of the `Plotly` plotting package. To do so, right-click on `Plotly` graphs, and save as image.

5. On the Individuals tab, users have the option of downloading Pairs data, as a `.csv` file.

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Walkthrough of Interface

The first tab of the application allows users to view kinship on a population level, whilst the second allows users to visualize the relationship between individuals of a given population.

The first tab looks like this:

The user may then import their data (or an R workspace), and then select the populations whose kinship they wish to view. The user must also select what process they wish to use in these visualizations. There are six options - for this walkthrough, we will use the first process (indep).

The application then plots these populations on an MDS Plot, as well as a bar graph that is ordered based on k-value.
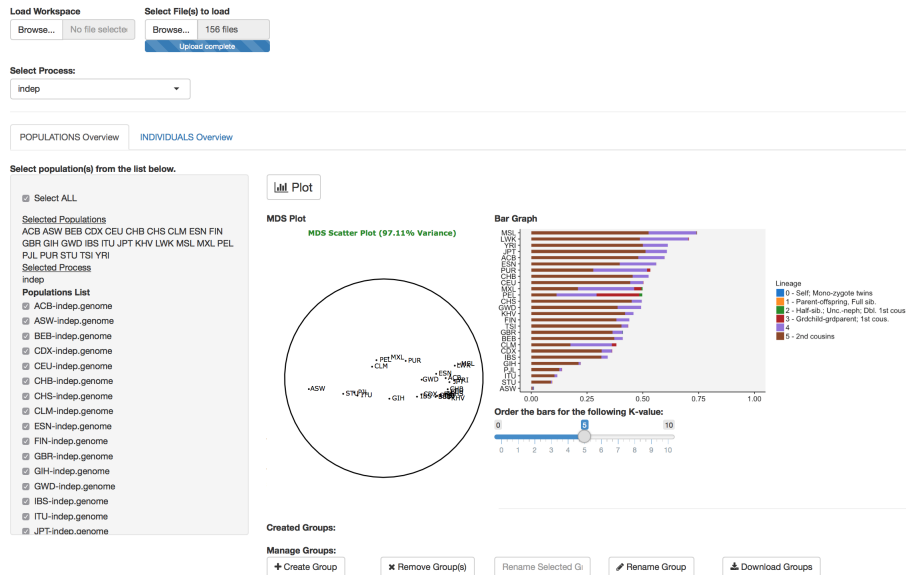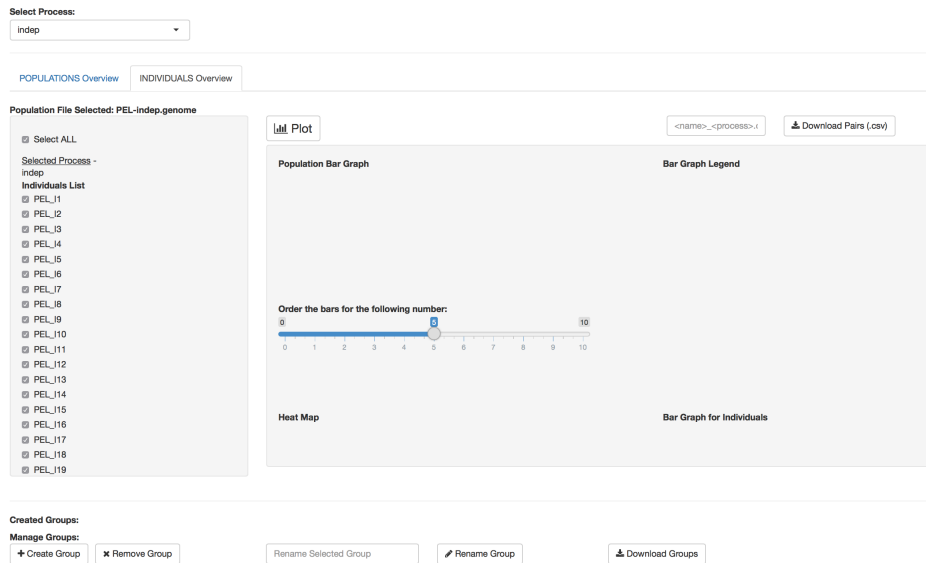
Users can then select a single population (either on the MDS Plot, or using the side bar), which can be further explored in the second tab.
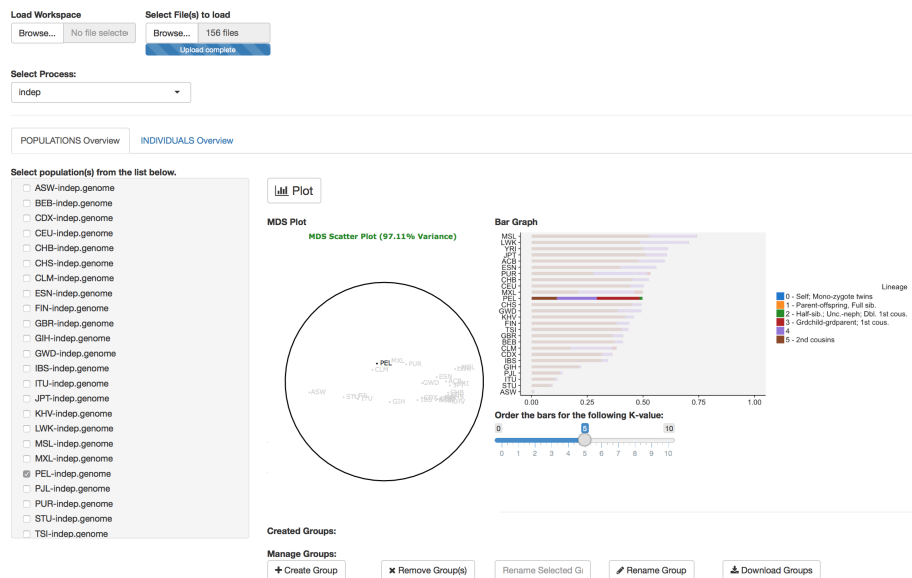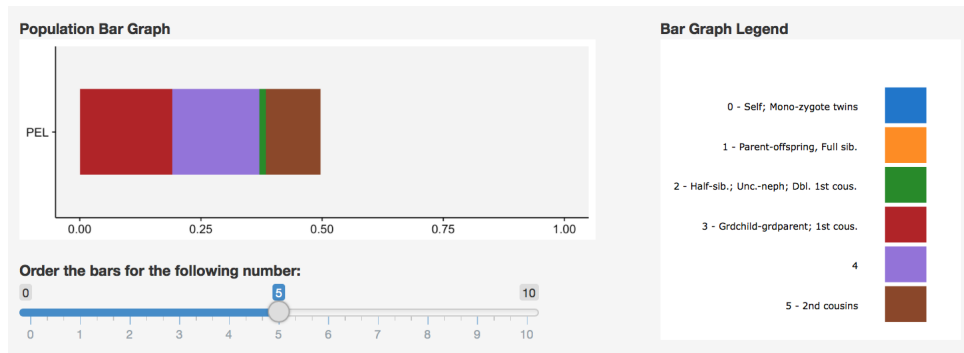

To switch to the second tab, simply select the relevant population, and then click on the second tab.
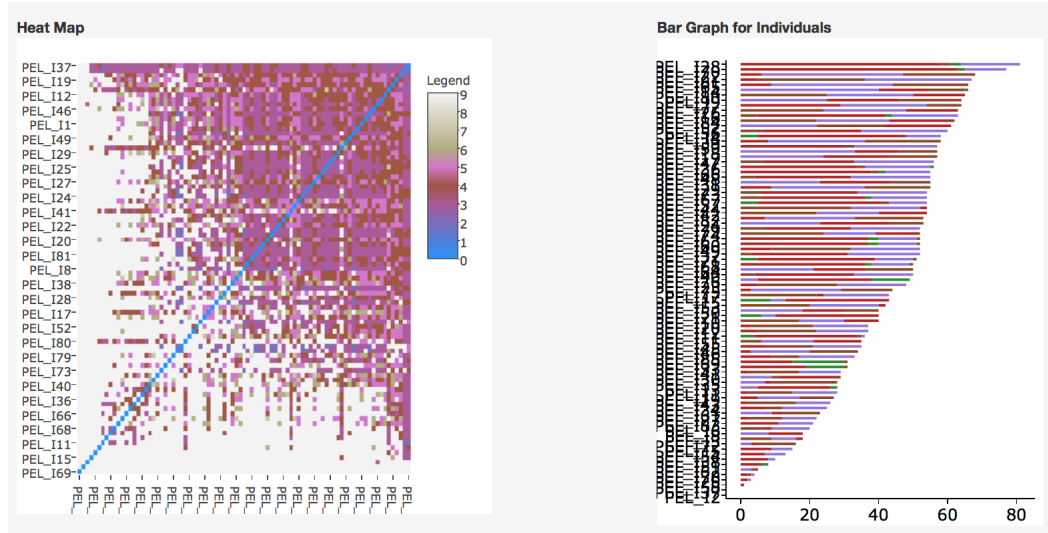
In this tab, users first see the breakdown of the population.

Scrolling down, they can see a heat map showing the kinship of every pair of individuals in the population, and a bar graph showing the kinship of each of the individuals in the population.

All the graphs on the second tab can be reordered based on the k-value.

Future Plans

In the next 1-2 months, we will be working towards fixing several bugs in KinVis, and releasing KinVis 1.1.0.