**1- Main Screen**

In this tutorial, we will familiarize ourselves with the KPDGUI main screen.

The main screen consists of 2 panels.

On the left is the visualization panel, which shows the network representation of our KPD pool.

Candidates in the network are represented by red nodes, their paired donors are represented by blue nodes next to their candidate. Non-directed donors are represented by purple nodes.

Matches between donors and potential recipients are represented by arrows between corresponding nodes.

On the right, we have lists of the full history of commands entered into the program, the pairings and non-directed donors, as well as each individual donor and candidate in the pool, all the matches in the pool, as well as all the possible exchanges and solutions found in match runs, which will be discussed in a later tutorial.

**2- Add Pairs and NDDs**

In this tutorial, we will learn how to add new pairings and non-directed donors to our KPD pool.

For this tutorial, we’re starting with a new, blank KPD.

To add a pair, click File->Add Donor-Candidate Pairing, or hit Ctrl+P from the keyboard. This will open up a dialog box where candidate information can be entered, namely name, age, blood type, PRA, along with other characteristics, including unacceptable HLA antigens.

Once all the desired information has been entered, click OK, and a second dialog box will be shown, where donor information can be entered similarly. Once the donor information is entered, click OK to add the pairing to the pool. Alternatively, if there are additional donors associated with this candidate, you can click the “OK and Add Additional Donor” button to enter information for the next donor.

The pair will be represented by a red candidate node, along with a blue node for each added donor. The information about the pair is also added to the corresponding lists on the right.

To add a new non-directed donor, click File->Add Non-Directed (Altruistic) Donor, or hit Ctrl+Shift+P from the keyboard, and a dialog box will open up where donor information can be entered once again. Once all the desired information has been entered, click OK, and the non-directed donor will be added to the pool, and represented in the visualization pane by a purple node.

In a later tutorial, we will show how to load multiple nodes at once, as well as saving and loading pools constructed through this program.

**3- Interaction with Visualization Panel**

In this tutorial, we will learn how to interact with the pairs and non-directed donors in our KPD pool.

For this tutorial, we’ve loaded the SmallKPDExample file, which is available in the software release.

There are a number of things you can do with individual donors and candidates in the visualization panel.

Click on a donor or candidate; the pairing will be selected and can then be moved around the screen at your leisure.

Right-clicking on a donor or candidate brings up a number of options:

The first is the ability to edit certain characteristics of any of the selected donors or candidate.

Clicking edit will bring up a dialog box with all of the donor or candidate information that can be updated. For example, we can make it so that a given donor or candidate is not included in future match runs that are performed.

Click Ok to accept the changes. Notice here that now the donor we have edited to not be included in future match runs is greyed out.

You can also add an additional donor to a pairing by clicking Add Additional Donor.

Notice the pairing now has an additional donor node attached.

By selecting a group of pairs or non-directed donors, you can move the entire group around the screen, and you can also cluster the selected pairs and non-directed donors into a circle.

Finally double-clicking matches brings up information about the match. You can also edit the match to, say, exclude it from future match runs, or add your own score value and success probability to be assigned during match runs.

**4- Display Settings**

In this tutorial, we will go over some of the display settings available for your KPD.

In this tutorial, we’re using the LargeKPDExample file, which is available in the software release.

The first thing one should know how to do is to zoom in and out of the pool. Simply click on the magnifying glasses in the toolbar to zoom in and zoom out. You can also use the slider, or you can hit Ctrl+= or Ctrl+- on the keyboard.

You’ll notice now that there are no matches being shown in this KPD pool. To change this, simply click the display menu, and choose from one of the many options available. Currently we have it set so that we show all matches amongst all selected pairings and non-directed donors. This can be changed to show all matches, all compatible donors and recipients for the selected matches, or you can show no matches at all.

How about we take a look at what happens when we display all compatibilities. Perhaps if we remove some of the pairings and non-directed donors from view, things will get a little easier to see.

Let’s say we want to remove pairs without any matches, or pairs that aren’t involved in any previously found solutions from view. Simply click Display->Node Display Settings…, or Ctrl+D on the keyboard, and we’ll get to choose which pairings we want to see in the visualization pane.

For example, if match runs have been run previously, we can choose to display only pairings and non-directed donors that are found in transplant arrangements or in solutions.

Perhaps we don’t want to see pairs that are being excluded from match runs, we can remove these by selecting Pair Subset. We can also remove pairs that have no matches, or that do not meet a minimum or maximum PRA threshold.

We can also condense pairings into single nodes for easier viewing. Let’s do that here.

Once the desired node display settings have been chosen, click OK, and pairings and non-directed donors will be added or removed from view accordingly. Notice now that pairings are represented as single red nodes. We can see now that this KPD pool is slightly easier to manage.

**5- Match Runs**

In this tutorial, we will learn how to perform match runs in order to find the optimal selections within your KPD.

For this tutorial, we’ve loaded the LargeKPDExample file, which is available in the software release.

Before performing a match run, you should set the parameters. Go to the Match Run menu, click Set Parameters, this will bring up a number of options available for the match run.

Start by choosing the optimization scheme, either Cycles and Chains, which will look for the best solution consisting of simple cycles and chains, or Cycles and Chains with Fallbacks, which further takes into account the ability to fallback to any sub-cycle or sub-chain in the case of donor, candidate or match failure, or Locally Relevant Subgraphs, which looks for the best solution of more general subgraphs of the KPD network, also accounting for fallback options. We’ll choose locally relevant subgraphs for this tutorial.

Next option is how we want to interpret utility, either in terms of total number of transplants, estimated 5-year survival based on donor and recipient characteristics, similarly for 10-year survival, total number of difficult-to-match pairs, or total assigned scores of the transplants involved. We’ll simply maximize in terms of number of transplants here.

You can set the maximum cycle and chain length, and the maximum subgraph size for locally relevant subgraphs. Then there are a number of numerical parameters that can be adjusted, such as the advantage to add to high PRA candidates, as well as the number of solutions you want to produce, as well as whether you want to estimate or calculate exactly the expected value to be assigned for fallback options.

Additional policy options can be found in the additional options tab if desired.

Once these parameters are set, click OK, and now we’re ready to perform our match run.

Either click the green arrow in the toolbar, or in the Match Run menu, click Perform Match Run, or hit Ctrl+R on the keyboard.

The solutions will automatically be populated into the solutions tab in the right panel of the screen, along with any previously found solutions.

Clicking any of these solutions will display the relevant nodes and matches in the visualization panel.

Right-clicking the solution gives the options to cluster the solution for easier viewing, or to see more detailed information about the solution.

Notice that in this case, since we have a fallback solution, the arrows are not restricted to simple cycles or chains.

**6- Saving and Loading**

In this tutorial, we will learn how to load pairs into the program, and save and load our progress when working with KPDs.

For this tutorial, we will begin with a blank KPD, and start by loading our KPDPairInformation.csv file, which is available in the software release.

Taking a look at that file for a moment, you can see that each row represents the information about a donor candidate pairing or a non-directed donor.

It contains entries such as the name, age, blood type for the donor as well as the transplant candidate, PRA information for the candidate, HLA information for both the donor and candidate, as well as some other characteristics.

This file is structured in such a way that it can be read in easily by the program. So feel free to add rows at your desire, or to come up with a totally separate file with the same headers, and enter the pairing information in the same order.

To load these pairs, click File->Load Pairings from File, or Ctrl+L from the keyboard. Then browse to that file in your system, click Open and then OK, and the pairs will now be loaded into the KPD, and be represented in the visualization panel.

To save this as a KPD file, click File->Save or Ctrl+S on the keyboard. Again, navigate to the folder where you want to save, rename your file, hit Save, and the KPD will now be saved in your system.

If you want to load a previously saved KPD file, we’ll click File->Open or Ctrl+O from the keyboard. Again, navigate to where your file is. You’ll notice the previous KPD file we had saved here. We’re going to load the LargeKPDExample file that we’ve been using in other tutorials. Click Open, and you’ll see that a new window pops up with the previously saved KPD program, with all of its saved information, including previous match runs.

**7- New Features**

In this tutorial, we’ll highlight some of the new aspects of this version of the KPDGUI platform that were not covered in previous tutorials.

For this tutorial, we’ve loaded the SmallKPDExample file, which is available in the software release.

In this version, matches take on different visual characteristics based on certain properties. If an O donor matches to a non-O candidate for example, the match is shown in yellow. Matches that have been excluded from match runs, or that are no longer compatible after editing donor or candidate characteristics of a previously compatible match, are now shown by a broken red arrow.

Display options, to either suppress these matches from view, or simply to remove this highlighting, can be accessed in the Display menu.

By adding a default donor-candidate pair, we’ll be able to see that donor nodes will now appear in green if they are found to be compatible with their paired candidate.

Finally, we can take a deeper look at the estimated survival probabilities assigned to individual matches. Click Tools->Survival Calculator to open the Survival Calculator screen. Here, you can manipulate the donor and candidate information of a hypothetical match and see the effect on the estimated survival probability.

You can also copy donor or candidate information from the pool and see the effect on estimated survival probability as well.