Importing Gel* projects to SeqMerge in GCG 11.0

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Background:

GCG 10.x users are familiar with the Gel* utilities (gelstart, gelassemble, geldisassemble, gelmerge, gelenter,...) in order to perform essential Fragment Assembly operations. Due to a bug with some internal libraries in version GCG 11.0, these utilities are currently not functioning with GCG 11.0. The GCG manual states that support for these utilities has been dropped by Release 11.0, but that does not mean that the utilities should not function at all. The software manufacturer Accelrys will address the issue of fixing the software error, so they are usable with a patch that is going to be released soon. Depending on customer feedback they might re-introduce support for them.

In the meantime, however, users could work with a much more refined application designed to replace the Gel* utilities. The application is called SeqMerge and represents the new evolved Fragment Assembly System introduced by Accelrys. We recommend that all users should switch to this utility, despite the fact that the Gel* utilities will be repaired. SeqMerge provides more suitable utilities to visualize and edit Fragment Assembly projects. This raises the question of how to access older project data (created by the Gel* programs) by SeqMerge. The remainder of this document describes how to perform this migration task.

Workstation Requirements for running SeqMerge:

SeqMerge relies on the X-Windows protocol, in order to function properly. Before following the instructions to launch SeqMerge, make sure that you have understood how to configure an SSH browser and an X-Windows server to perform 'X-Windows tuneling'. If you have run other graphical tools (SeqLab for example), your environment should be configured properly. If you have not run graphical tools but you mainly call command line programs, chances are that you won't have the proper configuration settings in place. EMBnet Norway has on line guide that explains how to achieve the desired configuration for Windows XP workstations in the following web page:

http://www.biotek.uio.no/EMBNET/SSHANDXtut.htm

Similar approaches are applicable for LINUX/UNIX and MACOSX workstations. If in doubt, send an email to admin@embnet.uio.no .

Launching SeqMerge and importing Gel* project data:
In order to launch 'SeqMerge', make sure that your X-Server emulation software is enabled and at the shell prompt type:
seqmerge &

and then hit enter. If your X settings are correct, you should enter the SeqMerge main screen which looks like Figure 1 below. The large white space area contains for me a couple of projects I am already working on, but if you launch it for the same time, it will be empty, so it will show no entries and no defined contigs or active projects.
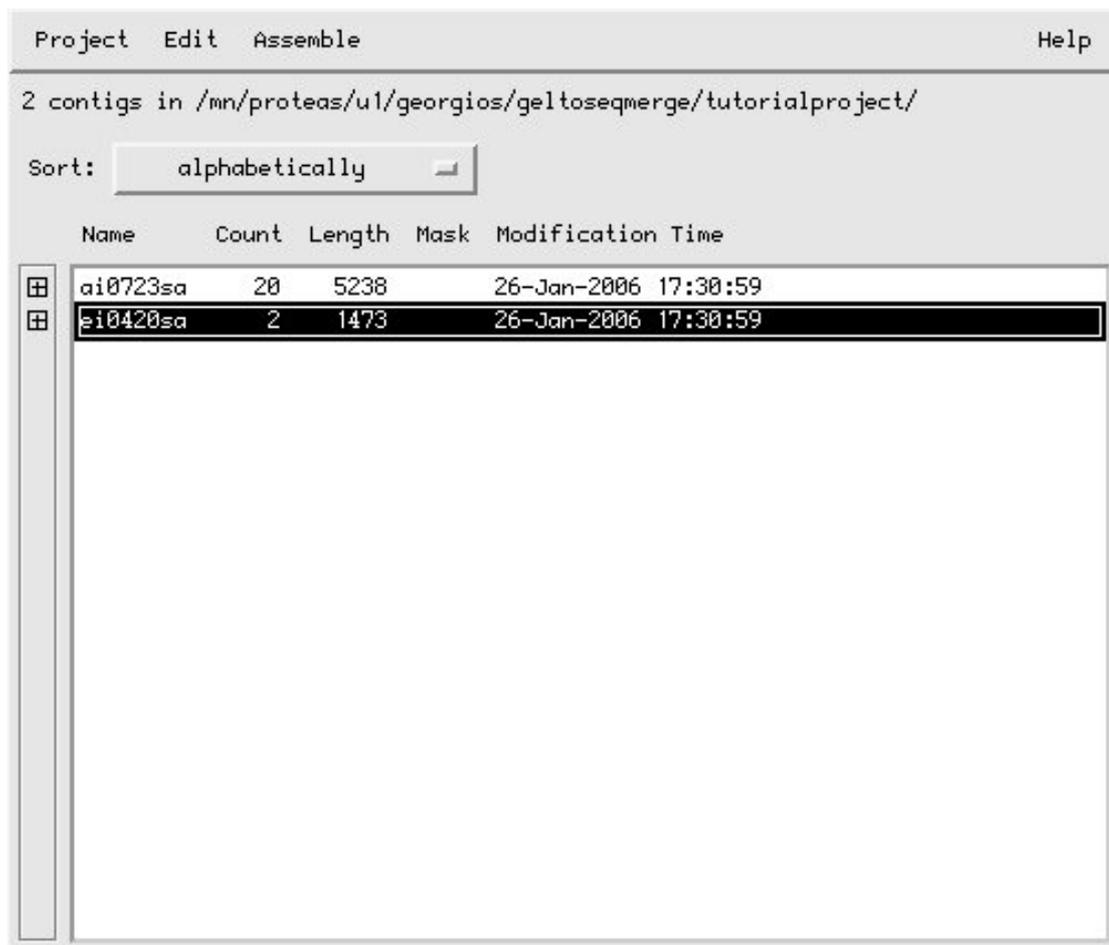
Figure 1: The SeqMerge main screen

Then, locate an old Gel* project (find the directory where the files reside) and **make a copy of it in another location in your home area**. That way you can try your data with the new SeqMerge environment and maintain the old project file format (SeqMerge will need to create a new directory structure). For example, if my original directory for the Gel* project data was ~/project1, I would type from the top level of my home directory the following:

cp -r project1 newproj1

This creates a replica of the old 'project1' directory with a new name 'newproj1'. We are now ready to import the old data (in their new location). From the main screen (see Figure 1), go to the top menu bar and from the '*Project*' menu select (left click) the second option from the top 'Open Project'. You will then see the 'Open Project' window appearing (Figure 2). Use the 'Navigate Field area to locate your existing projects and then point (on the right) to your new project directory 'newproject1' and click OK.


Figure 2: Open Project SeqMerge window

After clicking and if you copied a valid old Gel* project directory, the SeqMerge application should automatically recognize the old Fragment Assembly System (FAS) format 10 and give you the option of converting to the new FAS system of SeqMerge, as shown in Figure 3. Click on 'Yes' and then the system will generate the new FAS project directory structure. At that point, the main screen should contain older contig definitions that you can rearrange and you can assemble graphically, as shown in Figure 4.
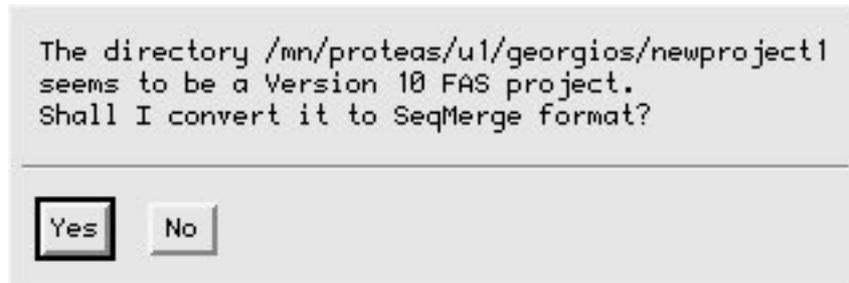
Figure 3: Gel FAS to SeqMerge FAS conversion prompt*
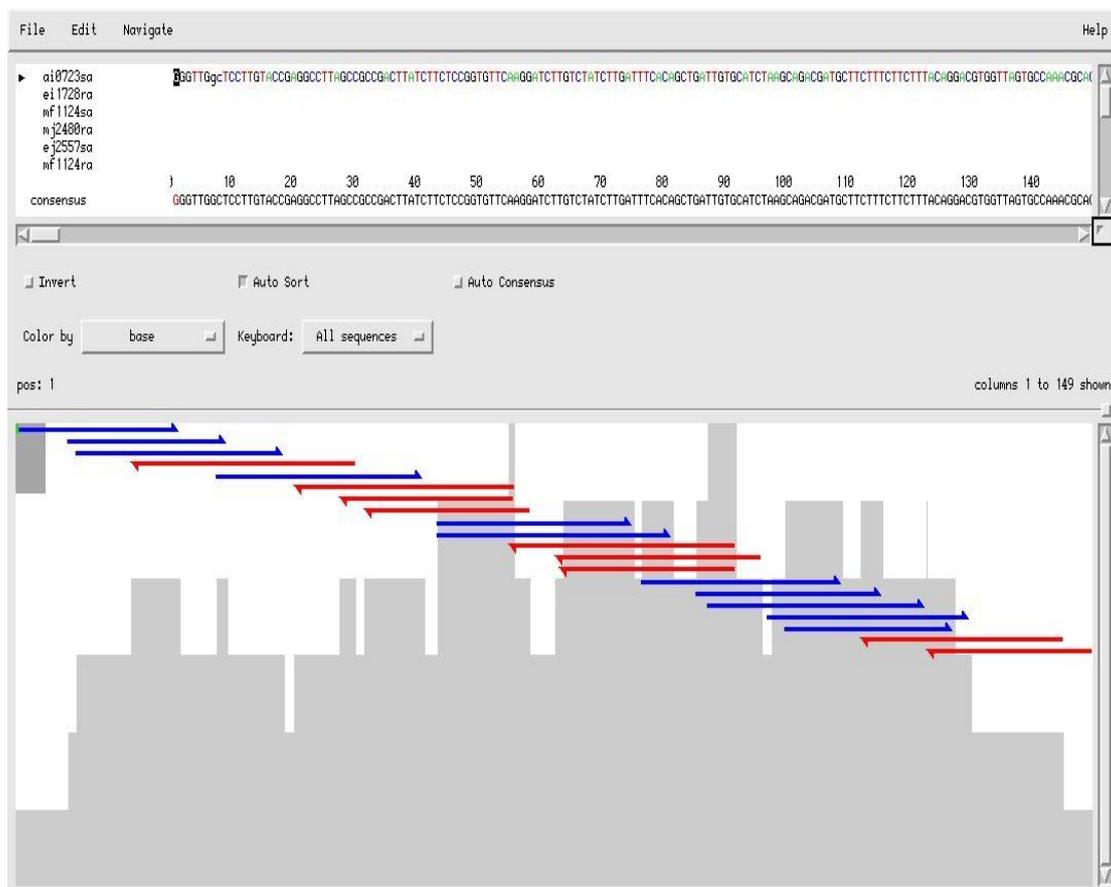
Figure 4: SeqMerge FAS workspace sample