Overview: Landmark

Landmarking Program to Create/Edit Landmark Points Between Samples

http://open2dprot.sourceforge.net/Landmark

Revised: 04-29-2005, P. Lemkin, G. Thornwall

Introduction

- Spot pairing between spots from two samples may require a small set of corresponding spots known to be the same in the two samples.

- Some pairing programs require landmark data.

- Set of landmark points must be created prior to spot pairing and are stored in a landmark database.

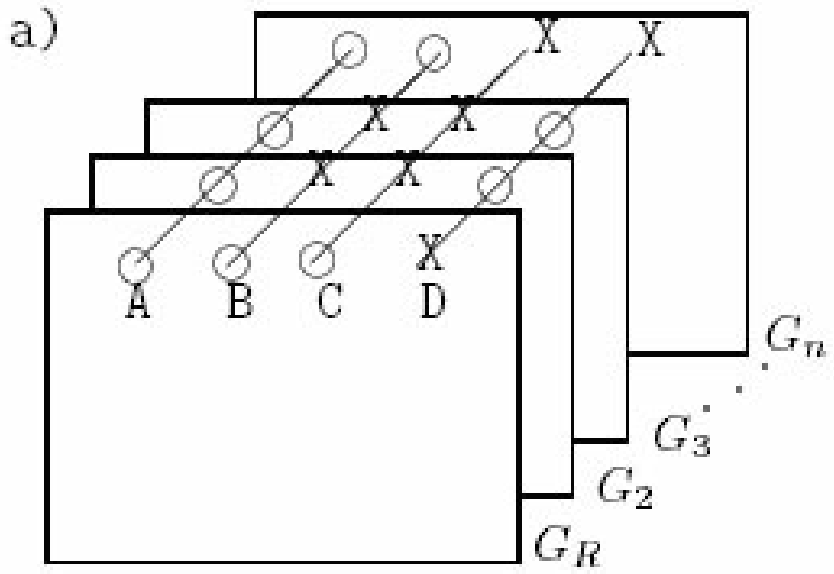
Introduction (cont.)

- Landmark program is a step [3] pipeline module used for creating and editing a set of landmarks between a reference sample and sample.

- It uses a graphical user interface to let the user interactively assign corresponding spots.

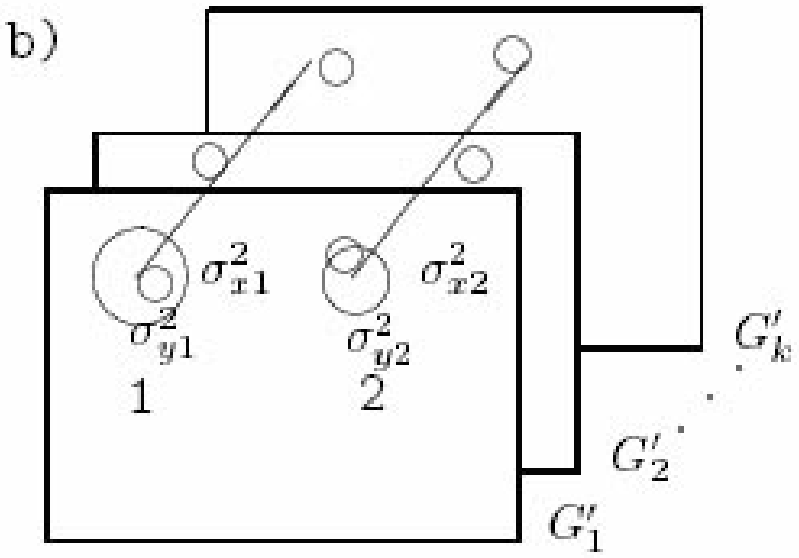
- It saves the landmark set data for a pair of samples in an XML landmark database used by the other Open2Dprot pipeline modules.

Composite Samples Database (CSD) Paradigm



Proteomic composite samples database (CSD) consisting of a set of n samples G_1, G_2, …,G_n with representative sample $G_r = G_1$

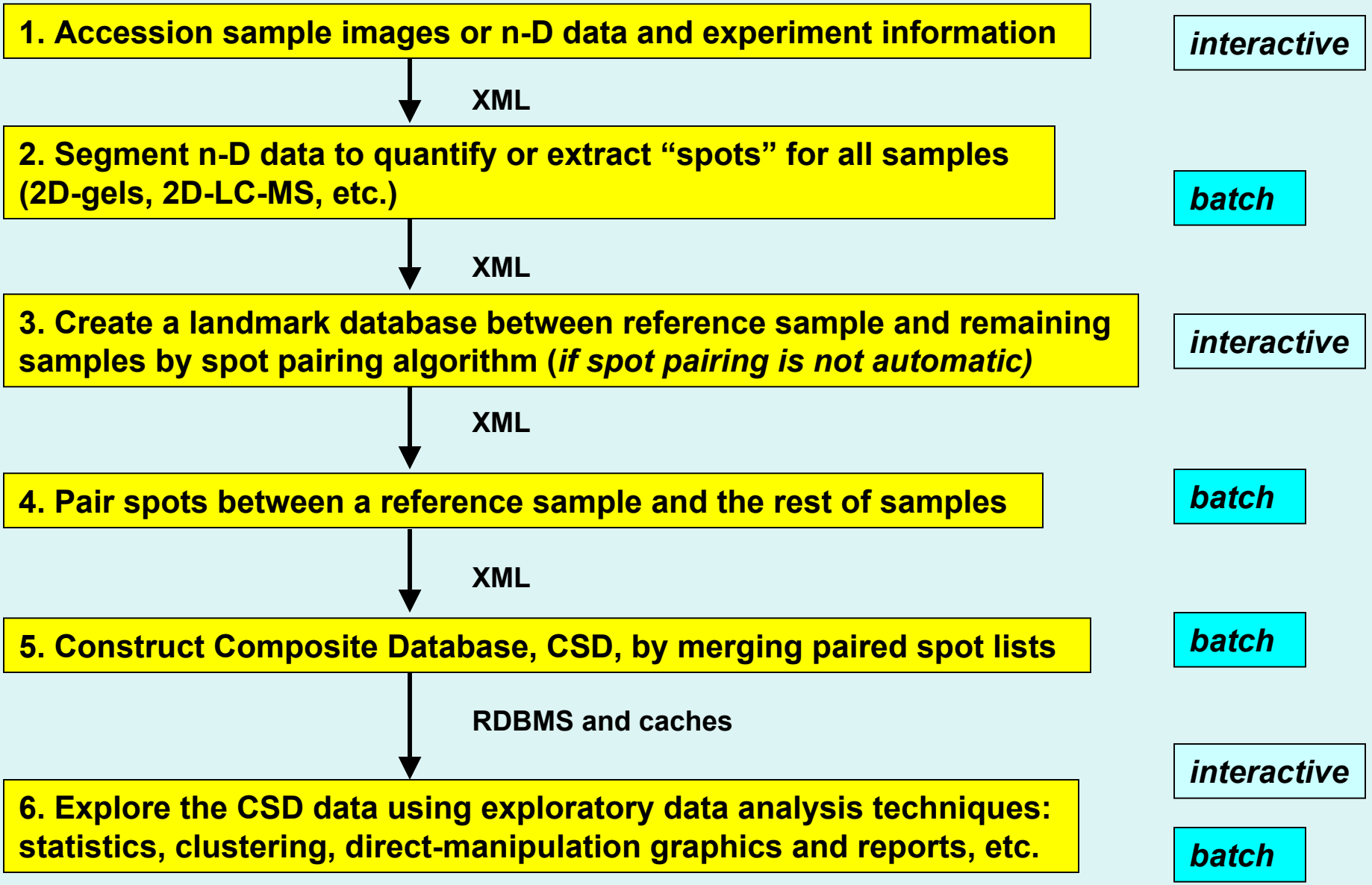
Expression profiles A,B,C, ...



A canonical sample database is a statistical representation of the CSD spot geometry and quantification that could be used for data mining

in Lemkin *et al.*, *Computers Biomedical Research*, 1981

Basic Open n-D Analysis Pipeline



Initial Open n-D Data-Mining Tools

- Accession n-D sample images or n-D data and experiment data
- Quantify 'spots' from sample images or peptide clusters
- Pair spots between samples and a reference sample
- Construct composite sample database for exploratory data analysis
- Manage subsets of proteins in the database
- Manage replicate samples and condition sets of samples
- Analyze expression profiles for multiple conditions
- Data-filter protein sets by statistics, clustering, set membership
- Direct-manipulation of data in graphics, spreadsheets
- Integrate R language statistical, clustering, classifiers, class prediction, and other methods
- Integrate access to Internet proteomic/genomic/function data servers for user-specified protein sets

Open2Dprot Pipeline Subprojects

Open2Dprot - Subprojects - Netscape

File Edit View Go Bookmarks Tools Window Help

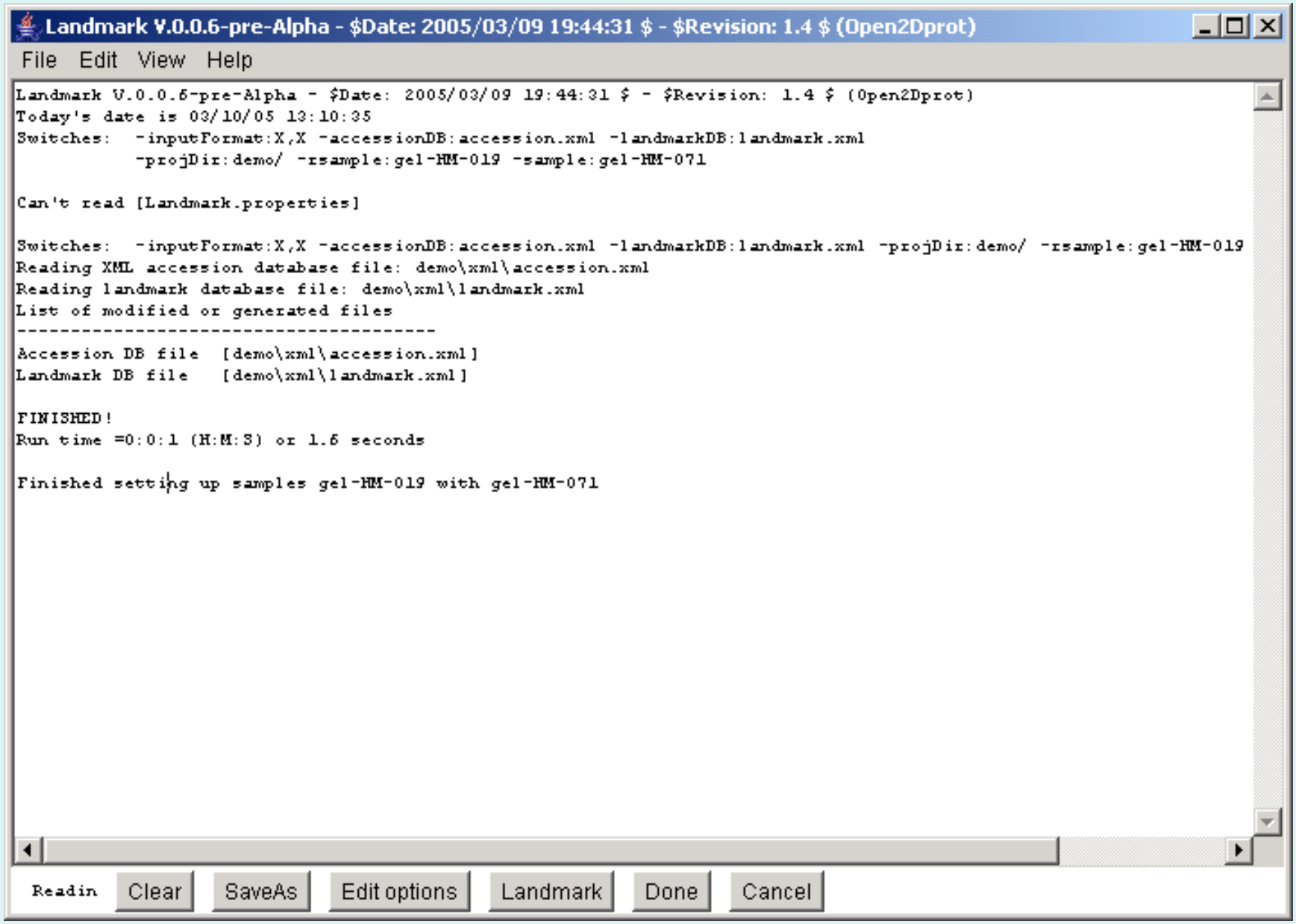
Open2Dprot pipeline subprojects

Open2Dprot consists of a series of coordinated Open2Dprot pipeline processing modules. The scheduler program, also called Open2Dprot, will schedule and run the modules in the pipeline after doing a data-dependency analysis. By using XML as the "glue" between modules, it is possible to substitute alternate modules at the various pipeline steps. As pipeline modules and alternate modules become available, they will be added to this table. *We encourage the donation of alternate pipeline processing modules which will be added to this table.*

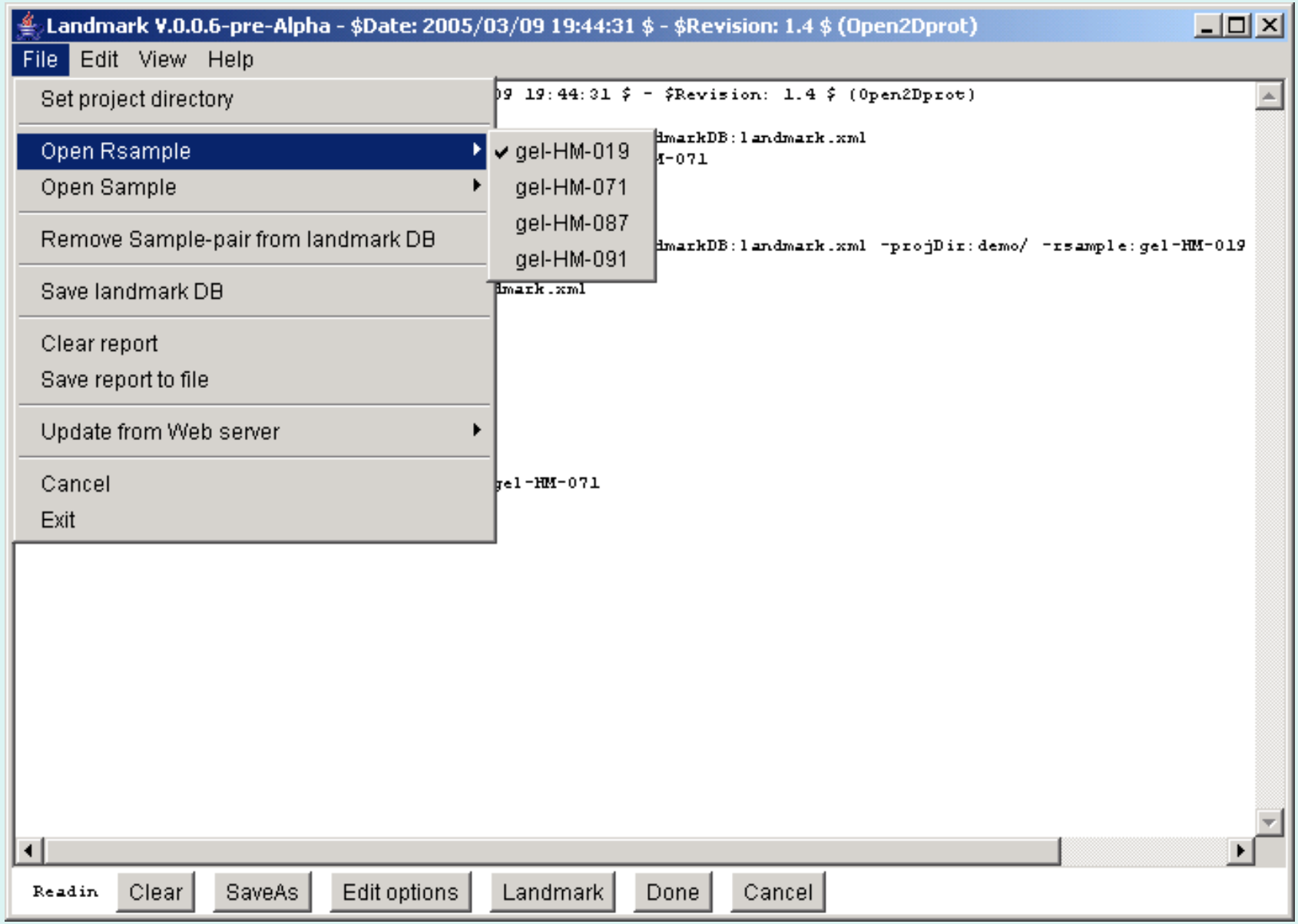
We will be using a common O2Plib library in the Open2Dprot pipeline modules. This will help ensure that they use the same conventions, data structures and XML data interchange formats.

Subproject Home	Download	Documentation	Overview (PDF)	PDF documents	Version	Revision history	Status	Pipeline step
Open2Dprot project	(see below)	Open2Dprot	Open2Dprot project	Open2Dprot project	Open2Dprot project	Open2Dprot project	Open2Dprot *design prototype*	-
Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot *pre-alpha* program	[scheduler]
Accession	Accession	Accession	Accession	Accession	Accession	Accession	Accession *pre-alpha*	[1]
Seq2Dgel	Seq2Dgel	Seq2Dgel	Seq2Dgel	Seq2Dgel	Seq2Dgel	Seq2Dgel	Seq2Dgel *pre-alpha*	[2]
Landmark	Landmark	Landmark	Landmark	Landmark	Landmark	Landmark	Landmark *pre-alpha*	[3]
CmpSpots	CmpSpots	CmpSpots	CmpSpots	CmpSpots	CmpSpots	CmpSpots	CmpSpots *pre-alpha*	[4]
BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD *design prototype*	[5]
CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer *design prototype*	[6]
O2Plib	O2Plib.jar	O2Plib	O2Plib	O2Plib	O2Plib	O2Plib	O2Plib *pre-alpha*	--common--

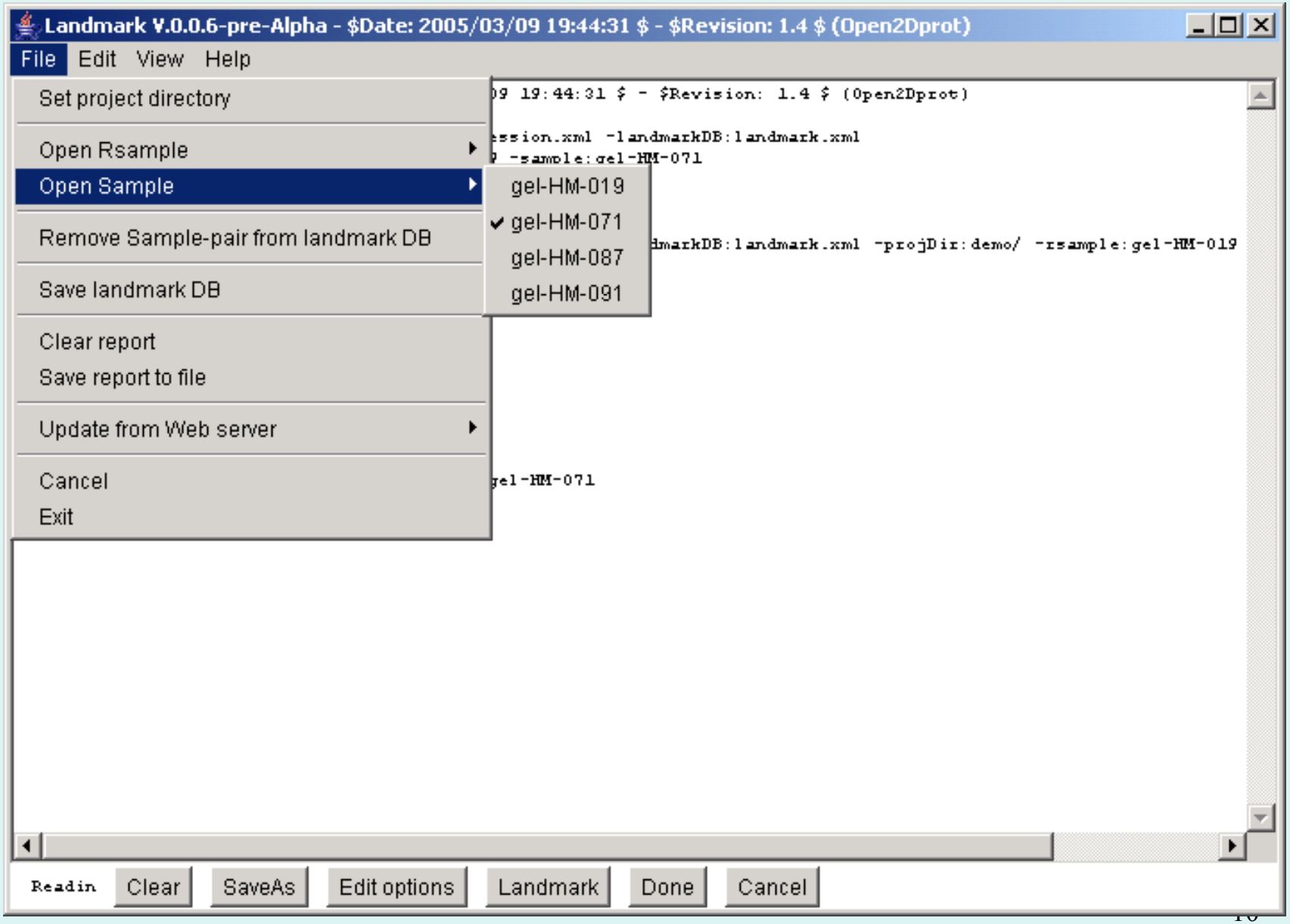
Main Window


Landmark V.0.0.6-pre-Alpha - $Date: 2005/03/09 19:44:31 $ - $Revision: 1.4 $ (Open2Dprot)
File Edit View Help
Landmark V.0.0.6-pre-Alpha - $Date: 2005/03/09 19:44:31 $ - $Revision: 1.4 $ (Open2Dprot)
Today's date is 03/10/05 13:10:35
Switches: -inputFormat:X,X -accessionDB:accession.xml -landmarkDB:landmark.xml
-projDir:demo/ -rsample:gel-HM-019 -sample:gel-HM-071
Can't read [Landmark.properties]
Switches: -inputFormat:X,X -accessionDB:accession.xml -landmarkDB:landmark.xml -projDir:demo/ -rsample:gel-HM-019
Reading XML accession database file: demo\xml\accession.xml
Reading landmark database file: demo\xml\landmark.xml
List of modified or generated files
Accession DB file [demo\xml\accession.xml]
Landmark DB file [demo\xml\landmark.xml]
FINISHED!
Run time =0:0:1 (H:M:S) or 1.6 seconds
Finished setting up samples gel-HM-019 with gel-HM-071
Readin
Clear
SaveAs
Edit options
Landmark
Done
Cancel

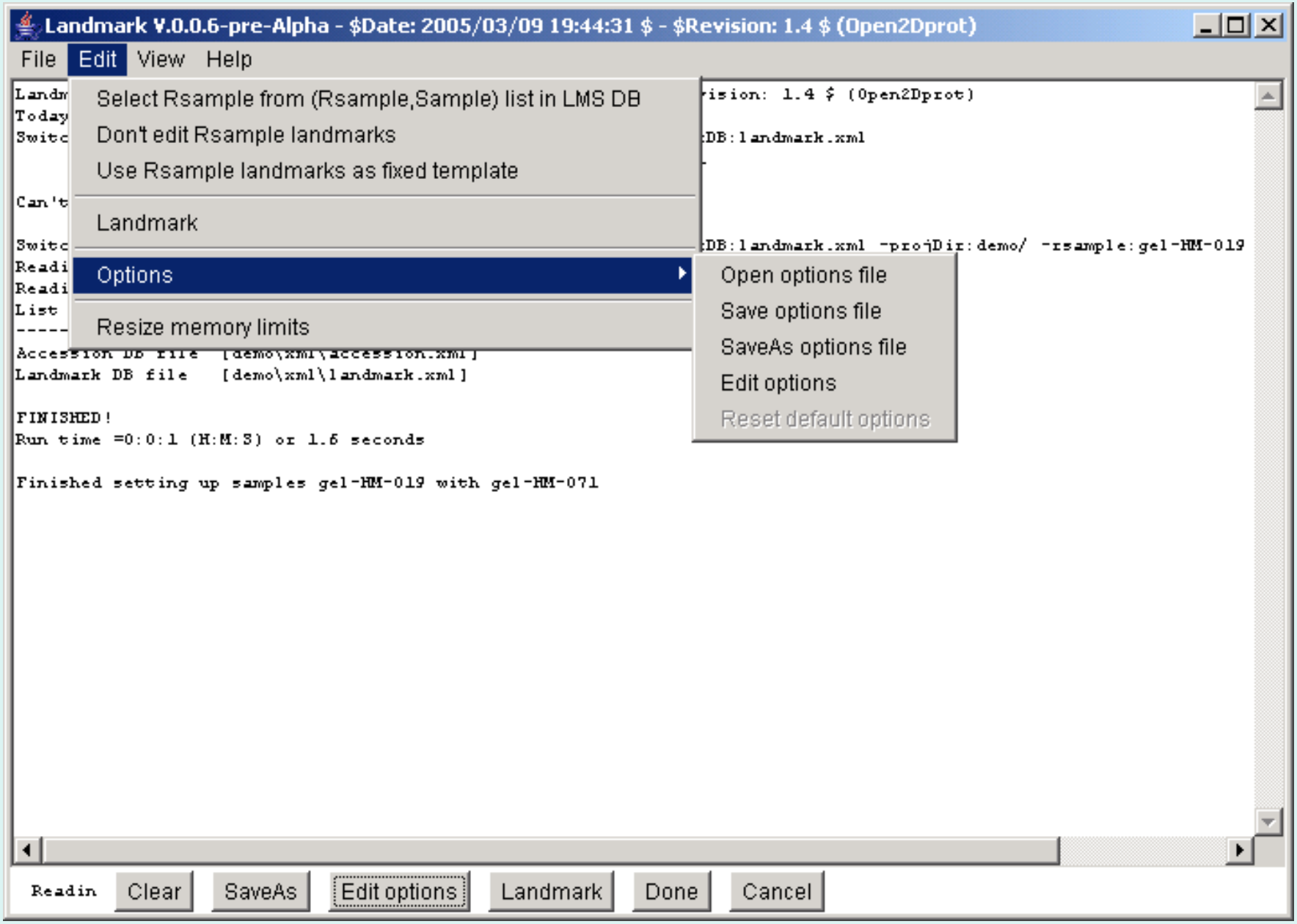
File Menu - Select Reference Sample



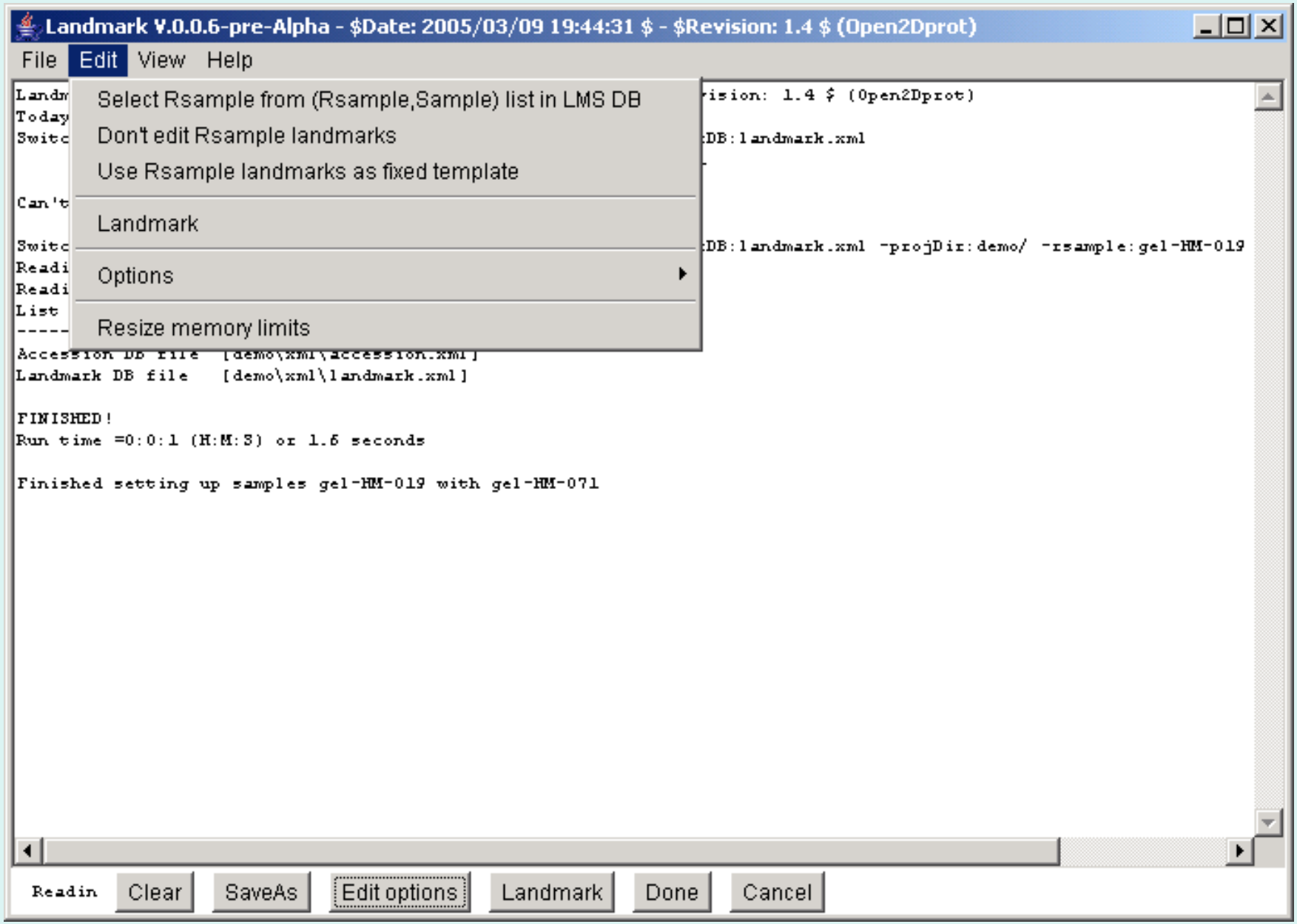
File Menu - Select Current Sample



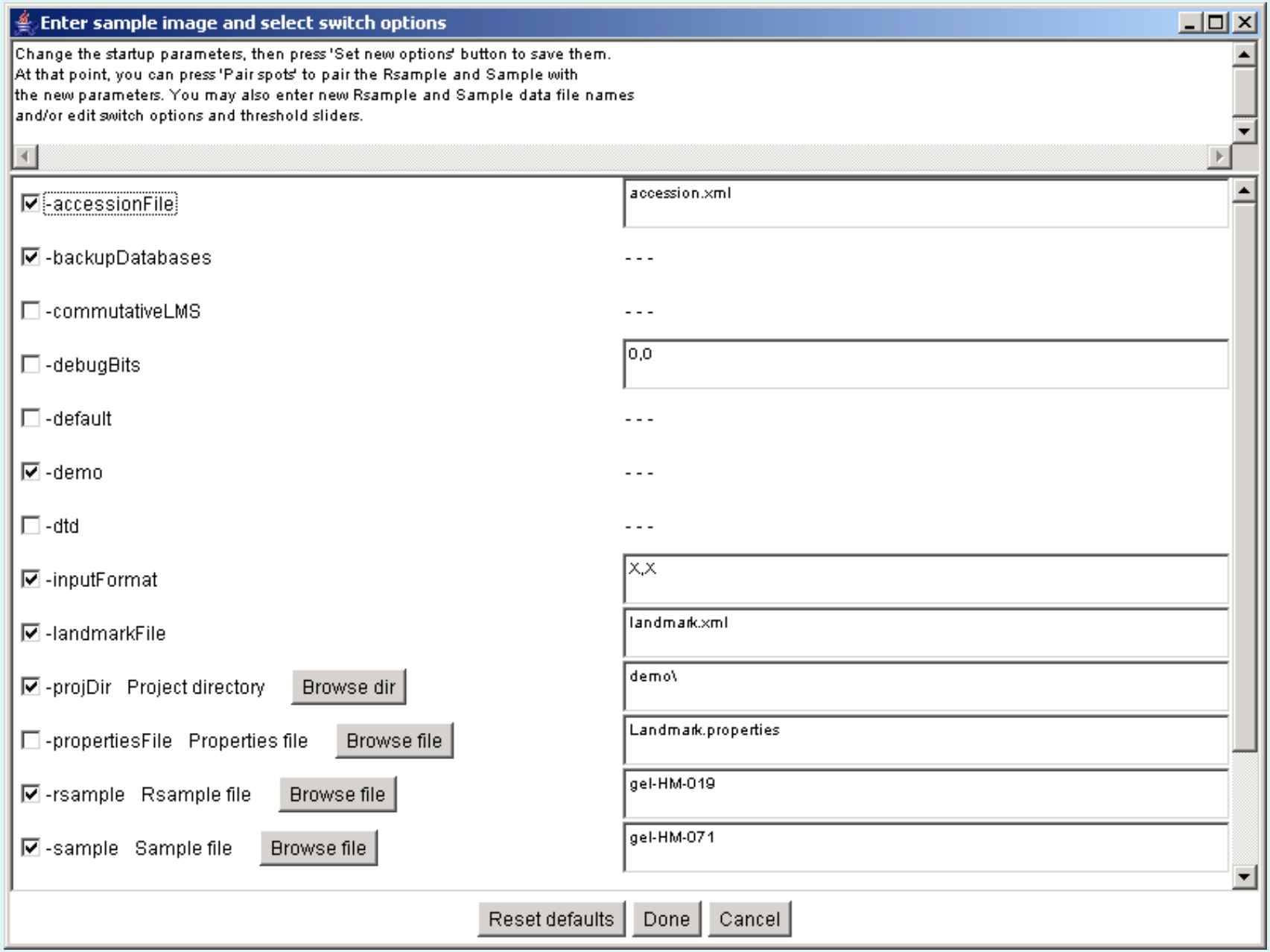
File Menu - Update From Web Server



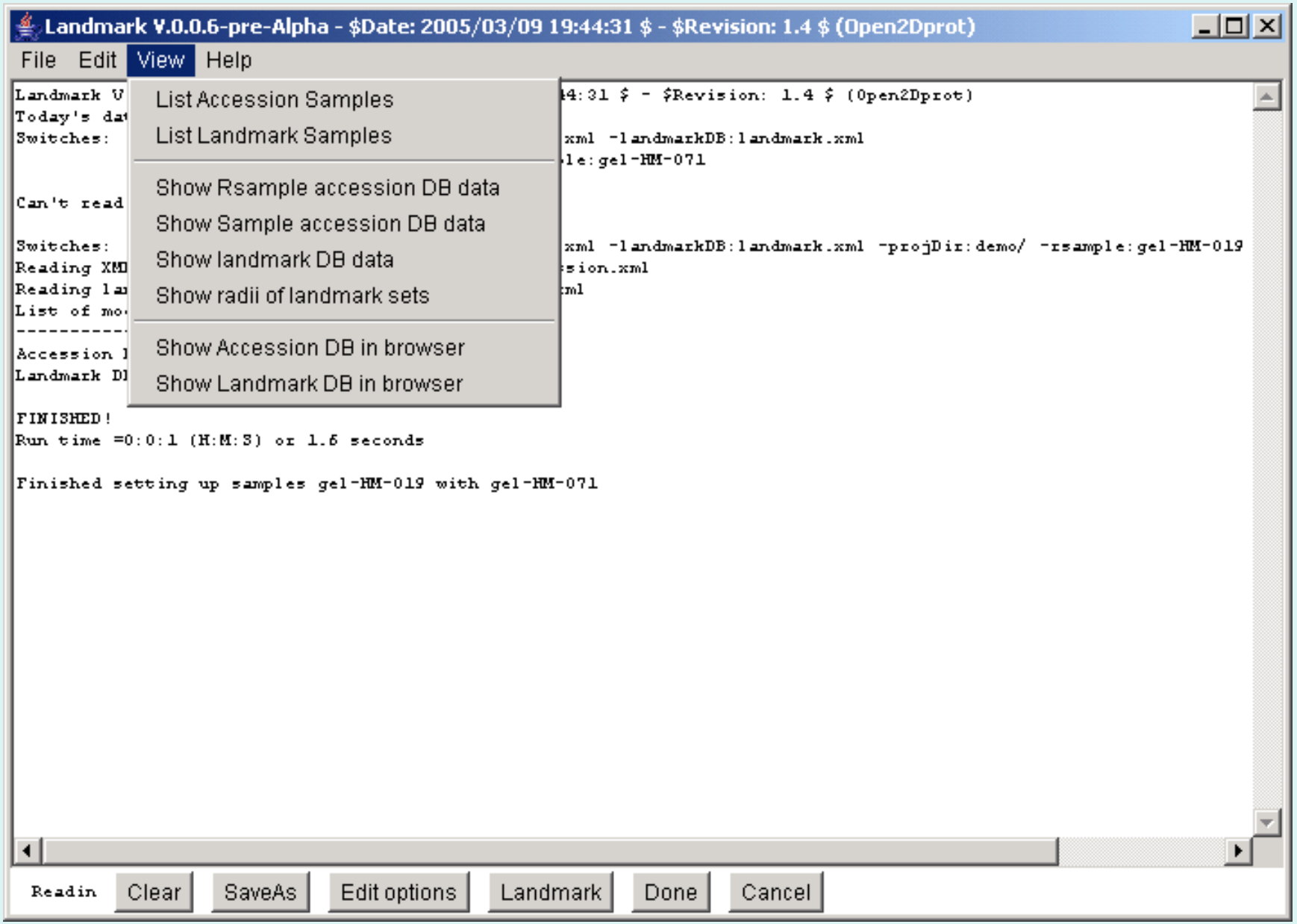
Edit Menu


Landmark V.0.0.6-pre-Alpha - $Date: 2005/03/09 19:44:31 $ - $Revision: 1.4 $ (Open2Dprot)
File
Edit
View
Help
Select Rsample from (Rsample,Sample) list in LMS DB
Don't edit Rsample landmarks
Use Rsample landmarks as fixed template
Landmark
Options
Resize memory limits
Accession DB file [demo\xml\accession.xml]
Landmark DB file [demo\xml\landmark.xml]
FINISHED!
Run time =0:0:1 (H:M:S) or 1.6 seconds
Finished setting up samples gel-HM-019 with gel-HM-071
Readin
Clear
SaveAs
Edit options
Landmark
Done
Cancel

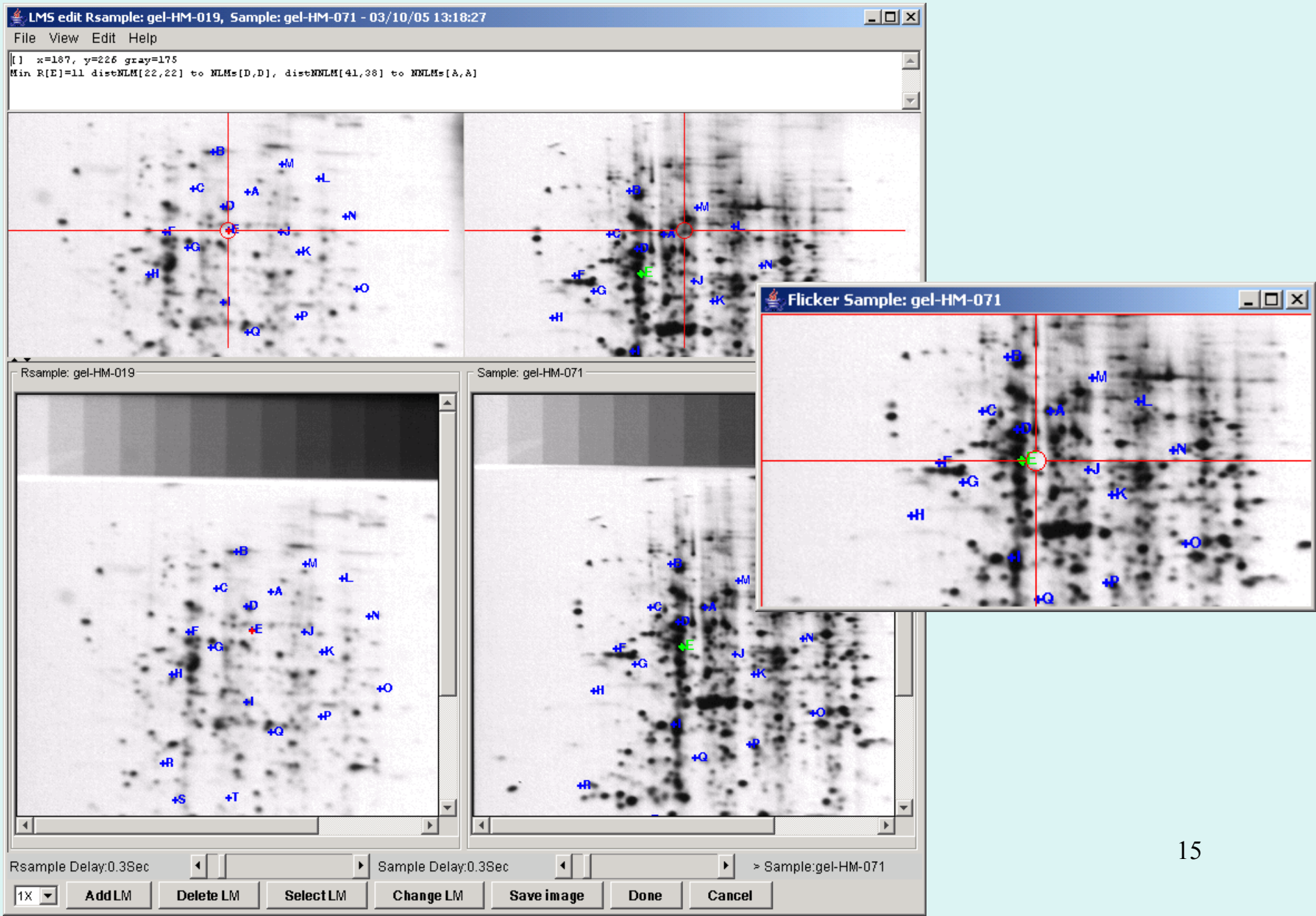
Edit Menu - command line options



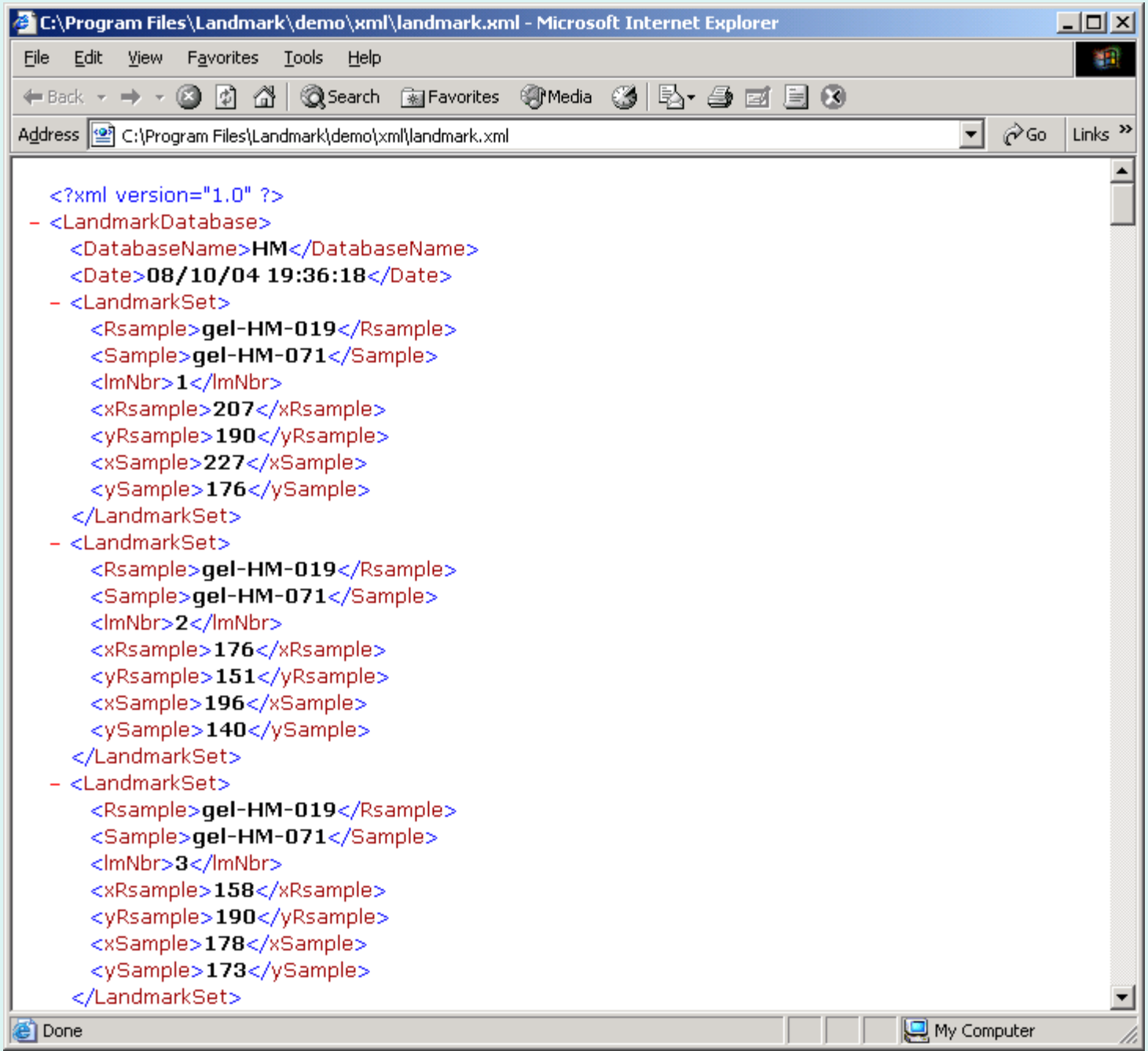
View Menu


Landmark V.0.0.6-pre-Alpha - $Date: 2005/03/09 19:44:31 $ - $Revision: 1.4 $ (Open2Dprot)
File
Edit
View
Help
List Accession Samples
List Landmark Samples
Show Rsample accession DB data
Show Sample accession DB data
Show landmark DB data
Show radii of landmark sets
Show Accession DB in browser
Show Landmark DB in browser
FINISHED!
Run time =0:0:1 (H:M:S) or 1.6 seconds
Finished setting up samples gel-HM-019 with gel-HM-071
Readin
Clear
SaveAs
Edit options
Landmark
Done
Cancel

Landmark popup window



Landmark XML DB in browser



Summary

- Landmark is a fully open-source landmark spot set editing program and is being developed at **http://open2dprot.sourceforge.net/**

- It uses a graphical user interface to let the user interactively assign corresponding spots.

- It saves the landmark set data for a pair of samples in an XML landmark database used by the other Open2Dprot pipeline modules.