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 4 Research, 1981

Basic Open n-D Analysis Pipeline



Initial Open n-D Data-Mining Tools

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

Open2Dprot Pipeline Subprojects

🔊 Open2Dprot - Subprojects - Netscape

<u>File E</u>dit <u>V</u>iew <u>G</u>o <u>B</u>ookmarks <u>T</u>ools <u>W</u>indow <u>H</u>elp

Open2Dprot pipeline subprojects

<u>Open2Dprot</u> consists of a series of coordinated <u>Open2Dprot pipeline processing modules</u>. 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 <u>O2Plib library</u> 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
<u>Open2Dprot</u> project	(see below)	Open2Dprot	<u>Open2Dprot</u> project	<u>Open2Dprot</u> project	<u>Open2Dprot</u> project	Open2Dprot project	Open2Dprot de <i>sign pr</i> ototype	-
Dpen2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot program	Open2Dprot <i>pr</i> e- <i>alpha</i> program	[scheduler]
ACE Accession	Accession	Accession	Accession	Accession	Accession	Accession	<u>Accession</u> pre-alpha	[1]
SG2 Seg2Dgel	<u>Seg2Dgel</u>	Seg2Dgel	<u>Seg2Dgel</u>	<u>Seg2Dgel</u>	<u>Seg2Dgel</u>	<u>Seg2Dgel</u>	<u>Seg2Dgel</u> pre-alpha	[2]
andmark	Landmark	Landmark	Landmark	Landmark	Landmark	Landmark	Landmark pre-alpha	[3]
CmpSpots	<u>CmpSpots</u>	<u>CmpSpots</u>	<u>CmpSpots</u>	<u>CmpSpots</u>	<u>CmpSpots</u>	<u>CmpSpots</u>	<u>CmpSpots</u> pre-alpha	[4]
BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD	BuildCSD de <i>sign pr</i> ototype	[5]
SDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer de <i>sigri pr</i> ototype	[6]
02Plib	<u>O2Plib.jar</u>	<u>O2Plib</u>	02Plib	<u>O2Plib</u>	<u>O2Plib</u>	<u>O2Plib</u>	<u>02Plib</u> pre-alpha	common

03-02-2005

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Main Window

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File Menu - Select Reference Sample

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File Menu - Select Current Sample

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Remove Sample-pair from landmark DB	✓ gel-HM-071 gel-HM-087	HM-019
Save landmark DB	gel-HM-091	
Clear report		
Save report to file		
Update from Web server	•	
Cancel	gel-HM-071	
Exit		
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File Menu - Update From Web Server

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File	Edit View Help		
Landr Tedar	Select Rsample from (Rsample,Sample) list in LMS DB	'ision: 1.4 \$ (Open2Dprot)	<u></u>
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	Use Rsample landmarks as fixed template	•	
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Swite		DB:landmark.xml -projDir:demo/	-rsample:gel-HM-019
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Edit Menu

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	Use Rsample landmarks as fixed template		
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Edit Menu - command line options

Enter sample image and select switch options					
Change the startup parameters, then press 'Set new options' button to save them. At that point, you can press 'Pair spots' to pair the Rsample and Sample with the new parameters. You may also enter new Rsample and Sample data file names and/or edit switch options and threshold sliders.					
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☑ -backupDatabases					
-commutativeLMS					
🗖 -debugBits	0,0				
🗆 -default					
🗹 -demo					
🗖 -dtd					
☑ -inputFormat	X,X				
🗹 -landmarkFile	landmark.xml				
✓ -projDir Project directory Browse dir	demo\				
-propertiesFile Properties file Browse file	Landmark.properties				
✓ -rsample Rsample file Browse file	gel-HM-019				
✓ -sample Sample file Browse file	gel-HM-071				
Reset defaults	Done Cancel				

View Menu

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Landmark popup window



Landmark XML DB in browser

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<pre><date>08/10/04 19:36:18</date></pre>		
- <landmarkset></landmarkset>		
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Summary

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