Overview: Accession

Data Accessioning Program

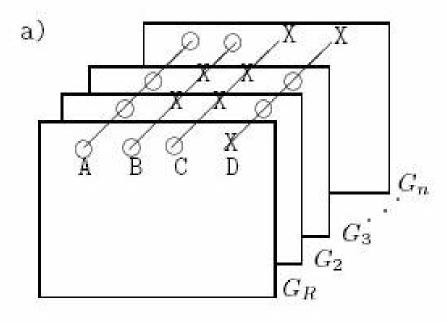
http://open2dprot.sourceforge.net/Accession

Revised: 03-01-2004, P. Lemkin

Introduction

- Data must be accessioned or entered into the program database. This consists of several activities:
- 1. Entering the name of the sample and sample information
- 2. Entering the Region Of Interest of sample
- 3. Entering sample calibration info if any

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 $G_r = G_1$

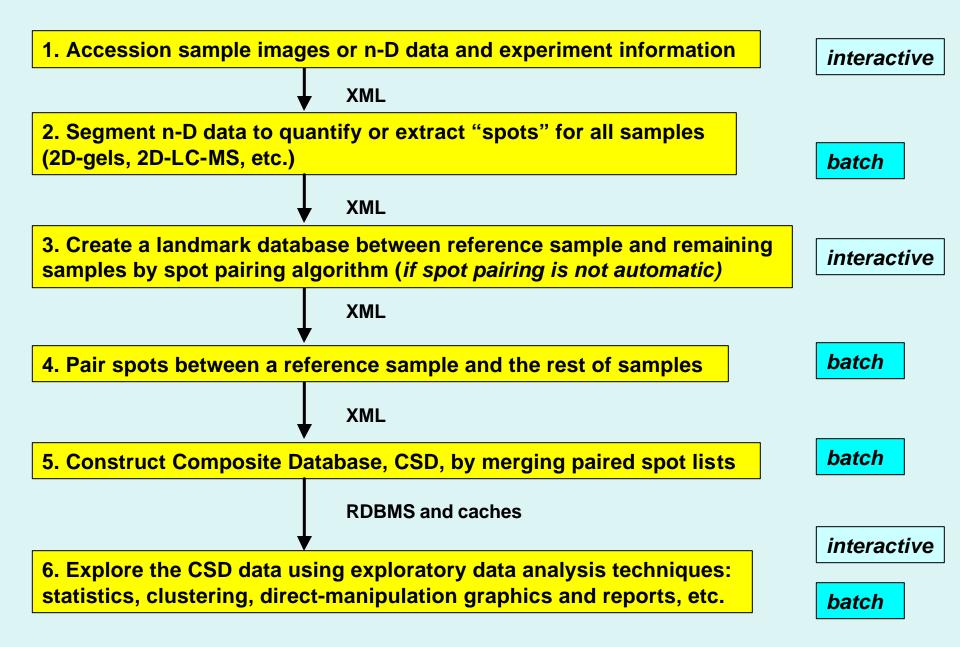
Expression profiles A,B,C, ...

b) O G'_{x1} O G'_{x2} G'_{x2} G'_{x1} G'_{x2} G'_{x1} G'_{x2} G'_{x1} G'_{x2} G'_{x1} G'_{x2} G'_{x1} G'_{x2} G'_{x1} G'_{x2} G'_{x2} G'_{x1} G'_{x2} G'_{x2} G'_{x2} G'_{x1} G'_{x2} $G'_$

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 3 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
- <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 pipeline subprojects

<u>Open2Dprot</u> consists of a series of coordinated <u>Open2Dprot pipeline processing modules</u>. 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
Open2Dprot	(see below)	Open2Dprot	Open2Dprot	Open2Dprot	Open2Dprot	Open2Dprot	Open2Dprot de <i>sign pr</i> ototype	-
Accession	Accession	Accession	Accession	Accession	Accession	Accession	Accession pre-alpha	[1]
Seg2Dgel	<u>Seg2Dgel</u>	<u>Seg2Dgel</u>	Seg2Dgel	Seg2Dgel	<u>Seg2Dgel</u>	Seg2Dgel	<u>Seg2Dgel</u> pre-alpha	[2]
Landmark	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 design prototype	[5]
CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer	CSDminer de <i>sign pr</i> ototype	[6]
<u>02Plib</u>	<u>O2Plib.jar</u>	<u>O2Plib</u>	02Plib	<u>O2Plib</u>	<u>O2Plib</u>	<u>O2Plib</u>	<u>02Plib</u> pre-alpha	common

6 **01-09-2005**

Associated or Related Projects

We had added some additional non-pipeline open source projects that may use similar data or common software modules. They may be useful for performing other types of analysis on data used by Open2Dprot or alternate types of analyses.

Contributed Project Home	Download	Documentation	Overview (PDF)	PDF documents	Version	Revision history	Status
Flicker	<u>Flicker</u>	<u>Flicker</u>	<u>Flicker</u>	<u>Flicker</u>	<u>Flicker</u>	<u>Flicker</u>	<u>Flicker</u>
MAE MAExplorer	MAExplorer	MAExplorer	MAExplorer	MAExplorer	MAExplorer	MAExplorer	MAExplorer
TIMAP ProtPlot	Protplot	TMAP (ProtPlot)	ProtPlot	ProtPlot	<u>ProtPlot</u>	ProtPlot	
xox	xxxx	XXXX	xxxx	xxxx	XXXX	2000	>>>>

09-12-2004

Main Window

Access	ion ¥.0.0.	.6-pre-Alpha	a - \$Date: 2005/	02/26 11:51:5	3 \$ - \$Revisio	n: 1.6 \$ (Ope	n2Dprot)			
File Edit	View	Help								
Today's d	ate is 0: -input)	3/01/05 12: Format:X,X	- \$Date: 2005/0 45:13 -accessionDB:ac sample:gel-HM-0	cession.xml -)	andmarkDB:la	100	pen2Dprot)			1
Can't rea	d [Acces:	sion.proper	ties]							
			-accessionDB:ac se file: demo\x			ndmark.xml	-projDir:demo) -isamp	le∶gel−HM	-019
										T
•										
Readin	Clear	SaveAs	Edit options	Accession	ROI Cal	ibrate wedge		Done	Cancel	

File Menu – Add New Sample

≜ Accession ¥.0.0.6-pre-Alpha - \$Date: 200	05/02/26 11:51:58 \$ - \$Revision: 1.6 \$ (Open2Dprot)	_ 🗆 🗙
File Edit View Help		
Create project (directory) Set project directory Change name of current accession DB Create new accession DB Add Sample to accession DB	2/26 11:51:58 \$ - \$Revision: 1.6 \$ (Open2Dprot) =ession.xml -landmarkDB:landmark.xml 19 -sample:gel-HM-071 =ession.xml -landmarkDB:landmark.xml -projDir:demo/ -rsample:gel-HM-019 -sa ml\accession.xml sher file.	umple:g
Remove Sample from accession DB Set Rsample Open Sample for editing Save accession DB Clear report Save report to file Update from Web server		
Cancel Exit	File name: Human-AML.gif Image: Files of type: All Files (*.*) Cancel	
Reading Sample image Clear Save/	As Edit options Accession ROI Calibrate wedge 📝 Done	Cancel

File Menu - Select Reference Sample

Add Sample to accession DB Remove Sample from accession DB Set Rsample Open Sample for editing Save accession DB Clear report Save report to file Update from Web server Cancel Exit	Create project (directory) Set project directory Change name of current accession DB Create new accession DB		- \$Revision: 1.6 \$ () ndmarkDB:landmark.xml M-071	Open2Dprot)		
Open Sample for editing gel-HM-071 Save accession DB gel-HM-087 Clear report gel-HM-096 Save report to file gel-HM-096 Update from Web server to file Cancel gel-HM-087		1.1.2. A 160 C - 3 S - 3 A - 1 A - 1 C - 2 C		-projDir:demo/	-rsample:gel	-HM-019
Bave accession DB gel-HM-087 Clear report gel-HM-096 Save report to file gel-HM-096 Update from Web server to file Cancel Cancel	Set Rsample	🕨 🗸 gel-HM-019				
Gave accession DB gel-HM-096 gel-	Open Sample for editing					
Clear report Save report to file Update from Web server Cancel	Save accession DB					
Cancel		gerrim coo				
	Jpdate from Web server	•				
Exit	Cancel					
	Exit					
	adin Clear SaveAs Edit options	Accession	ROI Calibrate wedg	e 🔽 Di	one Cance	4

File Menu - Select Current Sample

Create project (directory) Set project directory Change name of current accession DB Create new accession DB		\$ - \$Revision: 1.5 \$ (andmarkDB:landmark.xml -HM-071	openzuprot)		
Add Sample to accession DB Remove Sample from accession DB	cession.xml -1 ml\accession.xm	andmarkDB:landmark.xml ml	-projDir:demo/	-rsample:ge	1-HM-019
Set Rsample Open Sample for editing	▶ ▶ gel-HM-019	1			
Save accession DB	✓ gel-HM-071 gel-HM-087				
Clear report Save report to file	gel-HM-096				
Jpdate from Web server	•				
Cancel Exit					

File Menu - Update From Web Server

Accession ¥.0.0.6-pre-Alpha - \$Date: 2005/	/02/26 11:51:58 \$ - \$Revision: 1.6 \$ (Open2Dprot)	
File Edit View Help		
Set project directory	2/26 ll:51:58 \$ - \$Revision: 1.6 \$ (Open2Dprot) cession.xml -landmarkDB:landmark.xml 19 -sample:gel-HM-071	
Add Sample to accession DB Remove Sample from accession DB	ression.xml -landmarkDB:landmark.xml -projDir:demo/ -rsample:gel-HM ml\accession.xml	[-019
Set Rsample •		
Open Sample for editing		
Save accession DB		
Clear report Save report to file		
Update from Web server 🔹 🕨	Accession all files	
Cancel	Accession Program	
Exit	Accession demo files Accession documentation	
•		×
Readin Clear SaveAs Edit options	Accession ROI Calibrate wedge 🔽 Done Cancel	

Edit Menu

ces day itc	Accession info Regions of interest	02/25 11:51:58 \$ - \$Revision: 1.5 \$ (Open2Dprot) cession.xml -landmarkDB:landmark.xml				
- vitc adi	Calibrate by step wedge Calibrate by spot list Calibrate by file data Calibrate by manual entry Read calibration values from file	019 -sample:gel-HM-071 ccession.xml -landmarkDB:landmark.xml -projDir:demo/ -rsample:gel-HM-0. cml\accession.xml				
	Options Resize memory limits	 Open options file Save options file SaveAs options file Edit options Reset default options 				

Edit Menu - Accession

Accession edit sample [Sample] 03/01/0	5 12:52:28
File Edit Help	
Accession fields	
	in the accession file. It is also the name of the image file. I the entry in the accession file. It is also the name of the image s ated with the Sample.
Sample	gel-HM-071
Rsample	gel-HM-019
PatientNbr	34
Study	HEME MALIG-ALL, LYMPHOID (SCAN 1 OF 3)
ExperimentDate	T18 MONTHS
CultureReagent	CULT #2
AmpholyteAndGelGradientRange	3:10,5-20%
IntervalBeforeLabeling	0 HRS
LabelingIsotope	НЗ
DurationLabel	2 HRS
DurationExposure	96 HRS
Camera	VIDICON-AUTO,28MM,F8,76CM
Investigator	LESTER
wedgeCalList	.05,.20,.35,.50,.66,.80,.95,1.10,1.25,1.41,1.56,1.72,1.87,2.02,2.17
wedgeGrayList	028 051 075 098 118 138 155 169 183 192 200 208 215 225 229
cwx1	6
cwx2	450
cwy1	68
cwy2	503
calCWx1	0
calCWx2	0
calCWy1	0
calCWy2	0
PixWidth	512
PixHeight	512

Edit Menu – Accession editing options

File Edit Help		
Assign current Rsample entry to this sample Clear image computing window ROI entry Clear calibration wedge ROI entry		2
Sample	gel-HM-071	-
Rsample	gel-HM-019	
PatientNbr	34	
Study	HEME MALIG-ALL, LYMPHOID (SCAN 1 OF 3)	
ExperimentDate	T18 MONTHS	
CultureReagent	CULT #2	
AmpholyteAndGelGradientRange	3:10,5-20%	
IntervalBeforeLabeling	O HRS	
LabelingIsotope	НЗ	
DurationLabel	2 HRS	
DurationExposure	96 HRS	
Camera	VIDICON-AUTO,28MM,F8,76CM	
Investigator	LESTER	
wedgeCalList	.05,.20,.35,.50,.66,.80,.95,1.10,1.25,1.41,1.56,1.72,1.87,2.02,2.17	
wedgeGrayList	028 051 075 098 118 138 155 169 183 192 200 208 215 225 229	
cwx1	6	
cwx2	450	
cwy1	68	
evan/7	503	1

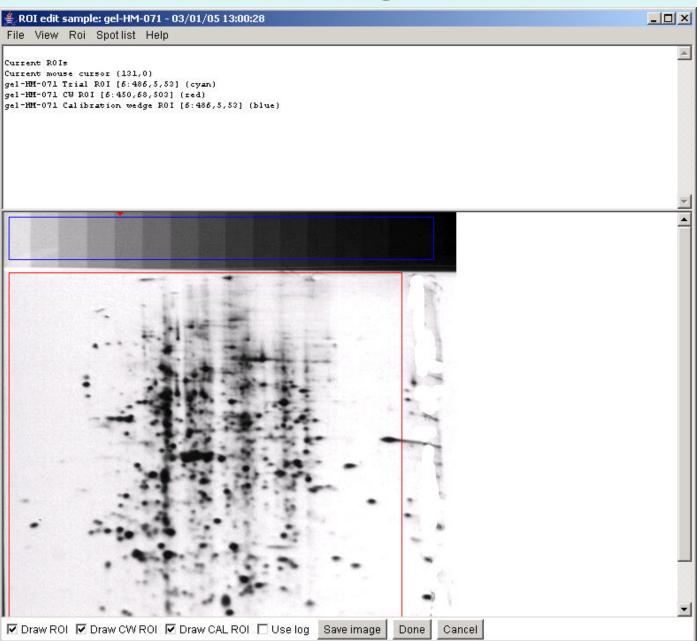
Edit Menu – Accession New Sample Using Old Sample Information as Template

Accession edit sample [Sample] 03	/01/05 12:54:16	×
File Edit Help		
Use values from template sample	gel-HM-019 gel-HM-071	<u>_</u>
Log text output to Report window	gel-HM-071 gel-HM-087	
Save accession DB	gel-HM-096	-
Cancel	✓ Human-AML	Human-AML
Exit		
PatientNbr		
Study		
ExperimentDate		
CultureReagent		
AmpholyteAndGelGradientRange		
IntervalBeforeLabeling		
LabelingIsotope		
DurationLabel		
DurationExposure		
Camera		
Investigator		
wedgeCalList		
wedgeGrayList		
cwx1		0
cwx2		511
cwy1		0
cwy2		511
calCWx1		0
calCWx2		0
calCWy1		0
calCWy2		0
PixWidth		512
PixHeight		512

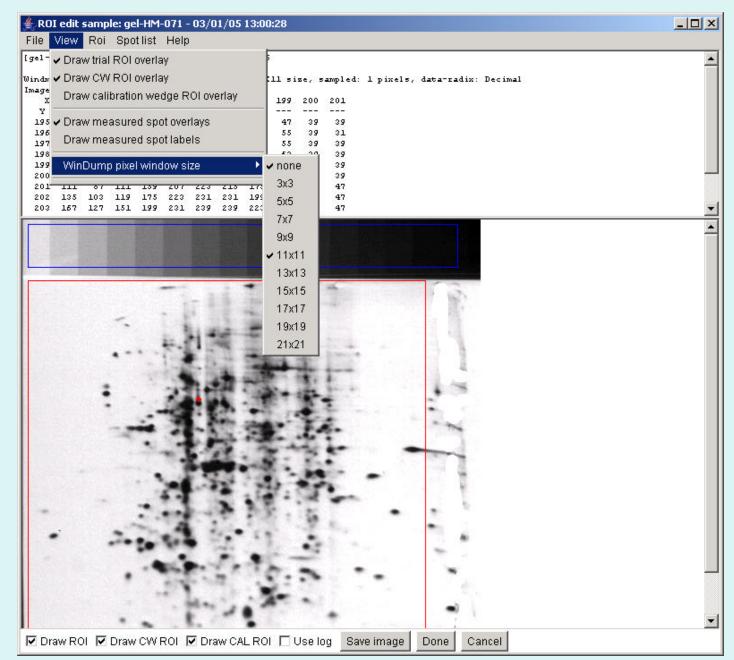
Edit Menu – Accession Sample after Template

File Edit Help		1.15
Using template [gel-HM-019] for Sample [Human-AML]		
Sample	Human-AML	
Rsample		
PatientNbr	41	
Study	HEME MALIG-AML, MYELOID (SCAN 1 OF 3)	
ExperimentDate	то	
CultureReagent	CULT #2	
AmpholyteAndGelGradientRange	3:10,5-20%	
IntervalBeforeLabeling	0 HRS	
LabelingIsotope	НЗ	
DurationLabel	2 HRS	
DurationExposure	96 HRS	
Camera	VIDICON-AUTO,28MM,F8,76CM	
Investigator	LESTER	
wedgeCalList	.05,.20,.35,.50,.66,.80,.95,1.10,1.25,1.41,1.56,1.72,1.87,2.02,2.17	
wedgeGrayList		
cwx1	0	
cwx2	511	
cwy1	0	
cwy2	511	
calCWx1	0	
calCWx2	0	
calCWy1	0	
calCWy2	0	
PixWidth	512	
PixHeight	512	_

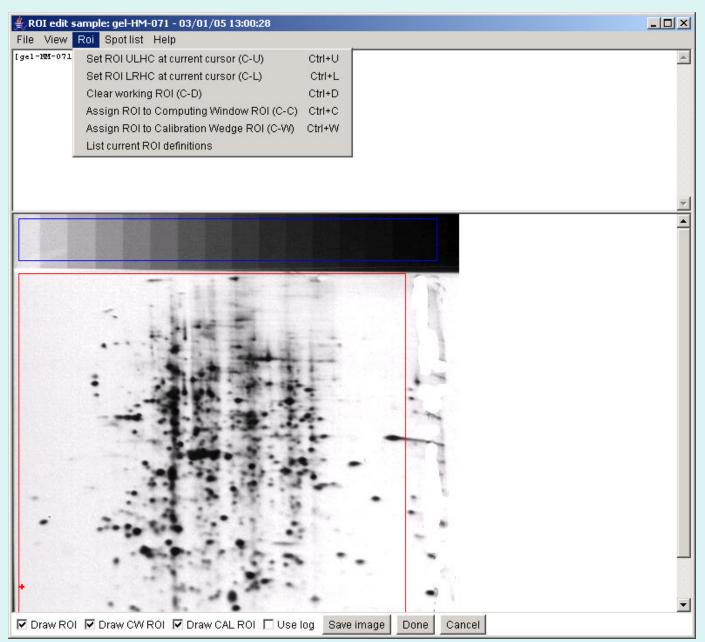
Edit Menu – Region Of Interest



Edit Menu – Region Of Interest overlay views



Edit Menu – Region Of Interest commands



Edit Menu – Region Of Interest Spot List

	le: gel-HM-071 - 03/01/05 13:00:28	
File View Roi [gel-HM-071] x=:	A CONTRACT OF A	
	Clear list of measured spots Clear background spot	
	Measurement square size ▶ ✓ Recompute spot-list measurements with common size Recompute spot-list measurements with background correction Sort spot-list measurements	1x1 3x3 5x5 7x7 9x9
		11x11 13x13 15x15 ✔17x17
:		19x19 21x21 23x23 25x25 27x27
		29x29
•		
+		
🔽 Draw ROI 🔽 I	Draw CW ROI 🔽 Draw CAL ROI 🗔 Use log 🛛 Save image 🔤 Done 🗌 Cance	91

Edit Menu – Calibrate Grayscale – OD, etc.

👙 Calibrate grayscale from step wedge ROI in Sample image gel-HM-071

File View Edit Help

*** UNDER CONSTRUCTION ***

Analyze wedge ROI

Add peak

Delete peak

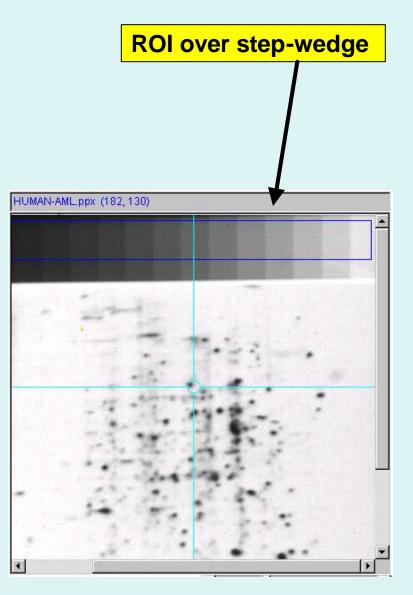
Calibr. units:	Optical density	Calibr. abbrev.:	od
Wedge ROI:	[-1:-1, -1:-1]		
Wedge ID#:	<opt. #="" part=""></opt.>		
Step #1 od:	0.00	Gray peak #1:	0
Step #2 od:	0.00	Gray peak #2:	0
Step #3 od:	0.00	Gray peak #3:	0
Step #4 od:	0.00	Gray peak #4:	0
Step #5 od:	0.00	Gray peak #5:	0
Step #6 od:	0.00	Gray peak #6:	0
Step #7 od:	0.00	Gray peak #7:	0
Step #8 od:	0.00	Gray peak #8:	0
Step #9 od:	0.00	Gray peak #9:	0
Step #10 od:	0.00	Gray peak #10:	0
Step #11 od:	0.00	Gray peak #11:	0
Step #12 od:	0.00	Gray peak #12:	0
Step #13 od:	0.00	Gray peak #13:	0
Step #14 od:	0.00	Gray peak #14:	0
Step #15 od:	0.00	Gray peak #15:	0
Step #16 od:	0.00	Gray peak #16:	0
Step #17 od:	0.00	Gray peak #17:	0
Step #18 od:	0.00	Gray peak #18:	0
Step #19 od:	0.00	Gray peak #19:	0
Step #20 od:	0.00	Gray peak #20:	0

- O ×

*

Flicker - Calibrating Grayscale with a ND Step-Wedge

- 1. The <u>ND step wedge</u> must be scanned with the image and the corresponding OD values known for each step
- 2. A <u>region of interest</u> (ROI) is overlaid on the step stepwedge
- 3. The <u>ND wedge calibration</u> wizard is invoked to analyze the data and estimate the calibration



Flicker - Calibrating Grayscale from ND Wedge Data

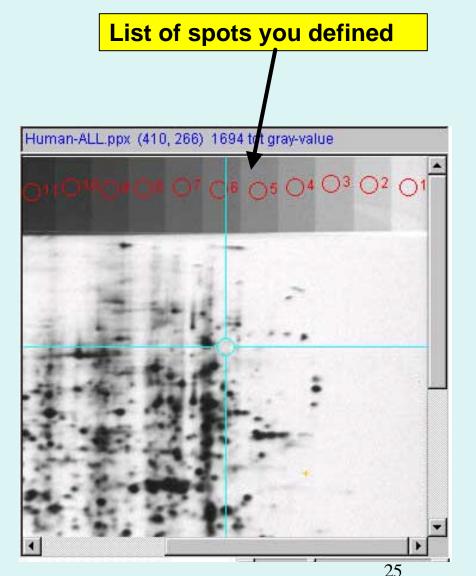
ROI histogram, peaks found and extrapolated calibration curve

OD vs gray-peaks table

leted peak from p	eaktable and calibration			_		
	Gel OD Calibration		Calibr. units:	Optical density	Callor, abbrev.;	od
			Wedge ROI:	[36:507, 7:51]		
2.5 od		<u>1</u> .375	Wedge ID#:	<opt. #="" part=""></opt.>		
-		₽ /F	Step #1 od:	0.06	Gray peak #1:	27
2.11		1 ² 1	Step #2 od:	0.20	Gray peak #2:	50
2.0 od 1.96		200	Step #3 od:	0.35	Gray peak #3:	73
map 1.80 - 1.67 -		11 / E	Step #4 od:	0.51	Gray peak #4:	95
1.5 od 1.54	e i e		Step #5 od:	0.64	Gray peak #5:	117
1.38 -	. 131	225	Step #6 od:	0.80	Gray peak #6:	136
1.24		V E	Step #7 od:	0.95	Gray peak #7:	155
1.0 od 0.95	Î I I I I I I	L 150	Step #8 od:	1.09	Gray peak #8:	168
libration o.so		F	Step #9 od:	1.24	Gray peak #9:	181
aks 0.64		H F	Step #10 od:	1.38	Gray peak #10:	192
0.5 od 0.51		_75	Step #11 od:	1.54	Gray peak #11:	200
0.20		ļ ļ	Step #12 od:	1.67	Gray peak #12:	208
0.06		E.	Step #13 od:	1.80	Gray peak #13:	214
- [- -			Step #14 od:	1.96	Gray peak #14:	219
edae 0	50 100 150 GrayScale	200 250	Step #15 od:	2.11	Gray peak #15:	223
equency	Grayscale range[16:243]		Step #16 od:	2.25	Gray peak #16:	0
stogram	Frequency range[1:377]		Step #17 od:	0.00	Gray peak #17:	0
83 	Region Of Interest [36:507, 7:5	51]	Step #18 od:	0.00	Gray peak #18:	0
	Active histogram bin ('not sele	cted]	Step #19 od:	0.00	Gray peak #19:	0
			Step #20 od:	0.00	Gray peak #20:	0

Flicker- Calibrating Grayscale with a Spot List of Calibrated Data

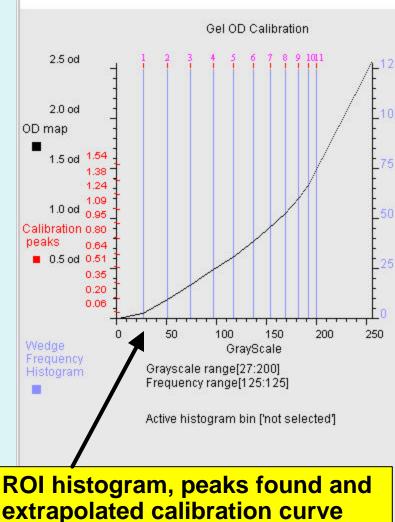
- 1. The image must contain <u>calibrated regions</u> with known concentrations or corresponding OD values <u>known for each spot</u>
- 2. You <u>define a set of spots</u> using (C-M) or (ALT-click)
- 3. The <u>Spot List Calibration</u> <u>wizard</u> is invoked to analyze the data and estimate the calibration



Flicker - Calibrating Grayscale from Spot List Data

🧶 Calibrate grayscale from spot list, image Human-ALL.ppx 🛛

OD vs gray-peaks table



Calibr. units:	Optical density	Calibr. abbrev.:	od
Mean spot values			
Wedge ID#:	<opt. #="" part=""></opt.>		
Step #1 od:	0.06	Gray peak #1:	27
Step #2 od:	0.20	Gray peak #2:	51
Step #3 od:	0.35	Gray peak #3:	74
Step #4 od:	0.51	Gray peak #4:	97
Step #5 od:	0.64	Gray peak #5:	117
Step #6 od:	0.80	Gray peak #6:	137
Step #7 od:	0.95	Gray peak #7:	154
Step #8 od:	1.09	Gray peak #8:	169
Step #9 od:	1.24	Gray peak #9:	182
Step #10 od:	1.38	Gray peak #10:	192
Step #11 od:	1.54	Gray peak #11:	200
Step #12 od:	1.67	Gray peak #12:	0
Step #13 od:	1.80	Gray peak #13:	0
Step #14 od:	1.96	Gray peak #14:	0
Step #15 od:	2.11	Gray peak #15:	0
Step #16 od:	2.25	Gray peak #16:	0
Step #17 od:	0.00	Gray peak #17:	0
Step #18 od:	0.00	Gray peak #18:	0
Step #19 od:	0.00	Gray peak #19:	0
Step #20 od:	0.00	Gray peak #20:	0

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 nam and/or edit switch options and threshold sliders.	
	Þ
✓[-accessionFile]	accession.xml
🗹 -backupDatabases	
🗖 -debugBits	0
🗖 -default	
🔽 -demo	555
🗖 -dtd	C.C.C.S.
🗹 -inputFormat 🛛 💌	×
	demo\
-propertiesFile Properties file Browse file	Accession.properties
✓ -rsample Rsample file Browse file	gel-HM-019
☑ -sample Sample file Browse file	gel-HM-071
□ -timer	
🗖 -update program 💌	program
Reset defaults	Done Cancel

View Menu

🛓 Accession	n V.O.O.6-pre	-Alpha - \$D	ate: 2005/0	2/26 11:51:58 \$	- \$Revision: 1.	6 \$ (Ope	en2Dprot)			_ 🗆 ×
File Edit	View Help									
List of sal	List Access	ion Sample	es							*
[0] gel-HM [1] gel-HM [2] gel-HM [3] gel-HM		mple acces: ple accessi	sion DB data on DB data	a						
[4] Human	Show Acce	ssion DB in	browser							
List of san [0] gel-HM [1] gel-HM	Show list o	fmeasured	spots							
[2] gel-HM-([3] gel-HM-([4] Human-AM	96									
List of samp [0] gel-HM-0 [1] gel-HM-0 [2] gel-HM-0 [3] gel-HM-0 [4] Human-A)19)71)87)95	ssionDB								•
				1	-	and the second second	F			
Reading Sa	mple image	Clear	SaveAs	Edit options	Accession	ROI	Calibrate wedge	1	Done	Cancel

View Menu - Show Current Sample Acc DB Data

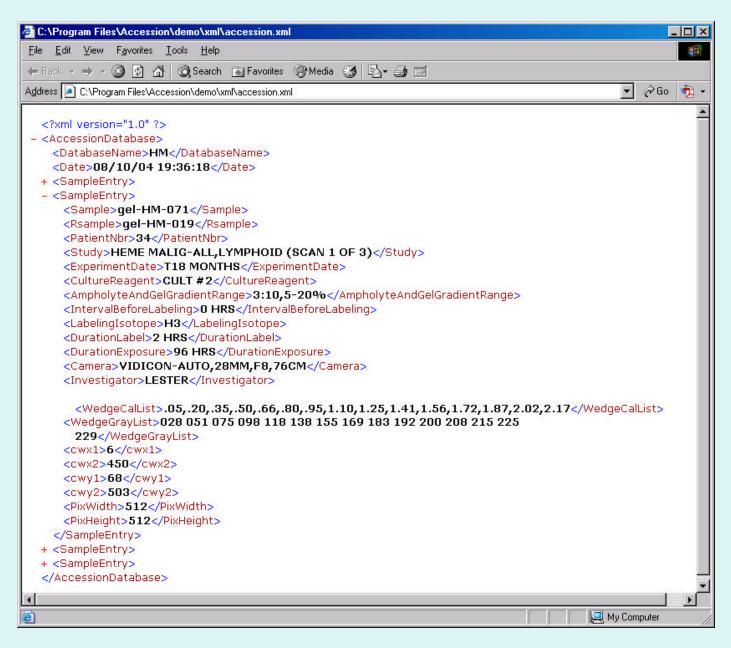
- 🗆 ×

Accession V.0.0.6-pre-Alpha - \$Date: 2005/02/26 11:51:58 \$ - \$Revision: 1.6 \$ (Open2Dprot)

File Edit View Help

```
Rsample[gel-HM-019]
Data Computing Window [14:475:74:509]
#0 Sample = 'gel-HM-019'
#1 Rsample = '-'
#2 PatientNbr = '41'
#3 Study = 'HEME MALIG-AML, MYELOID (SCAN 1 OF 3)'
#4 ExperimentDate = 'T0'
#5 CultureReagent = 'CULT #2'
#6 AmpholyteAndGelGradientRange = '3:10,5-20%'
#7 IntervalBeforeLabeling = '0 HR3'
#8 LabelingIsotope = 'H3'
#9 DurationLabel = '2 HRS'
#10 DurationExposure = '96 HR3'
#11 Camera = 'VIDICON-AUT0,28MM,F8,75CM'
#12 Investigator = 'LESTER'
#13 wedgeCalList = '.05,.20,.35,.50,.66,.80,.95,1.10,1.25,1.41,1.56,1.72,1.87,2.02,2.17'
#14 wedgeGravList = '027 049 072 095 117 136 153 168 181 192 200 208 213 220 225'
#15 cmx1 = '14'
#15 cmx2 = '475'
#17 cwyl = '74'
#18 cwy2 = '509'
#19 calCWx1 = ''
#20 calCWx2 = ''
#21 calCWy1 = ''
#22 calCWy2 = ''
#23 PixWidth = '512'
#24 PixHeight = '512'
                                    SaveAs
                                               Edit options
                                                                            ROI
                          Clear
                                                              Accession
                                                                                   Calibrate wedge
 Reading Sample image
                                                                                                              Done
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View Menu - XML Accession DB in Browser



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Summary

- Accession is an open-source sample accessioning Java program freely available at <u>http://open2dprot.sourceforge.net/Accession</u>
- Useful for adding sample experiment information, regions of interest and grayscale calibration (if available).
- It will be used as one of the step [1] alternative modules in the analysis pipeline in the Open2Dprot project at <u>http://open2dprot.sourceforge.net</u>