



# Image sequence (stack) analysis with PCA\_GUI in aXis2000

Adam Hitchcock (aph@mcmaster.ca)

- 1) Principles (slides courtesy Chris Jacobsen)
- 2) Example - core-shell microsphere (Stover) - 50:50 shell
  - \* forward fitting using SVD & OD1 reference spectra
  - \* PCA\_GUI analysis
  - \* Comparison

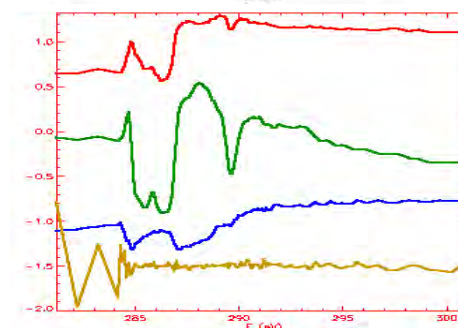
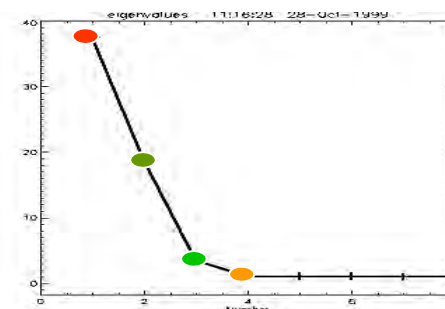
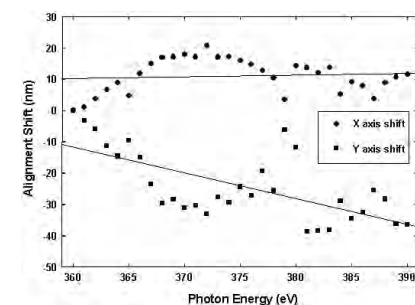
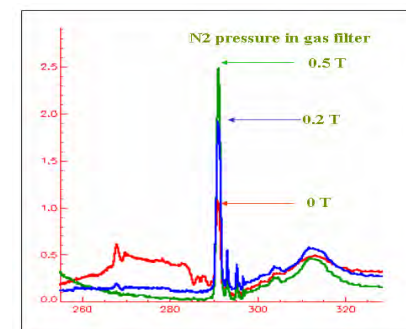
## REFERENCES:

- C. Jacobsen, M. Feser, M. Lerotic, S. Vogt, J. Maser, and T. Schäfer, *Cluster analysis of soft x-ray spectromicroscopy data*, Journal de Physique IV **104**, 623 (2003)
- M. Lerotic, C. Jacobsen, T. Schäfer, and S. Vogt, *Cluster analysis of soft x-ray spectromicroscopy data*, Ultramicroscopy **100**, 35 (2004)
- M. Lerotic, C. Jacobsen, J. B. Gillow, A. J. Francis, S. Wirick, S. Vogt, and J. Maser, *Cluster analysis in soft X-ray spectromicroscopy: Finding the patterns in complex specimens*, J. El. Spec. Rel. Phen. 144, 1137 (2005)
- H. Ade & A.P. Hitchcock, , *NEXAFS microscopy and resonant scattering: Composition and orientation probed in real and reciprocal space*, Polymer 49, 643-675 (2008) - describes this example

# Some challenges of quantitative mapping

## 1. Quality of data (spectra, linescan, image sequence)

Issue	Recommendation
linearity of absorption	avoid saturation (OD < 2-3)
spectral distortion	reduce or eliminate second order
energy calibration	check regularly; calibrate
alignment	interferometry; careful alignment
radiation damage	use as small a dose as possible
linear E-scale	check with known spectra



## 2. Suitability & quality of reference spectra

Situation	Recommendation
chemistry well known	record spectra of same or similar pure material (eg monomer unit)
chemistry poorly known but spatially well isolated	internal models guided by external models
chemistry complex	Principle component analysis to place limits on number of components
chemistry unknown	MSA and cluster analysis Lerotic & Jacobsen, J. El. Spec. 2005, 144, 1137
chemistry unknown	internal models by trial and error

*Rotating principal components to obtain real spectra using cluster analysis*

Problem: principal components are **abstract**. They are mixtures of the actual **real** spectra of the compounds present.

- PCA provides an orthogonalized representation of the data with less noise, fewer coordinates. Working with only significant components is an effective noise filter.
- We can find **groupings** of the data in the principal component coordinate system which relate to individual chemical components
- How ? => **Cluster analysis** or pattern matching

Slide courtesy of  
**Chris Jacobsen**  
SUNY Stony Brook

## *Cluster analysis: Euclidian distance learning algorithm*

- Data are in multidimensional principle component space; only 2 dimensions shown here.
- Ideally data are arranged in clusters in this space!
- Put down cluster centers at random positions.



PC-2

PC-1

Slide courtesy of  
**Chris Jacobsen**  
SUNY Stony Brook

## *Cluster analysis: Euclidian distance learning algorithm*

PC-2

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- Iterate:
  - Calculate distances from one cluster center to all data points.
  - Pick shortest distance.



PC-1

Slide courtesy of  
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PC-2

PC-1

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*Cluster analysis:  
Euclidian distance learning algorithm*

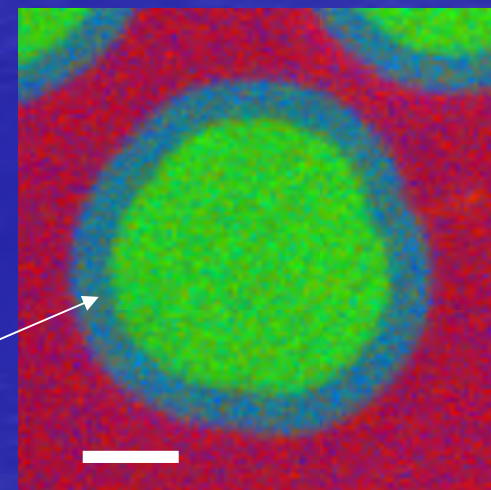
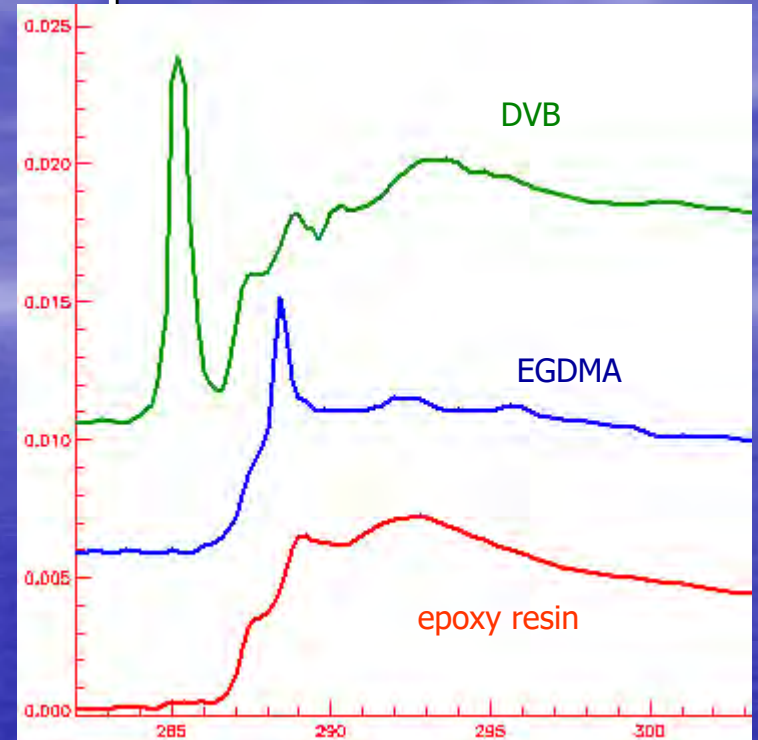
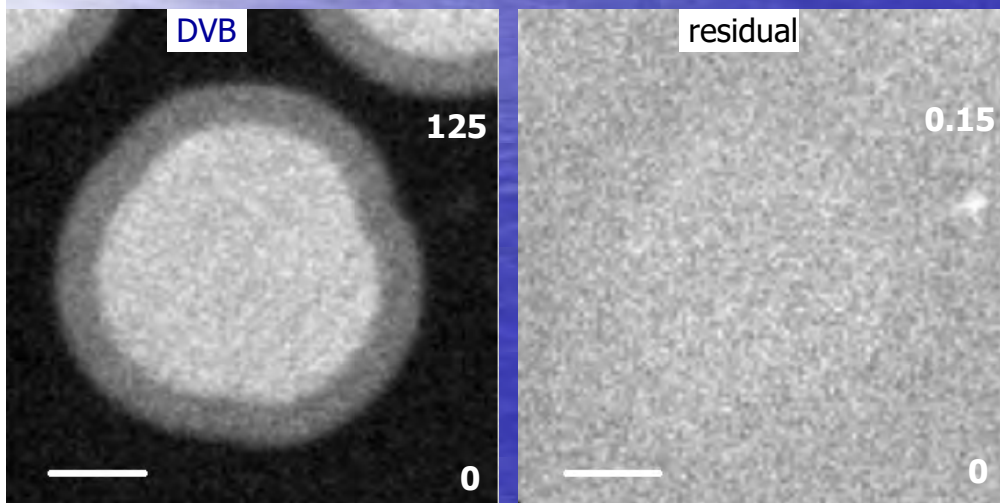
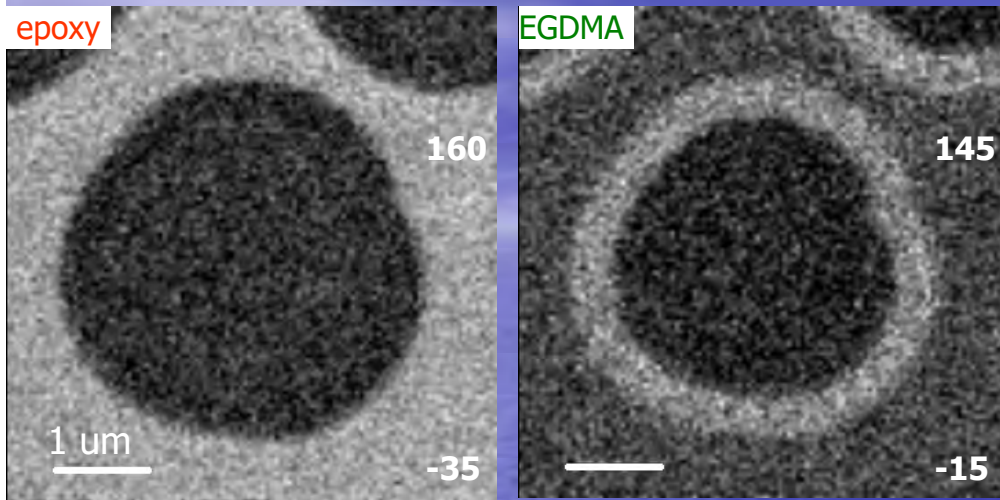
PC-2

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PC-1

# Example: core-shell microspheres

Datafile: cs50c-od.ncd/dat (stxm5322: 2003\_09\_28\_042)



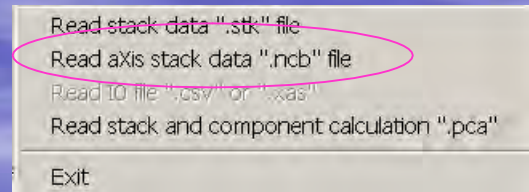
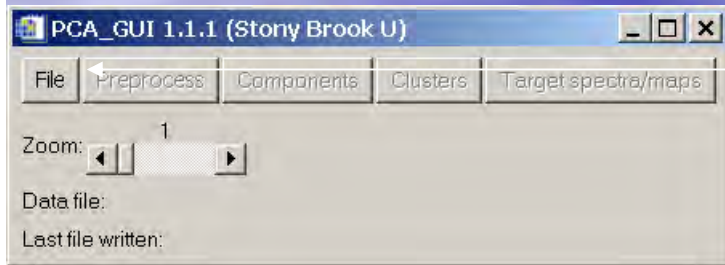
Turquoise color (B&G) indicates the shell is a MIX of DVB and EGDMA



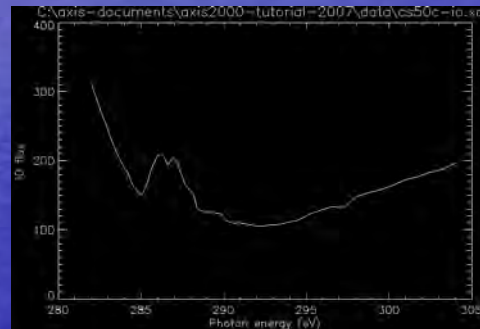
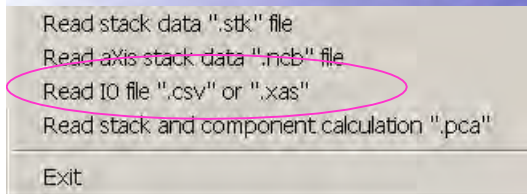
# Getting the stack into PCA\_GUI

0. LAUNCH stacks~statistical analysis~PCA\_GUI (CJJ Dec 2005)

1. Read in the TRANSMITTANCE file - cs50-c-1.ncb/dat



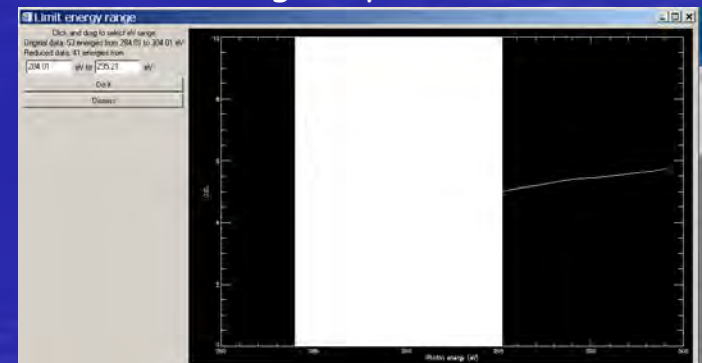
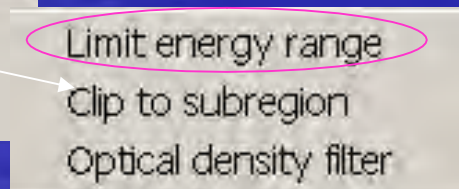
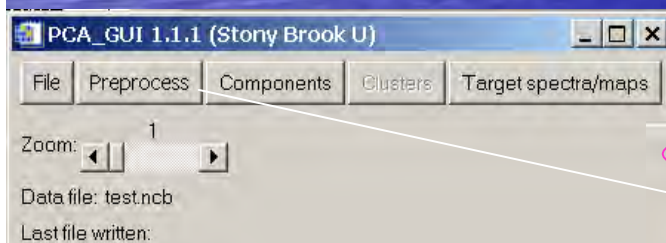
2. then, read in the I<sub>0</sub>, as the \*.xas file:



If you have only the stack in OD format, there is a comment on the stack\_process GUI (accessed by stacks~analyze~aXis\_binary) which converts OD stacks to transmittance stacks, with a whitel (I(E)=1.0 for all E) I<sub>0</sub> file

ONLY if you have both (I) and (I<sub>0</sub>) components successfully read in, do the next menu items become available

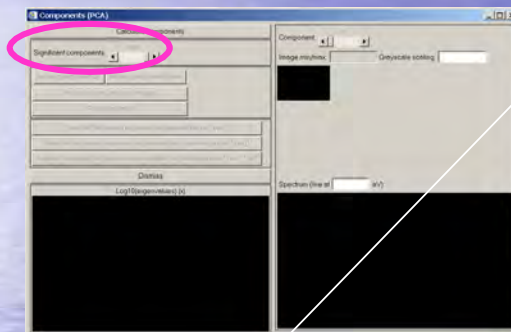
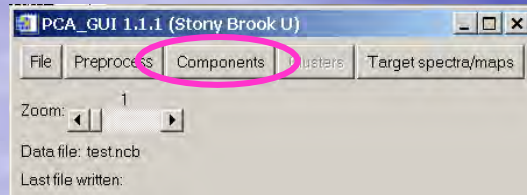
3. You can use PreProcess to reduce the ENERGY, SPATIAL, or INTENSITY range if you wish



in this case I chose to keep the full data range of the recorded data. It may be worthwhile to only include the energy range where the spectra of the chemical species differs the most, and to exclude any regions of noise, especially systematic noise

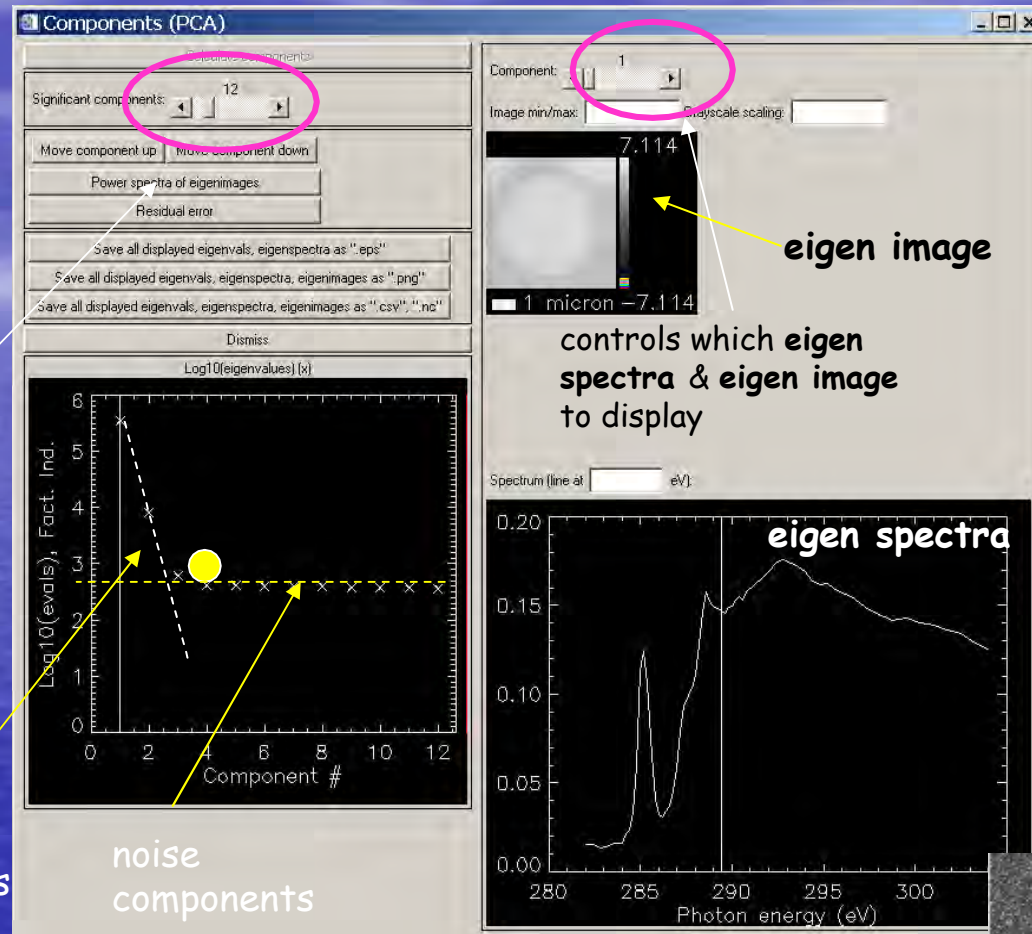
# Using PCA\_GUI – generating principle components

## 4. compute principle components



controls range of eigenvalues to display

significant components

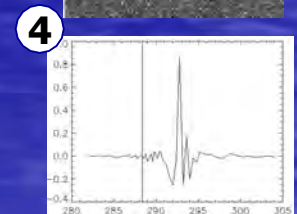
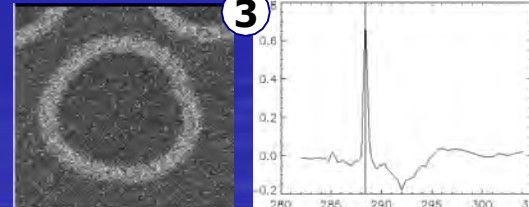
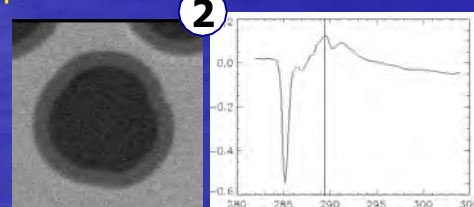
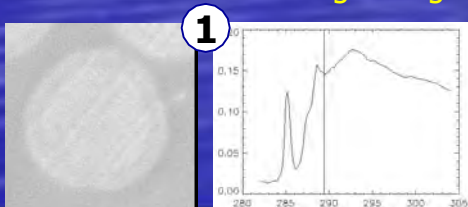


eigen image

controls which eigen spectra & eigen image to display

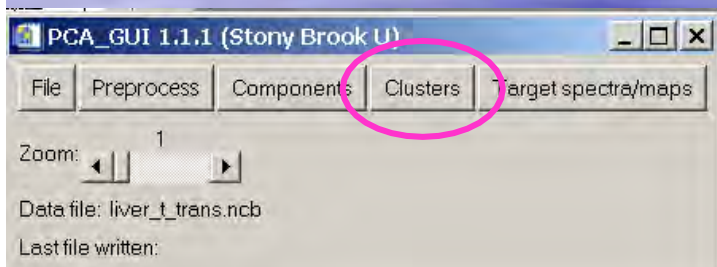
eigen spectra

In this case components 1 -3 are definitely significant - **but mix together all 3 components**  
 components 4-64 are noise; searching to component 15 just shows no pattern in the eigen-image, as for PC#4  
 If you regenerate the stack from PC#1, PC#2, PC#3 a very clean data set can be produced - this is a type of noise filtering  
**PC#1 is ALWAYS average image & spectrum**



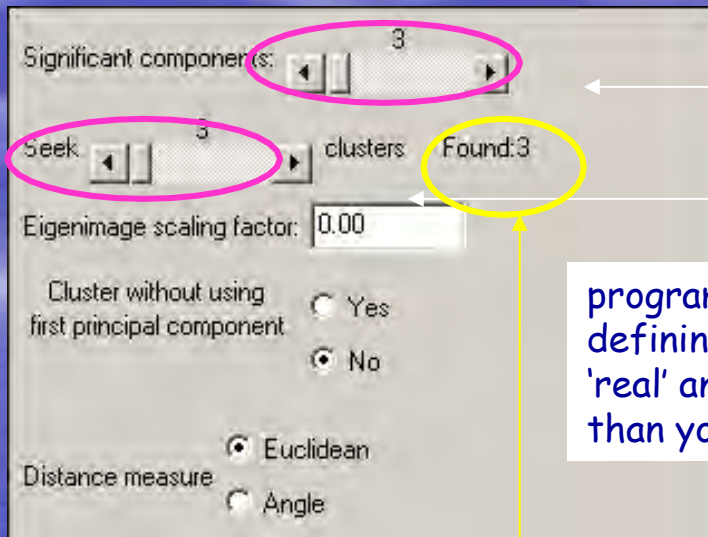
# Using PCA\_GUI cluster analysis to rotate PC

## 4. compute cluster components



This is where the 'art' comes in you have to select

- \* # of components to include
- \* WHICH components to include (you can move components up or down in the PC# listing in the 'components' panel)
- \* how many clusters to seek (= # of chemical components)
- \* method (Euclidian (r) or Angle)
- \* parameters of each method



I choose 3 as they are the only ones with meaningful signal

program has a way of defining which clusters are 'real' and often finds fewer than you ask for

this choice FINDS 3 components

All these choices affect the final result to some extent, which requires either experience, or some playing around to be happy that the set of parameters you choose is 'appropriate' for the data set. This is one of the 'Achilles heels' of the unsupervised approach - it needs supervision !!

I tend to use Euclidean, but Chris and his student Lerotic, have argued persuasively that angle is better

# Using PCA\_GUI cluster analysis to rotate PC

5. examine results

Significant components: 3

Seek: 3 cluster found: 3

Eigenimage scaling factor: 0.00

Cluster without using first principal component:  Yes  No

Distance measure:  Euclidean  Angle

Calculate:

- Scatterplots of pixel weightings
- Histogram of aggregate cluster distances
- Histograms of distances by cluster
- Dendrogram

Save cluster ".roi" files

Save all cluster spectra as ".eps"

Save all cluster spectra, images as ".png"

Save all cluster spectra, images as ".csv", ".nc", ".xas"

Dismiss

First 12 clusters:

Cluster number: 1

cluster #

Distances from cluster centers: max=1.27, rms=0.3604, 95%=0.6078

Distances image scaling factor: 0.00

Show outliers and spectra

Cluster 1 spectrum

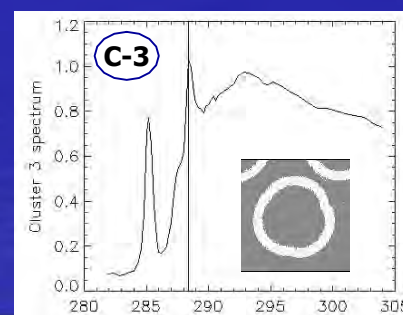
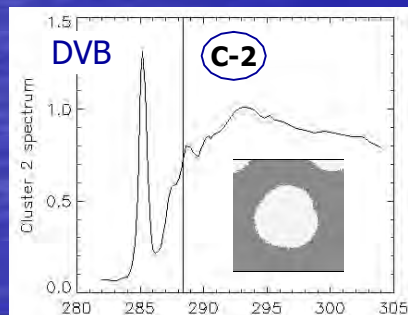
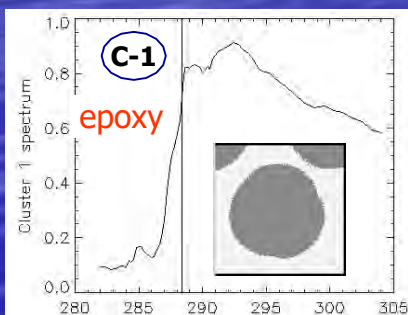
Photon energy (eV)

Component weights in cluster:

1:	-0.464	(36.37%)
2:	0.744	(58.32%)
3:	-0.0677	(5.31%)

PC composition

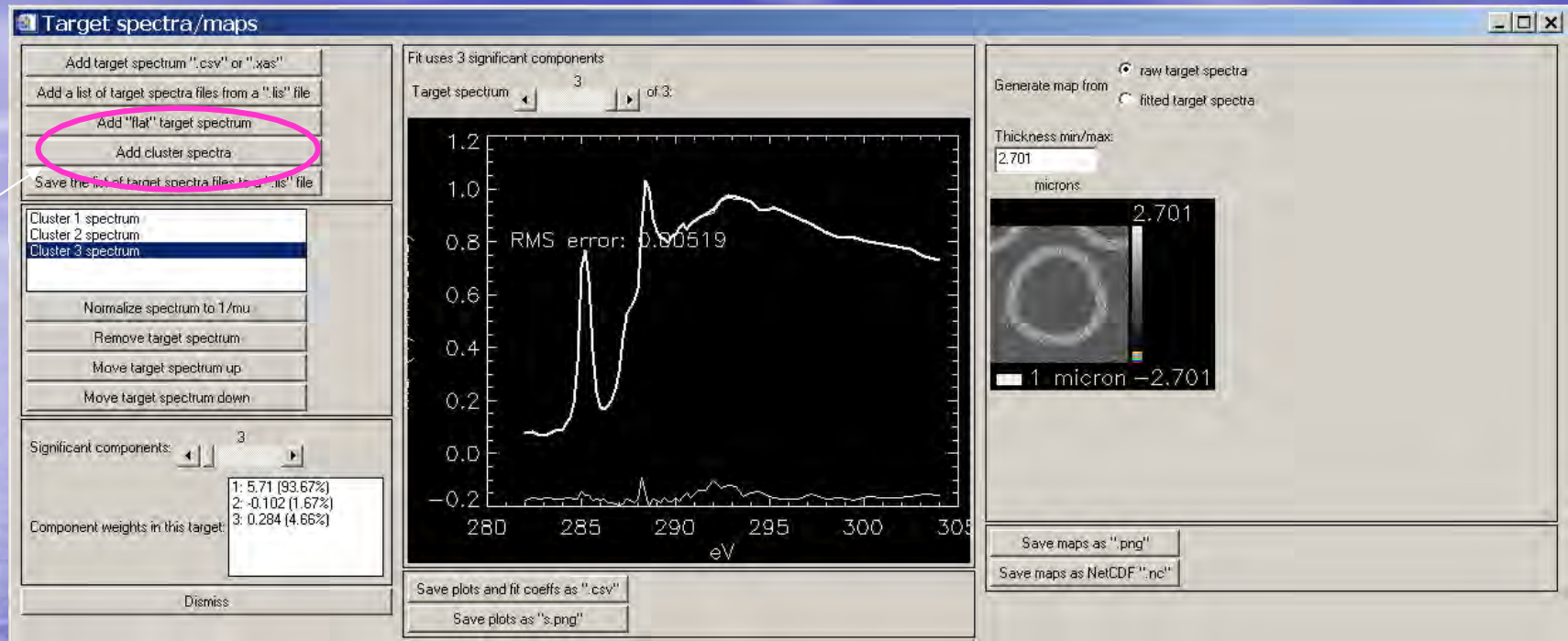
useful to look at this



Cluster 3 is the SHELL - which is spatially a well-defined component, but we know from the synthesis and comparison to pure-materials reference spectra that it is a mix of **DVB** and **EGDMA**

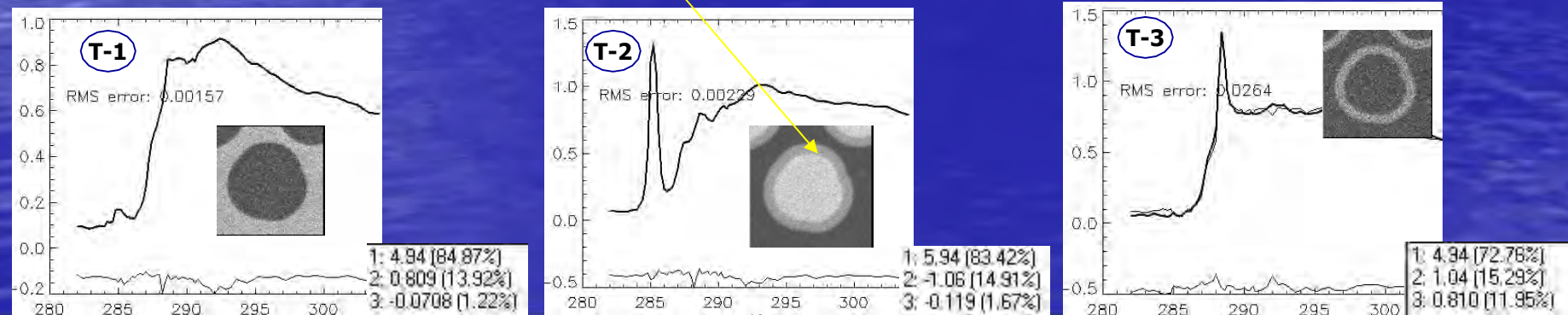
# Refining the analysis: target analysis

Auto adds the set of cluster spectra found from previous step



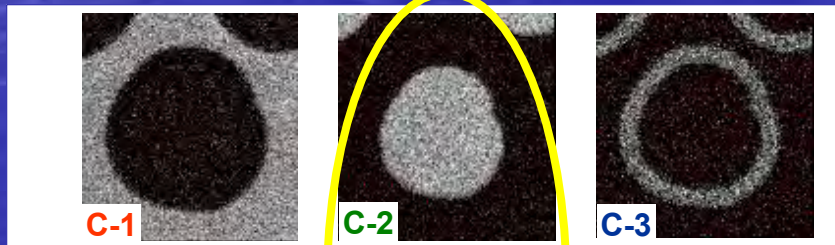
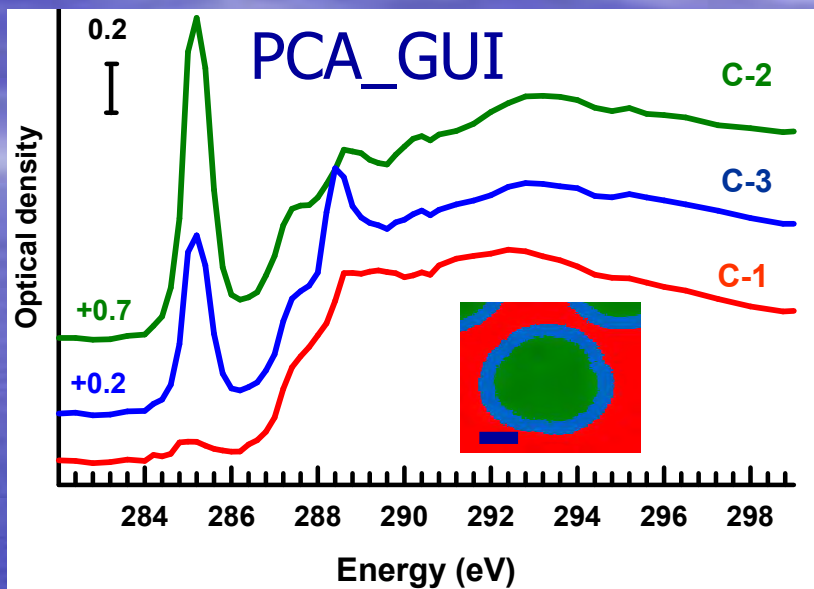
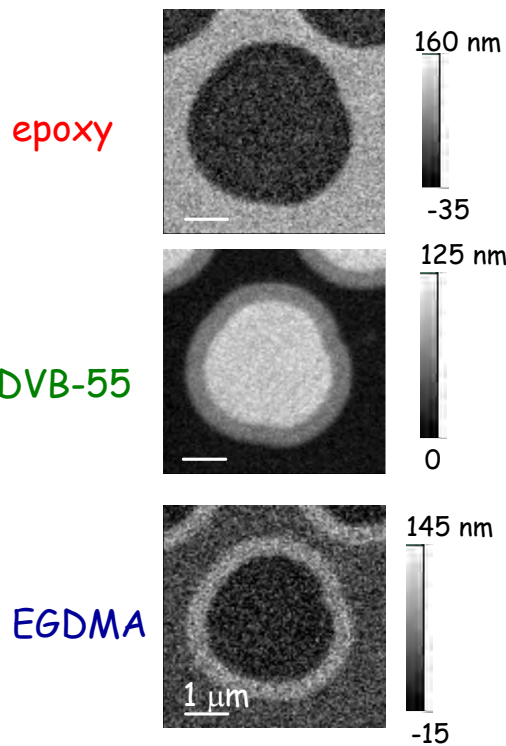
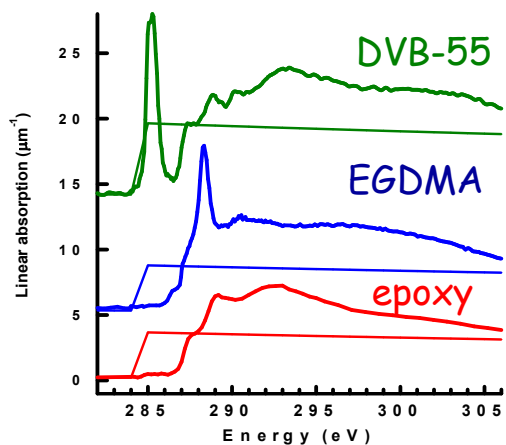
If you remove cluster#3 spectrum and add the spectrum of EGDMA (egdma-od-140.xas) then the analysis gets much better - it only finds EGDMA in the shell, and now finds **DVB** in the shell as well

Cluster 1 spectrum  
Cluster 2 spectrum  
egdma-od-140.xas



# Comparison of SVD and PCA\_GUI

## SVD



introduce EGDMA as a target spectrum

