

Dynamic Analysis Environment (DAE) – An Interactive GUI for Nuclear Forensics



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ABSTRACT

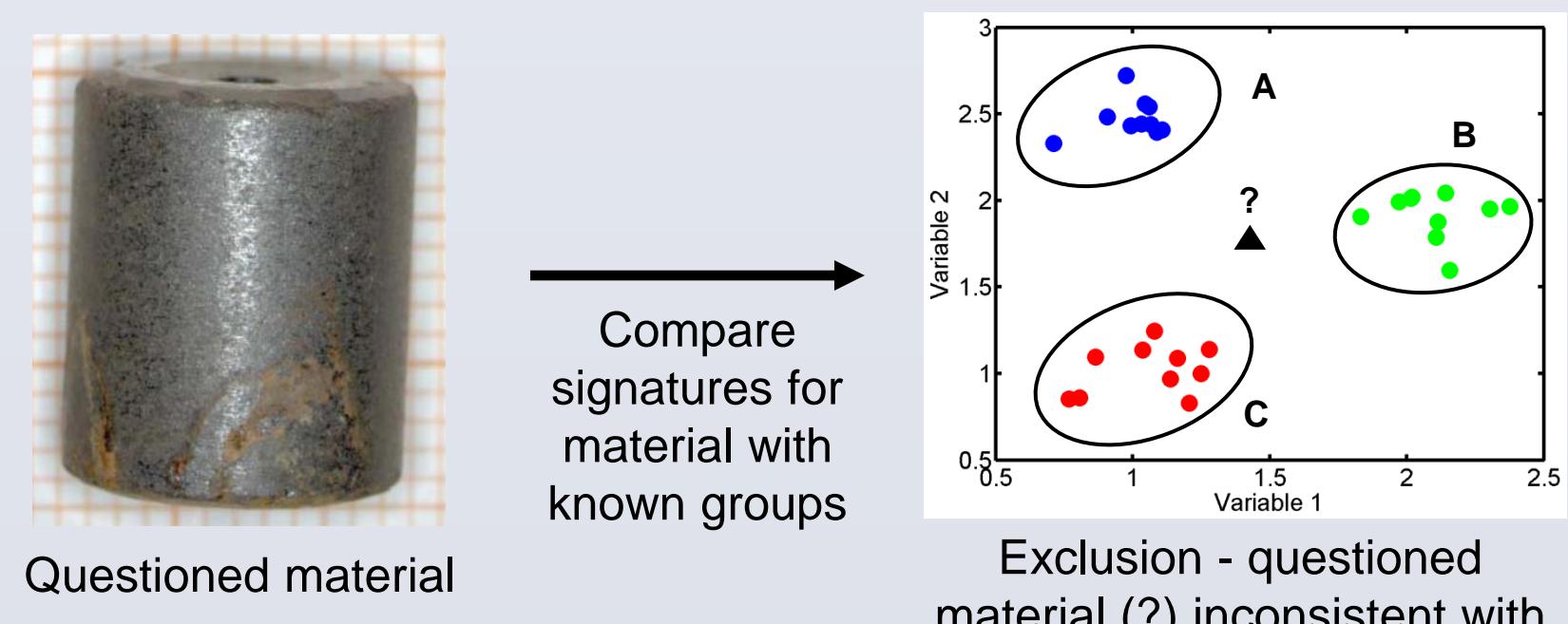
Dynamic Analysis Environment (DAE) is a graphical, user-interactive environment used to facilitate the analysis of data. Current efforts are focused on applying DAE to the analysis of nuclear forensics data. For this purpose, the following functionalities have been added to DAE: 1) the K-nearest neighbor supervised learning algorithm, and 2) numerous data-visualization tools to complement the principal component analysis supervised learning method already available in DAE.

INTRODUCTION

What is Nuclear Forensics? – Nuclear forensics is the characterization of intercepted nuclear materials to identify evidence of their source and intended use. The Domestic Nuclear Detection Office (DNDO) has supported the creation of national nuclear forensics libraries (NNFLs) of known nuclear materials against which to compare questioned materials as well as the development of multivariate group inclusion/exclusion algorithms to enable the linking of questioned materials/samples to their potential processes or facility of origin. Significant progress has been made in the creation of NNFLs and data analysis tools. However there has been little work done to integrate these data sets and tools into a single package to streamline group inclusion/exclusion analysis. DAE accomplishes this task.

What is group inclusion/exclusion?

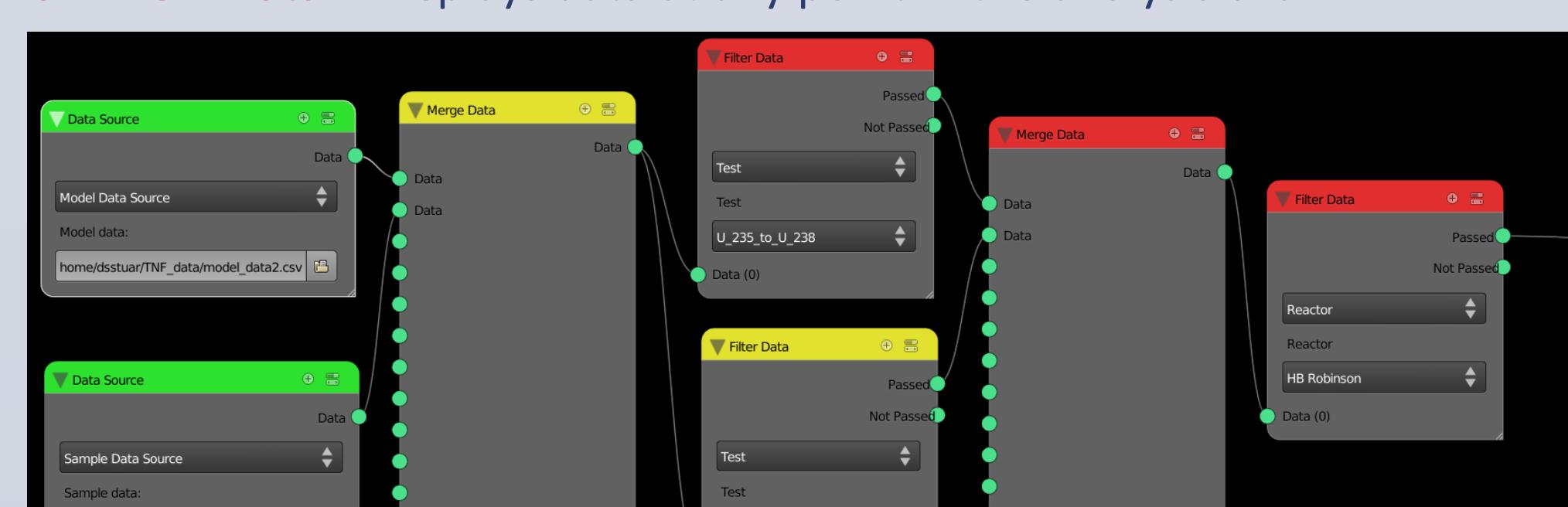
Inclusion: Identify a match between signatures of a questioned sample and that of a known group.



DAE – BASIC FUNCTION AND CAPABILITIES

DAE is an interactive, configurable environment that facilitates the analysis of very large data sets through the use of predefined analytical modules, called nodes. These nodes can be arranged into an analytical “chain” of data processing steps. Available nodes include:

- 1. Data Source** – Extracts known and unknown data from files.
- 2. Merge Data** – Combines data streams.
- 3. Filter Data** – Reduces data based on defined parameters (i.e. reactors or specific isotopic measurements).
- 4. Augment Data** – Prepares PCA or KNN model based on known/training data.
- 5. Relate Data** – Relates test data to PCA or KNN model.
- 6. View Data** – Displays data at any point in the analysis chain.



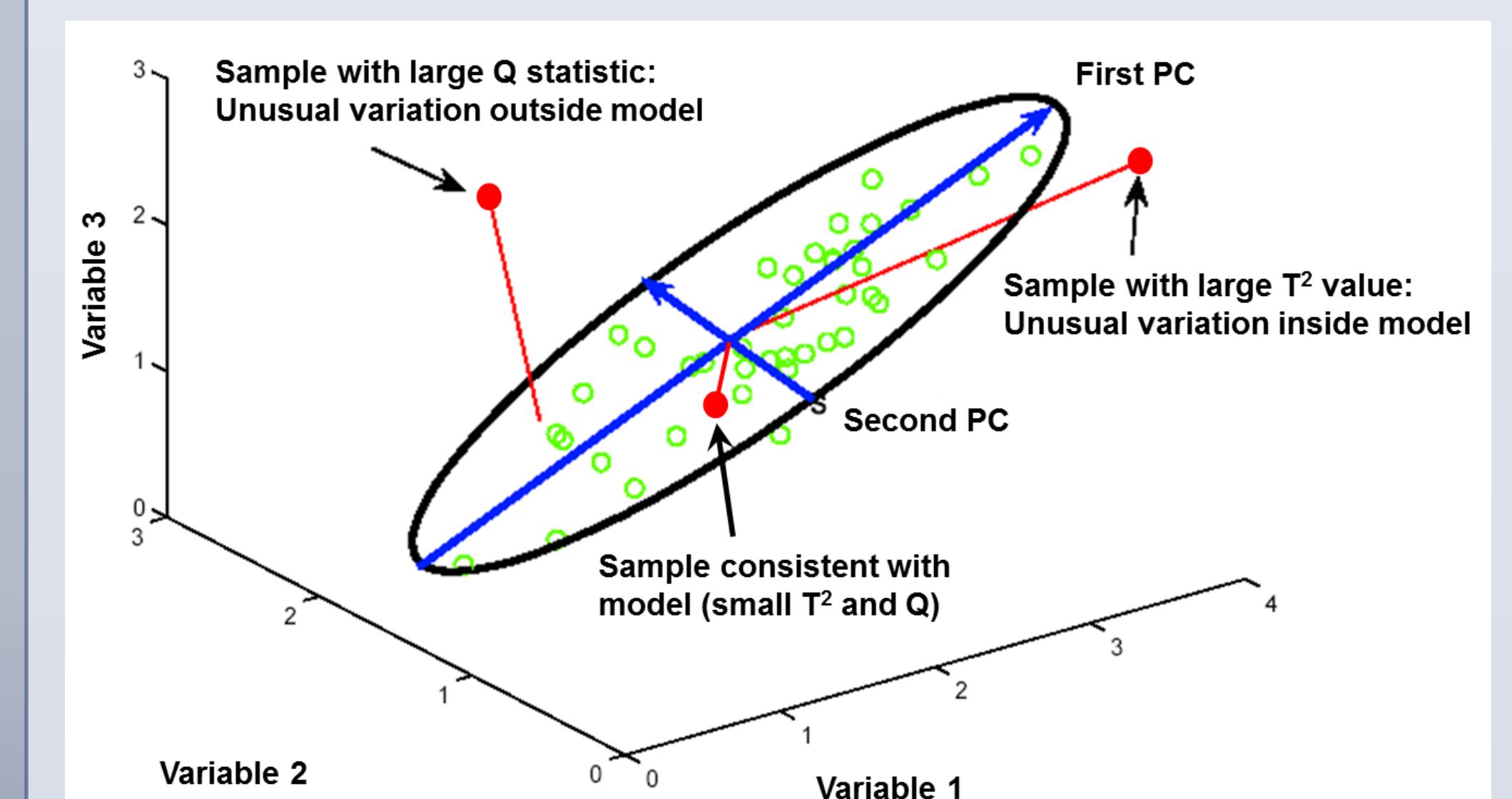
A data chain in DAE consisting of two data source nodes, a merge data node, two filter data nodes filtering on isotopic measurements, a second merge data node, and a filter node filtering on a reactor. Green nodes have completed their functions, yellow nodes are in the process of completing their functions, and red nodes have yet to begin their functions.

NUCLEAR FORENSICS DATA – SFCOMPO

In constructing and evaluating the performance of the PCA and KNN group inclusion/exclusion methods, known nuclear material data were taken from the open-source Spent Fuel Isotopic Composition (SFCOMPO) database, which consists of isotopic measurements of spent fuel samples from fourteen different nuclear reactors from around the world.

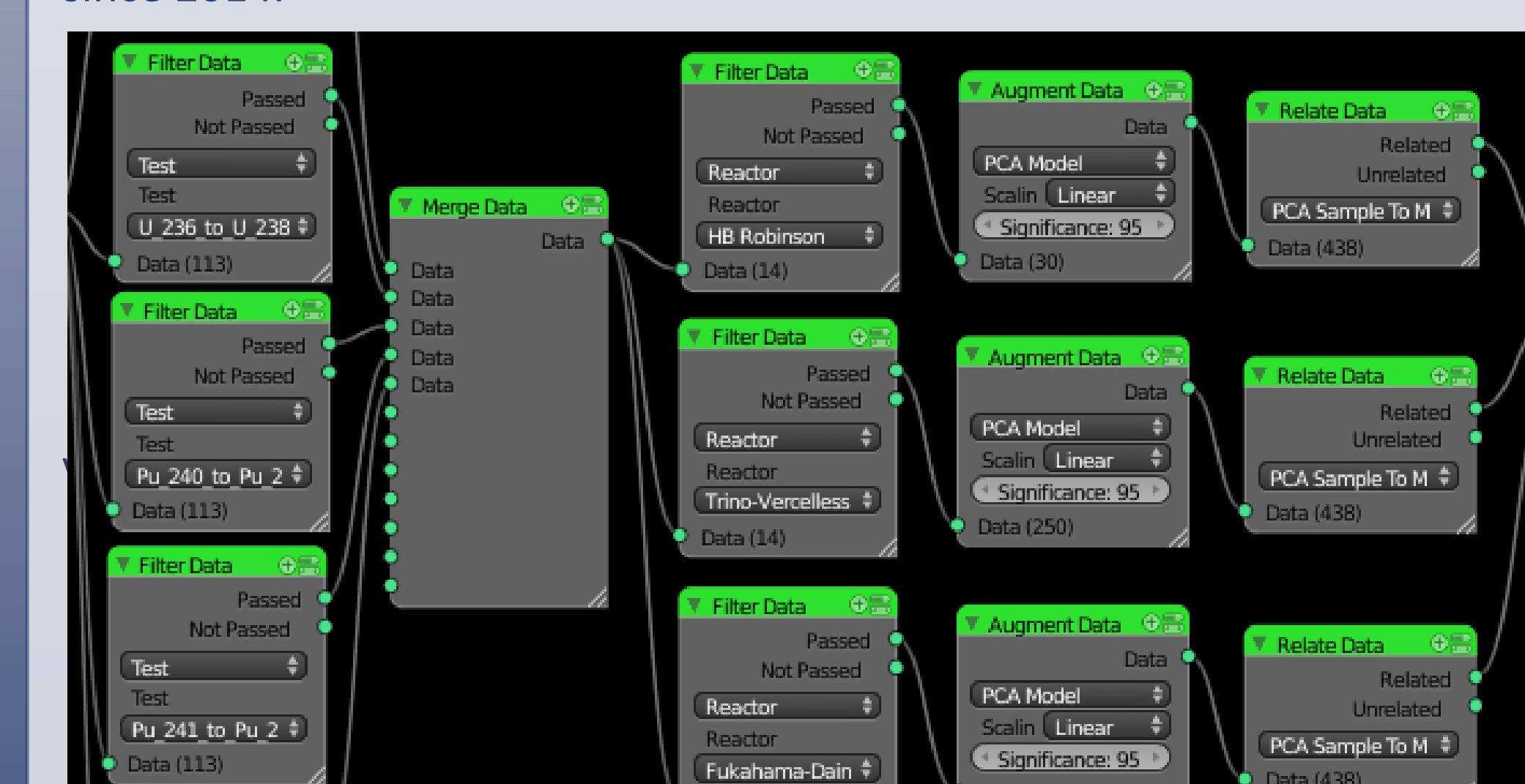
PRINCIPAL COMPONENT ANALYSIS (PCA)

Theory – The objective of PCA is to transform the coordinates of a data matrix to a new set of axes, called principal components, which optimally describe the data variance. Principal components (PCs) are assigned to the data matrix such that the first principal component explains the maximum amount of variation possible in the data set in one direction. Successive PCs are defined such that they are orthogonal to the previous PCs and describe the maximum amount of remaining variation in the data. Often, a small number of PCs describe a large percentage of the variance in the data, and subsequent PCs may be ignored. Once PCA is performed on model data, sample data can be compared to the model data by projecting the measurement variables of each sample into the PC space. Sufficiently small values of the Q , Hoteling's T^2 , and Hawkins' T_H^2 statistics indicate the sample is consistent with the model data.



An example of comparing sample data to a PC model using Q and T^2 values.

PCA has been available in DAE as a group inclusion/exclusion method since 2014.



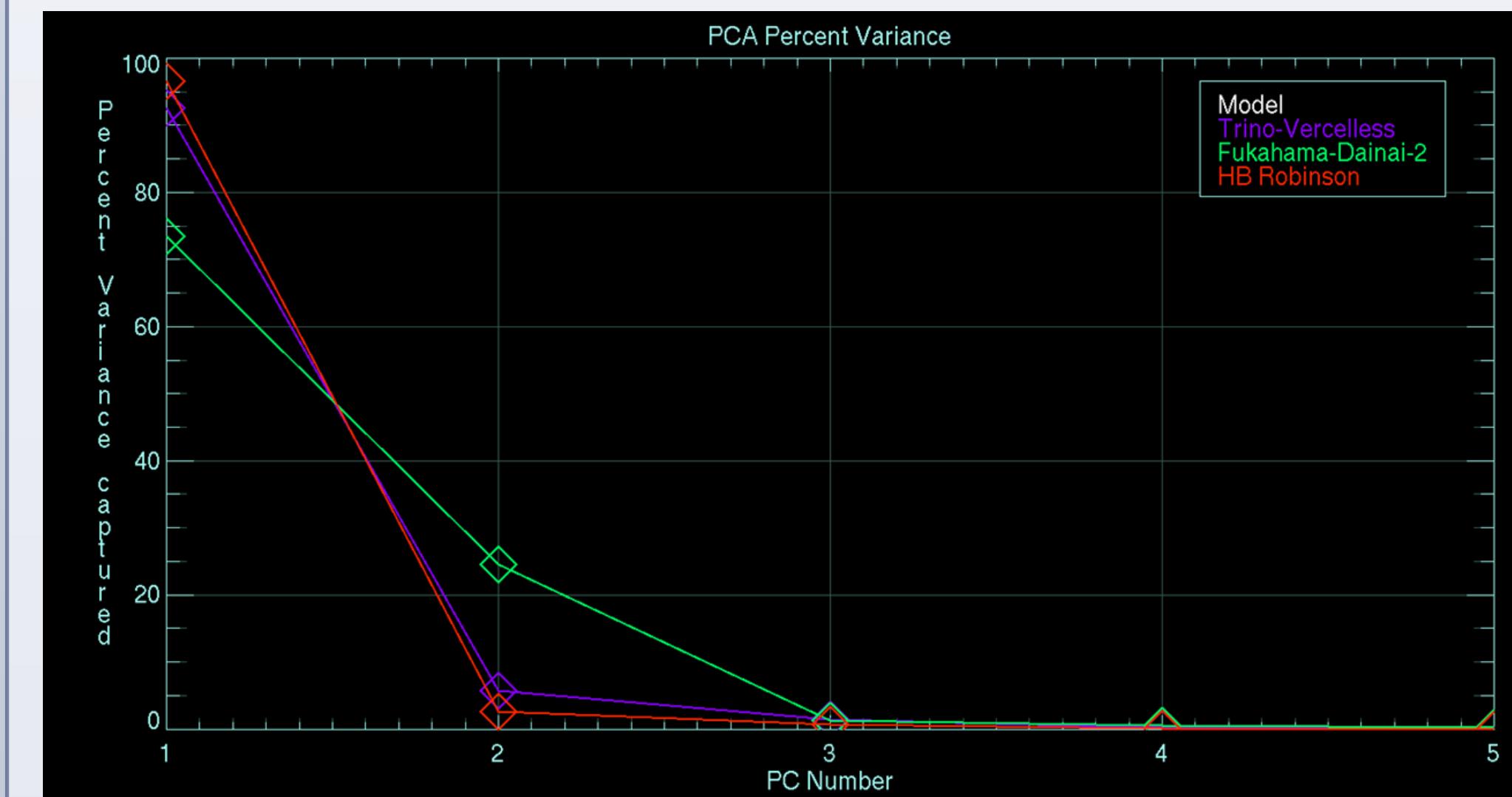
A data chain in DAE performing PCA on known and unknown data. Known and unknown data are filtered on various isotopic ratio measurements. “PCA Model” augment data nodes build PCA models for each of three reactors (specified with preceding filter data nodes). “PCA Sample To Model” relate data nodes compare the unknown sample data to each PCA model, calculating a Q , T^2 , and T_H^2 value for each unknown sample.

PRINCIPAL COMPONENT ANALYSIS (continued)

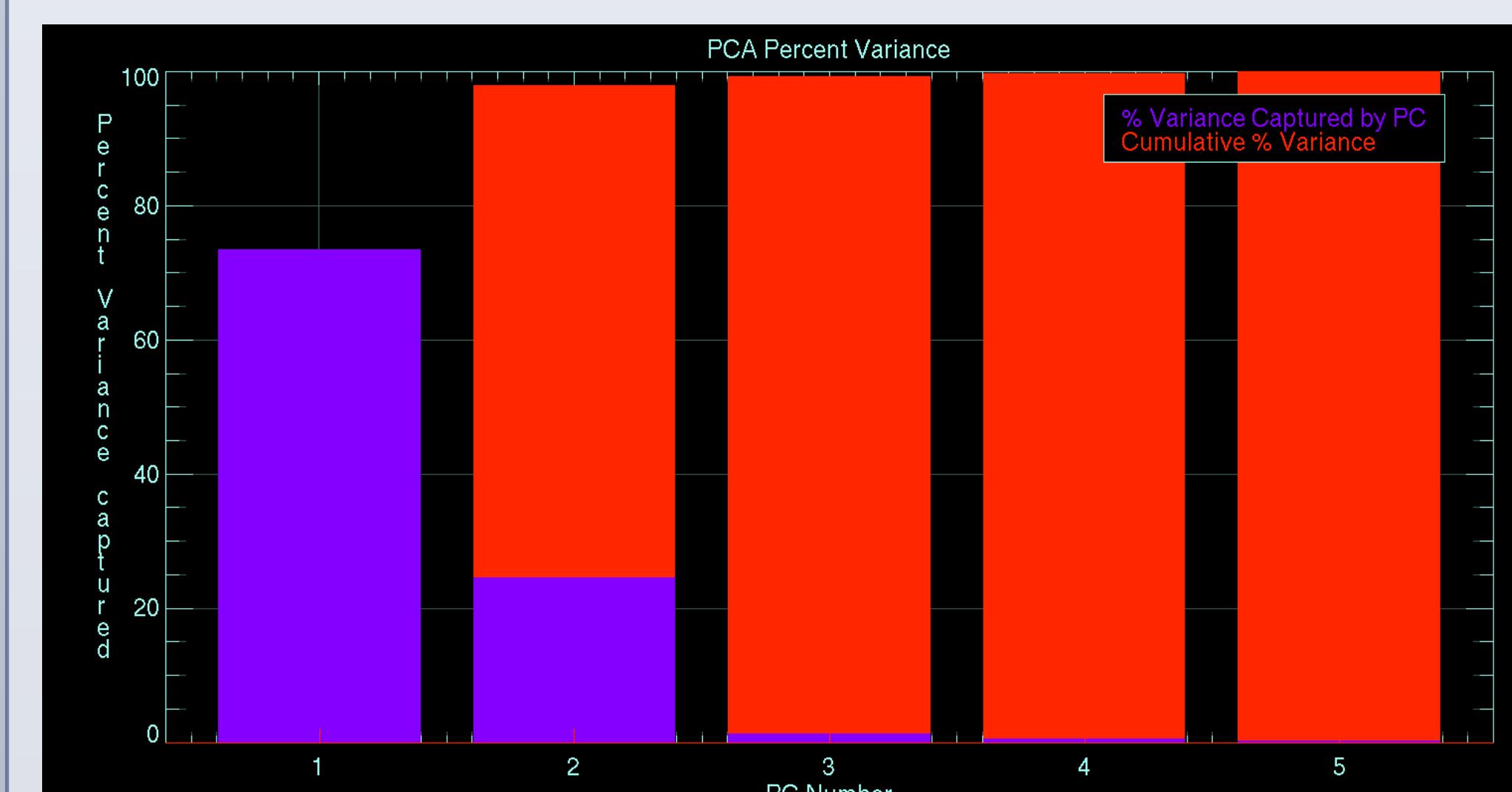
Model	RF	1	2	3	4	5	6	7	8	9	10	11
Fukushima-Daini-2	1	0.6354	0.3976	0.2017	0.5457	0.5799	0.0966	0.4430	0.2466	0.0444	0.0304	0.1993
HB Robinson	1	0.4286	0.6056	0.1934	0.4459	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Trino-Vercellese	1	0.0054	0.0000	0.0000	0.0003	0.4246	0.7450	0.3026	0.4599	0.5957	0.2493	0.3147

A PCA Sample to Model Correlation table output by DAE. The cells give each of 11 samples' Q -probability to PCA models formed by data from three reactors. Higher Q -probabilities indicate a close match with a model and are designated by brighter colors.

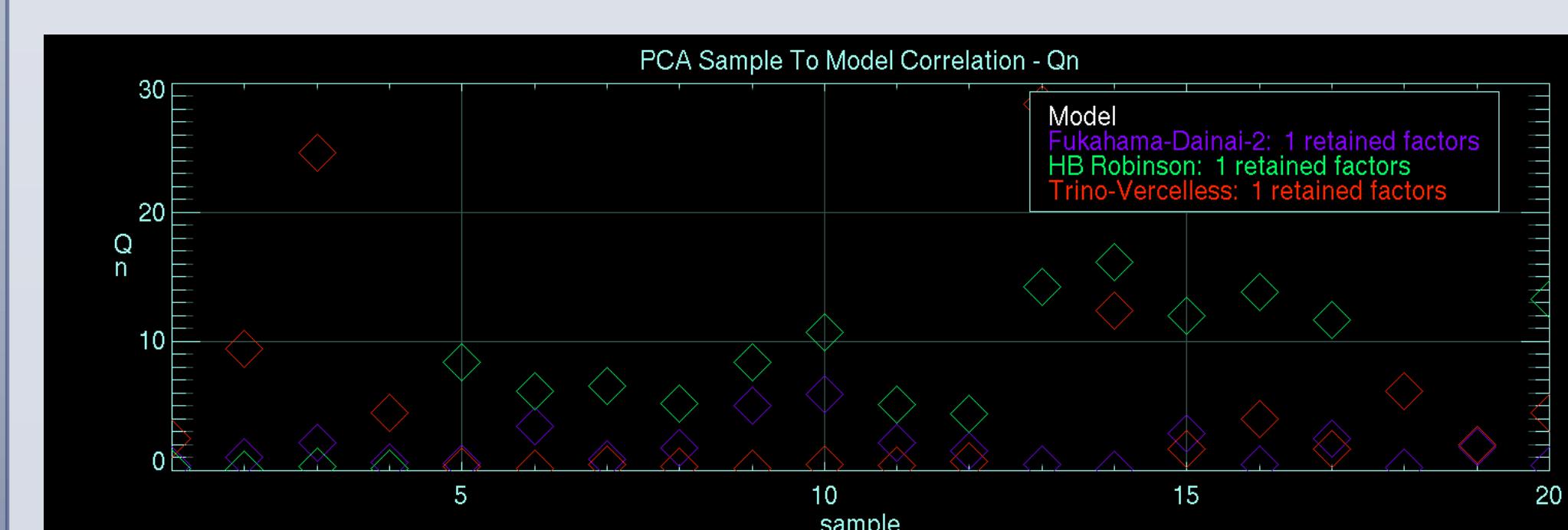
Additions to DAE – A number of data visualization tools have been added to DAE to complement the existing PCA capabilities.



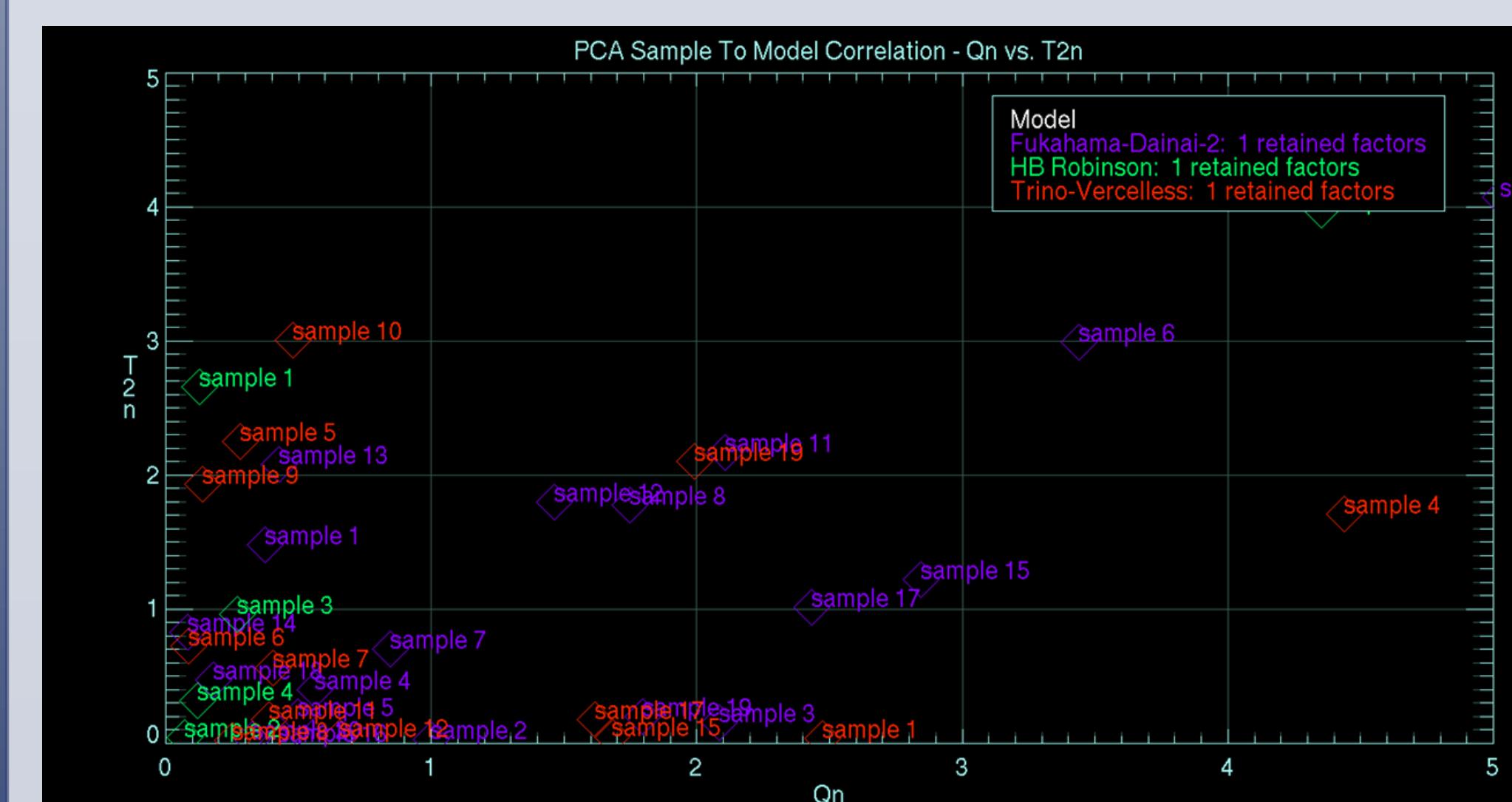
A newly-added visualization tool displays the percent variance captured by each of the five PCs for models formed using data from three reactors. This feature allows the user to determine how many PCs need to be retained in order to adequately model the data.



An additional tool which displays both the percent variance captured by each PC and the total variance captured up to that point by previous PCs in a bar graph.



A newly-added data visualization tool that plots the Q value of each sample, in this case for three different PCA reactor models. The tool can also produce identical plots for T^2 and T_H^2 .

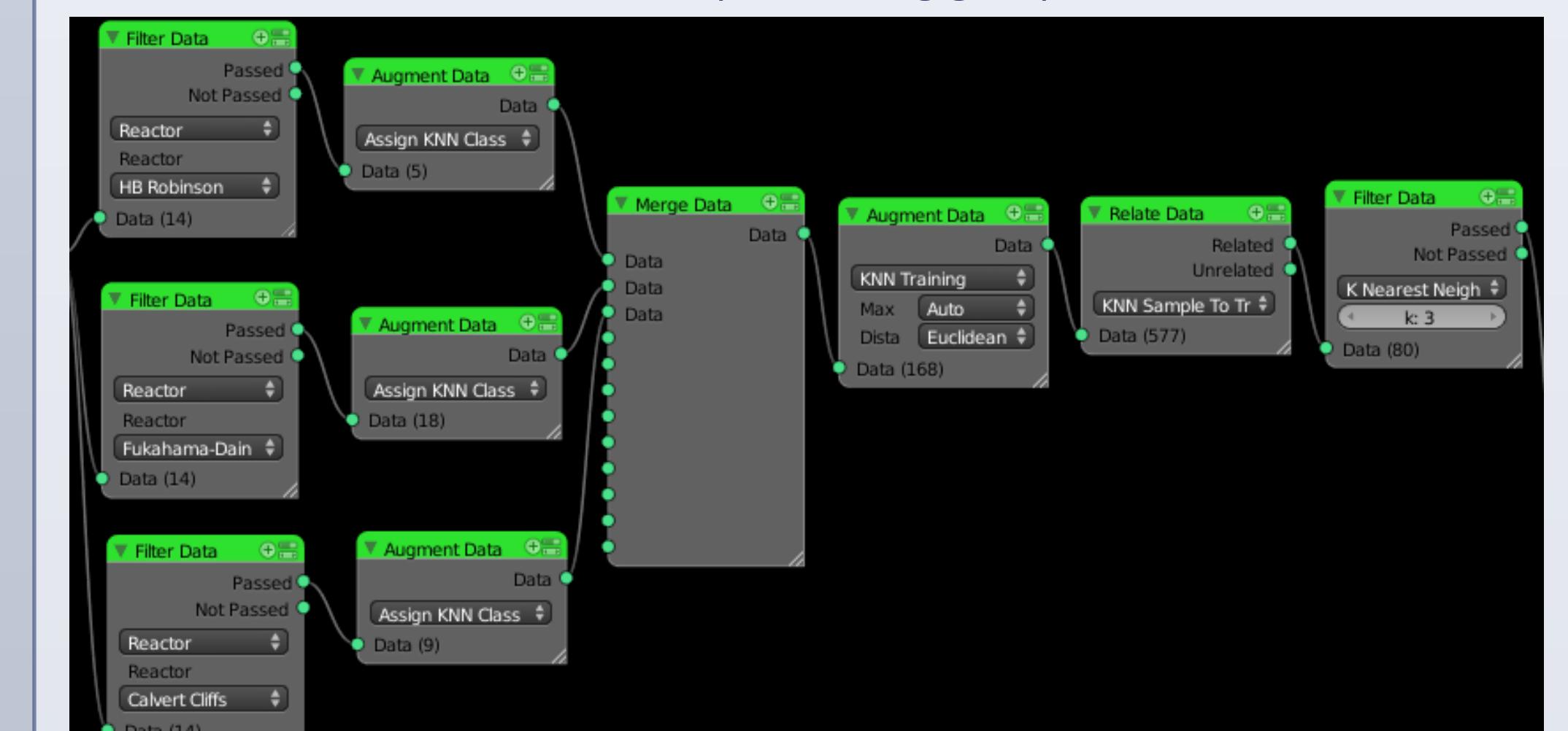


An additional tool which plots the Q value of each sample against its T^2 value.

K-NEAREST NEIGHBORS (KNN)

Theory – The KNN algorithm predicts the class of an unknown sample based on the majority vote of the known classes of the k sample(s) nearest to it. Each sample is then assigned a *goodness value*. A low goodness value indicates that a sample is well-contained by known samples in the class to which it is assigned. If a sample has a goodness value that exceeds the *goodness value threshold* of its assigned class, the sample is deemed to not be a member of that assigned class.

Addition to DAE – KNN is now available in DAE as a method for performing group inclusion/exclusion.



A data chain in DAE performing KNN. The “Assign KNN Class” augment data nodes assign a class ID to three sets of known data from three reactors. The data and class IDs are recombined, and a “KNN Training” augment data node both determines the goodness value threshold of each individual class as well as performs the KNN algorithm on each class, recording the percentage of known samples correctly classified for each value of k , thus allowing the user to choose an optimal value of k to use in subsequent calculations. The KNN Training augment node also allows users to choose a distance metric (i.e. Euclidean, City Block, Minkowski, etc.) for which to compute the k (also defined by the user) nearest neighbors of sample data points. A “KNN Sample to Training” relate data node assigns a class and goodness value to each unknown sample. If the goodness value of a sample exceeds the threshold of the class to which is assigned, the assignment is removed.

KNN Sample To Training Classification												
Training Class	K	1	2	3	4	5	6	7	8	9	10	11
Fukushima-Daini-2	3	NaN	0.202039	-1.20507	-1.18560	NaN	NaN	NaN	NaN	0.086031	0.040704	
Calvert Cliffs	3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	
HB Robinson	3	0.0000	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	

The KNN Sample to Training classification table output by DAE. The cells give each of 9 samples' goodness values for classes (formed by data from three reactors) to which they are assigned for $k = 3$. Lower (or negative) goodness values indicate a close match with a class and are designated by brighter colors. A value of NaN in a cell indicates that a sample has not been assigned to the corresponding class.

FUTURE PLANS

- Data visualization tools to complement the new KNN group inclusion/exclusion method will be added.
- Work will also be performed to evaluate and compare the success with which the PCA and KNN algorithms in DAE relate questioned data samples to reactors in the SFCOMPO database.

ACKNOWLEDGEMENTS

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