Undergraduate Research Report for Spring 2012

William K. Bittner*Florida Institute of Technology, Melbourne, FL
william.bittner@gmail.com

Abstract

This paper is in regards to the various research produced for Spring 2012 Undergraduate Research under Dr. Hohlmann, and in collaboration with Dr. Mitra, and the High Energy Physics Group A. The research this semester has covered a wide area. First focusing on getting results using POCLUST and CLUSTVIZ on real data that contained depleted Uranium and Lead. After that, the research principally focused on the future of Vx4D, POCLUST, CLUSTVIZ, and all the work done with Dr. Hohlmann and Dr. Mitra during my undergraduate career.

*Dr. Hohlmann, Dr. Mitra

.Contents

I. Introduction

The semester can essentially be split into two main parts:

1.1 Before FAS 2012 Annual Conference

This period of time was spent extending and concluding the research performed in the Fall of 2011, primarily focused on producing results from the world on POCLUST and CLUSTVIZ in order to present them at the FAS 2012 Annual conference. The target scenario was the "5 on a die" scenario, which featured 5 blocks of material including depleted Uranium in the middle. The goal was the be able to isolate the Uranium from the surrounding materials, using POCLUST, and to show that Muon Tomography and POCLUST is a viable solution for detecting Shielded Nuclear Weapons in Cargo

POCLUST POCLUST is a density based clustering algorithm, that was created by Dr. Mitra, originally based on the clustering of GEANT4 simulation data of the Muon Tomography station. It was created to be able to classify POCA points into "clusters" and with those clusters, calculate properties to be able to identify the material of the cluster. This is central for the detection of uranium inside lead shielding

CLUSTVIZ I created CLUSTVIZ in the Fall of 2011 to be able to visualize the output of POCLUST in comparison to the original target positions, using OpenGL and Linux, and to be able to calculate a metric for comparing results

1.2 After the FAS 2012 Annual Conference

After the FAS 2012 Annual Conference, efforts were mainly focused on bringing together all the research that I have done for Dr. Hohlmann over my Undergraduate Career and get it ready to be passed on to the future of the High Energy Physcis Group A. Furthermore, I wanted to continue my research while working at IBM, so directions were chosen that would align with both the Group's interest, and what would be possible, and most optimal while persuing my career at IBM. This period of research can be broken down into the following parts:

POCLUST rewrite The POCLUST code base originally obtained in the Fall of 2011 was long needed of a rewrite. Furthermore, with the consideration of future students continuing the research, I wanted the essential parts of the Algorithm to be easily abstracted, so that future students can do research on the Algorithm, without being concerned about the entirity of the working internals. This would allow students a low learning curve to get started with POCLUST, and therefore increase the probability of it being continued.

Parallel and Distributed Clustering using Hadoop Hadoop is growing in huge popularity in the sector of Big Data and Data Analytics, and runs seamlessly on a cloud infrastructure, all three of which belong to IBM's top 5 initiatives. Furthermore, if any complex methods of the optimization of POCLUST parameters were going to be used, much more computational power would be needed. Therefore, by bringing POCLUST to a parallel and distributed architecture through Apache Hadoop, this would align both the Group's interest, and that of my professional career. Therefore, much research was done in this area

The inclusion of Vx4D into ROOT ROOT is an object oriented data analysis framework built by CERN. All of the research students are familiar with ROOT, and it is used extensively

within the High Energy Physics Lab A. Vx4D is a stand alone software package I build for the High Energy Physics Group A initially. It is customized exactly to our needs, and had to be created because of the lack of 4D Voxelized Data visualization software available. ROOT was currently being used for doing 2D imaging on the data with "slices". In order to remove the necessity to maintain the framework of Vx4D, research was done to integrate Vx4D into ROOT. Therefore, future Undergraduate students can simply use ROOT's scripting ability to call Vx4D just like they would any other histogram.

II. POCLUST

2.1 POCLUST Overview

- POCA Points are read in, unvoxelized
- Simple thresholds applied to remove major noise
- Clustering of the POCA points begin
- Deletion or removal of âĂIJsporadicâĂİ clusters occurs on intervals
- Merging of Clusters that meet criteria
- When all the points have been processed, output is visualized in OpenGL and compared to original targets in wireframes

2.2 Key Parameters in POCLUST

MAX_POINTS_IN_CLUSTER This is the number of points at which, greater than this, the cluster no longer uses a euclidean measure, and uses a measure based euclidean distance multiplied by a factor of $Theta^2/ClusterVariance$ a.k.a DM Measure

MAX_L2_NORM_DIST This is the maximum distance a point can be from a cluster when using the euclidean measure

MAX_DM_NORM_DIST This is the maximum distance a point can be from a cluster when using the DM measure

angleThresh If the $Percent < 4$ and the number of points is greater than 50, then the cluster is "thrown" away, where $Percent =$The percent of POCA points within that cluster that has an average deflection angle of $<$ the parameter angleThresh

MinPercent two clusters are said to be similar if $abs($Percent of Cluster1 $-$ Percent of Cluster 2$) <$ MinPercent and also for MinVariance

MinVariance two clusters are said to be similar if $abs($Percent of Cluster1 $-$ Percent of Cluster 2$) <$ MinVariance and also for MinPercent

CENTROID_DISTANCE two clusters are said to be isClose() if the euclidean distance between the two centroids is $<$ CENTROID_DISTANCE

OVERLAP_PERCENTAGE two clusters are said to overlap() if $(overlapVolume/(volumeCluster1 + volumeCluster2)) >$ OVERLAP_PERCENTAGE

2.3 Building POCLUST and using POCLUST

To build POCLUST, it is quite easy. If you are in the `/poclust/algo/` directory, make sure you:

1. unvoxelized poca file is copied to the file input.txt
2. edit input.txt, and make sure the first line the in dimensions of the volume i.e. "300 300 300"
3. type in `./build.sh`
4. the `cluster_vis_output.m` is the file that CLUSTVIZ will take as a POCLUST output

III. CLUSTVIZ

3.1 CLUSTVIZ Overview

CLUSTVIZ was built in order to visualize the POCLUST output, and be able to compare it to the original target locations. It does this by take two files as parameters, one file being the original target location, and one being the output from the POCLUST `cluster_vis_output.m`. The white cubes inside of the volume represent the original targets, and the opaque objects represent the clustered objects. The color represents the mean scattering angle of that cluster / 15

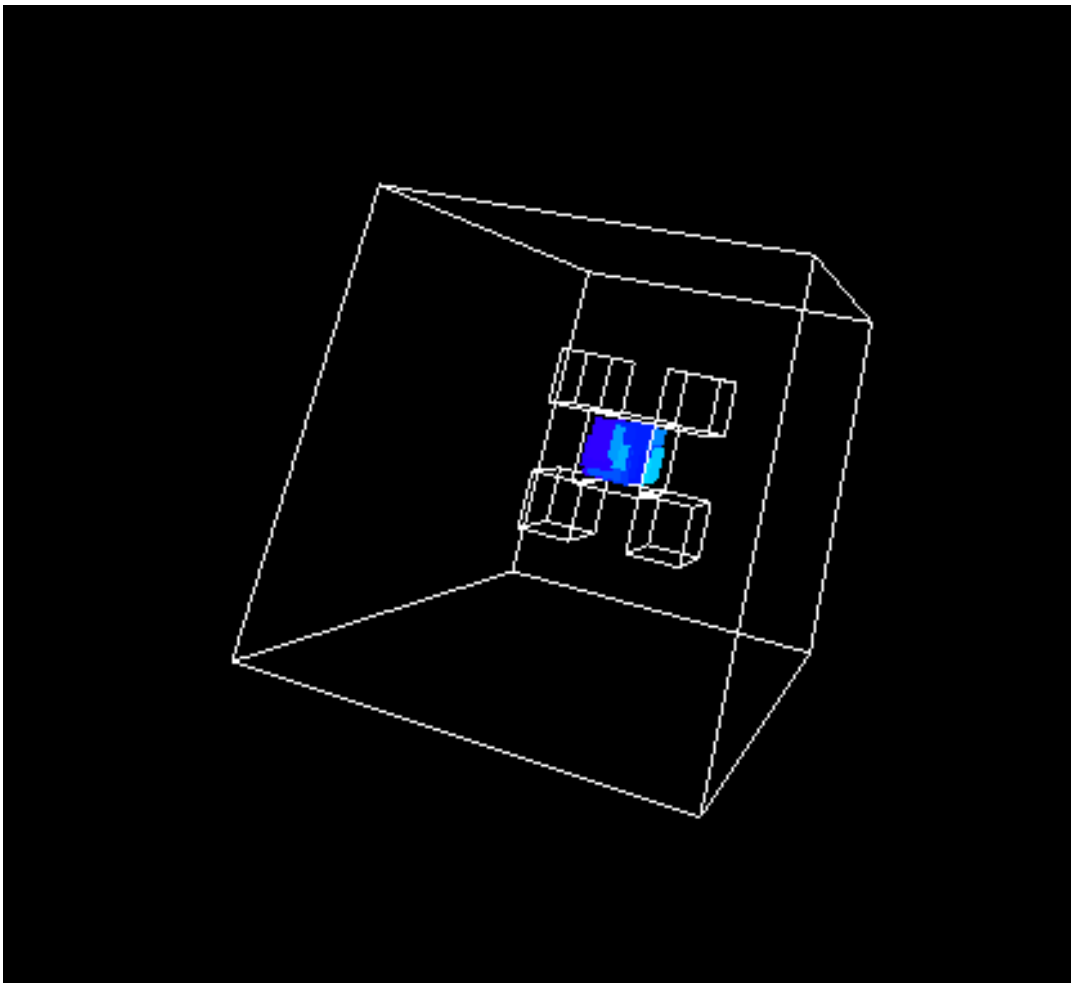


Figure 1: CLUSTVIZ example output, white boxes are the original target locations, and the opaque objects are the clusters from POCLUST

3.2 Building CLUSTVIZ

CLUSTVIZ, requires the same packages as Vx4D to be built. It also uses a make.sh file. The following packages are required:

- `directfb (libdirectfb-dev)`

- `stdc++ (libstdc++6-4.4-dev or apt-cache search libstdc++ for current version)`
- `libglu1-mesa-dev`
- `libglib2.0-dev`
- `libgl1-mesa-dev`
- `libx11-dev`
- `freeglut-dev (glutg3-dev)` After those development libraries are installed, go to the /verb!/poclust/visual/! directory and type:
  `./make.sh`
  After that, go to the bin directory, and you will see a file named:
  `pvis`
  That is the executable

3.3 Using CLUSTVIZ

When using CLUSTVIZ, you need two files, you need the `cluster_vis_output.m` file from POCLUST, and you need a file describing the original targets, Targets.dat or whatever you want to name it. Then you run it by:
`./pvis Targets.dat cluster_vis_output.m`
Of course, you can name the files what ever you want. The import thing is that Targets.dat is setup properly. Here is an example of the "5 on a die" scenario.

```
300 300 300
43 43 43 -48.8 -10.5 -45.5 1 1
43 43 43 47.5 -10.5 -46.5 1 1
43 43 43 -47.5 -10.5 44.5 1 1
43 43 43 47.5 -10.5 44.5 1 1
54 54 54 0 -5 0 1 1
```

The first line is ALWAYS the dimensions of the space. This must be the same dimensions you gave to POCLUST for the data. It goes X Y Z
Each line after that, the format is `ObjXLen ObjYLen ObjZLen ObjXPos ObjYPos ObjZPos 1 1`
Note: Y is the height, and Z is the distance from the viewer into the horizon, -z would be closer to you, this is the OpenGl coordinate system

IV. FAS 2012 Results

This section covers the results presented at the FAS 2012 Annual meeting, in which the latest POCLUST results were presented on the "5 on a die" real data, focusing on being able to distinguish between the Lead and the Depleted Uranium.

4.1 The dataset setup

The dataset was the "5 on a die" scenario, which was taken by Mike Staib, on the Cubic Foot MTS Station, around early February 2012. The targets were setup as follows:
The dimensions given to the POCLUST algorithm were "300 300 300".

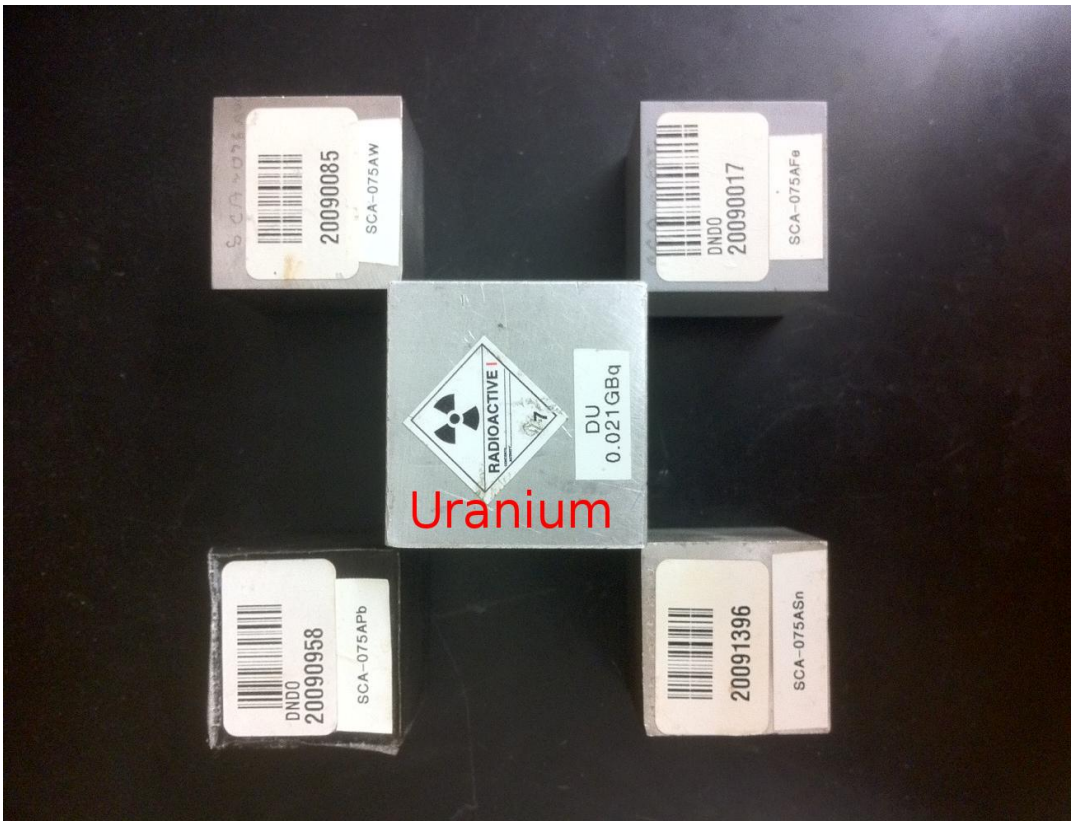


Figure 2: The top left is W , Top right is Pb, Bottom left is Sn, and bottom right is Fe

The original target positions for CLUSTVIZ were:

```
300 300 300
43 43 43 -48.8 -10.5 -45.5 1 1
43 43 43 47.5 -10.5 -46.5 1 1
43 43 43 -47.5 -10.5 44.5 1 1
43 43 43 47.5 -10.5 44.5 1 1
54 54 54 0 -5 0 1 1
```

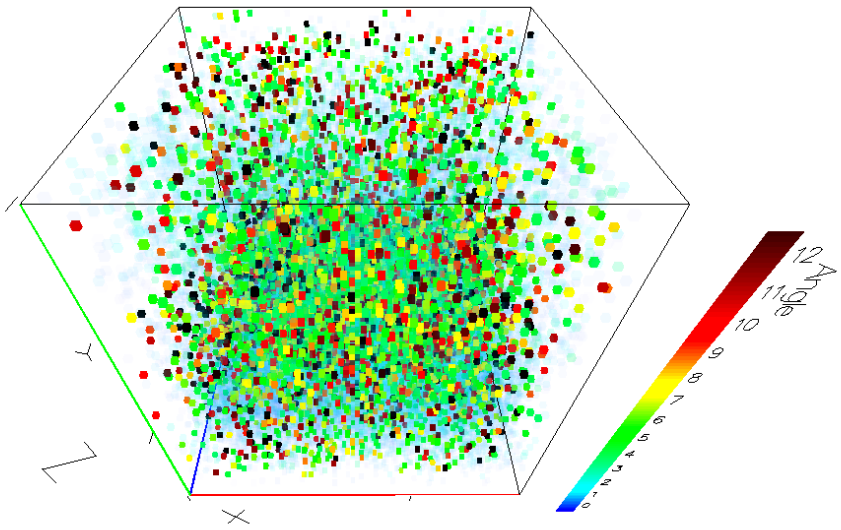


Figure 3: Vx4d output of "5 on a die" without any cuts applied

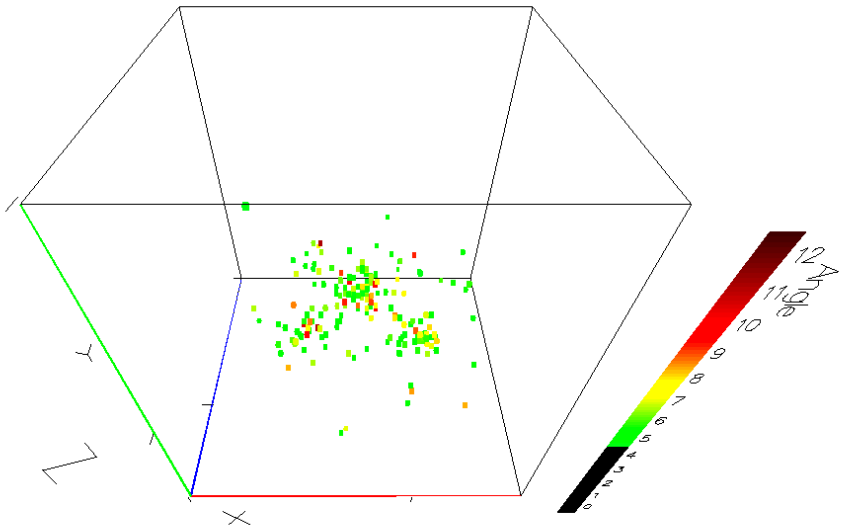


Figure 4: Vx4d output of "5 on a die" with manual cuts applied

Table 1: common.h

```
#define DOCA_cut 1
#define angThresh 4
#define MAX_L2_NORM_DISTANCE 100
#define MAX_DM_DISTANCE 1000
#define MAX_CLUSTERS 20000 //max no of clusters inside a voxel..
#define MinPointsInCluster 100 //this means that there should be 200 points inside a cluster, and af
#define MAX_OBJECTS 20000
#define P0 3
#define DENSITY_THRESH 1
#define TIME_STAMP 10000
#define OVERLAP_PERCENT 10
#define CENTROID_DISTANCE 250
#define MIN_VARIANCE 1
#define MIN_PERCENT 3
#define Ldeg 0.5
#define Udeg 15
#define MIN_ANG_CUT_ALL_TRACKS 1
```

Table 2: pocaStats.c parameters

```
#define Lcut 2
#define Ucut 15
#define DOCA_CUT 1
```

4.2 The raw data

Figure 3 is what the raw data from POCA output looks like, without any cuts applied:
After manual cuts were applied, in Figure 4, you can somewhat see the resemblance of the objects, but nothing that would be adequate for distinguishing Uranium from the Lead Shielding.

4.3 POCLUST Parameters settings

There are many parameters in POCLUST, but here are the main ones, and their current values, at the time these results were produced: Also, the final merging from "GeantPackage.cpp" was removed, along with other things:

4.4 CLUSTVIZ output

After tinkering around with the parameters and removing the final merging, which from the results seemed to be buggy, I was able to achieve the following output:

Table 3: GeantPackage.cpp diff

```
35 @@ -133,7 +133,7 @@ void Input_Geant_Data(char filename[]){
36     //for testing purpose NOW which basically finds non-sporadic clusters..
37     Find_objects_from_all_clusters(space.root,&Finclust,num);
38
39 -
40 +   //:NOTE: Removed the cluster merging and got a lot better result
41     //Merge the clusters with eachother..
42     //ClusterMerging(&Finclust);
44 @@ -270,13 +270,18 @@ void Output_to_File(data *ptr){
45         clusterDetail out;
46         double percent,factor,pr,lambda;
47         FILE *fout=fopen("output.txt","w");
48 -       FILE *matlab=fopen("5trgAir.m","w");
49 -
50 +       FILE *matlab=fopen("cluster_vis_output.m","w");
51 +
52 +       if (matlab == 0)
53 +       {
54 +           fprintf(stderr, "Could not open file for output");
55 +           exit(1);
56 +       }
57         factor=(10*(M_PI)*(M_PI)*10000)/(18*18);
58
59 -       fprintf(matlab,"function I=truck()\n");
60 -       fprintf(matlab,"rppd([400,300,300],[0,0,0],[0,0,0],[1,0,0],0);\n");
61 -
62 +       //fprintf(matlab,"function I=truck()\n");
63 +       //fprintf(matlab,"rppd([400,300,300],[0,0,0],[0,0,0],[1,0,0],0);\n");
64 +       fprintf(matlab,"%d %d %d \n",lenght,width,height);
65         for(int i=0;i< ptr->len;i++){
66
67                 c=ptr->object[i];
68 @@ -304,9 +309,14 @@ void Output_to_File(data *ptr){
69                 fprintf(fout,"\t\tEstimated density at last: %lf \n",lambda);
70
71                 //Printing the matlab code.
72 -               if(out.dX!=0 && out.dY!=0 && out.dZ!=0 && out.varTheta<15)
73 -                   fprintf(matlab,"rppd([%lf,%lf,%lf],
[%lf,%lf,%lf],[%lf,0,%lf],[0,0,0],1);\n",(2*out.dX)/10,
(2*out.dY)/10,(2*out.dZ)/10,(out.centroid.x)/10,(out.centroid.y)/10,
(out.centroid.z)/10,out.varTheta/15,
1-out.varTheta/15);
74 -
75 +               if(out.dX!=0 && out.dY!=0 && out.dZ!=0)
76 +                    //'&& out.varTheta<50)
77 +               //  fprintf(matlab,"rppd([%lf,%lf,%lf],[%lf,%lf,%lf],[%lf,0,%lf],[0,0,0],1);\n",(
78 +                   fprintf(matlab,"%lf %lf %lf %lf %lf %lf %lf 1\n",(2*out.dX)/10,(2*out.dY)/10,
79 +                    (out.centroid.x)/10,(out.centroid.y)/10,(out.centroid.z)/10,
80 +out.avgTheta/10);
81 +//out.varTheta/50);
82 +
83             }
```

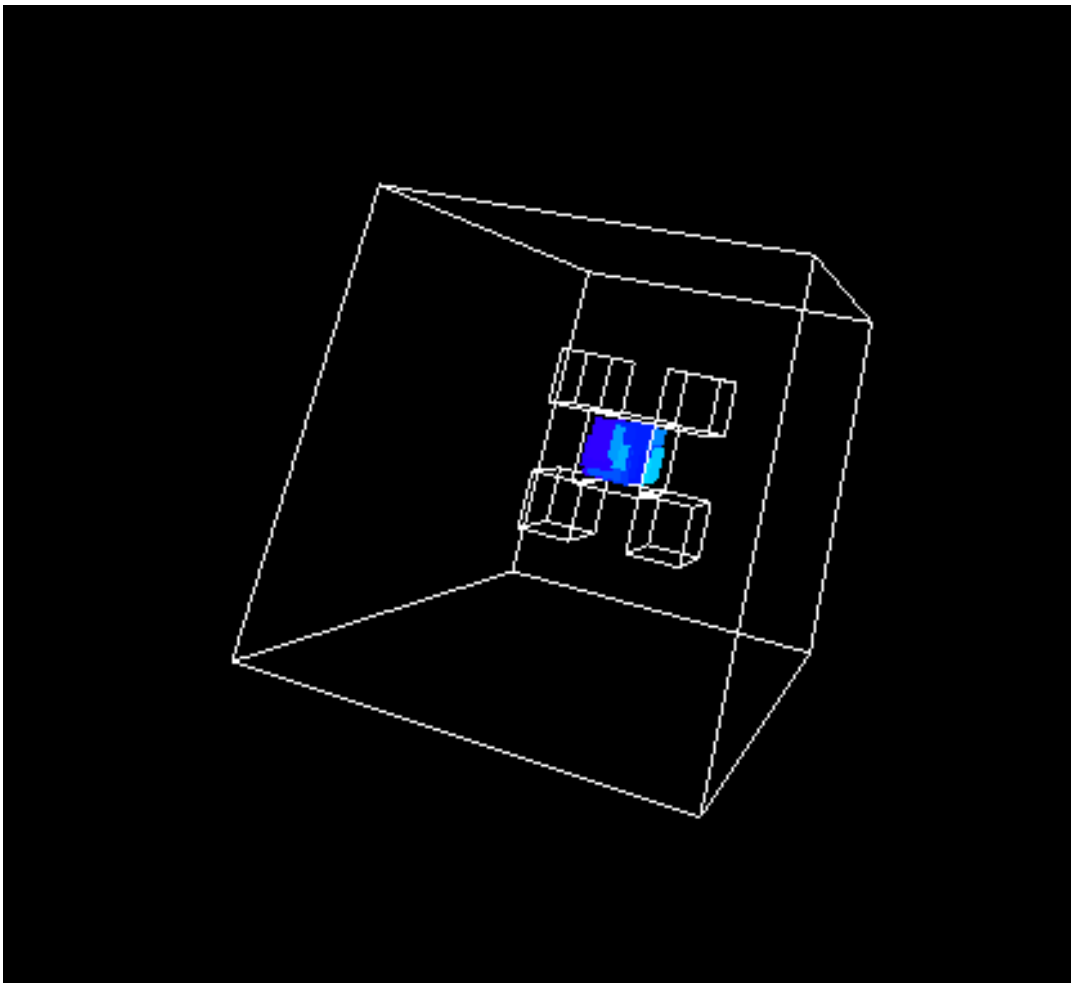


Figure 5: Output from the POCLUST algorithm, shows that only the Uranium was isolated, a success!

V. POCLUST Rewrite

After the FAS was done, the next goal was to create an clean Object Oriented Clustering Framework in $C++$ such that new students would have a minimal learning curve to be able to make changes to the current clustering algorithms and see the results. Though the framework was built, and other clustering algorithms were tested, POCLUST was only about 90% ported to the new framework. The reason is, it was soon realized that building a generic clustering framework that was not a parallel and distributed framework was simply a waste of time. This is because, in the future as the algorithm becomes more complicated and more data is presented, the current sequential model will not stand.

5.1 The Goals

The first a foremost goal was to clean up the code, followed by creating levels of abstraction would allow new students to easily make small changes to the algorithms and be able to notices the output from them. This would allow for a much smaller learning curve, and hopefully will

get more students interested. It was also designed to be a generic framework for making future Clustering Algorithms with minimal code, allowing the framework to do a majority of the internal operations like loading data, creating the space, merging and unmerging, managing the data, managing the clusters, output to a file.

5.2 The structure

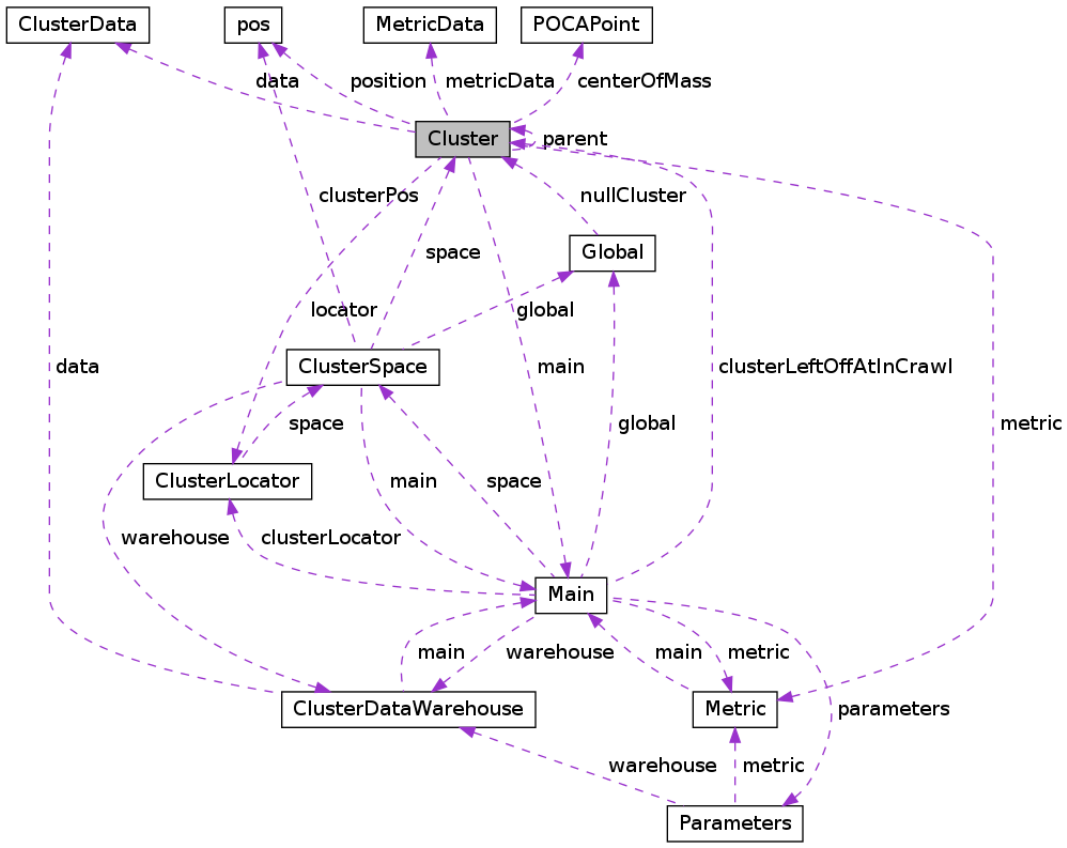


Figure 6: Structure of GenericCluster from POV of a Cluster

5.3 Abstracting Clustering Algorithms

Abstraction takes place by inheriting the following classes and modifying them:

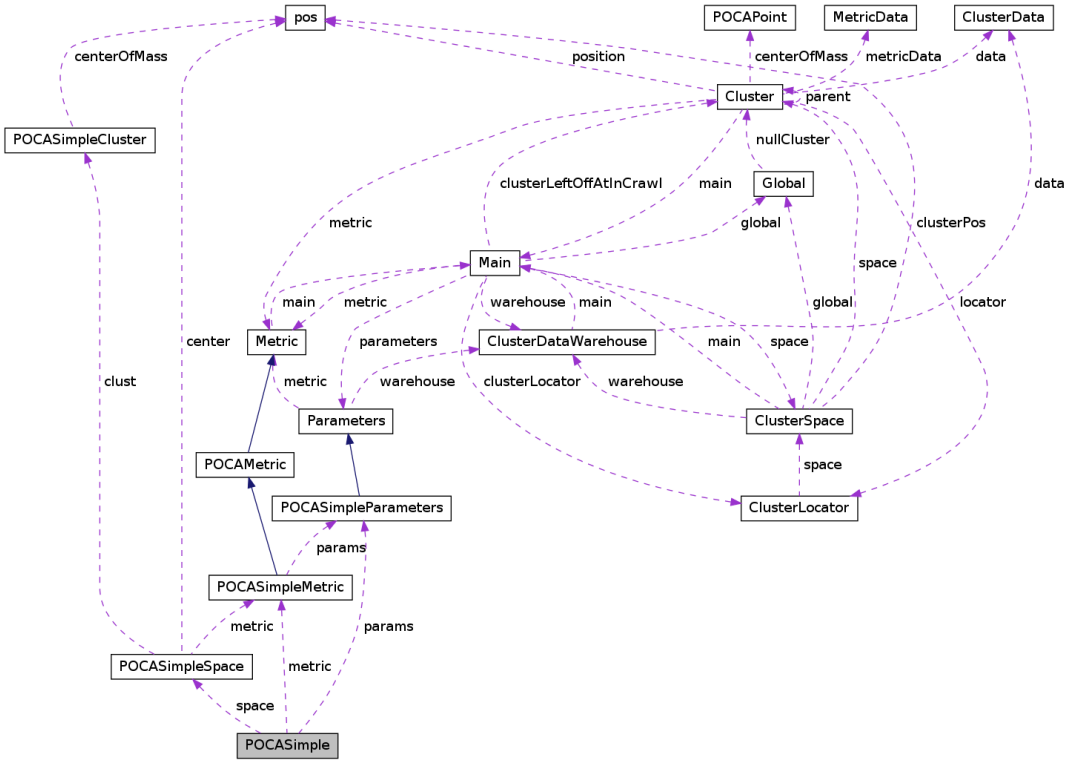


Figure 7: Abstraction of POCASimple from the Base Classes

As you can see, when a new algorithm called "POCA" was created, it created the new Classes from inheritance, Metric, Space, Cluster, Parameters. By manipulating those classes, you can achieve anything you want, without having to worry about the inside structure. Further information can be found on the documentation online.

VI. Parallel and Distributed Clustering using Hadoop

***Abstract*—Apache Hadoop is an open source frame work, that is intended to do parallel and distributed computing over large compute nodes or even in cloud environments such as Amazon EC2. Apache Mahout is the framework built on top of Hadoop that is composed of Machine Learning Algorithms for analysing large data sets. Of the tool kits available through Mahout, there exits a wide arrange of Clustering algorithms. Initial results of the "out of the box" clustering algorithms on real POCA data acquired from our cubic foot Muon Tomography station here at Florida Tech is presented, and to establish a baseline. Mahout's clustering algorithms allows the user to specify a "Measure" for each "Job" that runs, hence the ease to modify the Metric used for calculating distance between points and clusters. Since muon Coluomb scattering has an inherent Probability Distribution Function (PDF) that can be modelled many ways. Therefore the incorporation of the PDF into the Measure in order to create a space in which the Clustering Algorithms will run that is based more on the importance of the variables, will create a much better result. This has been seen is POCLUST, where the Euclidean measure was adjusted by the variance of the point with respect to the cluster, if the cluster is sufficiently large. Taking the concept, and laying out the background information and method on how to create a new measure for a Hadoop clustering algorithm based on a user trainable Probability Distribution Function and abstract it to N dimensional space was the point of this paper.**

I. Introduction

The following data set being used in the current analysis of developments on the DistanceMeasure in Hadoop Clustering algorithms, comes from our Muon Tomography Station in the High Energy Physics Lab A. It is a scenario containing 5 blocks of metal. Four of them are arranged on the corners of a square in the same plane, and the 5th is centred in the middle. The middle is depleted Uranium, and the surrounding metals range from Iron to Lead. The purpose of this scenario is to test our abilities to reconstruct the data and be able to distinguish the Lead from the other materials, without any previous knowledge of the placements.

Current research on the clustering of the POCA points has been done with POCLUST, which is a serialized on-line implementation of a density based clustering algorithm for POCA points similar. The algorithm has a tough time running as a single thread on a single machine as the dataset increases. If fast enough computation times, along with machine learning methods for parameter optimization is going to be used, we must move to a more power platform. We have access to a 30+ Node Tier 3 Computing Center that is run by the High Energy Physics Lab A, so implementing a parallel and distributed algorithm that can take advantage of every node would be to our advantage, and that was the prime motivation for the investigation into parallel clustering algorithms such a PDBSCAN, and those recently published that are based on Map/Reduce.

[1]

Fig. 1. $voidmap(Stringname, Stringdocument)$

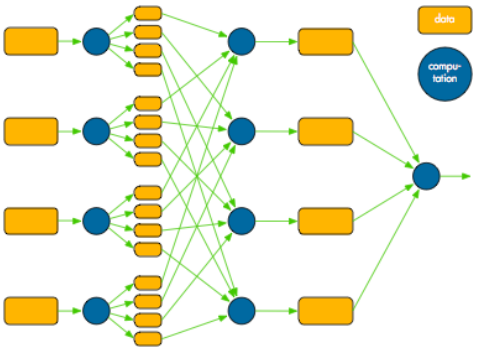
begin
  foreach *word w e of document* **do**
    $EmitIntermediate(w, "1")$
  end
end

A. Hadoop Map Reduce Paradigm

Fig. 2. void reduce(String word, Iterator partialCounts)

Data: word: a word and partial
Data: Counts: a list of aggregated partial counts
$intsum = 0$
foreach *pc e of partialCounts* **do**
  $sum+ = ParseInt(pc)$
$Emit(word, AsString(sum))$

[2]



B. Map/Reduce Cluster Algorithms

Map reduce clustering algorithms have come about just recently and have been exploding. With a map/reduce paradigm, you have shared nothing. That means, between processes or nodes, there is nothing shared. Therefore the functions have to be "self containing" and not access any global data. This can cause issues with synchronization. Synchronization plays a big role in the performance of parallel algorithms since if other threads or processes must wait and spin until another releases a resource, you are losing a lot of performance!

With the map reduce paradigm,for example take the traditional, and one of the most simple k-means clustering algortihms. Here are the two steps that you would need in a sequential word. The first step is:

Assignment Step

$$[h]S_i^{(t)} = \left\{x_p : \left\|x_p - m_i^{(t)}\right\| \leq \left\|x_p - m_j^{(t)}\right\| \; \forall \; 1 \leq j \leq k\right\} \tag{1}$$

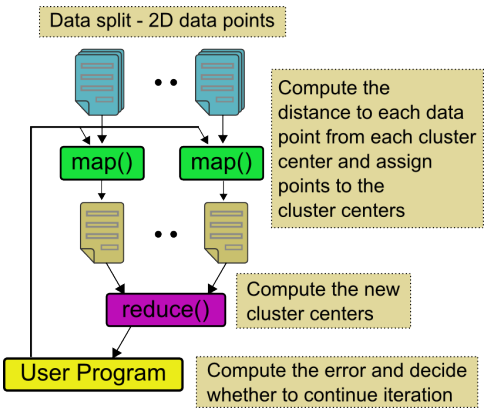
Essentially, the assignment step, each set S, contains points that joined S because out of all the other possible sets S, this one was the closest. As you can see, it is one dimensional, and uses a traditional euclidean measure. This could be the map stage, where each element coming in, will get mapped to an intermediate output.

Update Step

$$\mathbf{m}_i^{(t+1)} = \frac{1}{|S_i^{(t)}|} \sum_{\mathbf{x}_j \in S_i^{(t)}} \mathbf{x}_j \tag{2}$$

This step, essentially all you are doing is updating the mean value of the cluster with the addition of the new points. The reason that you would want to have this as your reduce step, is because Apache Hadoop, in the intermediate steps between map and reduce, sort your outputs, so that reduce gets all of the same outputs. In this situation, all of the same S, or cluster.

Though the k-means clustering may seem easy, actually implementing it is not. Coordinating the communication and synchronization between the parallel processes, and handling situations when clusters have to split among nodes, overlap, etc, it can become difficult. That is where Hadoop and mahout come in. Here is a diagram of a map/reduce k-mean clustering algorithm.



C. Mahout's Clustering Framework

Mahout is a algorithmic framework built on top of Hadoop. Essentially, Hadoop takes care of managing nodes, and file systems, and connections between them. It manages who has what jobs and when, where to transfer data and when, and orchestrates an entire parallel computer for you. The "hello world" for map/reduce is counting the frequencies of a word in a set of words such as a document. The mapper maps the portion of the document into 2 dimensional subset, the word, and the number of instances in that mapper, using the word as the "key". The Intermediate step sorts all the outputs from all the "nodes" or computers, by the word, and separates the data such that all the same words are given to a reducer. The reducer then adds up the number of the same words it was passed, and puts it into a "counter" that each processing node is allowed to have. The counters are all dumped to one file by each Reducer node, in order, and all the counts are therefore summed up for you.

So you created a parallel sorting algorithm for a sparse dataset, with about 4 lines of code added to the Hadoop base. The nature of the Map/Reduce paradigm just makes those sort of things really easy and fast, and some simple things really hard. So it is important to pick the most appropriate challenges by the Mahout team.

One of which, is classification, or the clustering of N dimensional unstructured or structured data. For clustering in Mahout, there are these major components:

D. The Abstract Vector Classifier

Mahout's clustering classifier on the lowest level is abstracted from AbstractVectorClassifier. This is an abstract class such that provides functions to take N-Dimensional vectors of data, and return their probabilities to be associated with each of the K groups, with the probabilities summing to 1. With the classifiers you either have to train them first, in which they build their own Probability Distribution Function. How this is down depends on the specific classifier.

E. The OnlineLearner

An OnlineLearner is a abstract class that supports two main functions, training and closing. For training, it accepts data, and updates its probability model based on the data it just accepted. It requires both the instance values and the actual values, so it can "learn" and compare to how well it is doing. This way it can learn the best model. Once the model and the parameters of the model have been satisfied by sufficient training, the user "Closes" the OnlineLearner, and can now store the model, and use it for classification.

F. The Cluster Classifier

This class inherits mainly from the AbstractVectorClassifier , and the OnlineLearner, and contains a ClusteringPolicy. The Cluster Classifier is given and ClusteringPolicy, which was constructed either by hand, or by training on previous data sets with a learner. It then uses this ClusteringPolicy to feed the VectorClassifier, to classify incoming data into the Clusters defined by the Clustering policy. With the adaptation of the OnlineLearner, it can activate and create multiple OnlineLearners, and not only classify data coming in, but can also adjust it's current clustering policy by closing a trained on-line learner, and feed it to the ClusterPolicy, which then adapts to the OnlineLearner's changes to the Probability Distribution Function and the model.

G. The Abstract Cluster

This is where the actual clustering goes on. A key thing about Hadoop, is that all these objects must be writeable and readable, similar to serializable, because they will be transmitted constantly over a transport that can't just do direct memory access. It stores and sends strings, or compact forms of the objects.

So the key parts of the abstract Cluster is first of all, here is the data that is shared globally amount clusters:

- CLUSTERED_POINTS_DIR - Path of Points already clustered
- CLUSTERS_DIR - Path of All living clusters
- FINAL_ITERATION_SUFFIX - File suffix of finish clusters
- INITIAL_CLUSTERS_DIR - Path of Initial Clusters

Since most clusters are based off a central point, and a volume definition around them, Mahout supports the methods of:

- getCenter - gets the "center" of the cluster
- getRadius - gets the "radius" of the cluster
- isConverged - returns if the converged (optional)

H. Model

The model is a small class with two purposes, to observe an event and retain it, and to construct a PDF (Probability Distribution Function) from that data it observers.

- double pdf(x) - returns the probability that the observation x based on its model
- observe(event) - retains information of this event, and observes it
- computeParameters() - computes a new set of posterior parameters based on the observations, recreates the PDF

I. Our focus:iterator DistanceMeasureCluster

This class is the grand daddy of all the Clustering Algorithms in the Examples. All the Clustering algorithms inherit this class. This class has three major traits:

1) A Model - to observe and generate the PDFs
2) ParameteredGeneralizations - contains the prefix of file, the Hadoop JobConf, cluster Parameters
3) pdf function - pass a vector, get back the probability of that vector based on its model
4) identifier - method of identifying the cluster
5) Data I/O readFields, write
6) get/set DistanceMeasure - This is the function we will be modifying

Program 1 WeightedEuclideanDistanceMeasure.java

```
public double distance(Vector p1,
Vector p2)
 {
    double result = 0;
    Vector res = p2.minus(p1);
    Vector theWeights = getWeights();
    if (theWeights == null) {
      Iterator<Vector.Element>
       iter = res.iterateNonZero();
      while (iter.hasNext()) {
        Vector.Element elt = iter.next();
        result += elt.get() * elt.get();
      }
    } else {
      Iterator<Vector.Element>
      iter = res.iterateNonZero();
      while (iter.hasNext()) {
        Vector.Element elt = iter.next();
        result += elt.get() * elt.get()
        * theWeights.get(elt.index());
      }
    }
    return Math.sqrt(result);
}
```

J. DistanceMeasure class - Our Focus

As of right now, the base abstact DistanceMeasure class has two distance functions:
1. distance(vector1, vector2)
2. distance(double centroidLenSquare, Vector Centroid, Vector V)
The first one is the typical distance measure of Euclidean spaces (or will be abstracted to be one)
The second one is for sparse higher dimensional matrices where the distance is proportional to the number of non-zero elements in the vector instead of the cardinality

So lets look at an abstracted example, the WeightedEuclideanDistanceMeasure:
As you can see the abstraction is pretty simple. that is really the only function created, the other one was empty. So in order to create our measure, all we need to do is abstract it.

Program 2 The Gaussian Model and Distance Measure

[bl]

```
public abstract class ProbDistanceMeasure
implements DistanceMeasure {

   public double pdf(VectorWritable vw) {
   // will use previous training values
   // to calculate the probability of vw
   // based on a gaussian pdf. Left out the
   // calculation.
    return Math.exp(...vw.get() ...);
}
public Model<VectorWritable>[]
sampleFromPrior(int howMany) {
..... pull from training array
}
    public double distance(Vector v1,
    Vector v2)
    {
    Parameters p = getPDFParams();
     return (Math.sqrt(super.distance(v1, v2))
     *p.variance
     *(Math.pow(2,f1(v1.get(p.Dims)/p.sigma))));
    }
    Parameters getPDFParams() {
    .... returns stddev, sigma, mean
    }
}
```

measure to gain wanted results.

II. Conclusion

As was shown throughout this paper, Apache Hadoop and Apache Mahout are two very powerful and flexible platforms. Thanks to the framework of Mahout for abstracting the Map/Reduce paradigm into something much easier to work with, parallel distributed clustering algorithms can take off. As far as the work described in this paper, the code is currently being tested on real data from the High Energy Physics Group's Muon Tomography station. Currently, it is only running on a single psuedonode, but there are hopes to run it on their Tier 3 Computing Cluster in the future, in order to take full advantage of Hadoop. At that point in time, the parameter optimizations will be run, for parameters (f1,f2,f...) scattered throughout the algorithms. Therefore allowing use to make fine adjustments.
As was demonstrated above, to create a parallel distributed clustering algorithm with a new distance measure only took a few lines of code. I hope this paper motivates people to begin experimenting with the options and power of these two platforms in respect to clustering in the Muon Tomography Reconstruction field.

Acknowledgment

Thanks to:

Dr. Hohlmann
: for changing my life in ways that I will never forget, and for finding me useful, even though I am always late and a dollar short, and for getting me on the IEEE publication that got me my career at IBM.

Ben Locke
: for getting me into the HEP Lab A, for my CERN T-shirt, and all the Monte Carlo Data

Dr. Mitra
: for getting me into clustering algorithms and allowing me to hack his algorithm POCLUST.

Dr. Dwyer

VII. The inclusion of Vx4D into ROOT

Due to the management complexity of keeping up with the dependencies, and multi-platform builds, it was decided that it would be much easier in the future to rewrite Vx4D in ROOT. This process is currently going on, and so is the inclusion of POCLUST eventually. Right now Vx4D is supported in ROOT, in beta, by using the:
`#include<TVxND.h>`
With a common constructor of: `TVxND(TFile *)` Using ROOT, a user interface will be created soon, allowing the user to manipulate, save, and load, all the previous options that Vx4D supported. All of this is still under development, and progress is being made. Once it is available in a public beta form, it will be available at:
TVxND Root Documentation, and Location of Code

7.1 The use of TVxND

TVxND will be an N-dimensional OpenGL Voxelized Visualization suite just like before, but now you can map an arbitrary amount of dimensions to the "Theta" variable.

I. Appendix A - Source Code Locations

A.1 CLUSTVIZ,POCLUST,GenericClust,Vx4D

POCLUST and CLUSTVIZ Full Documentation

GenericClust Full Documentation

Vx4D Full Documentation

A.2 ROOT with TVx4D and future additions

TVxND Root Documentation, and Location of Code

II. Appendix B - Source Code Manuals

III. GenericClust - the POCLUST rewrite

IV. POCLUST and CLUSTVIZ source documentation