#### Tracking change in Topology during Downsampling

A PROJECT REPORT SUBMITTED IN PARTIAL FULFIMENT OF THE REQUIREMENTS FOR THE DEGREE OF **Master of Engineering** IN

#### Computer Science And Engineering

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I, Raman Preet Kaur, with SR No. 04-04-00-10-41-14-1-11145 hereby declare that the material presented in the thesis titled

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### Abstract

We study the topological effects of downsampling in 3-D scalar fields represented over structured grids. To capture the extent of topological changes during downsampling, we consider Extended Branch Decomposition Graph (eBDG) based measure. While computing eBDG score of comparison between low resolution scalar fields and original scalar field, an additional parameter of position along with persistence is introduced. We compare and analyze the eBDG cost with Root Mean Squure Distance (RMSD) and Structural SIMilarity (SSIM) index.

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# Introduction

Scientific simulations and experiments such as study of objects or spaces which use scanning techniques like satellite imaging, medical imaging, 3D radar imaging, and various fields in physics where we need temperature distribution throughout space, pressure distribution in a fluid often generate scalar fields. These scalar fields are available as an array of values over the polygonal mesh (structured or unstructured). For space or low resolution requirements various applications require to downsample the structured or unstructured grids. Downsampling is common in image processing, scientific visualization of data in fields ranging from material science to medicine. But downsampling can introduce geometric or topological errors. Topological properties in scalar fields carry important information. These help to navigate in data, identify noise, used to compare, analyze and simplify volumetric data, check the quality and plausibility of extracted shapes and structures [3,6,13,18,19,24], so analyzing the change in topology while downsampling becomes critical.

The study aims to track and analyze the change in topology in 3D structured grids of scalar values as we move from high resolution data to low resolution data during downsampling. It helps to analyze various downsampling techniques by relatively comparing the topological changes introduced by each approach. This study also helps to visualize which topological properties/features are retained or lost during downsampling. Our work helped to quantify the extent of topological change introduced during downsampling.

### Motivation

Some work has been done in the field of topology aware or topology preserving dowsampling [4,10]. But none of them gives a guarantee to preserve topology. So we first study the standard sampling techniques and aim to capture the topology change during iterative downsampling. We analyze and quantify the change in topology at each iteration, which can help the user to stop at certain iteration where the topology change exceeds the permissible limit.

Also most of the applications require to retain the type of mesh during downsampling. The topology aware or topology preserving downsampling techniques apply mesh modifications. In 3D these techniques decompose the original mesh into tetrahedral mesh. Bong-Soo and Sohn [17] have shown topology preserving tetrahedral decomposition of trilinear cell where they decompose a cube with trilinear interpolation into a set of tetrahedra with linear interpolation, where they are trying to preserve isosurface topology. So modifying the original mesh type is an additional constraint imposed by topology aware downsamping techniques. But in our study we are using standard sampling techniques without modifying the mesh.

Further there is work done to capture the topology changes in unstructured grids but structured grids which are more ubiquitous need to be studied for the topological effects of downsampling.

# Background

The work builds upon methods developed that apply Morse theory to computer graphics and visualization. Morse theory studies the topology of manifolds by way of level sets of scalar fields defined over the manifolds. The topological properties of a scalar field refer to the topology of the level sets.

Let  $f : \mathbb{M} \longrightarrow \mathbb{R}$  be a piecewise linear function defined over a mesh  $\mathbb{M}$ . Let  $\mathbb{M}$  be a triangulated mesh. For a vertex v of  $\mathbb{M}$ , the *star* of v, denoted by St(v), consists of all triangles incident on v. The **link** of v, denoted by Lk(v), is the boundary of St(v) i.e., the cycle formed by edges of  $\mathbb{M}$  that are not incident on v but belong to the triangles of St(v). The lower(resp. upper) link of v,  $Lk^{-}(v)$ (resp.  $Lk^{+}(v)$ ), is the subgraph of Lk(v) induced by vertices u with h(u) < h(v)(resp. f(u) < f(v)) [2].

A minimum(resp. maximum) of  $\mathbb{M}$  is a vertex v for which  $Lk^+(v)(resp.Lk^-(v))$  is empty. A maximum or a minimum vertex is called a *extremal* vertex. A non-extremal vertex v is regular if  $Lk^-(v)$  (and also  $Lk^+(v)$ ) is connected, and saddle otherwise.

The **level set** for an isovalue  $v \in \mathbb{R}$  is defined as a set of points  $p \in \mathbb{M}$  where f(p) = v. The v-sublevel set and v-superlevel set of  $\mathbb{M}$  denoted by  $\mathbb{M}_{< v}$  and  $\mathbb{M}_{> v}$  respectively, consist of points  $p \in \mathbb{M}$  with f(p) < v and f(p) > v respectively. We refer to level set  $\mathbb{M}_v$  where v = f(p) for some critical vertex p as a critical level. A *contour* of  $\mathbb{M}$  is a connected component of a level set of  $\mathbb{M}$ .

**Contour tree** is an abstract way of representing a scalar field. It was introduced by Boyell and Ruston [4] as a summary of the evolution of contours on a map(i.e. in 2-D). Contour tree was used by Freeman and Morse to find terrain profiles in a contour map [7]. This was then introduced by Van Kreveld et al. [22] to compute isolines on terrain maps in geographic information systems. It captures the topological properties of a scalar field. The contour tree is a graph that tracks contours of the level set as they split, join, appear and disappear.



Figure 3.1: Contour tree tracks the contours of the level set as they split, join, appear and disappear. It can be created by merging the join tree and split tree. Adapted from [15].

It is obtained by contracting level set to a point. Formally, it is the quotient space under an equivalence relation that identifies all points within a connected component of a level set. Intuitively it is obtained by continuously collapsing each contour in the level set into a single point. One can imagine that for continuous function there is surjection map  $\phi : \mathbb{M} \longrightarrow \mathbb{T}_f$  such that  $\phi(x) = \phi(y)$  if and only if x and y are from the same contour. To obtain the contour tree, sweep through the input in decreasing order of function values. A vertex is a *join saddle* if two level set components merge at that vertex during the sweep. It is *split saddle* if a single component splits into two components at that vertex. The method is explained in Figure 3.1 [15]. The contour tree has been extensively used in image processing and geographic information systems. [9,11,16,18]. Contour trees are unrooted and can be computed by merging two rooted trees: the *join* tree and *split* tree, together referred as *merge* trees.

A join tree can be subdivided hierarchically into branches known as **branch decomposition tree (BDT)** according to the weight of the edges. Each node in BDT corresponds to branch of the join tree commenced by Pascucci et al. [14] shown in Figure 3.2 [15].



Figure 3.2: Branch Decomposition Tree. Adapted from [15].

### **Related Work**

Martin Kraus et al. [10] studied topology guided downsampling for structured volume grids. They have tried to preserve the scalar values of the critical points and not the critical points themselves. It is quite possible that the critical point might shift to the point in the neighborhood. And they have also assumed the relative importance of critical points to preserve the scalar values i.e. extremal points in their study have been given more importance than saddles and many more.

Renato Pajarola et al. [8] studied topology preserving and controlled topology simplifying multiresolution isosurface extraction based on recursive bisection of tetrahedra. There they modify the mesh and also they give no guarantee of topology being preserved.

Bong-Soo et al. [17] studied topology preserving tetrahedral decomposition of trilinear cell. Again there they give no guarantee for topology preservation.

There is work done on volume rendering of large scalar fields on low resolution devices (mobile devices) using subsampling techniques [20] where they propose sampling techniques that help to preserve topology during subsampling. But there too it is not guaranteed that the topology is preserved.

There exist approaches that deal with the comparison of topological structures. Beketayev et al. [12] compare two merge trees by means of branch decompositions. Large number of branch decompositions are considered to avoid instabilities resulting in long computation times. Cohen-Steiner at al. [5] introduced bottleneck distance between persistence diagrams. The measure is robust to noise but does not incorporate sub-level set nesting information. The sub-level set information is better captured by merge trees. The closest work to our study is due to Saikia et al. [15]. They compare all subtrees of two merge trees in an efficient manner exploiting redundancy. They introduce a novel data structure called the extended branch decomposition graph (eBDG) which is composed of the branch decompositions of all subtrees of the merge tree. An efficient algorithm based on dynamic programming has been provided to compare two eBDGs. Our study extends their work to include position of critical points along with the persistence to compute the comparison score.

### Methods

For tracking and quantifying the change in topology during downsampling, the idea is to use eBDG based measure.

#### eBDG Computation and Comparison

#### 1. Computation:

The first step is to compute the join trees for original scalar field and downsampled scalar fields. The join trees are computed using a fast and memory efficient parallel algorithm proposed in [1] with time complexity of  $O(V_{grid} + T \log T)$  where  $V_{grid}$  are the vertices in the structured grid and T are the critical points in the complete domain. The join tree is represented by (V, E)where V represents the critical points and  $V \subseteq T$  as it includes maxima, saddles and one global minimum and each edge is given by  $(v_i, v_j)$  such that  $v_i, v_j \in V$ .

The join trees obtained are used to compute the eBDGs. eBDG avoids redundancy by combining the branch decomposition trees (BDT) of all the subtrees of a join tree into a single graph structure. The **branch decomposition tree**  $B_{bdt_{-i}}$  is given by:

$$B_{bdt\_i} = (B_i, S_i)$$

with the nodes  $B_i = \{b : b = \{e_x, ..., e_y\}$  with  $e_x, ..., e_y \in E\}$  representing the branches and the edges  $S_i$  representing their hierarchy.

For **eBDG computation** we start with edges of the join tree that contain a maximum. The branch decomposition tree for these edges will be a single node representing the edge. The position  $P_i$  corresponding to these eBDG nodes will be the position of associated maximum. We initialize the eBDG with these trivial branch decompositions  $B_{bdt,i}$  for all maxima  $v_i \in V$ :

$$B_{bdt\_i} = (e_i, \{\})$$

where  $e_i = (v_i \rightarrow v_j) = (v_i, v_j)$  is the unique edge in the join tree starting from  $v_i$ . The weights

 $W_i$  of these trivially created nodes  $B_{bdt_i}$  and their levels  $L_i$  are given by:

$$W_i = w_i \qquad \qquad L_i = 0$$

where  $w_i$  is the weight of the edge  $e_i$ . This initialization creates the level 0 nodes of the eBDG. Then the algorithm visits every saddle of the join tree and updates the eBDG. The update of each saddle consists of adding a new node and number of edges to the eBDG.

The updation is done as follows:

Let  $v_i$  denotes a saddle with  $(v_k \to v_i) \in E$  and all  $B_{bdt,k}$  have already been computed. Then we can compute  $B_{bdt,i} = (B_i, S_i)$  as follows:

$$l = argmax\{W_x : (v_x \to v_i) \in E\}$$
  

$$B_i = e_i \cup B_l$$
  

$$S_i = S_l \cup \{(B_i \to B_k) : (v_k \to v_i) \in E \land k \neq l\}$$

with the weight of the root node of  $B_{bdt.i}$ , level and position given by

$$W_i = W_l + w_i$$
  

$$L_i = max(\{1 + L_k : (v_k \to v_i) \in E \land k \neq l\} \cup L_l)$$

 $P_i$  is the position of the maximum associated with the root node of  $B_{bdt.l}$ .

This computation at every saddle  $v_i$  can be interpreted as: the heaviest branch  $B_l$  is identified and combined with the edge  $e_i$  to form root node of  $B_{bdt.i}$ . All other branches are assigned as children. Also all children of heaviest branch are assigned as children of  $B_{bdt.i}$ .

#### 2. Comparison:

After computing the eBDGs for original and downsampled versions, the next step would be the comparison of the eBDGs. Bottom-up approach and memoization are used to compare an eBDG node to another - including their children.

Consider two eBDGs  $B^1$  and  $B^2$  where  $B^1$  represents the eBDG computed for original dataset and  $B^2$  represents eBDG computed for the downsampled version.

The cost between the **level-0** nodes  $B_i^1$  and  $B_j^2$  is given by the cost function:

$$c(B_i^1, B_j^2) = \frac{dist(P_i^1, P_j^2) + |W_i^1 - W_j^2|}{2}$$

where  $dist(P_i^1, P_j^2)$  is the  $L^2$  norm or  $L^2$  distance between  $P_i^1$  and  $P_j^2$ .

**Higher level** nodes have children which also need to be matched up such that it leads to the minimum cost. The key of the algorithm is memoization: if the minimum cost of matching a lower-level node is already computed, then it requires to match the immediate children. The eBDG nodes are visited in ascending order of the levels and compute the cost as:

$$c(B_i^1, B_j^2) = \frac{dist(P_i^1, P_j^2) + |W_i^1 - W_j^2|}{2} + c(F_i^1, F_j^2)$$

where  $c(F_i^1, F_j^2)$  is the cost of matching the two sequences of trees below  $B_i^1$  and  $B_j^2$ . The lower level are processed first, then this only requires to match up the sequences of values. The matching obtained must not have any crossings because if present, that implies higher valued saddles are getting matched to lower-valued saddles.

Matching two sequences without edge crossings can be solved by divide-and-conquer as proposed in [8]. There are three choices at any moment:

- 1. leave out the first node in the first sequence.
- 2. leave out the first node in the second sequence.
- 3. match the first two nodes.

Then this leads to following formulation,

$$c(F_i^1, F_j^2) = d_{0,0}(F_i^1, F_j^2)$$

where  $d_{p,q}(F_i^1, F_j^2)$  is the minimal cost of matching the two sequences of trees  $F_i^1$  and  $F_j^2$  at indices p and q respectively.

 $F_i^1$  and  $F_j^2$  are given by:

$$F_i^1 = \{B_{i,0}^1, B_{i,1}^1, B_{i,2}^1, \dots B_{i,m}^1\}$$
$$F_j^2 = \{B_{j,0}^2, B_{j,1}^2, B_{j,2}^2, \dots B_{j,n}^2\}$$

Here  $B_i^1$  has *m* children and  $B_j^2$  has *n* children. The  $d_{p,q}(\{B_{i,0}^1, B_{i,1}^1, B_{i,2}^1, \dots, B_{i,m}^1\}, \{B_{j,0}^1, B_{j,1}^1, B_{j,2}^1, \dots, B_{j,n}^1\})$  can be written as  $d_{p,q}$ . The **dynamic programming expression** can be written as:

$$d_{p,q} = min \begin{cases} d_{p+1,q} + c(B_{i,p}^{1}) \\ d_{p,q+1} + c(B_{j,q}^{2}) \\ d_{p+1,q+1} + c(B_{i,p}^{1}, B_{j,q}^{2}) \end{cases}$$

where  $p \in \{0, ..., m\}$  and  $q \in \{0, ..., n\}$ . The  $d_{p,n+1} = d_{m+1,q} = 0$ . Whenever a node is left, the cost of leaving that node also includes the cost of leaving all its children. That can be computed as:

$$c(B_i) = W_i + c(F_i)$$
  

$$c(F_i) = \sum c(B_k) \ \forall k \in children(i)$$

Thus an all to all score matrix is obtained. The rows and columns of the matrix correspond to the nodes of  $B^1$  and  $B^2$  respectively. Now from this matrix we find the minimum score column for the last row. The last row corresponds to the node of  $B^1$  which maps to complete join tree of the original scalar field. We backtrack and find the matchings for this node and its children. The cost of comparison (score) and the matched and unmatched nodes are analysed and plotted as graphs and visualized in **paraview** (an open source multiple-platform application for interactive scientific visualization).

The space complexity of the comparison algorithm is  $O(N_1N_2 + b_1b_2)$  where  $N_1$  and  $N_2$  denote the sizes of the two eBDGs and  $b_1$  and  $b_2$  denote the average branching factors. The time complexity is  $O(N_1N_2b_1b_2)$ .

#### <u>RMSD</u>

We compute the RMSD values for the downsampled versions on comparing with the original scalar field. The downsampled versions are tri-linearly interpolated to obtain the same number of points in the original scalar field.

RMSD is given by:

$$\text{RMSD}(\mathbf{X}, \mathbf{Y}) = \sqrt{\frac{1}{N} \sum_{i=1}^{N} |x_i - y_i|^2}$$

where X,Y are the original and interpolated downsampled scalar fields respectively.

#### **SSIM**

The third measure computed is SSIM, proposed by Wang et al. [17]. SSIM is a method to quantify the visibility of errors (differences) between a distorted image and a reference image. In our study we have extended it to 3D so as to use the same for the scalar fields defined on 3D structured grids. To compute SSIM, similar to RMSD, the downsampled scalar fields are tri-linarly interpolated. Suppose x and y are two set of scalar values on a subset of points of 3D structured grid (e.g., spatial subcubes extracted from original and downsampled scalar field). Here at each point, local statistics  $\mu_x$ ,  $\sigma_x$  and  $\sigma_{xy}$  are computed. Here  $\mu_x$  is mean intensity,  $\sigma_x$ 

is standard deviation and  $\sigma_{xy}$  is the correlation (inner product) cofficient between x and y, all are considered in a simple and effective way to quantify structural similarity.

SSIM is given by:

$$SSIM(x,y) = \frac{(2\mu_x\mu_y + C_1)(2\sigma_{xy} + C_2)}{(\mu_x^2 + \mu_y^2 + C_1)(\sigma_x^2 + \sigma_y^2 + C_2)}$$

The constants  $C_1$  and  $C_2$  are introduced to avoid instability when denominator is close to zero.

If X,Y are the original and interpolated downsampled scalar fields respectively;  $x_j$  and  $y_j$  are the scalar field values at the *j*th local window ( $11 \times 11 \times 11$  cube centered at *j*th grid point); M is the number of local windows of the scalar fields, then the Mean SSIM (MSSIM) is computed as:

$$MSSIM(X,Y) = \frac{1}{M} \sum_{j=1}^{M} SSIM(x_j, y_j)$$

The implementation and results are performed on Intel Core i5-3337U CPU 1.80GHz×4 processor with 4GB RAM and 100GB hard disk.

# Results

To compare and analyze the change in topology during downsampling, the experiment is performed on **Fuel dataset** (obtained from volvis.org).

The original fuel dataset shown in **Figure 6.1** has the resolution  $64 \times 64 \times 64$ , storing 8 bits per voxel. The dataset is simulation of fuel injection into a combustion chamber. The higher the density value, the less presence of air.



Figure 6.1: Experiments performed on Fuel dataset, resolution  $64 \times 64 \times 64$ , storing 8 bits per voxel. Shows simulation of fuel injection into a combustion chamber

The table in **Figure 6.2** shows the results for three measures considered that are eBDG based cost, RMSD and SSIM.

Downsampling of Fuel Dataset 64x64x64																					
Results based on EBDG, RMSD and SSIM when compared with orginal Fuel Dataset(64x64x64) with 175 Ebdg nodes and 86 Children																					
														Downsampled Data	a	EBDG					
	EBDG Nodes	Children	Matched	Cost	Persistence																
32x64x64	157	78	48	0.236	138.918 , 3.109	0.008	0.998														
64x32x64	135	66	47	0.007	0.682	0.013	0.994														
64x64x32	135	66	49	0.007	0.682	0.013	0.994														
64x32x32	109	53	23	0.236	138.918 , 3.109	0.018	0.988														
32x64x32	123	61	32	0.236	138.918 , 3.109	0.015	0.992														
32x32x64	121	60	35	0.236	138.918 , 3.109	0.015	0.992														
32x32x32	103	51	30	0.236	138.918 , 3.109	0.02	0.9867														
16x32x32	89	44	10	0.27	138.918 , 3.109	0.025	0.976														
32x16x32	65	33	11	0.256	138.918 , 3.109	0.034	0.943														
32x32x16	65	33	11	0.256	138.918 , 3.109	0.034	0.943														
16x16x32	53	27	7	0.291	138.918 , 3.109 , 10.975*3	0.038	0.933														
32x16x16	47	24	10	0.266	138.918 , 3.109 , 10.975	0.042	0.909														
16x32x16	53	27	6	0.292	138.918 , 3.109 , 10.975*3	0.038	0.933														
16x16x16	33	17	5	0.298	138.918 , 3.109 , 10.975*3	0.045	0.899														

Figure 6.2: Downsampling of Fuel Dataset

The results for various downsampled versions are computed when compared with original fuel dataset i.e.  $64 \times 64 \times 64$ .

The RMSD value 0 corresponds to identical datasets and greater than 0 and less than 1 implies different datasets. More the value of RMSD means more structural difference. SSIM value of 1implies structurally identical datasets. And as values goes towards 0, implies more difference. The first column in the table mentions the dimensions of various downsampled versions of fuel dataset. Under eBDG Column, in the first column it shows the total number of eBDG nodes, where each node refers to a unique sub tree in the join tree. And we are interested only in the last node (corresponds to whole join tree). The second column mentions the number of children of this special last node. And then in next column it shows the number of matched eBDG nodes. After that the table shows the eBDG cost. And next to it are the prominent persistence values of the unmatched eBDG nodes.

Next, the table has RMSD and SSIM values.

The table on a whole gives an idea for various downsampled versions as how the topology and structure of datasets change when we downsample the original scalar field.

The plots in Figures 6.3, 6.4, and 6.5 show the percentage change based on eBDG, RMSD and SSIM measures considered respectively, when we keep on downsampling the dataset start-

ing from  $64 \times 64 \times 64$  till we reach  $16 \times 16 \times 16$  resolution in Fuel.

The green line plot is for x-dimension, blue is for y-dimension and red is for z-dimension being downsampled gradually in above mentioned dimensions respectively.

On the x- axis of the plots, the cases are numbered as mentioned below:

- 1. x=0 for  $64 \times 64 \times 64$  fuel.
- 2. x=1 for  $32 \times 64 \times 64$  for green line,  $64 \times 32 \times 64$  for blue and  $64 \times 64 \times 32$  for red.
- 3. x=2 are for  $32 \times 32 \times 64$  and  $32 \times 64 \times 32$  for green and  $64 \times 32 \times 32$  and  $32 \times 32 \times 64$  for blue and  $64 \times 32 \times 32$  and  $32 \times 64 \times 32$  for red.
- 4. x=3 is for  $32 \times 32 \times 32$  fuel.
- 5. x=4 for  $16 \times 32 \times 32$  for green line,  $32 \times 16 \times 32$  for blue and  $32 \times 32 \times 16$  for red.
- 6. x=5 are for  $16 \times 16 \times 32$  and  $16 \times 32 \times 16$  for green and  $32 \times 16 \times 16$  and  $16 \times 16 \times 32$  for blue and  $32 \times 16 \times 16$  and  $16 \times 32 \times 16$  for red.
- 7. x=6 is for  $16 \times 16 \times 16$  fuel.



(a) Plot shows the percentage change of eBDG cost during downsampling. The indices on x-axis correspond to the downsampled versions of fuel dataset as mentioned earlier in Results section and y-axis shows the percentage of eBDG cost.

(b) Downsampled Versions on X-Axis

Figure 6.3: eBDG Cost Plot



(a) Plot shows the percentage change of RMSD values during downsampling. (b) Down-The indices on x-axis correspond to the downsampled versions of fuel dataset as sampled mentioned earlier in Results section and y-axis shows the percentage change of Versions RMSD values. on X-Axis





(a) Plot showing the percentage change of (1-SSIM) values during downsampling. (b) Down-The indices on x-axis correspond to the downsampled versions of fuel dataset as sampled mentioned earlier in Results section and y-axis shows the percentage of (1-SSIM) Versions values. on X-Axis

Figure 6.5: SSIM Plot



Figure 6.6: Left image shows  $64 \times 64 \times 64$  Fuel dataset and the right image shows the down-sampled  $32 \times 64 \times 64$  Fuel dataset.



Figure 6.7: Left and right image shows the matchings obtained based on only persistence and persistence and position considered together in  $64 \times 64 \times 64$  (left) when compared with  $32 \times 64 \times 64$  (right). For both images the larger spheres (less opaque ones) correspond to matches based on persistence. The smaller ones, more opaque spheres correspond for matches when both persistence and position are taken into account.



Figure 6.8: Children, of eBDG node that maps to the complete join tree of original  $64 \times 64 \times 64$  fuel dataset and eBDG node from eBDG of  $32 \times 64 \times 64$  downsampled dataset that has minimum eBDG score, are plotted in blue and green respectively. The lines are drawn between the ones matched.



Figure 6.9: The image shows the critical points corresponding to the children nodes of eBDG node that maps to the complete join tree of original  $64 \times 64 \times 64$  fuel dataset. The most opaque sphere corresponds to the eBDG node with highest persistence that did not match.

### Observations

Observations based on the plots shown in Figures 6.3, 6.4, 6.5 :

- 1. In Figure [6.3], the eBDG cost can be seen to substantially increase when we drop points in x-dimension. This is justified because in Fuel dataset, the data is concentrated along x-axis.
- 2. In Figure [6.3], at index 1 on the x-axis of the plot (for 32 × 64 × 64 resolution), there is sudden increase in topology change. This is due to a very high persistent feature (eBDG weight 138.918) being lost on dropping points in x-dimension. While for 64 × 32 × 64 and 64 × 64 × 32 at index 2 on the x-axis of the same plot, the percentage change is extremely less. The same can be verified from the details given under persistence column in Figure [6.2]. Further downsampling results in additional loss of topological features but all with less persistence.
- 3. While in RMSD plot and SSIM plot (Figure [6.4], Figure [6.5] respectively), dropping points in y and z dimension overshadows the cost of dropping points in x-dimension.

In Figure [6.6], the original fuel dataset i.e. with resolution  $64 \times 64 \times 64$  and the downsampled version with  $32 \times 64 \times 64$  resolution are shown in paraview. For the same datasets Figure [6.7] shows the matching obtained by eBDG measure, based on only persistence and persistence and position considered together.

For these we can observe:

1. The cardinality of matches obtained based on persistence and position together is less than the cardinality of matches obtained by considering only persistence. This can be justified because an additional constraint of position is included along with persistence which leads to less number of matches.

2. Few matches out of the ones obtained by considering both persistence and position are completely different from the ones obtained by considering only persistence. The same can be verified by seeing exclusively placed solid small spheres. This can be explained because it is more likely that the critical point has moved to a point in its neighborhood during downsampling and should be matched with a critical point nearby rather than matching it based on persistence alone. So considering position and persistence together can result in few matches that are different from matches obtained by considering only persistence.

Figure [6.8] shows the matchings between the children of eBDG node, from eBDG of original  $64 \times 64 \times 64$  fuel dataset, that maps to complete join tree and eBDG node from eBDG of  $32 \times 64 \times 64$  downsampled dataset that has minimum eBDG score. The plot clearly shows that there is one high persistent eBDG node (blue point located approximately at center) which is unmatched and rest unmatched nodes are with very low persistence. This unmatched high persistent node can be visualized in paraview as shown in Figure [6.9].

# **Conclusions and Future Work**

In the study we have considered one downsampling algorithm to see how the process of downsampling results in topology change. We considered eBDG measure to quantify the topology change and compared with RMSD and SSIM values. The matchings obtained by eBDG measure can be visualized and analysed in paraview.

In nutshell, considering these three measures together helps to compare topology and structural changes that results from downsampling. One can decide on sampling techniques to be considered that result in less topology change by analysing the costs. As the results help to visualize and quantify topology changes during downsampling, it can help to guide where one should stop during downsampling.

The work can be extended for other approaches where we require to compare scalar fields defined on the same domain like studying time varying scalar fields. This work can also contribute in the field of comparing and analysing multifield data.

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