# **Interpretability of Math produced Visualizations in Biology**

Summary of “The How and Why of Interpretability in the Biological Sciences — Lior Pachter”

Link: <https://www.youtube.com/watch?v=zg6vBHYMoKo>

This is a research paper explanation of the speaker in the above linked video. The speaker begins his lecture proving the below for a circle in a plane:



where L=Perimeter & Pi=Circumference/Diameter



But if we widen our horizon for all the shapes in a 2D plane,



Isoperimetric Inequality

And if we keep the perimeter fixed, the circle will have greatest area among all the closed shapes.

Another version of writing the Isoperimetric Inequality is the Isodiametric Inequality which is:



Isodiametric Inequality | where D=Diameter

Autoencoder is the combination of Encoder and Decoder. Encoder reduces the data points to a smaller dimension and Decoder gets back the data points(almost same as before) to the same size as before. But these Autoencoder are not Interpretable because usually the Neural Networks are not Interpretable because it contains non-linear functions. If you replace all the non-linear functions with the linear functions, then it can be interpretable; this is nothing but a PCA. So instead of using this PCA, I will keep the Encoder non-linear and change decoder with linear function. By doing this, accuracy is hampered a bit but the interpretability is enhanced drastically. Another drawback of PCA is that we cannot interpret the direction of the data points in the space, but we can do it with this method of Encoder + linear function.

From the Isodiametric Inequality, it is proved that, when you bring the data points from higher dimension to lower dimension, you will have some sort of distortion in terms of distance between the data points as per the Corollary mentioned below:

“Let’s say you have n points(where n≥3) in the 2D space, if d is the minimum distance among all the pairs of points and if D is the maximum distance between all the pairs of points(ie diameter of the circular region formed among the points) in the space; then the ratio of D and d is given by:”



Results of UMAP showed that the points which are close/far to each other in the 2D space may not be close/far in its real dimension(on the higher dimension), that means there are lot of information which is getting demolished. Therefore, it is hard to interpret the data through Visualization, but Visualization is not the only way for interpretability. Just by normalizing the data points in different ways, we get different interpretation of the data points in 2D space. So it is difficult to get interpretability from points in the 20,000 dimension transformed to 2D space.

Especially in biology, the data points are of high dimension; it is possible to get some sort of information from a single feature but clustering or segmenting specific group among the data points is really difficult because of the high dimension and the problems with interpretability when we reduce the points in high dimension to low dimension.

Since we have issues with interpretability for the data points in the high dimension, we try to use the models which are domain specific as mentioned the lecture like Stochastic Differential Equation Models. In this paper, the speaker studies these models to understand what kind of data these models would take to distinguish each feature in the dataset from one another.

So this is how we can build neural networks not just for prediction but for interpretability when we have high dimensional data.