

Comvi - Comparative Visualization of Molecular Surfaces using Similarity-based Clustering

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Abstract— The goal of this paper is to show the reader the abstract methods and concrete applications that were used to extract and compare features and rank the similarity of the molecular protein maps. Further we present a new method of how the won data can be visualized on high resolution and large displays with a The paper describes the process and the approaches that were taken to solve this task.

Index Terms—Clustering, Similarity, feature extraction, Visualization, high-resolution display, Powerwall, MegaMol, VISUS

1 INTRODUCTION

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Figure 1: lorem ipsum rasterized plus a longish caption spanning two lines

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2 RELATED WORK

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2.1 Approaches to the Clustering-Problem

Right of the start we had several ideas of how we could approach this problem. With the recent trend in machine learning we had a couple of ideas of how we could determine a similarity metric between two images or classify an image into a more usable vector of data.

Table 1: lorem ipsum tabulated

dataset	full performance (fps)	half performance (ms)
balls	1,243	0.1
buckets	23	23
bolts	23,312,134.3	22.1

We ended up using to determine the similarity between two protein maps because we didnt manage to train a custom model in the given timeframe, due to .

But our initial results with a pretrained Imagenet

cite imagenet

cite darknet publication

model let us to believe that it should be definetly possible for this specified task to find a machine learning solution.

2.2 Approaches to the Visualization-Task

Our aproaches to visualizing the given clusters were the following, the reader is reminded that we are not just visualizing the clusters on a "normal machine" but rather the POWERWALL, a projected display with effectively 6-24 times the resolution of a consumer grade display. Details on the POWERWALL can be found

cite powerwall publicatoin here if available

2.2.1 Ipsum

2.2.2 Dolor

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