Challenges in processing and knowledge discovery in specifications of scientific resources

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What's wrong with doing science?



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What's wrong with doing science?

Structural bioinformatics

Automatic recognition of ligands in electron density by machine learning

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for Structural Genomics of Infectiou ⁵Department of Crystallography, Fac

*To whom correspondence should be Associate Editor: Robert Murphy Received on March 24, 2018; revised on June

Abstract

Motivation: The correct identi cornerstone of structure-quide investigators into modeling fic maps, Ligand identification can on time-consuming iterative fitt



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Non-Maria eached by using multichaped backprope realistics on the popular benchmarks pr JOURNAL OF ISSN GLASS FILES, VOL. HL NO. & AUGUST 2515 andre Derman miner ersemiliere, einhe Beyond Self-attention: E

TransLoc3D : Point Cloud based Large-scale Place Recognition using Adaptive Receptive Fields

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Abstract

Place recognition plays an essential role in the field of autonomous driving and robot navigation. Although a namber of point cloud based methods have been proposed and achieved promising results, few of them take the size diffe



Recognizing and validating ligands with CheckMyBlob

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Received February 22, 2021: Revised April 04, 2021: Editorial Decision April 08, 2021: Accepted April 11, 2021

ABSTRACT

Structure-quided drug design depends on the correct identification of ligands in crystal structures of protein complexes. However, the interpretation of the electron density maps is challenging and often burdened with confirmation bias. Ligand identification can be aided by automatic methods such as Check-MyBlob, a machine learning algorithm that learns to generalize ligand descriptions from sets of moieties deposited in the Protein Data Bank, Here, we present the CheckMyBlob web server, a platform that can identify ligands in unmodeled fragments of electron density maps or validate ligands in existing models. The server processes PDB/mmCIF and MTZ files and returns a ranking of 10 most likely ligands for each detected electron density blob along with interactive 3D visualizations. Additionally, for each prediction/validation, a plugin script is generated that enables users to conduct a detailed analvsis of the server results in Coot. The CheckMv-Blob web server is available at https://checkmyblob. bioreproducibility.org Two Linear Lavers for Visual Tasks

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INTRODUCTION

outperform 2D or 2D-JD

morris. Also, we show that

works are robust to noise, outperform 3D convolutional neural networks and are faster than the 4D counterpart in

Many macromolecular crystal structures contain ligand molecules that can reveal the function of the protein or nucleic acid. Ligands are usually manually modeled by crystallographers, which requires good judgment and expertis

masses all discrete convo-					
nalized sparse controlation,	ID: Line	2D: Square	3D: Cabe	4D: Tessenet	
-differentiation library for tensive functions for high- al networks. ¹ We create 4D	Figure 2: 2D projections of hypercubes in various dimen- sions more affordable and widely used for robotics applications, 3D+videon became readily-available sources of input for robotics systems or ARVR applications. However, there are many technical challenges in using DD- videon for high-bed preception tasks. Find, DD data mapping				
neural networks using the rison 3D semantic segmen- d 4D datasets for 3D-video ges in the high-dimensional kernel, a special case of the aid the tribiteral-stationary					

alienates users or makes it difficult to interrate into larger systems. Second, the performance of the 3D convolutional neural networks is worse or on-par with 2D convolutional neural networks. Third, there are limited number of open source libraries for fast large-scale 3D data.

our problem and propose the generalized sparse convolu-

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Linguistic knowledge



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Image: A mathematical states and a mathem

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How it should look:



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