POCKETMÓN

SBI-PYTHON PROJECT

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POCKÉTMON DOCUMENTATION

PACKAGE OVERVIEW

*Pockétmon* is a computational tool developed to predict ligand-binding pockets in protein structures using deep learning methodologies. It leverages a three-dimensional Convolutional Neural Network (3D-CNN) trained on protein-ligand complexes to identify regions of interest with high spatial and functional relevance.

Unlike classical approaches based on geometric descriptors, energy minimization, or evolutionary conservation, *Pockétmon* adopts a data-driven strategy, capable of learning implicit biochemical patterns from atomic configurations. This makes it particularly effective in identifying non-obvious binding regions and generalizing across structurally diverse protein families.

KEY FEATURES AND ADVANTAGES

**Deep Learning-Powered Predictions**

Pockétmon employs a 3D-CNN capable of modeling complex spatial relationships between atoms within a protein structure. This allows the tool to detect subtle features often missed by rule-based or empirical scoring methods.

**Residue-Level Annotations**

In addition to generating voxel-based predictions in the form of pseudo-atom PDB files, Pockétmon maps predicted pockets back to protein residues. The output includes a curated list of candidate binding site residues, facilitating biological interpretation and experimental validation.

**Standalone and Efficient**

The tool is designed for local execution, with no reliance on external APIs or databases. It supports both CPU and GPU computation (including CUDA and Apple MPS), allowing efficient processing of large datasets or high-throughput screening pipelines.

**Tunable Trust Threshold**

Users may specify a confidence threshold (--trust) to control the model's sensitivity in classifying voxels. Lower thresholds increase detection breadth (useful for exploratory analysis), while higher thresholds yield more conservative and specific predictions.

APPLICATION SCOPE

*Pockétmon* can support a wide range of structural bioinformatics tasks, including:

* Identification of druggable sites in novel or under-characterized proteins
* Prioritization of residues for mutagenesis or functional studies
* Ligand placement and docking pre-processing
* High-throughput annotation of proteome-wide structural datasets

By combining machine learning robustness with interpretability and ease of use, *Pockétmon* provides a reliable and scalable solution for protein pocket prediction in both academic and applied research contexts.

INSTALLATION

To ensure optimal compatibility and performance, it is strongly recommended to use Python 3.10, especially when running on systems utilizing Apple's Metal Performance Shaders (MPS) or when working with PyTorch-based environments.

STEP 1: CLONE THE REPOSITORY

Begin by downloading the source code from the official GitHub repository:

git clone https://github.com/martagarnt/pocketmon.git  
cd pocketmon # navigate to the repository

STEP 2: SET UP A VIRTUAL ENVIRONMENT

Create and activate a virtual environment to isolate the installation:

python3.10 -m venv venv  
source venv/bin/activate

STEP 3: INSTALL REQUIRED DEPENDENCIES

Install the necessary Python packages using the provided requirements.txt file:

pip install -r requirements.txt

STEP 4: INSTALL POCKÉTMON AS A CLI TOOL

To use pocketmon as a global command from any directory, install the package locally:

pip install .

This installation exposes the pocketmon command in your terminal, enabling simple and direct usage.

STEP 5: VERIFY INSTALLATION

Finally, before running pocketmon, it is encouraged to check if the program and its dependencies have been installed successfully. To verify the installation, the following command can be run:

python -c "from pocketmon import predict; print('✓ Pockétmon installed successfully and ready to catch some pockets!'); predict.print\_banner('install')"

DOCUMENTATION

MODEL.PY

Header X

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PREDICT.PY

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Class Pocket3DCNN

class Pocket3DCNN(nn.Module):  
 def \_\_init\_\_(self, in\_channels=4):  
[…]  
 def forward(self, x):  
[…]

**Description:**

The Pocket3DCNN class defines a three-dimensional convolutional neural network (3D-CNN) tailored for the task of identifying ligand-binding pockets within protein structures. It accepts voxelized protein input data and returns a probability map highlighting regions likely to represent binding sites.

This architecture is designed to learn spatial and chemical patterns from volumetric representations of proteins and leverages multiple convolutional layers to capture hierarchical features.

**Constructor:**

Pocket3DCNN(in\_channels=4)

|  |  |  |
| --- | --- | --- |
| Parameter | Type | Description |
| in\_channels | int | Number of input channels, typically corresponding to different atomic types (e.g., C, N, O, S). Default is 4. |

**Network Architecture:**

The network consists of the following layers, organized in a nn.Sequential container:

1. Conv3D Layer 1
   * in\_channels → 32 filters
   * Kernel size: 3×3×3, Padding: 1
   * Followed by: BatchNorm3D + ReLU
2. Conv3D Layer 2
   * 32 → 64 filters
   * Kernel size: 3×3×3, Padding: 1
   * Followed by: BatchNorm3D + ReLU
3. Conv3D Layer 3
   * 64 → 128 filters
   * Kernel size: 3×3×3, Padding: 1
   * Followed by: BatchNorm3D + ReLU
4. Conv3D Layer 4 (Output Layer)
   * 128 → 1 filter
   * Kernel size: 1×1×1
   * Followed by: Sigmoid activation

This produces a single-channel voxel grid of the same spatial dimensions as the input, where each voxel’s value (between 0 and 1) represents the predicted likelihood of being part of a binding pocket.

**Forward pass:**

def forward(self,x):  
 return self.model(x)

|  |  |  |
| --- | --- | --- |
| Parameter | Type | Description |
| x | torch.Tensor | Input tensor of shape (batch\_size, in\_channels, D, H, W) representing voxelized protein structures. |

|  |  |  |
| --- | --- | --- |
| Returns | Type | Description |
| output | torch.Tensor | Output tensor of shape (batch\_size, 1, D, H, W) containing voxel-wise pocket probability scores. |

**Use Case:**

This model is optimized for protein binding site prediction by learning to associate structural patterns in 3D space with potential ligand interaction regions. It can be trained on protein-ligand complexes and later used to generalize predictions on unseen PDB structures.

**Remarks:**

The use of batch normalization and ReLU activation after each convolution layer enhances training stability and non-linearity.

The final Sigmoid function ensures output probabilities are bounded between 0 and 1, allowing for post-processing thresholding.

Function voxelize\_structure

def voxelize\_structure(pdb\_path, origin=None, grid\_size=32, voxel\_size=1.0, channels=['C', 'N', 'O', 'S']):

**Description:**

The voxelize\_structure function processes a protein structure from a PDB file and converts it into a 3D voxel grid representation suitable for input into a convolutional neural network (CNN). This spatial encoding enables machine learning models to learn local chemical environments from the atomic layout of the protein.

**Parameters:**

|  |  |  |
| --- | --- | --- |
| Parameter | Type | Description |
| pdb\_path | str | Path to the input PDB file containing the protein structure. |
| origin | np.ndarray or None | Coordinates for the grid origin. If None, the centroid of all atom coordinates is used as the center of the voxel grid. |
| grid\_size | int | Dimension of the cubic grid in voxels.  The output grid will be of shape (C, grid\_size, grid\_size, grid\_size). Default is 32. |
| voxel\_size | float | Physical size (in Ångstroms) of each voxel. Defines the resolution of the grid. Default is 1.0. |
| channels | list[str] | List of atomic element types (e.g., 'C', 'N', 'O', 'S') to encode into distinct channels of the voxel grid. |

**Returns:**

|  |  |  |
| --- | --- | --- |
| Return Value | Type | Description |
| grid | np.ndarray | 4D array with dimensions (C, X, Y, Z) representing the voxelized protein structure, where each channel corresponds to an atomic type. |
| origin | np.ndarray | The 3D coordinates of the grid origin used during voxelization. |
| structure | Bio.PDB.Structure | Biopython structure object of the protein, used for downstream analysis and residue lookup. |
| atom\_residue\_map | dict[tuple[int], Bio.PDB.Residue] | Dictionary mapping voxel indices (x, y, z) to their corresponding  Biopython Residue objects. This enables linking predicted voxel activations back to biological residues. |

**Use Case:**

This function is a critical preprocessing step in workflows involving 3D CNNs for protein-ligand interaction prediction. It allows atomic-level data to be spatially structured, making it accessible for deep learning models that leverage spatial convolution.

**Remarks:**

* The accuracy of downstream predictions can be affected by the chosen voxel\_size and grid\_size.
* The atom\_residue\_map is essential for residue-level interpretation of voxel-level predictions.

Function save\_predicted\_pocket\_to\_pdb

def save\_predicted\_pocket\_to\_pdb(pred\_grid, origin, voxel\_size, pdb\_filename, threshold=0.5, header\_name=None)

**Description:**

This function saves the predicted ligand-binding pocket as a 3D voxel-based PDB (Protein Data Bank) file. It converts voxels classified as part of the binding pocket (based on a confidence threshold) into pseudo-atoms in PDB format. Each pseudo-atom represents a voxel center within the predicted pocket volume.

This output can be visualized with molecular modeling software such as PyMOL or Chimera, enabling intuitive spatial inspection of predicted binding sites.

**Parameters:**

|  |  |  |
| --- | --- | --- |
| **Parameter** | **Type** | **Description** |
| pred\_grid | np.ndarray or torch.Tensor | 3D array of pocket prediction values (typically from a CNN). Values should be in the range [0, 1]. |
| origin | np.ndarray | The 3D coordinates of the origin (minimum corner) of the voxel grid, used to convert voxel indices into Cartesian coordinates. |
| voxel\_size | float | The physical size (in Ångströms) of a single voxel edge. |
| pdb\_filename | str | The file path where the output PDB will be written. |
| threshold | float, optional | A probability cutoff above which voxels are considered part of the binding pocket. Default is 0.5. |
| header\_name | str, optional | An optional protein name or identifier to be written in the PDB file header. |

**Returns:**

This function does not return any value. It writes a .pdb file to disk containing pseudo-atoms for all voxels with prediction scores above the specified threshold.

**PDB Formatting Details:**

* Each qualifying voxel is written as a HETATM entry in the PDB file.
* The pseudo-atoms are labeled with a generic atom name X and residue UNK (unknown).
* Coordinates are computed by scaling voxel indices from the origin using the voxel size.
* The output includes a final END statement, conforming to standard PDB format requirements.

**Usage example:**

save\_predicted\_pocket\_to\_pdb(  
 pred\_grid=cnn\_output,  
 origin=np.array([10.0, 15.0, 5.0]),  
 voxel\_size=1.0,  
 pdb\_filename="protein\_predicted\_pocket.pdb",  
 threshold=0.6,  
 header\_name="protein"  
)

Function save\_predicted\_residues

def save\_predicted\_residues(pred\_grid, origin, voxel\_size, residue\_lookup, output\_file, threshold=0.5)

**Description:**

This function extracts and saves the list of protein residues predicted to be part of a ligand-binding pocket. It maps high-confidence voxels (above the specified threshold) from the 3D prediction grid to corresponding residues using a voxel-to-residue lookup dictionary. The result is a residue-level annotation of the predicted pocket, saved in a human-readable text file.

This function complements the voxel-level .pdb output by providing biologically meaningful residue identifiers, which are easier to interpret and analyze.

**Parameters:**

|  |  |  |
| --- | --- | --- |
| Parameter | Type | Description |
| pred\_grid | np.ndarray or torch.Tensor | 3D array containing voxel prediction scores from the CNN. |
| origin | np.ndarray | The origin (minimum corner) of the voxel grid in 3D Cartesian coordinates. |
| voxel\_size | float | The physical edge length of each voxel in Ångströms. |
| residue\_lookup | dict | A dictionary mapping (x, y, z) voxel indices to their corresponding Bio.PDB.Residue objects. This is generated during voxelization. |
| output\_file | str | Path to the .txt file to write the residue list. |
| threshold | float, optional | Probability threshold for voxel classification (default: 0.5). Voxels with predictions above this value are included. |

**Returns:**

This function does not return a value. It writes a text file to disk with one line per residue, in the format:

# RESNAME RESID CHAIN

Example output:

LEU 6 A  
ASN 8 A  
LYS 10 A

**Implementation Details:**

* Converts PyTorch tensors to NumPy arrays if needed.
* Iterates through all voxels above the threshold.
* Uses the residue\_lookup dictionary to associate each qualifying voxel with a unique residue.
* Avoids duplicate entries using a set to track seen residues.
* Sorts the residue list first by chain, then by residue number for consistency.

**Usage example:**

save\_predicted\_residues(  
 pred\_grid=cnn\_output,  
 origin=np.array([0.0, 0.0, 0.0]),  
 voxel\_size=1.0,  
 residue\_lookup=voxel\_to\_residue\_dict,  
 output\_file="protein\_predicted\_residues.txt",  
 threshold=0.6  
)

**Remarks:**

* The output file is intended for downstream biological interpretation and validation.
* This residue-level output is especially useful when identifying potential ligand contact points or conducting mutagenesis studies.
* A well-constructed residue\_lookup is essential for accurate mapping; it must come from the same voxelization logic used for prediction.

Function main

The main() function orchestrates the entire workflow of the Pockétmon prediction tool. It serves as the command-line interface (CLI) entry point, handling user input, model loading, data preprocessing, inference, and output generation. It is designed to be invoked directly when the program is run from the command line using the pocketmon command.

**Workflow Overview:**

1. **Help Screen Display:**  
   If invoked with no arguments or with -h/--help, the function prints an ASCII art help screen summarizing usage, arguments, and example commands, then exits.
2. **Argument Parsing:**  
   Uses Python’s argparse library to parse the required and optional command-line arguments:
   * --input: path to the input PDB file (required)
   * --model: path to a .pt PyTorch model file (optional, defaults to best\_model\_refined.pt)
   * --output: base name for output files (default: predicted\_pocket)
   * --trust: voxel confidence threshold for classification (float, 0.0–1.0, default: 0.5)
   * --verbose: enables additional console output for debugging and transparency
3. **Device Detection:**  
   Automatically selects the most optimal computing device:
   * GPU via CUDA (if available)
   * Apple MPS (if on macOS, with fallback warning)
   * CPU fallback otherwise
4. **Model Loading:**  
   Initializes the 3D CNN architecture and loads the weights from the specified model file. The model is then moved to the selected device and set to evaluation mode.
5. **Input Preprocessing:**  
   Invokes voxelize\_structure() to parse the input PDB file and convert it into a voxel grid suitable for CNN input. Also retrieves the residue-to-voxel mapping.
6. **Prediction:**  
   Performs inference using the loaded model and converts raw sigmoid outputs into a binary mask based on the --trust threshold.
7. **Output Naming:**  
   Dynamically generates filenames based on the input PDB file:
   * <protein\_name>\_predicted\_pocket.pdb (voxel output)
   * <protein\_name>\_predicted\_residues.txt (residue list)
8. **Saving Results:**
   * The .pdb file is saved using save\_predicted\_pocket\_to\_pdb().
   * The .txt residue list is saved using save\_predicted\_residues().
9. **Logging & Exit:**  
   Prints output paths and key steps to the console, especially when --verbose is enabled. Ends execution gracefully.