Few-shot learning for classification of novel macromolecular structures in cryo-electron tomograms

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Supplementary Document

S1 Details about the metrics of classification results

The classification accuracy in our experiments is calculated as:

\[
\text{accuracy} = \frac{n_{\text{correct}}}{n_{\text{all}}}
\]

Where \( n_{\text{correct}} \) notes the number of samples of which the predicted label is the same with the ground truth label. And \( n_{\text{all}} \) notes the total number of samples that are predicted. The accuracy is calculated per episode with \( N_{C}N_{Q} \) samples, and the mean accuracy and the standard deviation are finally obtained through 100 episodes in the test period.

In the multi-class classification tasks, the accuracy we calculated in this way equals to the micro average precision since \( n_{\text{correct}} = \sum_{k=1}^{n} TP_{k} \) and \( n_{\text{all}} = \sum_{k=1}^{n} TP_{k} + FP_{k} \).

\[
\text{precision(\text{micro})} = \frac{\sum_{k=1}^{n} TP_{k}}{\sum_{k=1}^{n} TP_{k} + FP_{k}}
\]

Where \( n \) notes the total number of classes in the test set, \( TP_{k} \) notes the truly predicted samples in class \( k \), and \( FP_{k} \) notes the samples that are mistakenly classified as class \( k \).

The macro average precision is calculated as an additional reference for the performance of our methods as listed in Table A. Since the classes sampled in each episode may be different, we calculate the precision(macro) with all the samples tested through the test period.

\[
\text{precision(\text{macro})} = \frac{1}{n} \sum_{k=1}^{n} \frac{TP_{k}}{TP_{k} + FP_{k}}
\]

S2 Additional classification results

We have also analyzed the classification performance on different structural classes in Table B. Experiments were conducted on the three datasets and we provided examples of classified subtomograms from the classes with highest/lowest classification accuracy in Fig A. The results indicate that the structures with relatively clear outlines and larger difference between other structures in the test set are more likely to obtain a higher classification accuracy. As further proof of the superiority of our method, examples of subtomograms that are correctly classified by our method but wrongly classified by the baseline method are shown in Fig B. Our method outperforms the baseline method especially on the subtomograms with relatively indistinct structures.
Table A: The classification precision (macro) of the simulated and real datasets of subtomograms.

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Methods</th>
<th>5-shot</th>
<th>1-shot</th>
</tr>
</thead>
<tbody>
<tr>
<td>Simulated(0.1)</td>
<td>ProtoNet-CE</td>
<td>0.8727</td>
<td>0.7808</td>
</tr>
<tr>
<td>Simulated(0.1)</td>
<td>ProtoNet3D</td>
<td>0.8463</td>
<td>0.7645</td>
</tr>
<tr>
<td>Simulated(0.05)</td>
<td>ProtoNet-CE</td>
<td>0.7893</td>
<td>0.7102</td>
</tr>
<tr>
<td>Simulated(0.05)</td>
<td>ProtoNet3D</td>
<td>0.7792</td>
<td>0.6972</td>
</tr>
<tr>
<td>Simulated(0.03)</td>
<td>ProtoNet-CE</td>
<td>0.7109</td>
<td>0.5903</td>
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<tr>
<td>Simulated(0.03)</td>
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<td>0.6720</td>
<td>0.5511</td>
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<tr>
<td>Guo</td>
<td>ProtoNet-CE</td>
<td>0.9400</td>
<td>0.9180</td>
</tr>
<tr>
<td>Guo</td>
<td>ProtoNet3D</td>
<td>0.9258</td>
<td>0.8472</td>
</tr>
<tr>
<td>Noble</td>
<td>ProtoNet-CE</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>Noble</td>
<td>ProtoNet3D</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
</tbody>
</table>

Table B: Classification accuracy for different classes (all calculated in 5-shot case). (43: T20S proteasome (EMPIAR 10143); 73: insulin-bound insulin receptor (EMPIAR 10173); 35: DNAB helicase-helicase (EMPIAR 10135))

<table>
<thead>
<tr>
<th>Simulated(SNR=0.1)</th>
<th>Guo</th>
<th>Noble</th>
</tr>
</thead>
<tbody>
<tr>
<td>class</td>
<td>accuracy</td>
<td>class</td>
</tr>
<tr>
<td>3DY4</td>
<td>0.8315</td>
<td>ribosome</td>
</tr>
<tr>
<td>2BO9</td>
<td>0.9861</td>
<td>mitochondrial membrane</td>
</tr>
<tr>
<td>1VPX</td>
<td>0.6495</td>
<td>double capped proteasome</td>
</tr>
<tr>
<td>2GLS</td>
<td>0.6687</td>
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</tr>
<tr>
<td>1QO1</td>
<td>0.8645</td>
<td></td>
</tr>
<tr>
<td>4V4Q</td>
<td>0.9941</td>
<td></td>
</tr>
<tr>
<td>1A1S</td>
<td>0.9799</td>
<td></td>
</tr>
<tr>
<td>1F1B</td>
<td>0.9897</td>
<td></td>
</tr>
</tbody>
</table>

Figure A: Examples of classified subtomograms shown in 2D slices. a. 4V4Q (highest prediction accuracy in simulated dataset with SNR=0.1). b. 1VPX (lowest prediction accuracy in simulated dataset with SNR=0.1). c. Membrane (highest prediction accuracy in Guo dataset). d. Ribosome (lowest prediction accuracy in Guo dataset). e. Insulin-bound insulin receptor (prediction accuracy is 1.0 in Noble dataset). f. T20S proteasome (prediction accuracy is 1.0 in Noble dataset).
Figure B: Examples of subtomograms wrongly classified by baseline method but correctly classified by ProtoNet-CE (shown in 2D slices).