# Light Attention Predicts Protein Location from the Language of Life

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## Abstract

Although knowing where a protein functions in a cell is important to characterize biological processes, this information remains unavailable for most known proteins. Machine learning narrows the gap through predictions from expertly chosen input features leveraging evolutionary information that is resource expensive to generate. We showcase using embeddings from protein language models for competitive localization predictions not relying on evolutionary information. Our lightweight deep neural network architecture uses a softmax weighted aggregation mechanism with linear complexity in sequence length referred to as light attention (LA). The method significantly outperformed the state-of-the-art for ten localization classes by three to five percentage points (Q10). The novel models are available as a web-service and as a stand-alone application at OMITTED.com.

## 1. Introduction

Proteins are the machinery of life involved in all essential biological processes (biological background in Appendix). Knowing where in the cell a protein functions, referred to as its *subcellular localization* or *cellular compartment*, is important for unraveling biological function (Nair & Rost, 2005; Yu et al., 2006). Experimental determination of protein function is complex, costly, and selection biased (Ching et al., 2018). In contrast, the costs of determining protein sequences continuously decrease (Consortium, 2021), increasing the sequence-annotation gap (gap between proteins of known sequence and unknown function). Computational methods have been bridging this gap (Rost et al., 2003); one way has been to predict protein subcellular location (Goldberg et al., 2012; 2014; Almagro Armenteros et al., 2017; Savojardo et al., 2018). The standard tool in molecular biology, namely homology-based inference (HBI), accurately transfers annotations from experimentally annotated to sequence-similar un-annotated proteins. However, HBI is not available or unreliable for most proteins (Goldberg et al., 2014; Mahlich et al., 2018). Machine learning methods perform less well (lower precision) but are available for all proteins (high recall). The best methods use evolutionary information from families of related proteins as input (Goldberg et al., 2012; Almagro Armenteros et al., 2017). Although the marriage of evolutionary information and machine learning has influenced computational biology for decades (Rost & Sander, 1993), due to database growth, this information becomes increasingly costly to generate.

Recently, protein sequence representations (embeddings) have been learned from databases (Steinegger & Söding, 2018; Consortium, 2021) using language models (LMs) (Heinzinger et al., 2019; Rives et al., 2019; Alley et al., 2019; Elnaggar et al., 2020) initially used in natural language processing (NLP) (Radford, 2018; Devlin et al., 2019; Radford et al., 2019). Models trained on protein embeddings via transfer learning tend to be outperformed by approaches using evolutionary information (Rao et al., 2019; Heinzinger et al., 2019). However, embedding-based solutions can even outshine HBI (Littmann et al., 2021) and models predicting aspects of protein structure (Bhattacharya et al., 2020; Rao et al., 2020). Yet, for location prediction, embedding-based models (Heinzinger et al., 2019; Elnaggar et al., 2020; Littmann et al., 2021) remained inferior to the state-of-the-art using evolutionary information, e.g., represented by DeepLoc (Almagro Armenteros et al., 2017).

In this work, we leveraged protein embeddings to predict cellular location without evolutionary information. We proposed a deep neural network architecture using light attention (LA) inspired by previous attention mechanisms (Bahdanau et al., 2015; Vaswani et al., 2017).

## 2. Related Work

Previous state-of-the-art (SOTA) models for subcellular location prediction combined homology, evolutionary information, and machine learning, often building prior knowledge about biology into model architectures. For instance, LocTree2 (Goldberg et al., 2012) implemented profile-kernel SVMs (Cortes & Vapnik, 1995; Rui Kuang et al.,

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2004) which identified k-mers conserved in evolution and put them into a hierarchy of models inspired by cellular sorting pathways. BUSCA (Savojardo et al., 2018) combines three compartment-specific prediction methods based on SVMs using evolutionary information (Pierleoni et al., 2006; 2011; Savojardo et al., 2017). DeepLoc (Almagro Armenteros et al., 2017) uses convolutions followed by a bidirectional LSTM (Hochreiter & Schmidhuber, 1997; Schuster & Paliwal, 1997) that employs Bahdanau-Attention (Bahdanau et al., 2015). Using evolutionary information, DeepLoc rose to become the SOTA. Embedding-based methods (Heinzinger et al., 2019) have not yet outperformed this SOTA, although ProtTrans (Elnaggar et al., 2020), based on very large data sets, came close.

## 3. Methods

### 3.1. Data

**Standard set DeepLoc.** Following previous work (Heinzinger et al., 2019; Elnaggar et al., 2020), we mainly used a data set introduced by *DeepLoc* (Almagro Armenteros et al., 2017) for training and testing. The training set contained 13 858 proteins annotated with experimental evidence for one of ten location classes (nucleus, cytoplasm, extracellular space, mitochondrion, cell membrane, Endoplasmatic Reticulum, plastid, Golgi apparatus, lysosome/vacuole, peroxisome). Another 2 768 proteins made up the test set (henceforth called *setDeepLoc*), which had been redundancy reduced to the training set (but not to itself) at 30% pairwise sequence identity (PIDE) or to an E-value cutoff of $10^{-6}$. To tune model parameters and avoid overestimating performance, we further split the DeepLoc training set into a training set containing 9 503 sequences and a validation set (redundancy reduced to training by 30% PIDE) containing 1 158 sequences (distribution of classes in *Appendix: Datasets*).

**Novel *setHARD*.** To rule out that methods had been optimized for the static standard test set (*setDeepLoc*) used by many developers, we created a new independent test set from SwissProt (Consortium, 2021). Applying the same filtering mechanisms as the DeepLoc developers (only eukaryotes; only proteins longer than 40 residues; no fragments; only experimental location annotations) gave 5 947 proteins. Using MMseqs2 (Steinegger & Söding, 2017), we removed all proteins from the new set with more than 20% PIDE to any protein in DeepLoc (both training and testing data). Next, we mapped location classes from DeepLoc to SwissProt, merged duplicates, and removed multi-localized proteins (protein X both in class Y and Z). Finally, we clustered proteins to representatives at 20% PIDE and obtained a new and more challenging test set (dubbed *setHARD*) with 490 proteins. Class distributions differed between the two sets (see *Appendix: Datasets*).

*Table 1.* Parameters and implementation details of SeqVec (Heinzinger et al., 2019), ProtBert and ProtT5 (Elnaggar et al., 2020). The time it takes to embed a single sequence (sec per sequence) is averaged over embedding 10 000 proteins taken from the Protein Data Bank (PDB) (Berman et al., 2000). The number of sequences used for the pre-training task is detailed in "# sequences".

| | SEQVEC | PROTBERT | PROTT5 |
|---|---|---|---|
| PARAMETERS | 93M | 420M | 3B |
| # SEQUENCES | 33M | 2.1B | 2.1B |
| SEC PER SEQUENCE | 0.03 | 0.06 | 0.1 |
| ATTENTION HEADS | - | 16 | 32 |

### 3.2. Models

**Input: protein embeddings.** As input to the LA architectures, we extracted embeddings from three pre-trained protein language models (LMs; Table 1): the bidirectional LSTM SeqVec (Heinzinger et al., 2019) based on ELMo (Peters et al., 2018), the encoder-only model ProtBert (Elnaggar et al., 2020) based on BERT (Devlin et al., 2019), and the encoder-only model ProtT5 (Elnaggar et al., 2020) based on T5 (Raffel et al., 2020). We obtained embeddings for each residue (NLP equivalent: word) in a protein sequence (NLP equivalent: document) using the bio-embeddings software (Dallago et al., 2020). For SeqVec, the per-residue embeddings were generated by summing the representations of each layer. For ProtBert and ProtT5, the per-residue embeddings were extracted from the last hidden layer of the models. With a hidden size of 1024 for each LM, inputs to LA were of size $1024 \times L$, where $L$ is the length of the protein sequence.

**Light Attention (LA) architecture.** The input to the light attention (LA) classifiers (Figure 1) was a protein embedding $x \in \mathbb{R}^{1024 \times L}$. The input was transformed by two separate 1D convolutions with filter sizes $s$ parameterized by learned weights $W^{(e)}, W^{(v)} \in \mathbb{R}^{s \times 1024 \times d_{out}}$. The convolutions were applied over the length dimension to produce attention coefficients and value features $e, v \in \mathbb{R}^{d_{out} \times L}$.

$$e_{i,j} = b_i + \sum_{k=1}^{1024} \sum_{l=-\lfloor \frac{s}{2} \rfloor}^{\lceil \frac{s}{2} \rceil} W_{l,i}^{(e)} x_{:,j+l} \tag{1}$$

where $b \in \mathbb{R}^{d_{out}}$ is a learned bias and $x_{:,j}$ denotes the j-th residue embedding. Null vectors were set to $x_{:,j}$ for $j$ outside the interval $[0, L)$. To use the coefficients as attention distribution over all $j$, we softmax-normalized over protein length. The attention weight $\alpha_{i,j} \in \mathbb{R}$ for the j-th residue and the i-th feature dimension was calculated as:

$$\alpha_{i,j} = \frac{exp(e_{i,j})}{\sum_{l=1}^{L} exp(e_{i,l})} \tag{2}$$

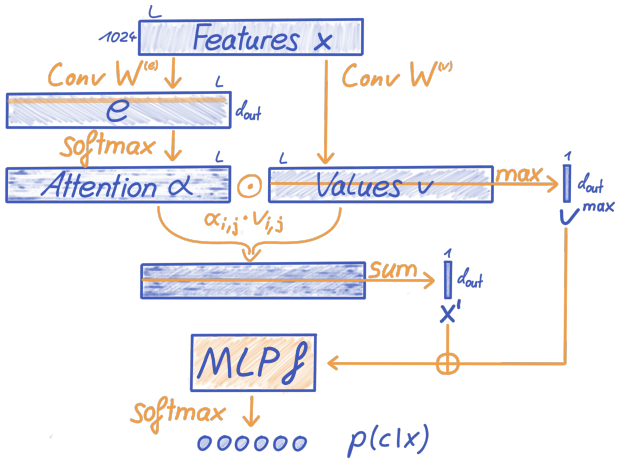


*Figure 1.* **Sketch of LA solution.** The LA architecture is parameterized by two weight matrices $W^{(e)}, W^{(v)} \in \mathbb{R}^{s \times 1024 \times d_{out}}$ and the weights of an MLP $f : \mathbb{R}^{2d_{out}} \mapsto \mathbb{R}^{d_{class}}$.

As the weight distributions for each feature dimension $i$ are independent, they might generate different attention patterns. We used the normalized attention distributions to compute weighted sums over the transformed residue embeddings $v_{i,j}$. Thus, we obtained a fixed-size representation $x' \in \mathbb{R}^{d_{out}}$ for the whole protein, independent of its length.

$$x'_i = \sum_{j=1}^{L} \alpha_{i,j} v_{i,j} \tag{3}$$

We concatenated $x'_i$ with the maximum of the values over the length dimension $v^{max} \in \mathbb{R}^{d_{out}}$, meaning $v_i^{max} = \max_{1 \leq j \leq L}(v_{i,j})$. This concatenated vector was input into a two layer multi-layer perceptron (MLP) $f : \mathbb{R}^{2d_{out}} \mapsto \mathbb{R}^{d_{class}}$ with $d_{class}$ as the number of classes. The softmax over the MLP output represents the individual class probabilities with classes indexed by $c$:

$$p(c|x) = softmax_c(f(x' \oplus m)) \tag{4}$$

where $\oplus$ denotes concatenation.

**Training models.** For the LA architecture, we trained three models, one for each protein embedding (SeqVec, ProtBert and ProtT5) for subsets of the training set. The models were trained using filter size $s = 9$, $d_{out} = 1024$, the Adam (Kingma & Ba, 2015) optimizer (learning rate $5 \times 10^{-5}$) with a batch size of 150 protein embeddings, and early stopping after no improvement in validation loss for 80 epochs. We selected the hyperparameters via random search (*Appendix: Hyperparameters*). Training was done on either an Nvidia Quadro RTX 8000 with 48GB vRAM or an Nvidia GeForce GTX 1060 with 6GB vRAM.

**Methods used for comparison.** For comparison, we trained a two layer feed-forward network (FFN) proposed previously (Heinzinger et al., 2019). Instead of per-residue embeddings in $\mathbb{R}^{1024 \times L}$, the FFNs used sequence-embeddings in $\mathbb{R}^{1024}$, which derived from residue-embeddings averaged over the length dimension (i.e. mean pooling). Furthermore, for these representations, we performed annotation transfer (dubbed AT) based on embedding similarity (Littmann et al., 2021). Following this approach, proteins in *setDeepLoc* and *setHARD* were annotated by transferring the class of the nearest neighbor in the DeepLoc training set (given by L1 distance).

### 3.3. Evaluation.

Following previous work, we assessed performance mostly through the mean ten-class accuracy (Q10), giving the percentage of correctly predicted proteins in one of ten location classes. Additional measures tested did not provide any additional insights and were, therefore, confined to the *Appendix: Additional Results*, e.g., Matthew's correlation coefficient (MMC) for multiple classes (Gorodkin measure (Gorodkin, 2004)). Error estimates were calculated over ten random seeds on both test sets. For previous methods (DeepLoc and DeepLoc62 (Almagro Armenteros et al., 2017), LocTree2 (Goldberg et al., 2012), MultiLoc2 (Blum et al., 2009), SherLoc2 (Briesemeister et al., 2009), CELLO (Yu et al., 2006), iLoc-Euk (Chou et al., 2011), YLoc (Briesemeister et al., 2010) and WoLF PSORT (Horton et al., 2007)) published performance values were used (Almagro Armenteros et al., 2017) for *setDeepLoc* and computed for *setHARD*. As a naive baseline, we used the majority classifier. All evaluation scripts to reproduce results are available[1].

## 4. Results

**Embeddings outperformed evolutionary information.** The simple AT approach already outperformed some methods using evolutionary information (Figure 2: *AT**). The FFN trained on ProtT5 (Elnaggar et al., 2020) outperformed *DeepLoc* (Almagro Armenteros et al., 2017) (Figure 2: *FNN ProtT5* vs. *DeepLoc*). Methods based on ProtT5 embeddings consistently yielded better results than ProtBert and SeqVec (Heinzinger et al., 2019) (*ProtT5 vs *ProtBert/*SeqVec in Figure 2). Results on Q10 are consistent with MCC (*Appendix: Additional Results*).

**LA architecture best.** The light attention (LA) architecture consistently outperformed other embedding-based approaches, irrespective of the protein LM used (LA* vs. AT/FFN* in Figure 2). Using ProtBert embeddings, LA outperformed the state-of-the-art (SOTA) (Almagro Armenteros et al., 2017) by $1-2$ percentage points (LA Prot-

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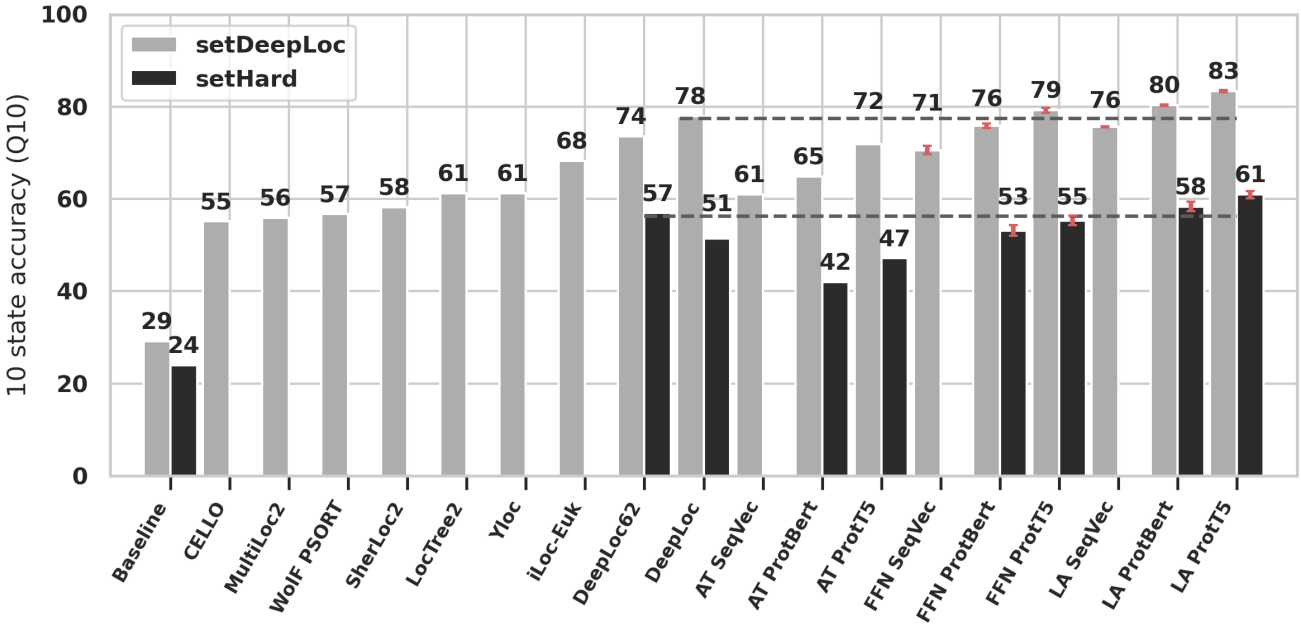


*Figure 2.* **LA architectures perform best.** Bars give the ten-class accuracy (Q10) for popular location prediction methods on *setDeepLoc* (light-gray bars) and *setHARD* (dark-gray bars). Baseline is the most common class in each set. Horizontal gray dashed lines mark the previous SOTA on either set. Estimates for standard errors are marked in orange for the methods introduced here. *setHARD* results are provided for a subset of methods that yielded the best results on *setDeepLoc* (Methods for detail on the external methods used; tabular data in *Appendix: Additional Results*). Two results stood out: (i) the LA approaches introduced here outperformed the top methods although not using evolutionary information (highest bars), and (ii) the performance estimates differed completely between the two data sets (difference light/dark gray).

Bert Figure 2) and by $3-5$ percentage points using ProtT5 (Figure 2) for *setHARD* and *setDeepLoc*, respectively.

**Overfitting by using standard data set.** The substantial drop in performance (around 22 percentage points) between results for the standard *setDeepLoc* and the new challenging *setHARD* (Figure 2: light-gray vs. dark-gray, respectively) suggests some level of overfitting. Mimicking the distribution of classes found in *setDeepLoc* by sampling with replacement from *setHARD* led to better results (in Q10: *DeepLoc62*=63%; *DeepLoc*=54%; *LA ProtBert*=62%; *LA ProtT5*=66%). *DeepLoc* performed worse on *setHARD* using evolutionary information than using simple sequence information (Figure 2: *DeepLoc* vs. *DeepLoc62*). Otherwise, the relative ranking and difference of models largely remained consistent between *setDeepLoc* and *setHARD*.

**Low performance for minority classes.** The confusion matrix of predictions for *setDeepLoc* using LA trained on ProtT5 embeddings highlighted how many proteins were incorrectly predicted in the most prevalent class, *cytoplasm*, and that even the two majority classes were often confused with each other (Figure 3: *nucleus* and *cytoplasm*). In line with the previous SOTA (Almagro Armenteros et al., 2017), the performance was particularly low for the most under-represented classes, namely *Golgi* apparatus, *lysosome/Vacuole*, and *peroxisome* (accounting for 2.6%, 2.3%, and 1.1% of the data, respectively).

**Light aggregation (LA) mechanism crucial.** To further evaluate the effectiveness of the LA architecture's aggregation mechanisms, we replaced the light attention that produced $x'$ with averaging the coefficient features $e$ over the length dimension. Performance using ProtT5 embeddings dropped from 83.37% to $81.54 \pm 0.13$% (Q10(*setDeepLoc*)). Similarly, we dropped the max-pooled values $v^{max}$ as input to the MLP such that only the aggregated light attention features were used. This reduced performance from 83.37% to $82.23 \pm 0.44$% (Q10(*setDeepLoc*)).

**Model trainable on consumer hardware.** After embeddings for proteins were generated, the final LA architecture, made of 18 940 224 parameters, could be trained on an Nvidia GeForce GTX 1060 with 6GB vRAM in 18 hours or on a Quadro RTX 8000 with 48GB vRAM in 2.5 hours.

## 5. Discussion

**Light attention beats pooling.** The central challenge for the improvement introduced here was to convert the

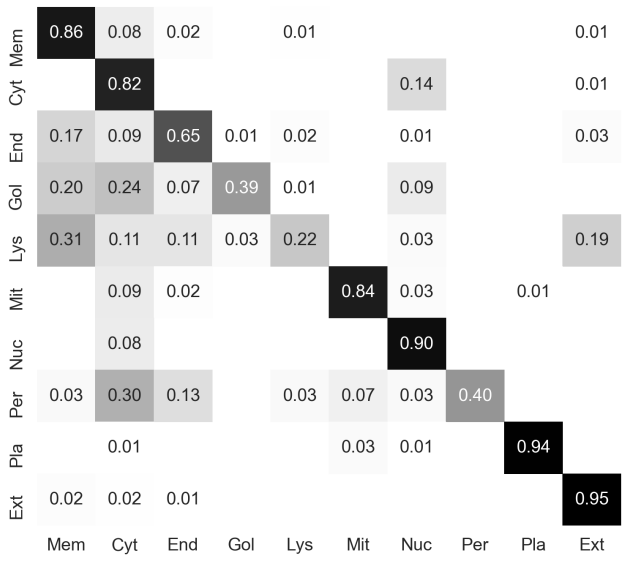


*Figure 3.* **Mostly capturing majority classes.** Confusion matrix of LA predictions on ProtT5 (Elnaggar et al., 2020) embeddings for *setDeepLoc* (Almagro Armenteros et al., 2017) annotated with the fraction of the true class. Y-axis (vertical): true class, X-axis (horizontal): predicted class. Labels: Mem=cell **Mem**brane; Cyt=**Cyt**oplasm; End=**End**oplasmatic Reticulum; Gol=**Gol**gi apparatus; Lys=**Lys**osome/vacuole; Mit=**Mit**ochondrion; Nuc=**Nuc**leus; Per=**Per**oxisome; Pla=**Pla**stid; Ext=**Ext**racellular

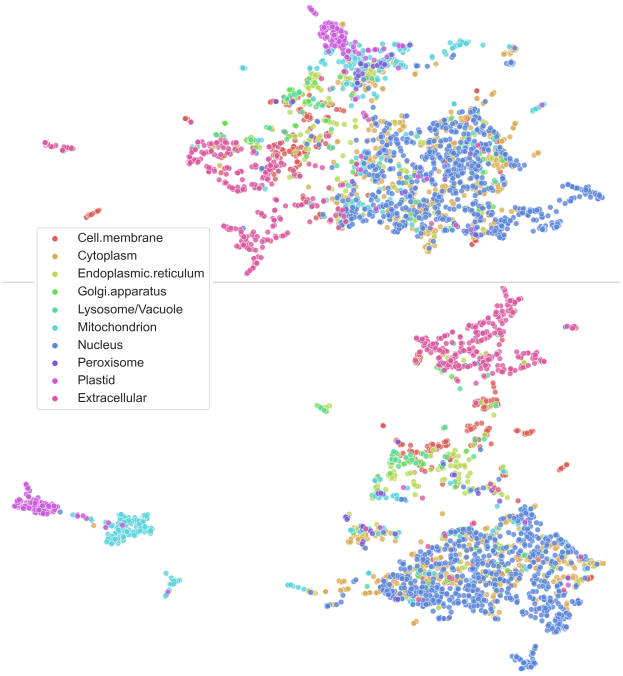


*Figure 4.* **Qualitative analysis confirms: attention effective.** UMAP (McInnes et al., 2018) projections of per-protein embeddings colored according to subcellular location (*setDeepLoc*). Top: ProtT5 embeddings (LA input; $x$) mean-pooled over protein length (as for FFN/AT input). Bottom: ProtT5 embeddings (LA input; $x$) weighted according to the attention distribution produced by LA (this is not $x'$ as we sum the input features $x$ and not the values $v$ after the convolution).

residue-embeddings (NLP equivalent: word embeddings) from protein language models such as SeqVec (Heinzinger et al., 2019), ProtBert, or ProtT5 (Elnaggar et al., 2020) to meaningful sequence-embeddings (NLP equivalent: document). A qualitative evaluation of the influence of the attention mechanism (Figure 4) highlighted its ability to steer predictions. Although averaging surpassed evolutionary-information-based methods using simple similarity-based annotation transfer (Figure 2: AT*) and in one instance even SOTA using a simple feed-forward network (Figure 2: *DeepLoc* vs. *FNN ProtT5*), LA was able to consistently distill more information from embeddings. Most likely, the improvement can be attributed to LA's ability to regulate the immense difference in lengths of proteins (varying from 30 to 30 000 residues (Consortium, 2021)) by learning attention distributions over the sequence positions. LA models appeared to have captured relevant long-range dependencies while retaining the ability to focus on specific sequence regions such as beginning and end, which play a particularly important role in determining protein location for some proteins (Lange et al., 2007; Almagro Armenteros et al., 2017).

**First win over evolutionary information.** Effectively, LA trained on protein LM embeddings from ProtT5 (Elnaggar et al., 2020) was at the heart of the first method that clearly appeared to outperform the best existing method (*DeepLoc*, (Almagro Armenteros et al., 2017; Heinzinger et al., 2019)) in a statistically significant manner on two test sets (Figure 2). To the best of our knowledge, this improvement was the first instance ever that embedding-based transfer learning substantially outperformed AI/ML methods using evolutionary information for function prediction. Even if embeddings are extracted from LMs trained on large sequence data originating from evolution, the vast majority of data learned originates from much more generic constraints informative of protein structure and function.

**Better and faster.** The embeddings needed as input for the LA models come with three advantages over evolutionary-information-based input essential for methods such as *DeepLoc* (Almagro Armenteros et al., 2017). Chiefly, embeddings can be obtained in far less time than is needed to generate evolutionary information and require fewer compute resources. Even considering the lightning-fast MMseqs2 (Steinegger & Söding, 2017), which is not the standard in bioinformatics (other methods 10-100x slower), in our experience required about 0.3 seconds to generate evolutionary information input for a large set of 10 000 pro-

teins. The slowest but most informative embedder (ProtT5) is 3x faster, while the second most informative (ProtBert) is 5x faster (Table 1). Additionally, these MMseqs2 stats derive from runs on a machine with $>$ 300GB of RAM and 2x40cores/80threads CPUs, while generating LM embeddings required only a moderate machine (8 cores, 16GB RAM) equipped with a modern GPU with >10GB of vRAM. Lastly, extracting evolutionary information relies on the use of tools (e.g., MMseqs2) that are sensitive to parameter changes, ultimately an extra complication for users. In contrast, generating embeddings doesn't require a parameter choice beyond which trained model to use (e.g., ProtBert vs. ProtT5).

**Overfitting through standard data set?** For protein subcellular location prediction, the data sets from *DeepLoc* (Almagro Armenteros et al., 2017) have become a standard in the field. Such static standards facilitate method comparisons. To further probe results, we created a new test set (*setHARD*), which was redundancy-reduced both with respect to itself and all proteins in the *DeepLoc* set (comprised of training data and *setDeepLoc*, used for testing). For this set, the 10-state accuracy (Q10) dropped, on average, 22 percentage points with respect to the static standard (Figure 2). We argue that this large margin may be attributed to some combination of the following coupled effects.

(1) All new methods may simply have been substantially overfitted to the static data set, e.g., by misusing the test set for hyperparameter optimization. This could partially explain the increase in performance on *setHARD* when mimicking the class distributions in the training set and *setDeepLoc*.

(2) The static standard set allowed for some level of sequence-redundancy (information leakage) at various levels: certainly within the test set, which had not been redundancy reduced to itself, maybe also between the training and test set. Methods with many free parameters might more easily zoom into exploiting such residual sequence similarity for prediction because proteins with similar sequence locate in similar compartments. In fact, this may explain the somewhat surprising observation that *DeepLoc* appeared to perform worse on *setHARD* using evolutionary information instead of a generic BLOSUM metric (Figure 2: *DeepLoc62* vs. *DeepLoc*). Residual redundancy is much easier to capture via evolutionary information than by BLOSUM (Urban et al., 2020) (for computational biologists: the same way in which PSI-BLAST (Altschul et al., 1997) outperforms pairwise BLAST).

(3) The confusion matrix (Figure 3) demonstrated how classes with more experimental data tended to be predicted more accurately. As *setDeepLoc* and *setHARD* differed in their class composition, even without overfitting and redundancy, prediction methods would perform differently on the two. In fact, this can be investigated by recomputing the performance on a similar class-distributed superset of *setHARD*, on which performance dropped only by 11, 24, 18, and 17 percentage points for *DeepLoc62*, *DeepLoc*, *LA ProtT5*, and *LA ProtBert*, respectively.

Overall, several overlaying effects caused the performance to drop between the two data sets. Interestingly, different approaches behaved alike: both for alternative inputs from protein language models (ProtVec, ProtBERT, ProtT5) and for alternative methods (AT, FFN, LA), of which one (AT) refrained from weight optimization.

**What can users expect from subcellular location predictions?** If the top accuracy for one data set was Q10 $\sim 60\%$ and Q10 $\sim$ 80% for the other, what can users expect for their next ten queries: six correct or eight, or 6-8? The answer depends on the query: if those proteins were sequence similar to proteins with known location (case: redundant): the answer is eight. Conversely, for new proteins (without homologs of known location), six in ten will be correctly predicted, on average. In turn, this implies that for novel proteins, there seems to be significant room for pushing performance to further heights, possibly by combining *LA ProtBert*/*LA ProtT5* with evolutionary information.

## 6. Conclusion

We presented a light attention mechanism (LA) in an architecture operating on language model embeddings of protein sequences, namely those from SeqVec (Heinzinger et al., 2019), ProtBert, and ProtT5 (Elnaggar et al., 2020). LA efficiently aggregated information and coped with arbitrary sequence lengths, thereby mastering the enormous range of proteins spanning from 30-30 000 residues. By implicitly assigning a different importance score for each sequence position, the method succeeded in predicting protein subcellular location much better than methods based on simple pooling. More importantly, for two protein LMs, LA succeeded in outperforming the state-of-the-art without using evolutionary-based inputs, i.e., the single most important input feature for previous methods. This constituted an important breakthrough: although many methods had come close to the state-of-the-art using embeddings instead of evolutionary information, none had ever overtaken as the methods presented here. Our best method was based on the largest protein LM, namely on ProtT5 (*LA ProtT5* in Figure 2). Many location prediction methods have been assessed on a standard data set (here: *setDeepLoc*) introduced a few years ago (Almagro Armenteros et al., 2017). Using a new, more challenging data set (*setHARD*), the performance of all methods appeared to drop by around 22 percentage points. While class distributions and data set redundancy (or homology) may explain some of this drop, over-fitting might have also contributed. Overall, the drop underlined

that many challenges remain to be addressed by future methods. For the time being, the best methods *LA ProtBert* and *LA ProtT5*, are freely available via a web-server[2] and as part of a high-throughput pipeline (Dallago et al., 2020).

## Acknowledgements

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# Appendix: Light Attention Predicts Protein Location from the Language of Life

**Anonymous Authors**[1]

## 1. Protein Preliminaries

**Protein Sequences.** Proteins are built by chaining and arbitrary number of one of 20 amino acids in a particular order. When amino acids come together to form protein sequences, they are dubbed residues. During the assembly in the cell, constrained by physiochemical forces, the one-dimensional chains of residues fold into unique 3D shapes based solely on their sequence that largely determine protein function. The ideal machine learning model would predict a protein's 3D shape and thus function from just protein sequence (the ordered chain of residues).

**Protein Subcellular Location.** Eukaryotic cells contain different organelles/compartments. Each organelle serves a purpose, e.g., ribosomes chain together new proteins while mitochondria synthesize ATP. Proteins are the machinery used to perform these functions, including transport in and out and communication between different organelles and a cell's environment. For some compartments, e.g., the nucleus, special stretches of amino acids, e.g., nuclear localization signals (NLS), help identifying a protein's location via simple string matching. However, for many others, the localization signal is diluted within the whole sequence, requiring sequence-level predictions. Furthermore, some organelles (and the cell itself) feature membranes with different biochemical properties than the inside or outside, requiring protein gateways.

**Homology-inference.** Two highly similar protein sequences will most likely fold in similar 3D structures and more likely to perform similar functions. Homology based inference (Nair & Rost, 2002; Mahlich et al., 2018), which transfers annotations of experimentally validated proteins to query protein sequences, is based on this assumption (Sander & Schneider, 1991). Practically this means searching a database of annotated protein sequences for sequences that meet both an identity threshold and a length-of-match threshold to some query protein sequence. Sequence homology delivers good results, but its stringent requirements render it applicable to only a fraction of proteins (Rost, 1999).

**Machine learning Function Prediction.** When moving into territory where sequence similarity is less conserved for shorter stretches of matching sequences (Mahlich et al., 2018; Rost, 2002), one can try predicting function using evolutionary information and machine learning (Goldberg et al., 2012; Almagro Armenteros et al., 2017). Evolutionary information from protein profiles, encoding a protein's evolutionary path, is obtained by aligning sequences from a protein database to a query protein sequence and computing conservation metrics at the residue level. Using profiles leads to impressively more accurate predictions for sequences with no close homologs and has been the standard for most protein prediction tasks (Urban et al., 2020), including subcellular localization (Goldberg et al., 2012; Almagro Armenteros et al., 2017; Savojardo et al., 2018). While profiles provide a strong and useful inductive bias, their information content heavily depends on a balance of the number of similar proteins (depth), the overall length of the matches (sequence coverage), the diversity of the matches (column coverage), and their generation is parameter sensitive.

## 2. Hyperparameters

The following describes the search space used to find hyperparameters of our final LA and FFN models. We performed random search over these parameters. The evaluated learning rates were in the range of $[5 \times 10^{-6}$ - $5 \times 10^{-3}]$. For the light attention architecture, we tried filter sizes $[3, 5, 7, 9, 11, 13, 15, 21]$ and hidden sizes $d_{out} \in [32, 128, 256, 512, 1024, 1500, 2048]$, as well as concatenating outputs of convolutions with different filter sizes. For the FFN, we searched over the hidden layer sizes $[16, 32, 64, 512, 1024]$, where 32 was the optimium. We maximized batch size to fit a Quadro RTX 8000 with 48GB vRAM, resulting in the batch size of 150. Note that the memory requirement is dependent on the size of the longest sequence in a batch. In the DeepLoc dataset, the longest sequence had 13 100 residues.

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*Table 1.* Accuracy and Matthew's correlation coefficient (MCC) on *setDeepLoc*.

| METHOD | ACCURACY | MCC |
|---|---|---|
| LOCTREE2 | 61.20 | 0.525 |
| MULTILOC2 | 55.92 | 0.487 |
| SHERLOC2 | 58.15 | 0.511 |
| YLOC | 61.22 | 0.533 |
| CELLO | 55.21 | 0.454 |
| ILOC-EUK | 68.20 | 0.641 |
| WOLF PSORT | 56.71 | 0.479 |
| DEEPLOC62 | 73.60 | 0.683 |
| DEEPLOC | 77.97 | 0.735 |
| AT SEQVEC | 60.97 | 0.508 |
| AT PROTBERT | 64.85 | 0.567 |
| AT PROTT5 | 71.89 | 0.661 |
| FFN SEQVEC | 70.57± 0.93 | 0.636± 0.011 |
| FFN PROTBERT | 75.88± 0.45 | 0.702± 0.006 |
| FFN PROTT5 | 79.20± 0.55 | 0.749± 0.007 |
| LA SEQVEC | 75.63± 0.11 | 0.705± 0.002 |
| LA PROTBERT | 80.29± 0.21 | 0.762± 0.002 |
| LA PROTT5 | **83.37**± 0.24 | **0.800**± 0.003 |

*Table 2.* Accuracy and Matthew's correlation coefficient (MCC) on *setHARD*.

| METHOD | ACCURACY | MCC |
|---|---|---|
| DEEPLOC62 | 56.94 | 0.476 |
| DEEPLOC | 51.36 | 0.410 |
| AT PROTBERT | 42.04 | 0.306 |
| AT PROTT5 | 47.14 | 0.368 |
| FFN PROTBERT | 53.16± 1.19 | 0.429± 0.014 |
| FFN PROTT5 | 55.31± 1.04 | 0.457± 0.012 |
| LA PROTBERT | 58.36± 1.02 | 0.490± 0.012 |
| LA PROTT5 | **60.92**± 0.82 | **0.522**± 0.010 |

## 3. Additional Results

We provide results for both *setDeepLoc* (Table 1) and *setHARD* (Table 2) in tabular form, including the Matthew's Correlation Coefficients (MCC).

## 4. Datasets

Table 3 shows the distribution of subcellular localization classes in the *setDeepLoc* and our new *setHARD*.

### 4.1. New test set creation

In the following, we lay out the steps taken to produce the new test set (*setHARD*). The starting point is a filtered UniProt search with options as selected in Figure 1. Python code used is available here: *OMITTED*.

- Download data as FASTA & XML:

```
wget "https://www.uniprot.org/uniprot/?query=taxonomy:%22Eukaryota%20[2759]%22%20length:[40%20TO%20*]%20locations:(note:*%20evidence:%22Inferred%20from%20experiment%20[ECO:0000269]%22)%20fragment:no%20AND%20reviewed:yesformat=xmlforce=truesort=scorecompress=yes"
wget "https://www.uniprot.org/uniprot/?query=taxonomy:%22Eukaryota%20[2759]%22%20length:[40%20TO%20*]%20locations:(note:*%20evidence:%22Inferred%20from%20experiment%20[ECO:000026%22)%20fragment:no%20AND%20reviewed:yesformat=fastaforce=truesort=scorecompress=yes"
```

- Download deeploc data:

```
wget http://www.cbs.dtu.dk/services/DeepLoc-1.0/deeploc_data.fasta
```

- Align sequences in swissprot to deeploc that have more than 20% PIDE:

*Table 3.* Number of proteins and percentage of dataset for each class for the DeepLoc dataset and our *setHARD*. ER abbreviates Endoplasmatic Reticulum

| LOCATION | DEEPLOC | | SETHARD | |
|---|---|---|---|---|
| | # | % | # | % |
| NUCLEUS | 4043 | 28.9 | 99 | 20.2 |
| CYTOPLASM | 2542 | 19.3 | 117 | 23.8 |
| EXTRACELLULAR | 1973 | 14.0 | 92 | 18.8 |
| MITOCHONDRION | 1510 | 11.8 | 10 | 2.0 |
| CELL MEMBRANE | 1340 | 9.5 | 98 | 20.0 |
| ER | 862 | 6.2 | 34 | 6.9 |
| PLASTID | 757 | 5.4 | 11 | 2.6 |
| GOLGI APPARATUS | 356 | 2.6 | 13 | 2.6 |
| LYSOSOME/VACUOLE | 321 | 2.3 | 13 | 2.2 |
| PEROXISOME | 154 | 1.1 | 3 | 0.6 |

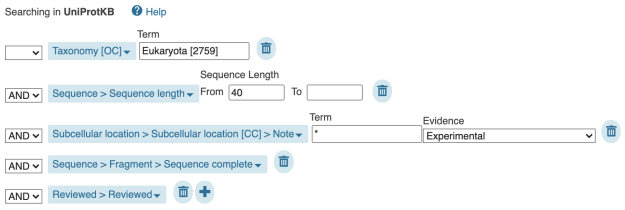


*Figure 1.* Screenshot of the filtering options applied to the advanced UniProt search (uniprot.org/uniprot).

```
mmseqs easy-search swissprot.fasta
deeploc_data.fasta -s 7.5
--min-seq-id 0.2 --format-output
query,target,fident,alnlen,mismatch,
gapopen,qstart,qend,tstart,tend,
evalue,bits,pident,nident,qlen,tlen,
qcov,tcov alignment.m8 tmp
```

- Extract localizations from SwissProt XML:

```
python extract_localizaiotns_from_
swissprot.py
```

- Map deeploc compartments on swissprot localizations & remove duplicates ([P123, Nucleus] appearing twice), remove multilocated ([P123, Nucelus] and [P123, Cytoplasm] –> remove P123) empty or not experimental annotations:

```
python map_and_filter_swissprot_
annotations.py
```

- Create FASTA like deeploc from sequences not in alignment:

```
python extract_unaligned_
sequences.py
```

- Redundancy reduce new set to 20%:

```
mmseqs easy-cluster --min-seq-id
0.2 new_test_set_not_redundancy_
reduced.fasta new_hard_test_set_
PIDE20.fasta tmp
```

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