



SHORT REPORT

Open Access

Interpol: An R package for preprocessing of protein sequences

Dominik Heider* and Daniel Hoffmann

* Correspondence: dominik.heider@uni-due.de
Department of Bioinformatics,
Center for Medical Biotechnology,
University of Duisburg-Essen,
Universitaetsstr. 2, 45141 Essen,
Germany

Abstract

Background: Most machine learning techniques currently applied in the literature need a fixed dimensionality of input data. However, this requirement is frequently violated by real input data, such as DNA and protein sequences, that often differ in length due to insertions and deletions. It is also notable that performance in classification and regression is often improved by numerical encoding of amino acids, compared to the commonly used sparse encoding.

Results: The software "Interpol" encodes amino acid sequences as numerical descriptor vectors using a database of currently 532 descriptors (mainly from AAindex), and normalizes sequences to uniform length with one of five linear or non-linear interpolation algorithms. Interpol is distributed with open source as platform independent R-package. It is typically used for preprocessing of amino acid sequences for classification or regression.

Conclusions: The functionality of Interpol widens the spectrum of machine learning methods that can be applied to biological sequences, and it will in many cases improve their performance in classification and regression.

Findings

Machine learning techniques have been widely applied to biological sequences to gain insights into biological function, for instance Rost and Sander [1], Dubchak *et al.* [2], Karchin *et al.* [3] and Nielsen *et al.* [4]. Nanni and Lumini [5] have found improved performance of classifiers based on numerically encoded amino acid sequences as compared to classifiers based on the typically used standard orthonormal representation, i.e. a vector containing twenty indicator variables (one for each amino acid) for each sequence position, resulting in a matrix containing the amino acid distributions for each position in the input sequence. For numerical encoding, each amino acid (or nucleotide) of a sequence is mapped to a numerical descriptor value, such as hydropathy [6], molecular weight, or isoelectric point.

One major limitation of almost all machine learning algorithms is the fixed input dimension, making these algorithms incapable of handling data which varies in its dimension. This is unsuitable for many biological applications as there are often sequence deletions and insertions.

We have developed a preprocessing approach for machine learning that combines the use of numerical descriptor values with a normalization of sequences to a fixed length by numerical interpolation. This procedure has already been applied to

coreceptor usage prediction in HIV-1 [7], functional protein classification [8,9], and HIV-1 drug resistance prediction [10] were it led to marked improvements of prediction performance. Although many machine learning algorithms are available as software, no package for the described preprocessing of amino acid sequences is available to date. We have therefore developed Interpol, a flexible and easy to use open source package for the statistical language R <http://www.r-project.org/>. Currently, Interpol provides encoding of amino acid sequences with 531 different numerical descriptors from the AAindex database [11] and one additional empirical descriptor. Moreover, it allows normalization of encoded sequences to a specific length with five different linear or non-linear interpolation procedures.

Interpol is included in the Comprehensive R Archive Network (CRAN) and can be directly downloaded and installed by using the following R command:

```
install.packages("Interpol")
```

In the following example, we introduce Interpol's two commands `AAdescriptor` and `Interpol` applied to a set consisting of 1351 HIV-1 V3 loop sequences from Dybowski *et al.* [7] for the prediction of coreceptor usage (see also Table 1). After loading the set of sequences, the first V3 sequence is encoded using the `AAdescriptor` command:

```
library(Interpol)
data(V3) #load V3 data
data.new <- AAdescriptor(V3[1]) #numerically encode
sequence 1
```

Optional parameters are the applied descriptor (default `descriptor = 151`, i.e. the hydrophathy scale of Kyte and Doolittle [6]) and an interval normalization (default `normalize = 0`, i.e. no normalization). The list of available descriptors can be found in `data(list)`.

After encoding the amino acid sequence as numerical vector, it can be normalized to a specific length for subsequent classification. In our example, the V3 sequence lengths vary between 33 and 38 amino acids due to deletions or insertions. The following commands translate the amino acid sequences into numerical sequences using the hydrophathy descriptor, and then normalize the sequences to a fixed length of 35:

```
library(Interpol)
data(V3) #load V3 data
L.norm <- 35 #desired length
data.new <- matrix(nrow = length(V3),
                  ncol = L.norm)
for(i in 1:length(V3)) {
  #AAdescriptor encodes sequences
```

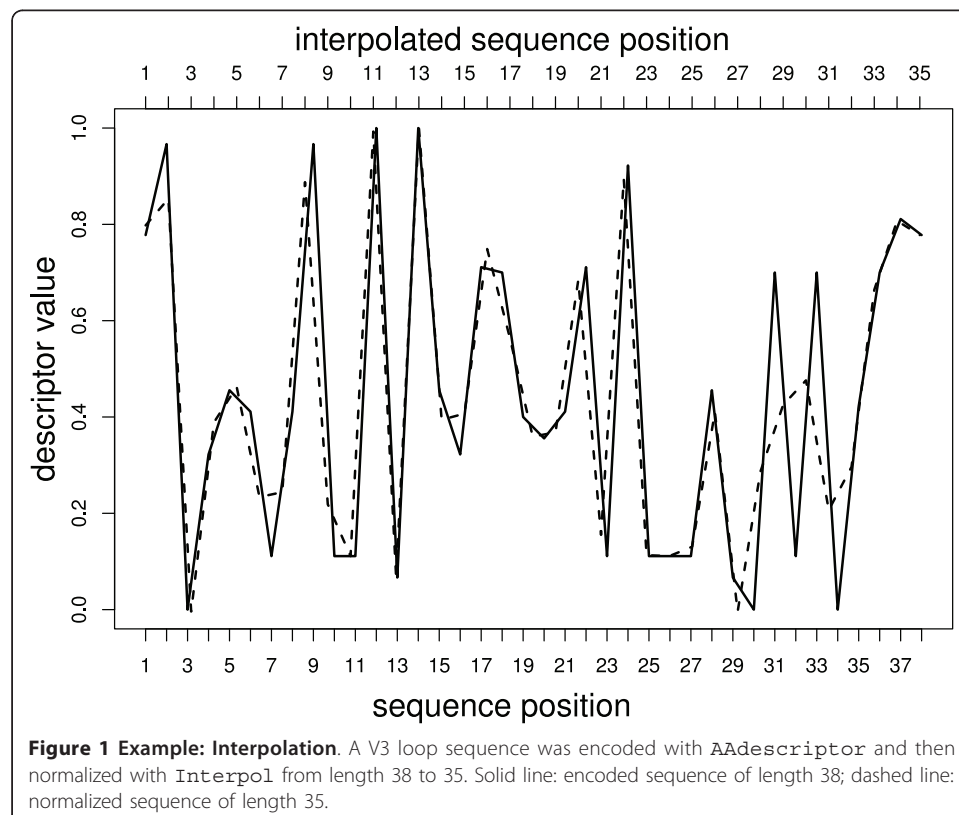
Table 1 Method overview

command	parameters	information
AAdescriptor	data	amino acid sequence
	descriptor (optional)	1-532; default = 151 [6]
	normalize (optional)	0: no; 1:[-1,1]; 2:[0,1]; default = 0
Interpol	data	encoded amino acid sequence
	dims	desired length
	method (optional)	default = linear, spline, periodic, natural, fmm

```
#Interpol normalizes to length L.norm  
data.new[i,] <- Interpol (AAdescriptor (V3[i]),  
                        dims = L.norm)  
}
```

Sequence 782 in the V3 dataset has a length of 38 amino acids. In the following example the code for normalization from 38 to 35 amino acids, and for visualization of the interpolation is demonstrated (see Figure 1):

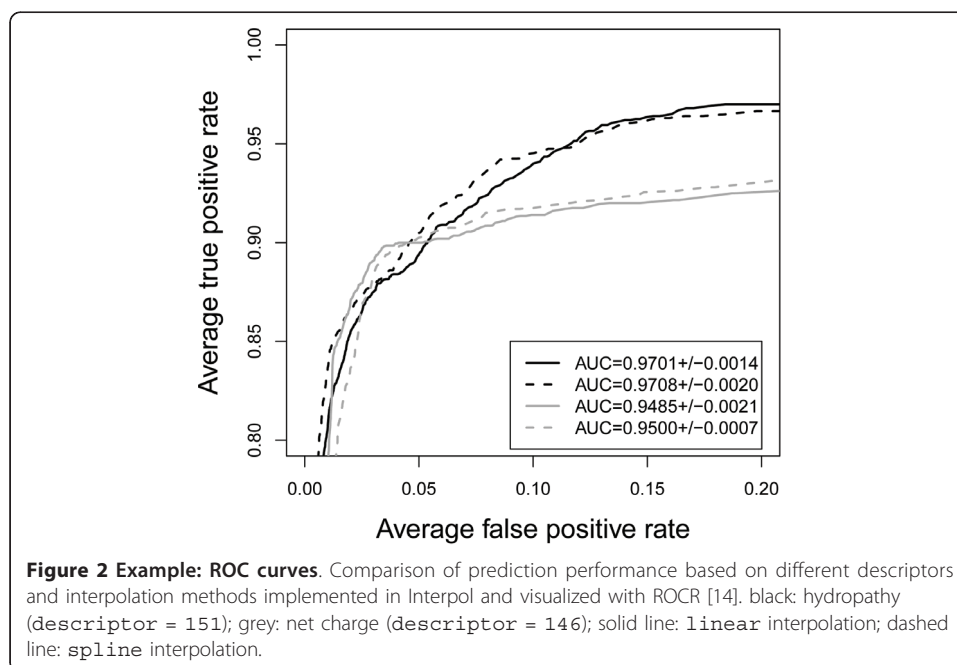
```
library(Interpol)  
data(V3) #load V3 data  
sequence <- AAdescriptor(data = V3[782], #numerically  
encoding  
                        descriptor = 151, #hydropathy descriptor  
normalize = 2) #interval normalization [0,1]  
sequence.35 <- Interpol(data = sequence, #normalize sequence  
                        dims = 35, #desired length 35  
method="spline") #spline interpolation  
plot(sequence, type="l", ylim = c(0,1), #plot sequence 782  
      ylab="descriptor value",  
      xlab="sequence position",  
      lty = 1, lwd = 2)  
lines(seq(1,38,(38/35)),sequence.35, #plot normalized  
sequence  
      lty = 2, lwd = 2)
```




```
rf <- randomForest (as.factor (classes)~, , #build
forest
                    data = data.new)
pred <- prediction (rf$votes[,2], classes) #prediction
object
perf <- performance (pred, "auc") #AUC estimation
```

Using the Interpol package, it is very easy to retrieve and compare the performance of different descriptors, e.g. hydrophobicity and net charge, and different interpolation methods (e.g. linear and spline interpolation), by just changing line `desc <- 151` to `desc <- 146` and `inter <- "linear"` to `inter <- "spline"`, respectively, in the above code (see also Figure 2). The complete list of descriptors can be found on the help pages (`help (Interpol)`) and in `data(list)`. Note that the above code somewhat overestimates the true performance as it does not include the leave-one-patient-out scheme used by Dybowski *et al.* [7].

There are several potential limitations of the Interpol method for protein classification. First, normalizing to lengths of less than 50% of the original sequence length will in general lead to loss of information. Thus, we suggest to stretch short sequences to a certain length instead of squeezing longer sequences. However, stretching can also cause problems as the normalized sequence space has a higher dimension and thus classification is more prone to overfitting. A more general limitation of normalization is that in some cases the sequence length itself can carry some information. For instance, classifying sequences of huntingtin protein [16] for induction of Huntington's disease critically relies on the length of a Glutamine repeat, an information that can be partly lost in sequence normalization.



Availability and requirements

- Project name: Interpol
- Project home page (CRAN): <http://cran.r-project.org/web/packages/Interpol/>
- Operating system (s): Platform independent
- Programming language: R ($\geq 2.10.0$)
- License: GPL (≥ 2)
- Any restrictions to use by non-academics: none

Acknowledgements

We thank the reviewers for their fruitful suggestions. Funding by Deutsche Forschungsgemeinschaft TRR60/A6 is gratefully acknowledged.

Authors' contributions

DH* has implemented and tested the software, and drafted the manuscript. DH has revised the manuscript. All authors read and approved the final manuscript.

Competing interests

The authors declare that they have no competing interests.

Received: 27 March 2011 Accepted: 17 June 2011 Published: 17 June 2011

References

1. Rost B, Sander C: **Combining evolutionary information and neural networks to predict protein secondary structure.** *Proteins* 1994, **19**:55-72.
2. Dubchak I, Muchnik I, Holbrook SR, Kim SH: **Prediction of protein folding class using global description of amino acid sequence.** *Proc Natl Acad Sci* 1995, **92**:8700-8704.
3. Karchin R, Karplus K, Haussler D: **Classifying G-protein coupled receptors with support vector machines.** *Bioinformatics* 2002, **18**:147-150.
4. Nielsen M, Lundegaard C, Worning P, Lauemøller SL, Lamberth K, Buus S, Brunak S, Lund O: **Reliable prediction of T-cell epitopes using neural networks with novel sequence representations.** *Protein Sci* 2003, **12**(5):1007-1017.
5. Nanni L, Lumini A: **A new encoding technique for peptide classification.** *Expert Systems with Applications* 2011, **38**(4):3185-3191.
6. Kyte J, Doolittle R: **A simple method for displaying the hydropathic character of a protein.** *J Mol Biol* 1982, **157**:105-132.
7. Dybowski JN, Heider D, Hoffmann D: **Prediction of co-receptor usage of HIV-1 from genotype.** *PLoS Comput Biol* 2010, **6**(4):e1000743.
8. Heider D, Appelmann J, Bayro T, Dreckmann W, Held A, Winkler J, Barnekow A, Borschbach M: **A computational approach for the identification of small GTPases based on preprocessed amino acid sequences.** *Technology in Cancer Research and Treatment* 2009, **8**(5):333-342.
9. Heider D, Hauke S, Pyka M, Kessler D: **Insights into the classification of small GTPases.** *Advances and Applications in Bioinformatics and Chemistry* 2010, **3**:15-24.
10. Heider D, Verheyen J, Hoffmann D: **Machine learning on normalized protein sequences.** *BMC Research Notes* 2011, **4**:94.
11. Kawashima S, Pokarowski P, Pokarowska M, Kolinski A, Katayama T, Kanehisa M: **AAindex: amino acid index database, progress report 2008.** *Nucleic Acids Res* 2008, **36** Database: D202-D205.
12. Forsythe GE: *Computer Methods for Mathematical Computations* Prentice Hall; 1977.
13. Breiman L: **Random Forests.** *Machine Learning* 2001, **45**:5-32.
14. Sing T, Sander O, Beerewinkel N, Lengauer T: **ROCR: visualizing classifier performance in R.** *Bioinformatics* 2005, **21**(20):3940-3941.
15. Karatzoglou A, Smola A, Hornik K, Zeileis A: **kernlab - An S4 Package for Kernel Methods in R.** *Journal of Statistical Software* 2004, **11**(9):1-20.
16. Walker FO: **Huntington's disease.** *Lancet* 2007, **369**(9557):218-228.

doi:10.1186/1756-0381-4-16

Cite this article as: Heider and Hoffmann: Interpol: An R package for preprocessing of protein sequences. *BioData Mining* 2011 **4**:16.