The new SignalP

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The SignalP method for prediction of secretory signal peptides [1] has been updated. In addition to the original Neural Network-based method (SignalP-NN), which has been retrained on a newer data set, the server now includes a Hidden Markov Model (SignalP-HMM).

SignalP-HMM is a slightly modified version of the HMM architecture presented at ISMB '98 [2,3]. It has a better performance than SignalP-NN in dicriminating between cleaved signal peptides and uncleaved signal anchors (transmembrane helices). On the other hand, SignalP-NN is better at predicting the exact location of the cleavage site. Here, we show how the output of both methods can be combined to give the best overall predictions.

In addition, we show the expected accuracy and false positive rate of SignalP on different types of protein data sets: Multispanning membrane proteins, partial sequences, and ORFs with wrong or missing start codons.

The new SignalP provides not only a prediction of the presence of a signal peptide and the position of the cleavage site, but also (through the HMM approach) an assignment of n-, h- and c-regions within the signal peptide. These assignments can be used to further characterise signal peptides from different organisms.

References

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[2] H. Nielsen and A. Krogh: Prediction of signal peptides and signal anchors by a hidden Markov model. *ISMB*, **6**, 122–130, June 1998.

[3] H. Nielsen, S. Brunak, and G. von Heijne: Machine learning approaches to the prediction of signal peptides and other protein sorting signals. *Protein Engineering*, **12**, 3–9, Jan. 1999.

SignalP: http://www.cbs.dtu.dk/services/SignalP/