ProteinPrediction II

PPII Ex5 - Week 5

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Merging Trees

- merging happens the same way as last week
- every node (hpo annotation) gets attribute e.g.:
 - ▶ blast found sequence P18465 with this annotation
 - hhblits found sequence Q24365 with this annotation

What we really did

Validation

- created homology reduced data set with CD-Hit
- cross validation on this dataset

Predictor training

- create attributes
- train neural network with pybrain

Schaul, Tom and Bayer, Justin and Wierstra, Daan and Sun, Yi and Felder, Martin and Sehnke, Frank and Rückstieß, Thomas and Schmidhuber, Jürgen: PyBrain; Journal of Machine Learning Research

Validation

Lots of open questions:

- ► Take annotations and all parent annotations as true positive?
- Weigh level in HPO tree?
- **.**..

Is there a unified performance measure for our different methods before CAFA?