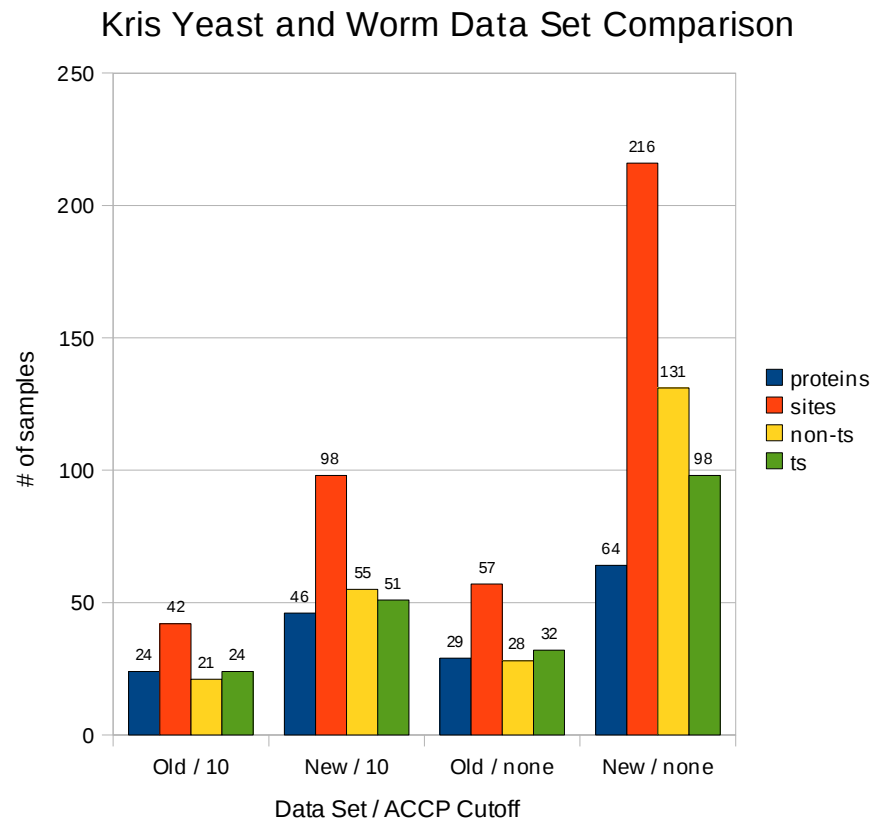


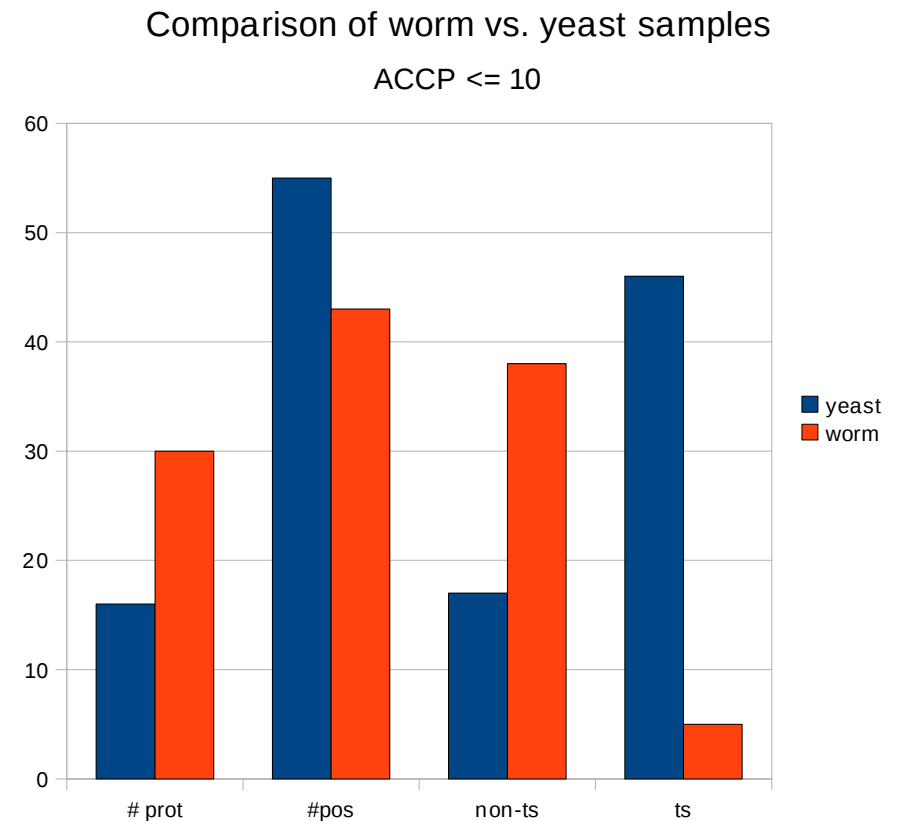
Updated Worm/Yeast Data

- Substantial increase in data set size
 - more samples
 - more proteins and sites with multiple samples



Updated Worm/Yeast Data

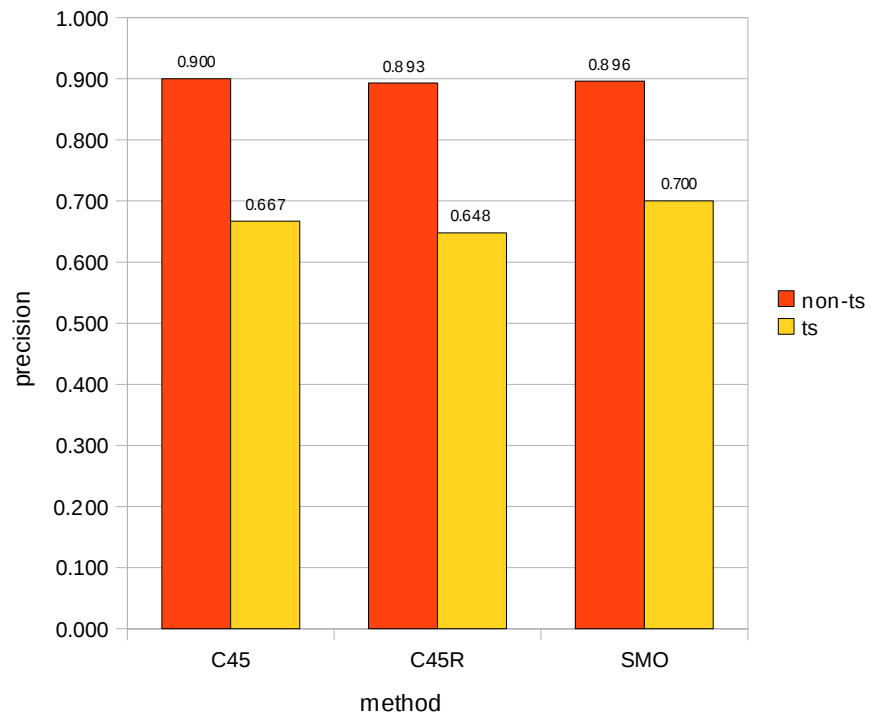
- Sample distribution varies per species
 - Yeast: 3:1 ts:non-ts
 - Worm: 1:8 ts:non-ts



Updated Worm/Yeast Results

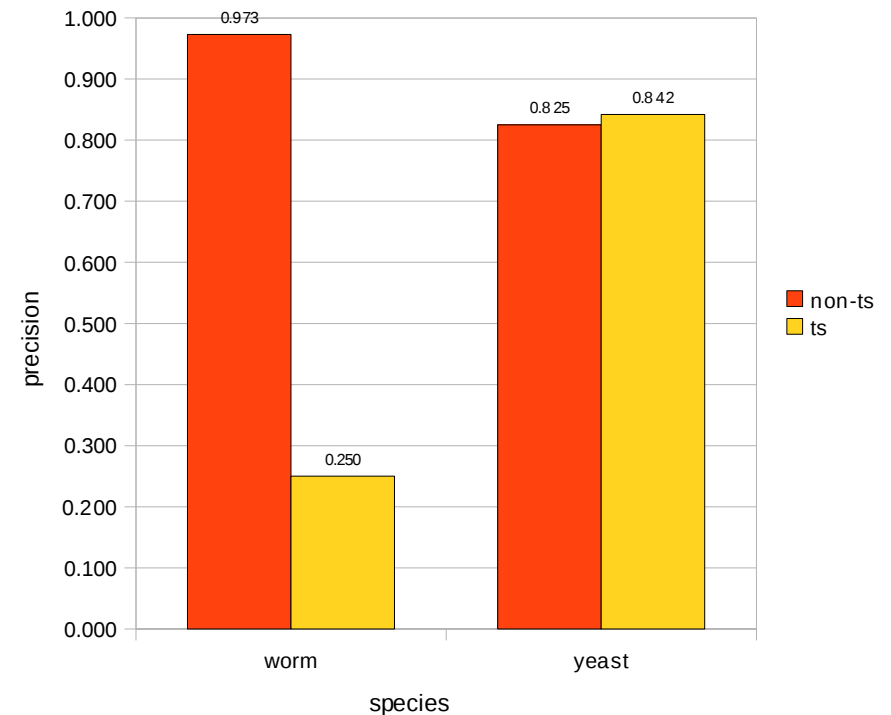
Precision on combined worm+yeast data by ML method

10x cross-validation, run3, ACCP <= 10



Precision on full worm+yeast set, split out by species

10x cross-validation, run3, method SMO, ACCP <= 10

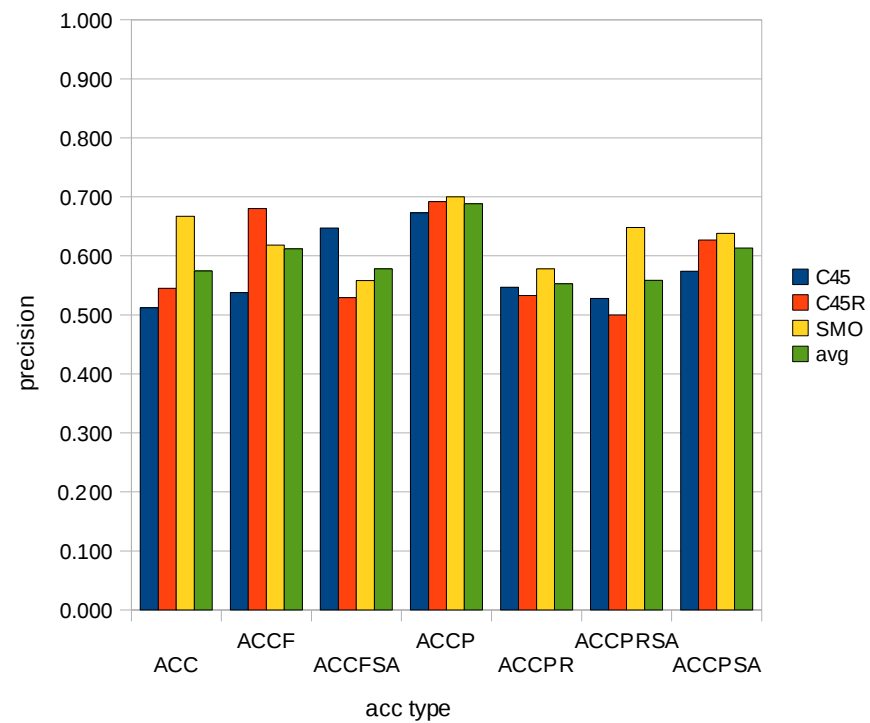


Cross-validation was performed on the full worm+yeast set; precision was then calculated for each species (a per-species breakdown of the SMO column of the chart to the left).

Accessibility Method Comparison

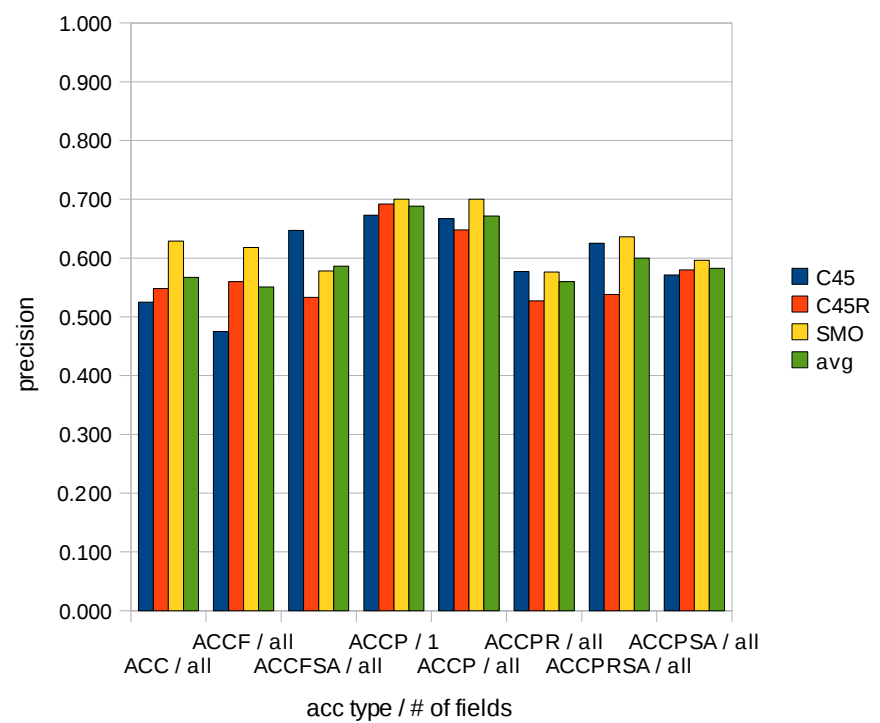
Precision by acc method

acc field and cutoff by acc type, acc <= 10



Precision by acc method

all or 1 acc field(s), cutoff by acc type

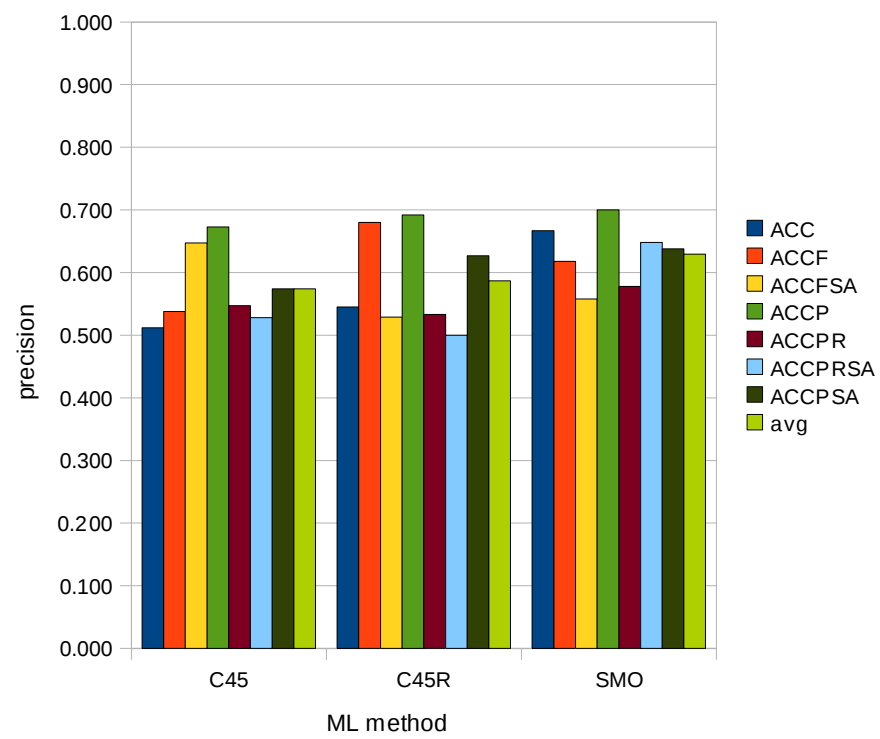


Best performance in each case is using only ACCP method for cutoff and training (ACCP or ACCP / 1 columns)

Accessibility Method Comparison

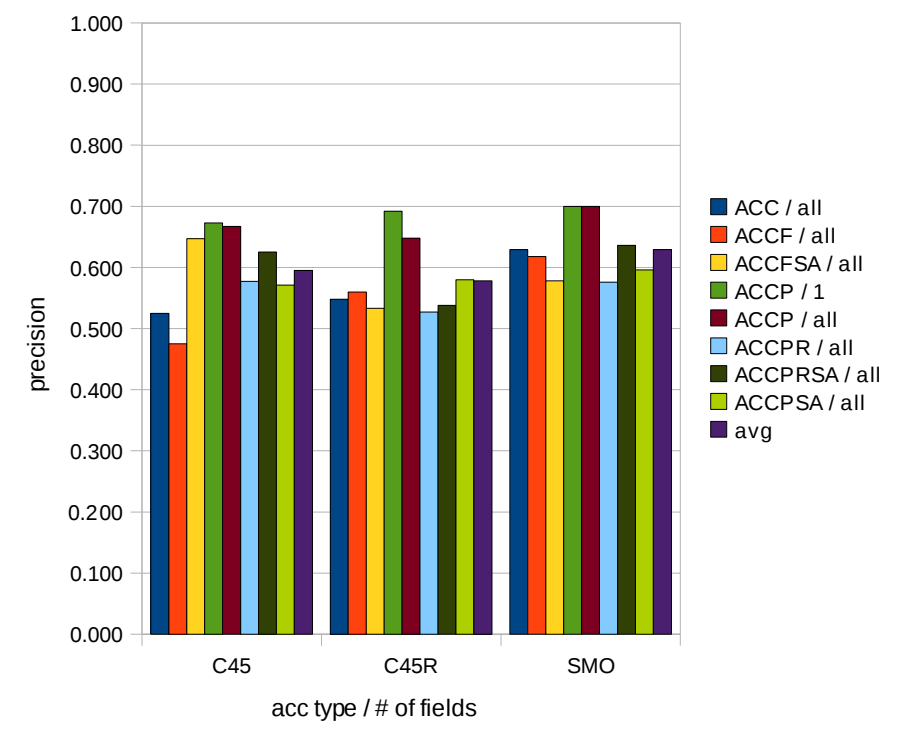
Precision by ML method

acc field and cutoff by acc type, acc <= 10



Precision by ML method

all or 1 acc field(s), cutoff by acc type



Best performance in each case is using only ACCP method for cutoff and training (ACCP or ACCP / 1 columns)