

CONSORF system benchmark results

In addition to being a free and reliable system for predicting microbial CDSs for large bioinformatics providers, CONSORF's advantage is its high accuracy achieved as a consensus prediction system. Based on stop position match (evaluation level 1, Table 1), the prediction accuracy of CONSORF ('representative CDSs' against the overall 'public CDSs') was compared to the previously reported results of other well-known and/or high-accuracy CDS prediction programs such as Glimmer, Critica, GeneMarkS, YACOP, and GeneLook. We used thirteen common organisms reported in at least two prediction programs (Table 2). On average, CONSORF showed higher accuracies than other prediction programs. CONSORF had the highest accuracy (F-measure; the harmonic average of sensitivity and specificity) in the CDS prediction of ten organisms and had the same (highest) accuracy with YACOP for *Bacillus subtilis* and *Helicobacter pylori* 26695. The accuracy of CONSORF for *Clostridium acetobutylicum* ranked the second highest after YACOP.

In a detailed comparison between CONSORF and YACOP, CONSORF had the highest accuracy with four out of seven common organisms and the same accuracy with *Bacillus subtilis* and *Helicobacter pylori* 26695. The average sensitivities and specificities and their F-measures (the harmonic average of sensitivity and specificity) of CONSORF and YACOP for the seven organisms were: 97.0%, 97.1%, and 97.0% for CONSORF and 98.4%, 94.6%, and 96.5% for YACOP. As the sequences of closer

neighbors of presently low-accuracy organisms become available and the accuracies of *ab initio* prediction programs, such as GeneLook and GeneMarkS, improve, we expect that CONSORF's accuracy will continue to increase due to its consensus nature.