

For *S. cerevisiae* occupies almost one-third of five species, the benchmark dataset S can be divided into parts: one is the dataset S_3 only composed of sequence samples from *S. cerevisiae*, and the other is the dataset S_4 consisting of the rest sequences from the other four species. Thus, we constructed a SVM-based prediction model training by the dataset S_3 and then used the dataset S_4 as the independent testing dataset to examine the constructed model performance.

The dataset S_3

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>P_S.cerevisiae_21
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>P_S.cerevisiae_22
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>P_S.cerevisiae_23
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>P_S.cerevisiae_24
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The dataset S₄

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