Analyzing the symmetrical arrangement of structural repeats in proteins with CE-Symm [S4 Tab]

Spencer E Bliven, Aleix Lafita, Peter W Rose, Guido Capitani, Andreas Prlić, Philip E Bourne

Method	Precision	Cramer V
GraphComponent	0.598	0.652
DeltaPosition	0.783	0.728
ROTATIONANGLE	0.754	0.642

**S4 Tab.** Performance measures of the symmetry order detection methods for domains in the benchmark dataset with closed symmetry. Precision measures the total fraction of correct predictions and Cramer V measures the correlation between actual and predicted classes. Both measures have values in the [0,1] interval, where 1 means perfect precision and correlation.