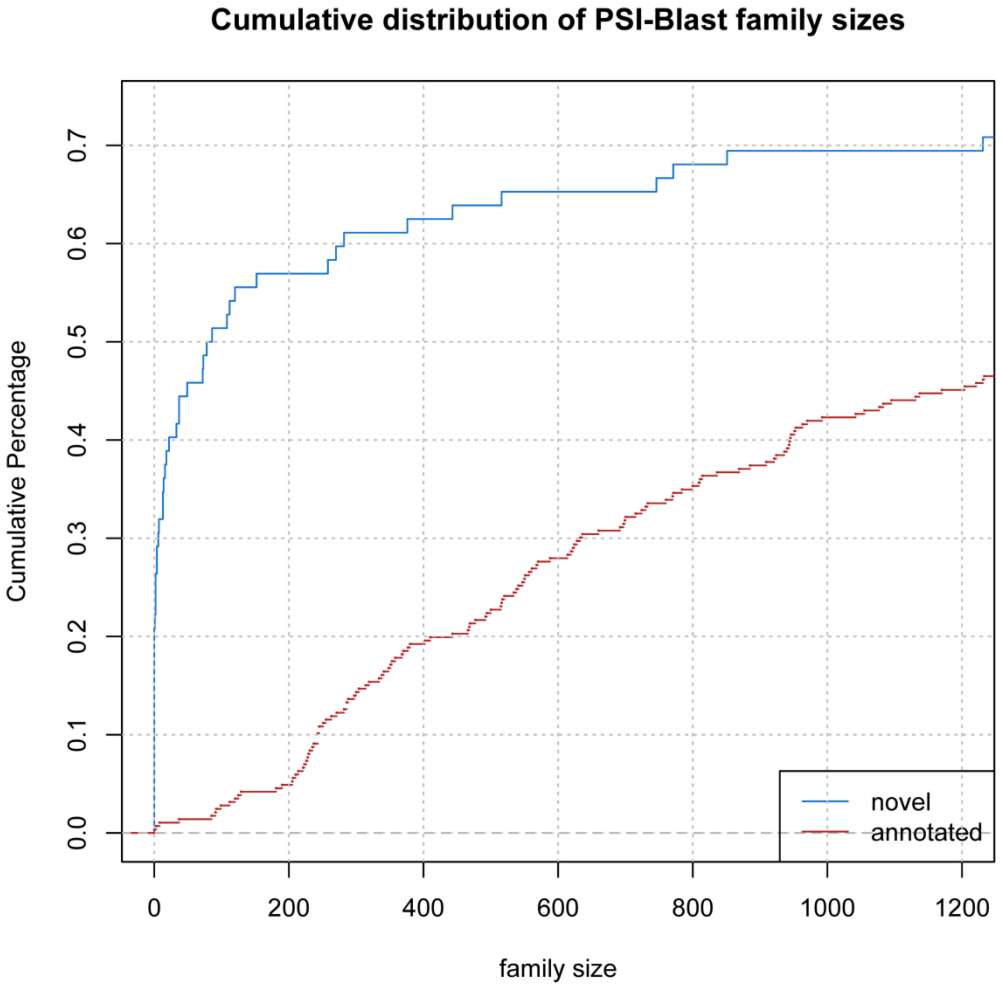
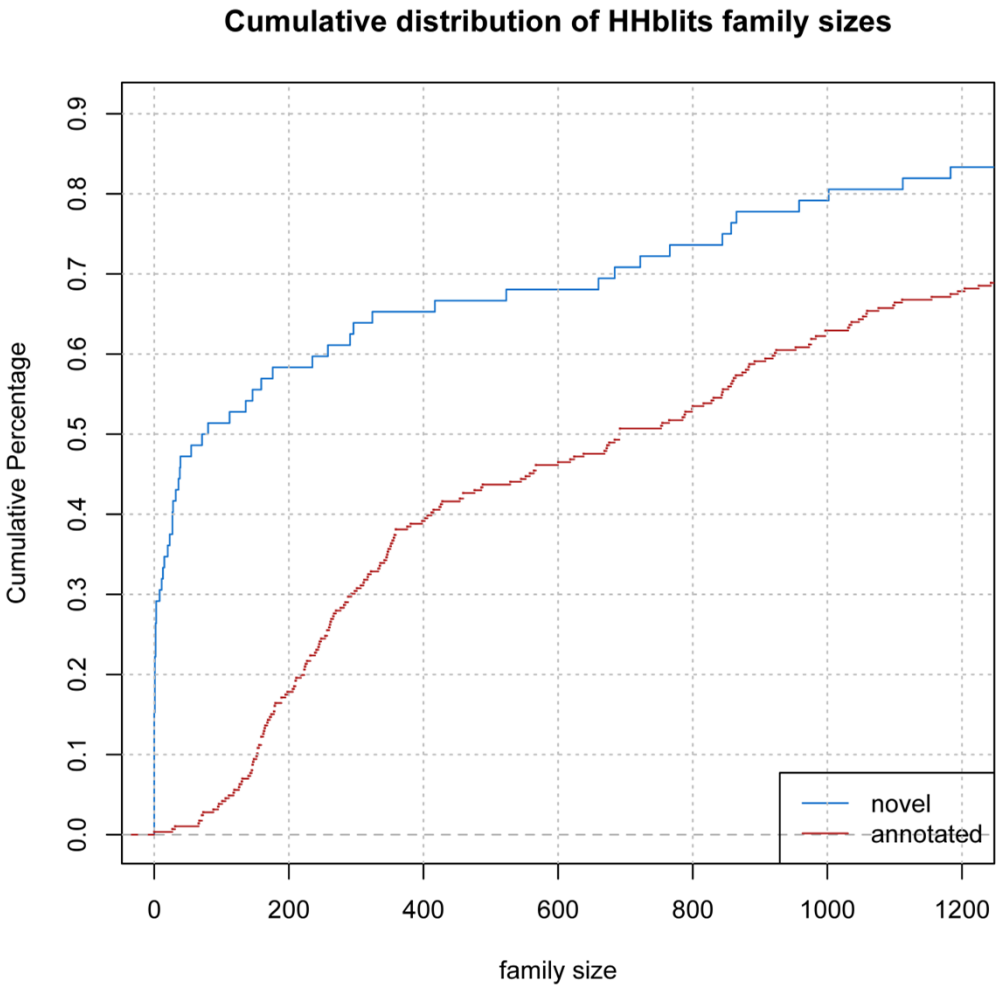


PSI-Blast search at an E value of ≤10^{-3}. At this E-Value cut-off we count for each query how many subjects we receive in Uniprot, which is defined as „family size“. Shown is on the y-axis the cumulative percentage of the proteins (novel, blue; annotated, red) which have a family size of the same size or smaller than this given percentage of the proteins. E.g., at a family size of 200, about 57% of the novel proteins have a family size of 200 or less, but only about 5% of the annotated proteins have a family size of 200 or less. More important than the actual values is the trend, since the E-value or any chosen percentage / family size combination are of arbitrary choice. However, most of the novel proteins have small family sizes compared to the annotated.



HHblits search at an E value of ≤10^{-3}. At this E-Value cut-off we count for each query how many subjects we receive in Uniprot, which is defined as „family size“. Shown is on the y-axis the cumulative percentage of the proteins (novel, blue; annotated, red) which have a family size of the same size or smaller than this given percentage of the proteins. E.g., at a family size of 200, about 59% of the novel proteins have a family size of 200 or less, but only about 18% of the annotated proteins have a family size of 200 or less. More important than the actual values is the trend, since the E-value or any chosen percentage / family size combination are of arbitrary choice. However, most of the novel proteins have small family sizes compared to the annotated.