





Figure 3: Pipelines for both DomSerf and BioSerf. The BioSerf pipeline makes three searches of the PDB using PSI-BLAST, pGenTHREADER and HHSearch. Each produces a set of models. The TMJury method then selects the cluster of most similar structures and these are used to generate a consensus model. The DomSerf method uses PSI-BLAST against the PDB and CATH database. Any whole PDB chain matches are parsed to divide the match in to domains. If the query sequence has sufficient coverage the match alignments are passed to MODELLER and the final models are produced. If the query sequence has little coverage pDomTHREADER is used to recognise CATH domains and any overlapping domains are resolved using DomainFinder. The set of best matching domains are then passed to MODELLER to produce the final models.