



Figure 1. Schematic of the Linear Motif Discovery Strategy

Interaction maps are probed for interaction sets (A): Partners of proteins with multiple interactions are clustered together when there are no known sequence features present (B). Domains and homologous regions are then identified (B) and removed prior to running exhaustive pattern discovery (C) to produce a list of motifs ranked by their probabilities P (D). Hypothetical motifs are shown as coloured squares in (C) and (D). “Proteins” in (D) gives the set of proteins containing at least one copy of the motif.