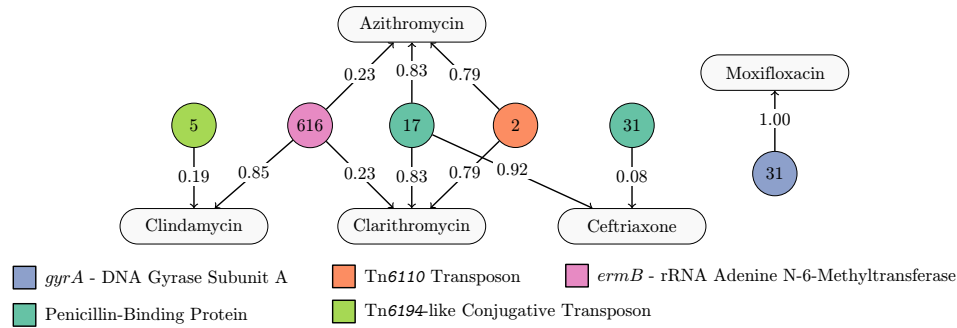
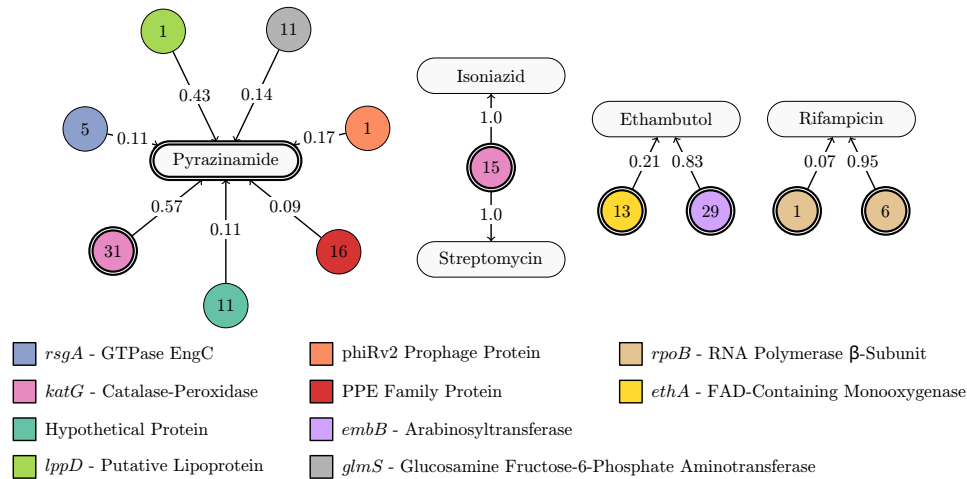


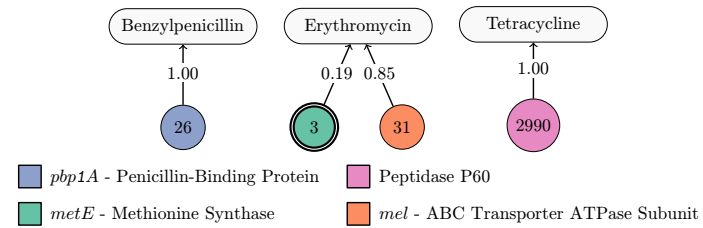
a) *C. difficile*



b) *M. tuberculosis*



c) *S. pneumoniae*



d) *P. aeruginosa*

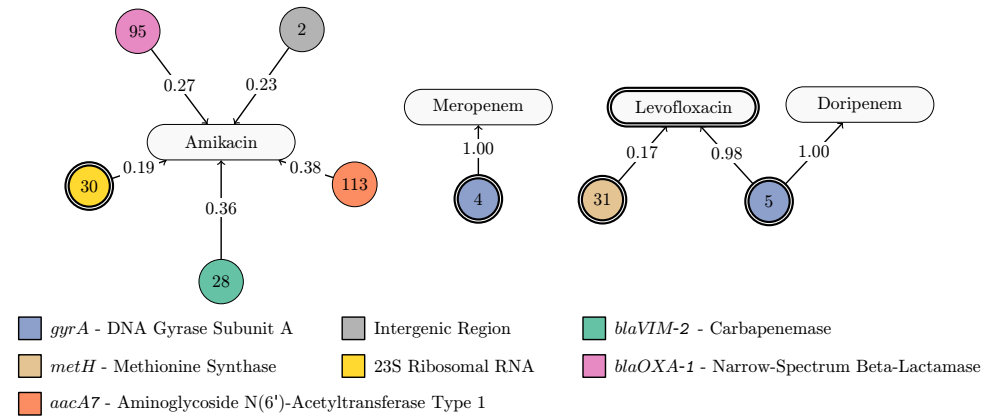


Figure S1: The antibiotic resistance models learned by the SCM for each dataset. The rounded rectangles correspond to antibiotics. A single border indicates that the model is a disjunction (logical-OR), whereas a double border indicates that the model is a conjunction (logical-AND). The circular nodes correspond to  $k$ -mer rules. A single border indicates a presence rule and a double border indicates an absence rule. The numbers in the circles show to the number of equivalent rules. A rule is connected to an antibiotic if it was included in its model. The weight of the edges gives the importance of each rule.