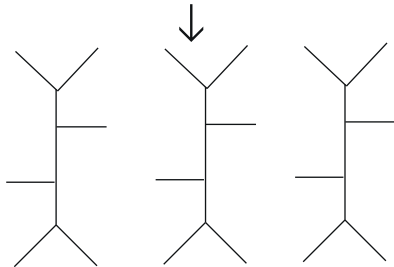
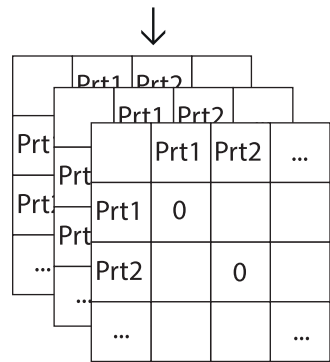


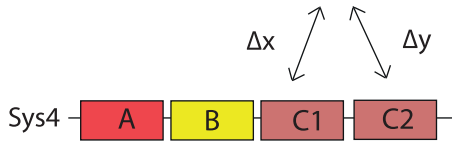
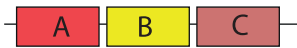
Step 1: Take all the systems representatives



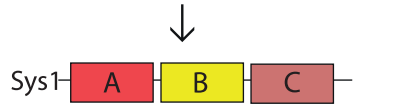
Step 2 : Inferring ML tree for each "core protein" family of the systems



Step 3a : Extracting patristic distances for all the trees



Step 3b : Comparing the distances between the proteins in multi copies with the homolog in the closest systems



Step 4 : Choosing for each system the copy with the smallest distance

