Figure 1: Total solution times of `CBICL-BB` on real-world gene expression datasets under constraint configurations (Constr.) $(n/4, n/4, 0, 0)$, $(0, 0, m/4, m/4)$, $(0, 0, m/4, m/4)$, $(n/4, n/4, m/4, m/4)$ and violation percentages (Viol.). Each bar represents the average over three sets of constraints corresponding to the same configuration.
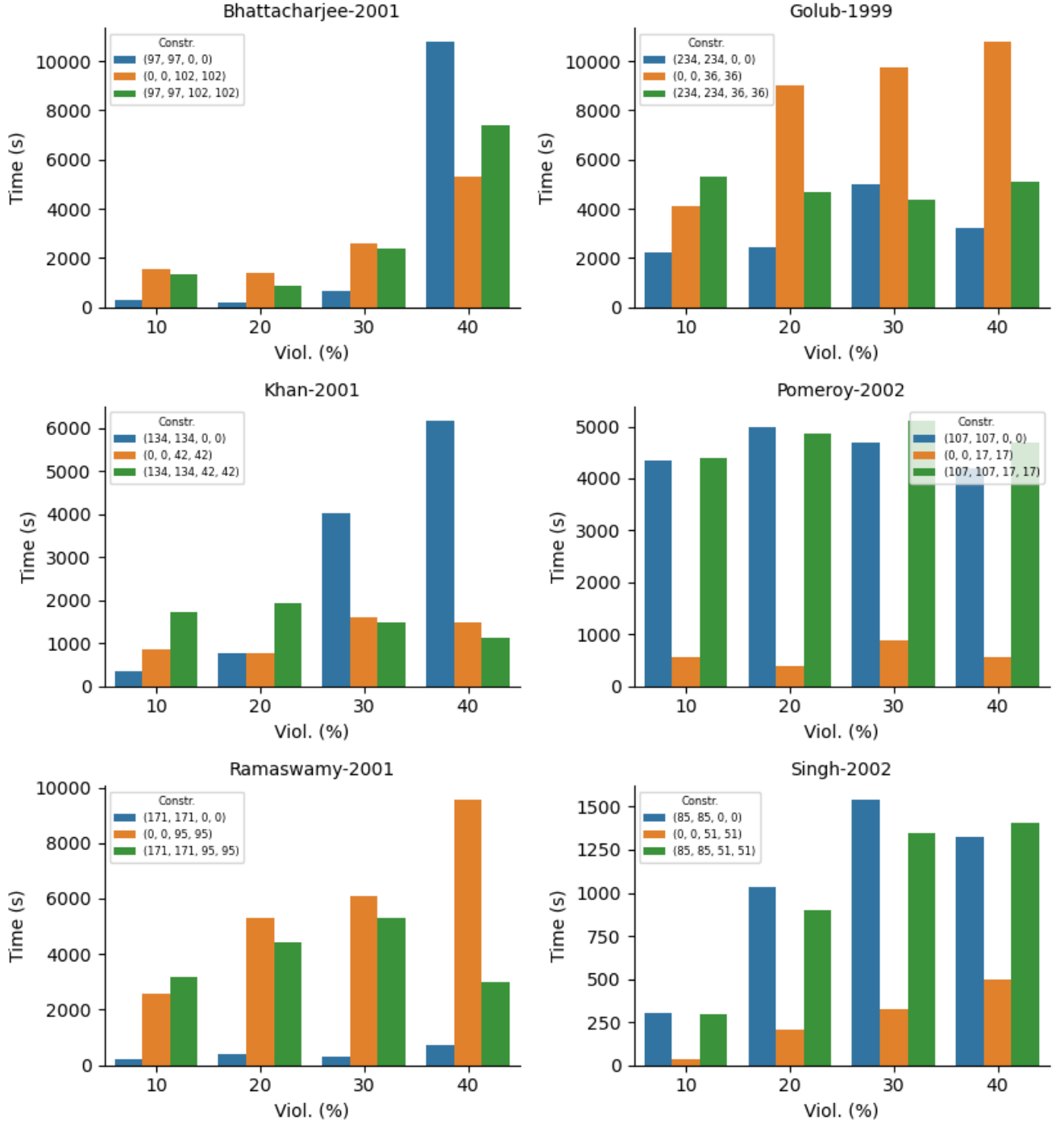
Figure 2: Total solution times of `CBICL-BB` on real-world gene expression datasets under constraint configurations (Constr.) $(n/2, n/2, 0, 0)$, $(0, 0, m/2, m/2)$, $(0, 0, m/2, m/2)$, $(n/2, n/2, m/2, m/2)$ and violation percentages (Viol.). Each bar represents the average over three sets of constraints corresponding to the same configuration.
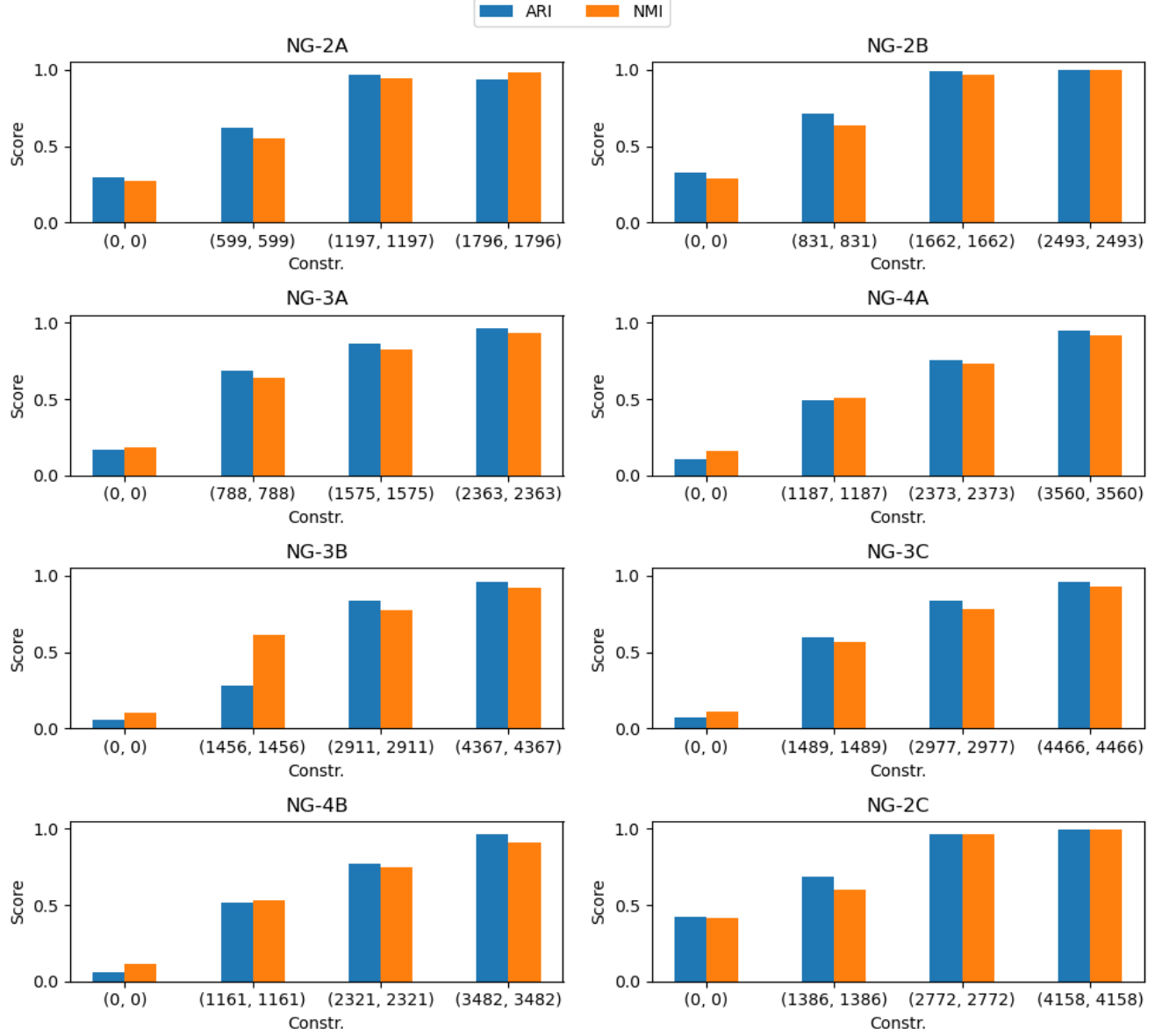
Figure 3: ARI and NMI scores of `CBICL-LR` on real-world document clustering datasets under varying constraint configurations (Constr.). Each bar represents the average over three sets of constraints for each configuration.