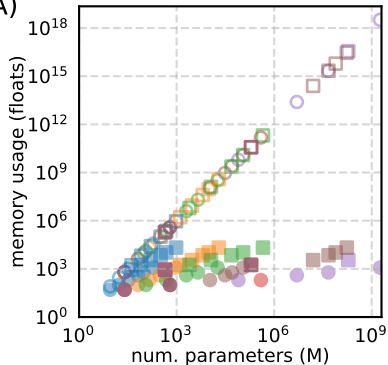
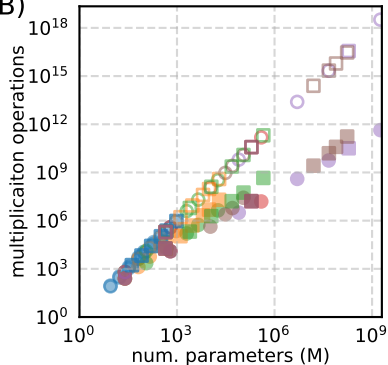


(A)



(B)



model type

- additive
- neighbor
- pairwise
- allorder
- K-order (K=5)
- K-adjacent (K=5)

alphabet size

- 4 (DNA/RNA)
- 20 (protein)

algorithm

- standard
- GaugeFixer