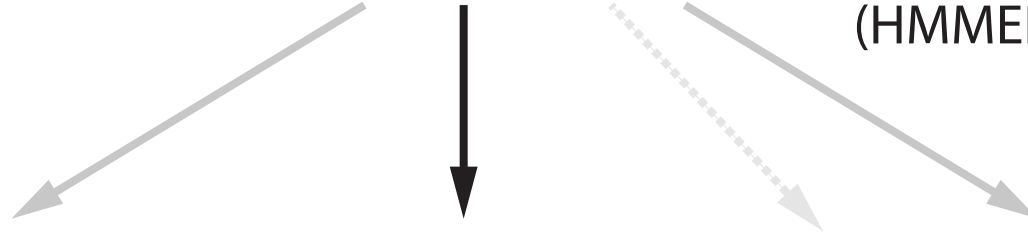


input sequences:



## ***Stage 1: Classification***

Score each sequence  
with all models  
(HMMER3 shortened pipeline)



### Model 1 (HMM)

RefSeq sequence and features    Group: Norovirus  
Subgroup: IV



low HMM score

### Model 2 (HMM)

RefSeq sequence and features    Group: Dengue  
Subgroup: 1



highest HMM score

***best-matching model  
used in remaining stages***

### Model N (HMM)

RefSeq sequence and features    Group: *NONE*  
Subgroup: *NONE*



low HMM score