

Segment sequence: ATTCGG.....CGGTAA

Codon feature extraction

AAA

AAG

AAC

AAT

.....

TTT

H_1

H_2

H_3

H_4

All features form a 61-dimensional feature vector

H_{61}

self-organizing
map

wining node

Define genotype based on clustering results

genomeID	info	PB2	PB1	PA	HA	NP	NA	MP	NS
xxx	...	PB2_12	PB1_21	PA_35	HA_43	NP_58	NA_62	MP_77	NS_83

Reassortment detection

parent1

+

parent2

reassort

xxx