

Supplementary file Text S1

RV-Typer: a web server for serotyping of *Rhinoviruses* using alignment-free approach

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Detailing of method to compute Return time distribution (RTD)

Sample protein sequence:

TLALAPAAPNPDKWNDFTAFFKVGAAACATTGTGAAYNCFYDGAACA

Computing RTD for 'A'

TLALPAAPNPDKWNDFTAFFKVGAAACATTGTGAAYNCFYDGAACA

1-1-0-10-5-0-0-1-5-0-7-0-1

Return times for 'A'

RTD for 'A' in above sample sequence

Return time for A (X)	Frequency (F)
0	5
1	4
5	2
7	1
10	1

Parameters of RTD for 'A'

$$\mu(A) = 2.38 \text{ and } \sigma(A) = 3.27$$

Similarly, we can compute μ and σ of RTDs of other amino acids for $k = 1$.

- At $k = 2$, there will be 400 k-mers (di-mers) of 20 amino acids, hence 400 RTDs can be computed using the same approach.
- So in general for other integer values/size of k , 20^k RTDs will be computed.