Improved (DFT) Generalized k-nearest information systems on Molecular QSAR-QMMM Cryptographic Mining and Chern-Simons Weighted neuron(ι):=φ[?]D[?]R2[?]S[?]R1 Topologies for the generation of the Roccustyrna Ligand Targeting SARS-COV-2 D614G Binding Sites.

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Abstract

SARS coronavirus 2 (SARS-CoV-2) in the viral spike (S) encoding a SARS-COV-2 SPIKE D614G mutation protein predominate over time in locales revealing the dynamic aspects of its key viral processes where it is found, implying that this change enhances viral transmission. In this paper, we strongly combine topology geometric methods for generalized formalisms of k-nearest neighbors as a Tipping–Ogilvie and Machine Learning application within the quantum computing context targeting the atomistic level of the protein apparatus of the SARS-COV-2 viral characteristics. In this effort, we propose computer-aided rational drug design strategies efficient in computing docking usage, and powerful enough to achieve very high accuracy levels for this in-silico effort for the generation of AI-Quantum designed molecules of GisitorviffirnaTM, Roccustyrna_gs1_TM, and Roccustyrna_fr1_TM ligands targeting the COVID-19-SARS-COV-2 SPIKE D614G mutation by unifying Molecular Pairs (MMP), Lindenbaum-Tarski logical spaces and Adaptive Weighted KNN Positioning for Matched Bemis and Murko (BM) driven eigenvalue statements into Shannon entropy quantities as composed by Tipping–Ogilvie driven Machine Learning potentials on a (DFT) neuron(ι):=φ[?]D[?]R2[?]S[?]R1 02(1+[?]=1{-20<[?]===¡ψ*——ps*¿=[?]Ni,j=1¡ψi——($^{-}r^{0}$)||yj > [?]$Ni,j = 1dij$ − [?]$Ni,j = 1 < yi||r^{0}||yj > N - Tr[r^{r^{0}}]-[?]Ni=1,j[?]i<yi||r^{0}||yj>1-2R[?]Ni=1,j$

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